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SCIENCE ADVICE FOR GENETIC EFFECTS FROM MARINE FINFISH AQUACULTURE IN SOUTHERN CALIFORNIA AND THE GULF OF AMERICA

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Science Advice for Genetic Effects from Marine Finfish Aquaculture in Southern California and the Gulf of America

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Executive Summary

This report contains a discussion of potential candidate species for aquaculture of finfish in the regions of Southern California and Gulf of America and describes potential sources of genetic risks to wild populations from the escape of fish or gametes from cages. The consideration of effects from aquaculture is limited to genetic effects related to cultured-wild interactions and loss of genetic diversity due to culture-origin escapes surviving in the wild. This report does not address potential ecological risks due to non-native species outcompeting native species, disease, or other factors. However, information about dispersal of genetic material provided in this report can be used to inform evaluations of ecological risk.

Candidate species for marine aquaculture were selected by NOAA based on known industry interest, potential for significant industry development, environmental suitability in each respective region, and environmental and technical feasibility for farming offshore in federal waters. Species included here do not represent an exhaustive list of potential species that could be cultivated in federal waters, nor an explicit endorsement by NOAA of these species for cultivation.

This report includes a series of genetic risk modeling case studies using OMEGA, a scientific decision-support tool. OMEGA case studies were completed for three candidate species in each of the two regions to evaluate potential genetic effects to wild conspecific populations from a theoretical aquaculture farm for two production scales: 10,500 and 17,500 metric tons. Each case study used a single trait fitness model and used model responses to evaluate effects to wild fitness and genetic diversity. Model scenarios were parameterized according to aquaculture operations, natural population dynamics, growth rates, survival in culture and post-escape, and probability of encounter. OMEGA case studies were completed for California Yellowtail (*Seriola dorsalis*), White Seabass (*Atractoscion nobilis*), and Striped Bass (*Morone saxatilis*) in the Southern California region, and for Red Drum (*Sciaenops ocellatus*), Almaco Jack (*Seriola rivoliana*), and Cobia (*Rachycentron canadum*) in the Gulf of America region.

Based on a synthesis of each of the candidate species (presented in Chapters 2 and 3), an assessment of the influence of species and population dynamics on the genetic risk level was determined for each species as a qualitative assessment of potential for genetic effects to wild populations from commercial finfish culture. A summary of findings related to genetic risk for each of the species in the Southern California and Gulf of America regions are shown in the tables below. More detailed factors contributing to these findings are tabulated in Chapter 4.

The genetic risk level is based on specific risk factors that would influence genetic effects to wild populations from aquaculture, based on species and population characteristics. The risk factors are: potential for maturity in culture (e.g. harvest after maturity age would present greater genetic risk), wild population abundance (low abundance of the local population would result in greater demographic contribution for each escaped fish, with potential for greater genetic risk), biological/life history characteristics (cultured fish more likely to migrate away from cages would present greater genetic risk; and/or longer-lived fish may promote a cumulative effect of culture traits persisting through multiple generations), and knowledge on genetic structure and population structure of the species on a region level.

The evaluation of uncertainty in the risk level is based on available data to support findings on the wild population status and genetic diversity. The Low/Moderate/High assessment for the genetic risk level and uncertainty presented in the tables is based on a broad review of the available research and scientific literature regarding wild population dynamics and characteristics for each species. The risk levels do not account for culture production levels, escape rates or other operational factors. As such the genetic risk levels in the table can be considered as factors that influence risk but should not be construed as a full assessment of genetic risk from aquaculture.

Southern California Candidate Finfish Species for Aquaculture: Summary of Risk Factors, Uncertainty in assessment, and Priorities to Minimize Genetic Effects

Species name	Common name	Influence of Species and Population Dynamics on Genetic Risk Level	Uncertainty in Risk Level	Management Priorities to Minimize Genetic Effects
Seriola dorsalis	California Yellowtail	Low to Moderate: can be harvested before maturity; status of wild population is unknown but presumed to be healthy	Moderate: stock is presumed to be healthy based on limited data	Broodstock genetic management plan
Atractoscion nobilis	White Seabass	High: harvest size occurs before maturity; replenishment is contributing to stability of population, but more data is needed on abundance and genetics of the admixed population	High: stock is rebuilding through enhancement efforts, but effect on genetic diversity needs to be better understood. Stock assessments are needed to estimate biomass and identify the geographical extent of the Southern California population	Broodstock genetic management plan, genetic diversity monitoring
Morone saxatilis	Striped Bass	Low to Moderate: unlikely to mature in culture, replenishment is contributing to stability of population abundance, but more data is needed	Moderate: stock is rebuilding but there is limited data on stock status	Broodstock genetic management plan, genetic diversity monitoring

Species name	Common name	Influence of Species and Population Dynamics on Genetic Risk Level	Uncertainty in Risk Level	Management Priorities to Minimize Genetic Effects
Anoplopoma fimbria	Sablefish	Low to Moderate: harvest size occurs before maturity, status of wild population is healthy, however potential for encounter is high	Low: genetic research and stock assessments have been done recently	Broodstock genetic management plan, genetic diversity monitoring
Paralichthys californicus	California Halibut	High: harvest size occurs before maturity; population status is uncertain	Moderate: Updated stock assessment is needed	Management of sexual dimorphism, management of gamete releases in culture, broodstock genetic management plan, genetic diversity monitoring
Paralichthys olivaceus	Olive Flounder	Low: nonexistent wild population in the U.S.	Low	Not applicable; nonexistent wild population in the U.S., however this species presents potential ecological risks

Gulf of America Candidate Finfish Species for Aquaculture: Summary of Risk Factors, Uncertainty in assessment, and Priorities to Minimize Genetic Effects

Species name	Common name	Influence of Species and Population Dynamics on Genetic Risk Level	Uncertainty in risk assessment	Management priorities to minimize genetic effects
Sciaenops ocellatus	Red Drum	Low: escapement rates indicate recovery, harvest size occurs before maturity, there is evidence that the wild population is resilient to selection pressures	Moderate: Stock assessments are needed to characterize the stock status for the Gulf at large	Broodstock genetic management plan
Seriola rivoliana	Almaco Jack	High: harvest size occurs before maturity, catch data suggests a low level of wild abundance	High: Stock assessment is needed for nearshore and offshore populations	Broodstock genetic management plan, genetic diversity monitoring
Rachycentron canadum	Cobia	Low: harvest size occurs before maturity; stock is not considered to be overfished	Low: Stock assessment update conducted in the last 5 years	Broodstock genetic management plan, siting, genetic diversity monitoring
Seriola dumerili	Greater Amberjack	High: status of wild population is unknown, but is overfished and considered to have low abundance	High: Updated stock assessment and more information about stock genetics are needed	Broodstock genetic management plan, siting, genetic diversity monitoring
Trachinotus carolinus	Florida Pompano	Moderate: harvest size occurs before maturity, but status of wild population is unknown	High: Updated stock assessment is needed	Broodstock genetic management plan, delayed maturation, genetic diversity monitoring

Species name	Common name	Influence of Species and Population Dynamics on Genetic Risk Level	Uncertainty in risk assessment	Management priorities to minimize genetic effects
Centropristis striata	Black Sea Bass	High: harvest size is coincident with maturity age; stock is overfished	High: more information is needed about life history, biology, stock status, and population structure in the Gulf	Management of hermaphroditism in cultured stock, broodstock genetic management plan, siting, genetic diversity monitoring
Cynoscion nebulosus	Spotted Seatrout	Low: supplementation programs stabilize wild abundance; however, population abundance is more vulnerable to degradation of habitat	Moderate: ecology of estuaries may influence abundance of species over time; genetic diversity at a subregion level is unknown	Management of cannibalism, broodstock genetic management plan, siting
Lobotes surinamensis	Tripletail	Moderate: harvest size may be coincident with maturity age, but abundance of wild population is unknown	High: research is needed on many aspects of life history, behavior, and population connectivity in the Gulf population	Fertilization in culture, broodstock genetic management plan, siting
Paralichthys lethostigma	Southern Flounder	Moderate: harvest size is coincident with maturity age, and abundance is vulnerable to degradation of habitat, but studies support a genetically diverse population	Moderate: more fine-scale speciated research is needed on life history and stock structure	Management of sexual dimorphism and hermaphroditism, broodstock genetic management plan, siting, genetic diversity monitoring

1.0 How Cultured Organisms Escape and Consequences of Escape

The purpose of this report is to present a synthesis of knowledge about aquaculture of marine finfish in the context of potential cultured-wild interactions and subsequent genetic effects on wild populations. The scope of effects from aquaculture in this report is focused on genetic effects related to cultured-wild interactions and loss of genetic diversity due to escaped/dispersed culture-origin individuals surviving and successfully interbreeding with wild conspecifics.

The purpose of this report is to 1) define primary genetic risks to wild fish from aquaculture, 2) provide managers with information about characteristics of candidate species to inform an evaluation of risk factors, 3) synthesize information about risk factors for each species, and 4) demonstrate the utility of the OMEGA model to quantify genetic risk of aquaculture for three candidate species in each region.

This document describes the types of escape and interactions that occur, potential competitive and genetic effects on wild species, and measures that may be implemented to minimize adverse effects from escapes. Potential genetic effects of aquaculture escapes include the introduction of maladaptive genes, reduced fitness, loss of within-population genetic diversity, and loss of among-population genetic diversity.

In considering risk, Kaplan and Garrick (1981) suggested defining and addressing three questions: (1) what can go wrong? (2) what is the likelihood of that happening? and (3) what are the consequences? With that guidance in mind the following sections describe how cultured organisms escape, the likelihood that they may escapes (Section 1.1, *Escape Background and* Categories), and the consequences of their escape (Section 1.2, *Consequences of Escape*).

Candidate species for marine aquaculture were selected by NOAA based on known industry interest, potential for significant industry development, environmental suitability in each respective region, and environmental and technical feasibility for farming offshore in federal waters. Species included here do not represent an exhaustive list of potential species that could be cultivated in federal waters, nor an explicit endorsement by NOAA of these species for cultivation.

1.1 Escape Background and Categories

Fish escapes are inevitable in aquaculture and have been reported in almost every country where aquaculture occurs (Jackson et al. 2015, Glover et al. 2017, McIntosh et al. 2022). These escape events occur at all levels, ranging from the escape of a single fish to large-scale escapes where most or all fish in net pens escape (Naylor et al. 2005, Leggatt et al. 2010, Atalah and Sanchez-Jerez 2020). Based on extensive monitoring and reporting of fish escapes in Norway, structural failures are the most common way Atlantic Salmon (*Salmo salar*) escape followed by operational-related failures (e.g., day-to-day operations such as inventorying of fish, nursery net replacement, detaching and towing harvest pens, vessel mooring, etc.; Jensen et al. 2010). The frequency and magnitude of different escape pathways determines, in part, the level of impact escaped fish may pose to conspecific wild populations and to the broader ecosystem.

Figure 1.1 shows the five ways fish escape from cages as conceptualized in the OMEGA model. Type one and two represent leakage and the escape of 10s to 100s of fish at a time. Type three represents episodic escapes resulting in intermediate escape numbers of 1,000s to 10,000s, and type four represents the rare complete failure of multiple cages or a catastrophic equipment failure and loss of 100,000s to millions of fish. The fifth category is more difficult to quantify fifth category and involves gametes released from mature fish held in cages. Each escape type is discussed in detail in the following sections.

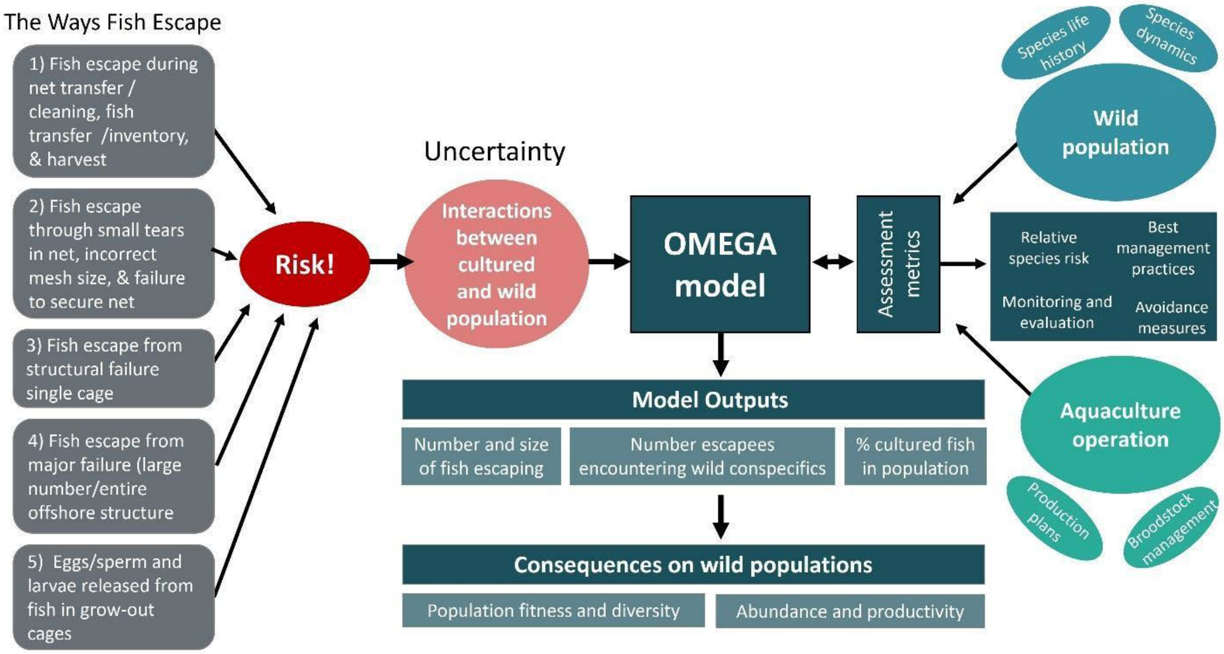

Figure 1.1. The ways fish escape, and OMEGA model conceptual design.

1.1.1 Leakage Escape

Leakage refers to the loss of one to possibly 100s of fish at a time. This type of escape results from processes associated with daily operations such as feeding, maintenance, handling/transferring maneuvers, and other such activities (Glover et al. 2017, Føre and Thorvaldsen 2021, Yang et al. 2022). While this type of loss is inevitable in aquaculture, determining the cause(s), or detecting the losses is difficult given the low number of fish involved at any one time (Naylor et al. 2005). This type of escape is the most frequent in terms of the number of occurrences (Skilbrei et al. 2015, Glover et al. 2017). As reported in Yang et al. (2022), out of 300 total recorded escape events that included a detectable loss of fish, approximately 59% of those events (or 176 events) would have been considered leakage-level events, but this accounting is likely incomplete. Even though any one leakage event results in a small number of fish escaping, the rate of occurrence and cumulative effect of fish escaping over time could have a considerable impact on a conspecific wild population (Baskett et al. 2013). This has been demonstrated in previous sensitivity analyses using OMEGA (ICF 2018).

Because leakage occurrences are often not recorded, quantifying escapes from leakage is more difficult than for any other type of escape (Leggatt et al. 2010). It is difficult to detect small numbers of fish escaping from a system, and as such, there is a considerable level of under-reporting, leading to as much as 50% of reportable incidents not being reported (Yang et al. 2022). An analysis conducted on Atlantic Salmon in Norway found that the actual number of escaped fish was two- to four-fold higher than the numbers reported by the industry (Skilbrei et al. 2015), and this 2-4x multiplier has now been used in recent modeling of salmon escapes in Canada and Iceland (Bradbury et al. 2020, MFRI 2020) to account for this under-reporting.

1.1.2 Episodic Escape

Episodic escapes often result from individual or multi-cage failures, or other malfunctions where all or a portion of fish escape from a cage(s) (Naylor et al. 2005). Advances in farm technology have reduced the incidence of escape overall, and particularly for catastrophic failures (Føre and Thorvaldsen 2021), but these episodic events may still happen at sites using some of the most advanced technology (e.g., Ocean Farm 1 in Norway lost 16,000 Atlantic Salmon in 2018 when water entered an inspection hatch that was accidentally left open; Fujita et al. 2023, https://www.fishfarmingexpert.com/escape-ocean-farm-1-salmar/ocean-farm-1-escape-total-worked-out-at-16000/1323127). This type of escape often occurs during vulnerable maneuvers such as inventorying of fish, nursery net replacement, detaching and towing harvest pens, initial seeding of pens, size-grading of fish using crowders, well-boat operations, net cleaning and repair, use of equipment to remove dead fish from pens, vessel mooring, bottom weight handling, and float line handling (Jensen et al. 2010, Atalah and Sanchez-Jerez 2020, Føre and Thorvaldsen 2021, Holmen et al. 2021). These events may occur due to human error during these activities, although unfavorable and unexpected weather and wave conditions (e.g., rogue waves) are also contributing factors (Føre and Thorvaldsen 2021). Analyses of Norwegian fish farm escapes found that net holes accounted for many escape events (e.g., 47% of escape events and 76% of escaped fish; Holmen et al. 2021); submerged nets due to operational and structural failures were another large contributor of escape events (Holmen et al. 2021, Yang et al. 2022). In addition to the operational and external factors above leading to escapes and possible holes in the net, the behavior of the species in culture also has a significant impact on escape risk. Atlantic Cod (*Gadus morhua*) for example, are more likely to bite at nets than salmon, and as a result, have a higher rate of escape (Moe et al. 2009, Jensen et al. 2010). Similarly, Gilthead Sea Bream (*Sparus aurata*) are also more prone to biting at the net, while European Seabass (*Dicentrarchus labrax*) do not bite the net, but are more opportunistic than Sea Bream in escaping from sea cages (e.g., through small holes or operational errors; Sanchez-Jerez et al. 2008, Arechavala et al. 2018). Predators may also contribute to episodic events through net breakage, enlargement of pre-existing holes, and/or distress of fish in the pens (Arechavala et al. 2018).

The design of individual aquaculture operations will have implications for the expected frequencies and magnitudes of episodic escape events. If it is assumed that the likelihood of an episodic escape occurrence is similar for large and small cages, then sites with more cages (regardless of size) will have a higher risk of an episodic escape event. However, a site with fewer, but larger cages, may have a lower overall frequency of episodic escapes, but a greater impact in terms of magnitude if an escape occurs (McIntosh et al. 2022). McIntosh et al. (2022) illustrated the effect of risk-consequence trade-offs by plotting the average number of cages per farm against the mean surface area (m^2) of those cages across different regions. The analysis showed that while Japan and Chile had the highest average number of cages per site, their mean cage surface areas were small to medium (relative to other regions), respectively. Consequently, these regions face a relatively high risk of escape due to cage losses but only a low to moderate impact from escaped fish because of the lower number of fish per cage. In contrast, Norway and Iceland had among the lowest average numbers of cages per site, but their mean cage surface areas were relatively large. As a result, these regions experience a lower risk of escape due to cage failures but face a high potential consequence if escapes occur, given the large number of fish per cage (McIntosh et al. 2022). In the Yang et al. (2022) analysis, out of the 300 recorded events that included loss of fish, approximately 41% of those events (or 124 events) would have been considered episodic-scale events. The magnitude of episodic escapes is much less than large-scale or catastrophic failures, but large enough that pulses of fish escaping into the environment in this way should be modeled in addition to impacts from chronic leakage. Accounting for both the frequency and magnitude of episodic escape events helps evaluate the risk of escape from an operation.

1.1.3 Large-scale Escape and Catastrophic Events

Large-scale losses from catastrophic events are the headline grabbing occurrences that the public unfortunately associates with offshore aquaculture. This type of loss may result from extreme storm and weather events or other disasters such as fires, collisions, or tsunamis that cause the failure of the mooring system and/or grid infrastructure (Yang et al. 2022, Føre and Thorvaldsen 2021, Jackson et al. 2015). Although large-scale escape events are rare, they have historically occurred, releasing hundreds of thousands to millions of cultured fish into the environment in a short time. Notable instances include 500,000 Atlantic Salmon in Norway in 2005, ~155,000 in Scotland in 2014, ~250,000 in Washington State, U.S. in 2017, and 120,000-130,000 in Tasmania in 2020, and 1.5 million European Seabass (90%) and Sea Bream (10%) in the Canary Islands between 2009 and 2010 (Jensen et al. 2010, Toledo-Guedes et al. 2014, Jackson et al. 2015, Atalah and Sanchez-Jerez 2020, Lyle 2021, Yang et al. 2022; http://aquaculture.scotland.gov.uk/data/fish_escapes_record.aspx?escape_id=64). Improvements in engineering, equipment technology (e.g., submersible cages, copper-alloy mesh pens), and industry standards (e.g., Norwegian Standard NS 9415) have reduced the frequency of these events (Føre and Thorvaldsen, 2021, McIntosh et al. 2022). The sudden presence of such large fish biomasses in the natural environment represents a unique environmental risk compared to other types of escape (Arechavala-Lopez et al. 2018) and the ability of a wild population to buffer against a high level of escape biomass will vary. Therefore, the impacts of these events warrant independent evaluation from other forms of escape.

1.1.4 Gamete-based Escape

Gamete-based escape involves the release of viable, fertilized eggs from sexually mature cultured fish inside of grow-out cages in an open setting within the natural environment (Leggatt et al. 2010, Arechavala-Lopez et al. 2018). This phenomenon is known to occur in Atlantic Cod where genetically tagged, culture-origin larvae were reported to make up between 20 and 25% of the total Atlantic Cod larvae sampled in the Norwegian fjord where the net pens were located (Jorstad et al. 2008). Modeling simulations indicated that from a standard pen holding 60,000 Atlantic Cod, between 1.4 and 21 tons of 3-year-old 'escaped' farm-origin Atlantic Cod may be produced through spawning in the net pens (Uglem et al. 2012). Similarly, a report by Somarkis et al. (2013) estimated that cultured Gilthead Sea Bream released between 3.5×10^{11} and 7.0×10^{11} eggs from pens in the Mediterranean based on assumptions of 5 to 10% mature fish and 130,000 tons of annual production. Sexual maturation is usually detrimental to the growth and fillet quality of the cultured fish, and if possible, it is avoided in most farming operations (Taranger et al. 2010). However, precocious maturity can be an issue for some cultured fish species (e.g., salmonids and Cod) (McClure et al. 2007, Karlsen et al. 2006). While preventing the physical escape of eggs and larvae would be nearly impossible, the risk from gamete-based escape is negligible if fish are harvested before reaching sexual maturity.

1.1.5 Recapture Rates

Leakage of 10s to 100s of fish are generally not recorded until final inventory of fish in cages during harvest and are calculated as the difference between the number of fish stocked and the number at harvest. Some of this difference may be attributed to mortalities during grow-out but a significant proportion may be unnoticed escapes that occurred during the grow-out period. Thus, tracking escapes from leakage may be incomplete and recapture of escaped fish from leakage is generally not possible. Some recovery may be possible if operators notice farmed fish in the immediate vicinity of the cages and escapees remain long enough to allow recapture.

Escapes from episodic and large-scale events may be mitigated by attempts to recapture escaped fish. However, Dempster et al. (2018) found that the overall recapture rate across various species was low (8% of fish that escaped), and this value exhibited large variance based on the species, the number of fish, and the size of fish escaping. Experimental Atlantic Cod recapture rates have varied widely among studies. For adult Cod, rates between 28 and 52% were reported by Uglem et al. (2008, 2011) and 11% by Zimmerman et al. (2013). Much lower rates are reported for juvenile Cod (up to 4.5%; Serra-Llinares et al. 2013). As reviewed in Dempster et al. (2018), Atlantic Salmon recapture rates have varied as high as 69% for experimental releases of fewer than 100 large fish, whereas recapture rates following large-scale escape events of smaller salmon was much lower (1.5 to 10%), which may be partially due to higher predation on smaller sized escapees. In the Mediterranean, single events have resulted in higher levels of recapture. For example, 64.7% of Gilthead Sea Bream were recaptured following a large-scale escape (Izquierdo-Gomez and Sanchez-Jerez 2016), and 20% of the Gilthead Sea Bream and European Seabass were recaptured following a different large-scale escape event (Toledo-Guedes et al. 2014). However, Arechavala-Lopez et al. (2018) reported lower recapture rates overall for

European Seabass (5.4%), Gilthead Sea Bream (7.1%), and Meagre (*Argyrosomus regius*; 8.7%) in the Mediterranean.

Generally, recapture rates improve with increasing size of escapees (Dempster et al. 2018), but it is difficult to determine whether this is due to more effective fishing or recapture methods for larger fish, or if it is due to higher mortality for smaller escaped fish, but both factors are likely important. Dempster et al. (2018) found a negative correlation between escapee size and the number of escaped fish, meaning that generally a greater number of smaller fish escape than larger fish. As noted across several studies, recapture efforts that started as soon as possible, and ideally within 24 hours, were more successful (Uglem et al. 2011, Dempster et al. 2018).

1.1.6 Summary

While escape events will continue to occur in aquaculture, their magnitude and frequency can (and has) improved with advancing technologies and adaptive regulations. Detailed reporting infrastructure is critical to assessing improvements and developing mitigation measures. For example, in Norway, fish escape incidents must be reported with information regarding the number of fish lost, type of fish farm, operational and technical contributing causes, and sea and weather conditions; these are reported with the goal of helping to further develop industry recommendations for best practices (Holmen et al. 2021, Yang et al. 2022).

1.2 Consequences of Escaped Fish

The previous section described the first and second aspects of risk assessment: 1) things that can go wrong (different ways cultured organisms escape), and 2) the likelihood of each of these types of events. The third component of assessing risk from escaped cultured organisms revolves around the potential consequences of those escapes.

Cultured fish are subject to selection pressures while in culture that differ from their wild counterparts. Different selection pressures occur at all stages of culture including during spawning, early growth, and grow-out to harvest. Cultured organisms may also be from just a few parents and thus they are closely related and have much lower genetic diversity compared to their wild counterparts.

The potential consequences of escaped, cultured organisms are dependent on their interactions with their wild counterparts. In considering the consequence of escaped organisms, we focus on three possible impacts: 1) the fitness effects on the wild population(s); 2) the effects on genetic diversity to the wild population(s) (both within- and among-population diversity); and 3) the ecological effects on multiple species, including the conspecific species. Each of these potential impacts is discussed below. Generally, the extent of the impact varies depending on the number of cultured organisms escaping, the life stage when they escape, the frequency of escape events, cultured population husbandry and genetic management, and the size and health of the wild conspecific population (Lorenzen et al. 2012, Atalah and Sanchez-Jerez 2020).

In the following section, we address risk in the context of factors that contribute to the likelihood of escaped/dispersed organisms interacting with wild populations.

1.2.1 Interactions

The potential consequences of escaped cultured organisms is dependent on their interactions with their wild counterparts. These include their ability to survive to reproductive age, the probability they will encounter their breeding wild counterparts, and their ability to effectively reproduce with their wild counterparts.

1.2.1.1 Survival of Escaped Fish

Survival of escaped fish may be lower than similarly sized wild counterparts (Lorenzen et al. 2000, Arechavala-Lopez et al. 2012, Arechavala-Lopez et al. 2014), and this may occur for a few reasons. First, farmed fish are raised on manufactured pelleted food and thus they are unaccustomed to finding live food once in the natural environment (Glover et al. 2017). Olsen and Skilbrei (2010) and Abrantes et al. (2011) reported high mortality in escaped salmonids due to starvation from failing to acclimate to wild food sources. In a 2003 report by the South Australian Research and Development Institute, a sampling effort on escaped Yellowtail Kingfish (*Seriola lalandi*) determined that the stomachs of these fish were either empty or contained atypical contents (e.g., plant material) compared to diets of wild conspecifics (Fowler et al. 2003). This acclimation challenge would likely apply to all sizes of escaped fish with subsequent starvation-induced mortality. However, acclimation success to wild food sources varies by species and some are capable of rapidly acclimating to wild conditions. For example, escaped Gilthead Sea Bream have been shown to feed on natural prey after only one week in the wild (Arechavala-Lopez et al. 2012).

Second, predation pressure on escapees may be quite high from the large and diverse fish assemblages often found near pens, leading to high mortality of any escaped fish (Dempster et al. 2009). Interestingly, this “wall of predatory mouths” has been suggested as an escape mitigation approach that could be amplified by limiting fishing on piscivorous fish in the vicinity of pens (Dempster et al. 2018, Arechavala et al. 2018). Mortality associated with predation is likely to be associated with escapee size, with smaller escapees being more vulnerable to predators and having a higher predation mortality. Predation from marine mammals may be significant on larger escapees.

Third, the cultured fish may be more susceptible to capture by fishing gear than wild counterparts (Lorenzen et al. 2012). Mezzera and Largiader (2001) report angling efforts disproportionately caught cultured Brown Trout (*Salmo trutta*) compared with electrofishing. Behavioral differences in cultured fish compared to wild fish may increase their vulnerability to fishing efforts. Härkönen et al. (2014) reported that higher ‘moving activity’ among cultured fish predicted vulnerability to angling in Brown Trout, but the study could not determine the role of hunger in this increased activity. Greater vulnerability of cultured fish to angling has also been reported in the Common Carp (*Cyprinus carpio*), which has been attributed to differences in both genetic factors and behavioral differences (increased boldness) in the cultured fish (Klefoth et al. 2013).

1.2.1.2 Probability of Escaped Fish Encountering Wild Populations

The probability of escaped, cultured fish encountering wild conspecifics is strongly influenced by the location of the pens in relation to suitable habitat for the species, the geographical range of the species and the habitats they utilize at different life stages, size of fish at escape in terms of proximity to similar sizes of wild conspecifics, and timing of the escape occurrence (Dempster et al. 2018). Much work has been conducted with dispersal of cultured Atlantic Salmon in the Northeast Atlantic (e.g., Hansen and Jacobsen 2003), the Northwest Atlantic (e.g., Whoriskey et al. 2006), the North Pacific (e.g., McKinnell and Thomson 1997), and the coastal waters of Chile (Soto et al. 2001). Whoriskey et al. (2006) reported the rapid dispersal of tagged Atlantic Salmon released from aquaculture sites where most fish had left the vicinity of the pens within a day. They found that the dominant tidal circulation was important in fish dispersal direction. Jensen et al. (2013) found that at least a portion of Atlantic Salmon that escaped during the post-smolt period migrated and dispersed in the sea in a manner similar to wild Atlantic salmon. A study following the escape of farmed Atlantic Cod discovered that they rapidly dispersed over large areas and had a distribution that overlapped with wild Cod populations (Uglem et al. 2008). Moreover, the escaped Atlantic Cod were later found at local Atlantic Cod spawning locations during the spawning season (Uglem et al. 2008). Similarly, Zimmerman et al. (2013) suggested there is potential for interactions between cultured and wild Atlantic Cod based on their study which found rapid and long-distance dispersal of escaped Atlantic Cod (e.g., 157 km).

Multiple studies have found that in the Mediterranean, escaped (or simulated escaped) Gilthead Sea Bream and European Seabass may disperse long distances over time (Arechavala-Lopez et al., 2012, 2014, 2018). Studies of post-escape behavior of Gilthead Sea Bream and the European Seabass have shown that fish move towards coastal areas at varying dispersal distances based on the species and location of escape (Arechavala-Lopez et al. 2018). Toledo-Gudes et al. (2009) found that escaped European Seabass dispersed up to 11 km along the coast, while Toledo-Guedes et al. (2014) found that Gilthead Sea Bream moved as much as 50 km from the point of escape. Other studies have reported slightly shorter dispersal distances for Gilthead Sea Bream (Izquierdo-Gomez and Sanchez-Jerez 2016, Segvić-Bubić et al. 2018). Izquierdo-Gomez and Sanchez-Jerez (2016) reported that the farthest recapture recorded was 30 km from the pens and that most recaptures were within 3 km. Segvić-Bubić et al. (2018) found that Gilthead Sea Bream in the eastern Adriatic Sea displayed short-term farm fidelity, with 70% of tagged individuals remaining near the escape site after two weeks. The Meagre, another farmed species in the Mediterranean, was found to rapidly disperse from the farm location within a short 24- to 48-hour window following the escape event, showing little-to-no farm fidelity (Arechavala-Lopez et al. 2017).

In summary, most studies found evidence that either a portion of escaped cultured fish find their way into wild conspecific populations or are capable of dispersal at distances where encountering wild conspecific populations is possible. The weight of evidence indicates it is appropriate to account for this likelihood unless specific information exists to refute this possibility (e.g., location of the farm-site or biology of the wild population).

1.2.1.3 Relative Reproductive Success

Relative reproductive success (RRS) describes the reproductive fitness of escapees (as it relates to spawning success). RRS generally is a value between 0 (reproductively sterile escapees) to 1.0 (same spawning contribution as wild fish). It is possible that escapees may have a RRS that exceeds 1.0 if evidence supports a higher contribution to the next generation per individual as compared to wild fish. RRS can be both a function of environmental effects (i.e., non-genetic factors such as culture methods or sterilization of farmed fish) and genetic factors resulting from domestication selection (e.g., time of spawning or fecundity). It has been suggested that RRS improves with the length of time at liberty in the wild following the escape event (i.e., younger escapees surviving to maturity may have higher RRS; Jonsson 1997, Glover et al. 2017).

RRS data are scarce with only one study examining RSS in a fully marine species (Leggatt et al. 2010). That study was a laboratory experiment and found that cultured Atlantic Cod had lower reproductive success than wild Atlantic Cod. Almost all direct evidence for reduced RRS in cultured fish comes from experimental work in salmonids. In a particularly compelling study, fifth generation farmed Atlantic Salmon had greatly reduced RRS as compared to their wild conspecifics; cultured females were only one third as reproductively successful as wild females, and farmed males only exhibited 1 to 3% of the reproductive success that wild males achieved (Fleming et al. 1996). A later study by Fleming et al. (2000), found that farmed Atlantic Salmon had less than one third of the reproductive success of wild fish, with males again performing relatively poorly. Jonsson (1997) and Weir et al. (2004) found the RRS of cultured male Atlantic Salmon in general was lower than in corresponding cultured females. Specific mechanisms resulting in the lower RRS in cultured Atlantic Salmon as compared to wild counterparts was reviewed in Weir and Grant (2005). In experiments with Chinook Salmon (*Oncorhynchus tshawytscha),* cultured males had significantly lower reproductive success relative to wild males in egg-to-fry survival due to competition with wild offspring (Lehnert et al. 2013).

1.2.2 Fitness Effects

Because of the differences between the wild and cultured environments, fish, even if spawned directly from wild caught broodstock, will develop trait differences that are adapted to culture conditions (Glover et al. 2004, Liu et al. 2015, Bolstad et al. 2017). These differences, or phenotypes, may be caused by genetic changes in the captive population, or may be due to phenotypic plasticity where a single genotype may be expressed differently under varying environments (Wringe et al. 2015, and references therein). In addition, traits that are advantageous under culture conditions, or traits that are economically beneficial, can be intentionally targeted through selective breeding of captive broodstock or unintentionally selected for during successive generations.

As heritable fish phenotypes become optimized towards culture conditions, escaped cultured fish would experience lower fitness in the natural environment as compared to their wild counterparts due to any number of maladaptive morphological, behavioral, or physiological traits (Lorenzen et al. 2012, Wringe et al. 2015). When escaped cultured fish survive to encounter and reproduce with wild fish, there is a potential risk that cultured-wild hybrids will have associated maladaptive traits, and thus also have lower fitness in nature (McGinnity et al. 2003, Naylor et al. 2005, Yang et al. 2019). Over successive generations, as there is continued influx of cultured fish and interbreeding between cultured and wild fish, the fitness of the natural population would be reduced through introduction of maladapted traits and fixation of deleterious alleles (Basket et al. 2013, Boltstad et al. 2017, Glover et al. 2017, Yang et al. 2019, Bradbury et al 2020). Most evidence for reduced fitness, lowered population viability, and changes to the wild population demography resulting from escaped cultured-wild fish interbreeding comes from salmonids (McGinnity et al. 2003, Bolstad et al. 2017, Sylvester et al. 2019), although it is reasonable to expect similar consequences for other species interbreeding with escaped conspecifics.

The extent of the fitness consequences will vary based on the number of fish escaping from culture that survive and breed with their wild counterparts, the degree of domestication of the cultured fish, and the size and resilience of the wild population. Overall, the greater the number of escaped fish, the higher the level of interbreeding and introgression into the wild population is to be expected (Glover et al. 2017). However, there are differing opinions as to whether a constant low-level leakage of escapes (Baskett et al. 2013, Yang et al. 2019) or less-frequent larger-scale escape events (Hindar et al. 2006, Sylvester et al. 2019) will have a greater impact on the wild population fitness. The interpretation of the impacts of these two types of events depends on whether the focus is the longer-term population equilibrium or short-term fitness outcomes (Glover et al. 2017). The constant influx of cultured fish from leakage leads to long-term consequences whereas episodic escape events may result in short-term reductions in fitness with natural selection removing maladapted traits between escape events. In the latter case the frequency of events is important as well as the generation length of the species (escapees of long-lived species persisting longer in the breeding population).

The degree of domestication of escapees also directly impacts the fitness outcomes for the wild population. Cultured fish recently derived from wild broodstock have the greatest potential to interbreed with the wild counterparts because theoretically they would be more similar to their wild counterparts (Lorenzen et al. 2012). Because selection in the culture environment has not occurred over multiple generations, the genetic differences between the cultured and wild fish are likely to be minor and thus have a lower effect on the fitness of the wild population (Glover et al. 2017). When cultured fish have undergone multiple generations of breeding within the culture environment, selection (intended or unintended) results in traits that are potentially maladapted to the natural environment. However, in this case, a long history of domestication is also thought to reduce the ability to successfully survive and reproduce with the wild population (Baskett et al. 2013). It is hypothesized that domestication intermediate to those two points actually poses the greatest risk to the population, where escaped cultured fish are likely to have accumulated heritable traits maladapted to the natural environment, but that also retain the ability to survive and reproduce with their wild counterparts (Baskett and Waples 2013, Lorenzen et al. 2012, Baskett et al. 2013, Glover et al. 2017).

The size and resilience of the wild conspecific fish population is also significant when considering the extent of fitness impacts from escaped cultured fish. The larger the wild population size, the lower the proportions of escaped farmed fish will be in that population (Diserud et al. 2022), so population size in terms of absolute numbers is an important factor. Escapes are most damaging when wild populations exist at naturally low abundances or are depleted due to excessive fishing pressure or environmental factors (Lorenzen et al. 2012, Baskett et al. 2013). The population genetic structure of the wild population is another consideration for evaluating fitness impacts (Lorenzen et al. 2012). For species exhibiting significant spatial genetic structuring, escaped fish may alter (e.g., homogenize) distinct locally adapted populations, potentially leading to the loss of fitness. By definition, locally adapted populations have higher fitness within their native region relative to an introduced population (Savolainen et al. 2013). Genomic swamping from escaped cultured fish could eradicate localized genomic adaptation in distinct populations, and lead to lowered fitness across the formerly adapted populations.

1.2.3 Genetic Diversity Effects

Genetic diversity, which refers to the genetic variation among individuals of a population or in a species, is the material which evolutionary forces act upon to shape variation in phenotypic traits over time (Frankham 1996, Palstra and Ruzzante 2008, Sonsthagen et al. 2017). Genetic diversity within populations or species is influenced primarily by the biology and ecology of a species (e.g., distribution, population size, dispersal behavior, mating system, and generation time), but may also be influenced by anthropogenic actions such as harvest, species introductions, species propagation or culture, and habitat loss and fragmentation (Amos and Hardwood 1998). Evolutionary forces can also generate genetic diversity in a population in many ways such as through mutations (creation of new genetic variants), and reduce diversity through genetic drift (stochastic events and gradual change), and selective sweeps (e.g., rapid natural selection for an adaptive trait) (Amos and Hardwood 1998, Waples et al. 2012). Immigration of individuals from another population may also act to rapidly increase genetic diversity in a population.

There are many factors that govern demographic and evolutionary processes for a given species, and the ability of a species to withstand or recover from a loss of genetic diversity varies (Milinkovitch et al. 2013, Sonsthagen et al. 2017). Genetic diversity provides long-term resilience to natural populations from future stressors. A genetically diverse population where some genotypes (and resulting phenotypes) would provide a degree of additional benefit to withstand the novel stressors and help a species or population survive (Waples et al. 2012). Accordingly, the loss of genetic diversity in a population or species may result in the inability to respond to new selective pressure (e.g., environmental changes or novel pathogens) (Tringali and Bert 1998, Araki and Schmid 2010, Lorenzen et al. 2012, Waples et al. 2012). Rare alleles, which may be those best suited to unexperienced stressors, are the most vulnerable to being lost rapidly when genetic diversity is reduced (Roman and Darling 2007). Genetic diversity may also reflect locally adaptive genetic variation among populations. In that case, there is concern about escaped fish causing homogenization across populations, instead of, or in addition to, reduction in diversity within a population (Waples et al. 2012). Although loss of genetic diversity in artificially propagated populations has been documented for multiple species, the extent to which a reduction in genetic diversity has an impact on a species' or a population's viability is not fully understood and difficult to quantify (Araki and Schmid 2010, Gruenthal and Drawbridge 2012, Hornick and Plough 2019).

1.2.3.1 Effective Population Size

The effective population size (N_e) is a metric which estimates the idealized population size that shows the same rate of genetic drift as the census population (N) assuming random mating, and no selection, immigration, or mutation. (Ryman and Laikre 1991, Tringali and Bert 1998, Husemann et al. 2016). It can be thought of as a way to measure the fraction of the gene pool passed on to the next generation of offspring (Franklin et al. 1980). As Waples et al. (2018) succinctly described, census population size (N) influences demographic and ecological processes (e.g., population growth, competition, predation, pathogen transfer), and effective population size (N_e) influences population processes such as inbreeding, genetic drift, genetic diversity, and adaptive potential. The ratio between the census and effective population size predicts the rate or extent to which those population processes may change under different scenarios (Waples et al. 2018).

Large effective populations are predicted to have higher genetic diversity and maintain that genetic diversity more effectively. Natural selection is considered to be most effective in these larger populations, whereas small effective populations have less genetic diversity and lose genetic diversity at a higher rate. Small effective populations are considered more susceptible to stochastic genetic drift randomly fixing alleles that could result in lower overall fitness for the population; there is also a greater likelihood for inbreeding depression in smaller effective populations (Roman and Darling 2007, Ponzoni et al. 2010; Waples et al. 2012, Yáñez et al. 2014, Sonsthagen et al. 2017).

There is often a large discrepancy between the effective and census population sizes due to the biological characteristics of the species or population (e.g., unequal sex ratios, spawning or mating strategies) or unequal reproductive success where not all individuals contribute or contribute equally to the next generation (Waples et al. 2012, Sonsthagen et al. 2017). In marine fish and invertebrates, for example, N_e is often smaller, sometimes by two to six orders of magnitude, than the census population size (Hauser and Carvalho 2008, Waples et al. 2012). This phenomenon is believed to be due to large variances in reproductive success among individuals (Hedgecock and Pudovkin 2011). This results in N_e/N ratios much smaller than 0.01 (Hedgecock and Pudovkin 2011), and extremely low ratios have been reported in a variety of marine fish (for example: Atlantic Cod (4×10^{-5}; Hutchinson et al. 2003), Red Drum (*Sciaenops ocellatus*, 1×10^{-3}; Turner et al. 2002), Red Snapper (*Lutjanus campechanus*, 1×10^{-3}; Saillant and Gold 2006), New

Zealand Snapper (*Pagrus auratus*, 2x10^{-5}; Hauser et al. 2002), Plaice (*Pleuronectes platessa*, 2x10^{-5}; Hoarau et al. 2005), and Striped Bass (*Morone saxatilis*, 3x10^{-4}; Diaz et al. 2000).

However, more recent research has indicated substantial downward biases in the N_e/N ratios (incorrectly reflecting smaller effective population sizes than is the reality) due to inadequate sample sizes and violations in the assumptions for the N_e calculation (Waples et al. 2016). Waples (2016) evaluated scenarios necessary to produce small N_e/N ratios in populations and found that even after accounting for longevity, fecundity, variance in reproductive success (that increases with age), and variation in egg quality, even more extreme conditions (or extreme types of variances) were required to reduce the N_e/N below approximately 0.01.

Recent approaches to understanding population estimates that utilize very large sample sizes revealed much higher N_e/N ratios in the few marine species where this approach has been applied (e.g., the Southern Bluefin Tuna (*Thunnus maccoyii*) (>0.1 and approaching 0.5; Waples et al. 2018), Red Drum (*Sciaenops ocellatus*) (~0.21; Tringali and Lowerre-Barbierri 2023), and New Zealand Snapper (*Chrysophrus auratus*) (0.33; Jones et al. 2019). While this does not discount that smaller N_e/N ratios are possible, the similar life-history characteristics in those species and the lower samples sizes in the earlier studies with low N_e/N ratios, suggests that the estimates of N_e/N ratios in the species with the earlier estimates may have been downwardly biased (Waples et al. 2018). This downward bias is not easily corrected for as simulations have indicated that approximately 1% of the census population needs to be sampled over a sufficient temporal range to provide more precise estimates of N_e, and for many marine species this could mean sampling many thousands to many hundreds of thousands of individuals which is rarely feasible (Marandel et al. 2019).

1.2.3.2 Effective Population Size and Genetic Diversity of Cultured Fish

Cultured populations often show reduced genetic diversity compared to wild populations because the small subset of individuals used for broodstock may only contain a fraction of the wild diversity of the source population (Lorenzen et al. 2012). Araki and Schmid (2010) reviewed 32 studies of effective population size and genetic diversity in cultured populations and in 21 of those studies lower effective population sizes and lower diversity compared to wild conspecifics were reported. Species in that review included Atlantic Salmon (Blanchet et al. 2008), Japanese Flounder (*Paralichthys olivaceus*) (Sekino et al. 2002, Shikano et al. 2008), Red Drum (Gold et al. 2008, Karlsson et al. 2008), Red Sea Bream (*Pagrus major*) (Kitada et al. 2009), Spotted Halibut (*Verasper variegatus*) (Ortega-Villazán Romo et al. 2006), and Black Sea Bream (*Acanthopagrus schlegelii*) (Blanco Gonzalez et al. 2008). Loss of genetic variation has also been documented in farmed Turbot (*Scophthalmus maximus*) stocks (Danancher and Garcia-Vazquez 2011, Prado et al. 2018) and in Coho Salmon (*Oncorhynchus kisutch*) (Yáñez et al. 2014). A similar pattern of loss of genetic diversity is also seen in many cultured shellfish species, for example in Pacific Oysters (*Magallana gigas*) (Appleyard and Ward 2006, Miller et al. 2012), Suminoe Oysters (*C. ariakensis*) (Xiao et al. 2011), the South African Abalone (*Haliotis midae*), Black Lip Abalone (*H. rubra*) (Evans et al. 2004), and the Eastern Oyster (*Crassostrea virginica*) (Hornick and Plough 2019).

Selection during culture can lead to even smaller effective population sizes (in comparison to wild conspecific effective sizes) leading to further loss of genetic diversity. It is known that reducing genetic diversity too much in a cultured population can make a breeding program unstable (Ponzoni et al. 2010) and can reduce the additive genetic variance that selective breeding programs would target for economic benefit. However, the extent to which loss of genetic diversity in a cultured population may be acceptable is not well understood (Araki and Schmid 2010), and likely depends on the species' biology and the wild population.

Artificial propagation of fish is different from most other types of breeding programs because of the much larger number of individuals produced, their relatively higher fecundities, and high mortality at early-life stages (Fisch et al. 2015). Further, only a relatively small number of fish (compared to wild population) are brought into a breeding program and high reproductive variance contributes further to disproportionate offspring production (Tringali and Bert 1998). Consistently, a much smaller number of mate-pairings are represented in the offspring compared to the potential maximum number of breeders. This has been detected in Red Drum (Gold et al. 2008, Karlsson et al. 2008), Steelhead Trout (*O. mykiss*) (Christie et al. 2012), Atlantic Halibut (*H. hippoglossus*) (Jackson et al. 2003), Japanese Flounder (Sekino et al. 2003), and California Yellowtail (*Seriola dorsalis*; Schmidt et al. 2021). Differential survival in the larval and juvenile stages and size grading may further skew how many broodstock fish are represented by the offspring (Frost et al. 2006, O'Leary et al. 2022). These factors create a setting where the effective population size of cultured fish may be greatly reduced compared to the number of broodstock individuals (Appleyard and Ward 2006, Waples et al. 2012). It may, in some cases, be half as large as the actual broodstock number or represent a small fraction of the total potential pairings (Jackson et al. 2003, Frost et al. 2006, Christie et al. 2012, Hornick and Plough 2019).

The effective population size of the broodstock and resulting offspring may be further reduced by intended or unintended selection in captivity (Fisch et al. 2015). Long-term sustainability and prevention of inbreeding due to small effective population size is a chief concern in aquaculture (Danancher and Garcia-Vazquez 2011, Prado et al. 2018), particularly as there is a trend toward lower genetic diversity with increasing time since founding of a cultured population (Aho et al. 2006). Additionally, a small effective population size often leads to rapid accumulation of genetic differentiation between cultured and wild populations (Janssen et al. 2017). Strategies to achieve a large effective population size and maintain a high genetic diversity in a cultured population may be difficult because of the costs and resources necessary to include a larger number of breeders in a program.

1.2.3.3 Risk of Escaped Fish on Genetic Diversity

There is a risk to wild populations when cultured fish escape, survive, and reproduce with wild fish and contribute a large proportion of offspring the next generation (Laikre et al. 2010, Lorenzen et al. 2012). The result can be a significant reduction in the total effective population size (N_{eT}; combined escapee-wild population) and loss of genetic diversity in the wild population (Laikre et al. 2010, Waples et al. 2016). This type of risk from the escape of cultured individuals and the resulting loss of genetic diversity in the mixed population is termed the Ryman-Laikre effect (1991) and occurs when few captive parents produce large numbers of cultured offspring (Waples et al. 2016). While the effect may pose greater risk to population viability of small or fragmented populations, the Ryman-Laikre effect can reduce the total effective population size to a fraction of the wild effective size even in species with large effective sizes, and thus should be taken into consideration for aquaculture operations with the potential for cultured fish to interact with wild conspecifics (Waples et al. 2016).

The degree of risk from the Ryman-Laikre effect depends on the species' population biology, demographics, and genetic structure in the wild as demonstrated in Tringali and Bert (1998). That study explored the potential for a Ryman-Laikre effect from supplementation programs for Red Drum and the Gulf Sturgeon (*Acipenser oxyrinchus desotoi*), two species with quite different life-histories and population dynamics. They found that effects on genetic diversity may be low to negligible for some geographically widespread species with modest cultured fish contributions to the wild population. However, in other instances (e.g., species that have experienced population crashes), release of cultured fish into the wild may lead to large reductions in N_e with negative effects for the population (Tringali 2023).

Despite losses of genetic diversity in cultured populations, no loss of genetic variation was detected in wild populations of Red Drum (Tringali and Bert 1998, Laikre et al. 2010, Katalinas et al. 2018), Pacific Herring (*Clupea pallasii*) (Kitada et al. 2009), Japanese Spanish Mackerel (*Scomberomorus niphonius*) (Nakajima et al. 2014), Steelhead Trout (Gow et al. 2011), and Eastern Oyster (Hornick and Plough 2019) when cultured animals were introduced into the wild. However, admixed populations have resulted in reduction in genetic diversity or genetic differentiation due to introgression from cultured conspecifics, for example, in Coho Salmon (*O. kisutch*) (Eldridge and Naish 2007, Eldridge et al. 2009), Red Sea Bream (Kitada et al. 2009), and populations of Steelhead Trout (Christie et al. 2012).

In thinking about the Ryman-Laikre effect, it is important to consider consequences from the reduction in the total effective size of the mixed population (i.e., the ratio of N_{eT}/N_{eW}). While the absolute value of N_{eT} may be large enough to maintain population diversity and thus viability (according to theoretical models), N_e may be reduced by a few orders of magnitude, potentially resulting in a considerable loss of genetic diversity and adaptive potential that previously existed in the wild population. Wild populations at the greatest risk from Ryman-Laikre effects are those with large effective sizes (Waples et al. 2012) because of the potential for a substantial reduction in N_e. This aspect of risk to genetic diversity is often overlooked (Christie et al. 2012). Under some circumstances N_e may only need to be 'large enough' for selection, rather than genetic drift, to be the greater force acting on the population; if so, the population may retain its adaptive potential as long as both the lifetime variance in reproductive success among breeders and the generation length are adequately large for the species (Tringali 2023). There are also instances where the Ryman-Laikre effect may be of secondary concern. Loss of genetic diversity would be less important if the fitness of the population had been greatly affected by introgression with escaped cultured fish (i.e., the loss of fitness from introgression would be a more immediate concern). Finally, a Ryman-Laikre effect may not be a concern if cultured fish do not survive and reproduce well in the natural environment. In that case there would be little to no Ryman-Laikre effect on N_e from the escaped fish (Lorenzen et al. 2012, Waples et al. 2012, Waples et al. 2016, Glover et al. 2017).

1.2.3.4 Potential for Mitigation

Certain life-history characteristics may buffer or minimize Ryman-Laikre effects on wild populations. These include long adult lifespans, overlapping generations, and large census population sizes (Tringali and Bert 1998, Katalinas et al. 2019). Migration from neighboring populations or from the outer population range may help to rebuild genetic diversity in a cultured-wild admixed population much more quickly than through mutational processes. However, that process may eventually work in the opposite direction where genetic diversity is lost across the species through migration away from the admixed population (Ingvarsson 2001, Waples et al. 2012). To minimize Ryman-Laikre effects, it has been recommended that the genetic contribution from cultured fish to the next generation in the admixed population remains below 10%, however, a more conservative threshold of 5% has also been proposed (Waples et al. 2012, Waples et al. 2016). As described for potential fitness effects of escaped fish, if cultured fish do not survive or reproduce well in the natural environment then their genetic contribution will be much lower than a simple estimate of proportion based on census data (Waples et al. 2016). A rigorous monitoring program is important to evaluate the annual proportion of escaped fish in the admixed population, annual genetic contribution of cultured fish to the next generation in the admixed population, and to establish a genetic baseline in the wild population and regular genotyping of the admixed population to evaluate any changes over time (Waples et al. 2016).

Best practices during the culture phase to help mitigate possible Ryman-Laikre effects include steps to maximize effective number of adults used for broodstock, minimize inbreeding (e.g., through pedigree-reconstruction using genetic markers or careful tracking of family lines ahead of planning breeding crosses), and incorporate long-term genetic goals into the breeding program to preserve genetic diversity of the brood population (Ryman and Laikre 1991, Ponzoni et al. 2010, Yáñez et al. 2014, Fisch et al. 2015, Hargrove et al. 2015). Collecting broodstock that represent the genetic variation of the wild population across broad spatial and temporal scales would help capture a more representative portion of the existing natural variation (Waples et al. 2012). Breeding practices in a culture setting should aim to increase the effective population size in the cultured offspring by maximizing potential mating combinations per spawn (to account for spawning dynamics), equalizing numbers of progeny generated per spawning event during larval grow out period, and increasing the number of spawning events represented in the fingerlings transferred to offshore grow out pens (Gold et al. 2008, Christie et al. 2012, Schmidt et al. 2021). In stock supplementation programs (the intentional release of cultured fish to augment natural production), it has been suggested that a range of between 50 and 200 breeders is able to maintain genetic variability in a cultured population and that it could possibly represent up to 99% of population diversity (Tringali and Bert 1998). Gruenthal and Drawbridge (2012) explored this idea for a White Seabass (*Atractoscion nobilis*) stock supplementation program and found that 74 effective breeders were able to represent 99% of wild genetic diversity in the surveyed population. Given spawning dynamics, mortality, and reproductive variance observed for White Seabass, this would translate to maintaining between 140 and 200 broodstock fish distributed evenly across a free-breeding system where a subset of males and females are held in a tank to broadcast spawn. While the exact numbers would vary by species, it may be possible to retain most of the existing genetic diversity of the population using reasonable broodstock sizes for commercial operations even if the effective population size (N_{eT}) is reduced by orders of magnitude. This still carries a risk, however, that low frequency gene variants in the wild population (e.g., those alleles under a frequency of 0.02 based on the White Seabass example) would l likely be lost (Tringali and Bert 1998, Gruenthal and Drawbridge 2012).

1.2.4 Ecological Effects

Ecological effects from escaped fish fall primarily into three categories: 1) competition, 2) predation, and 3) disease and each of these may impact wild populations of conspecifics independently from, or in combination with, cultured-wild fish interbreeding (Bradbury et al. 2020). Ecological interactions may have immediate effects, acting on temporally co-occurring populations and may also affect the selective landscape experienced by other species in the ecosystem resulting in multi-generational (or even permanent) changes to allele frequencies that have adapted to these new selective pressures (Bradbury et al. 2020). One example of a 'non-reproductive genetic interaction' described by Bradbury et al. (2020) is hypothesized to impact gene diversity associated with immune functioning (e.g., major histocompatibility complex or MHC) in non-conspecific wild fish (e.g., major histocompatibility complex or MHC) due to shifting selective pressures from pathogens carried by cultured fish (Bradbury et al. 2020, and references therein). While the OMEGA modeling does not explicitly examine ecological impacts from escapes (see section 1.3, Assessing Risks of Escape using Modeling Methods), we touch on some potential impacts in the next sections

1.2.4.1 Competition

As a result of escaped fish, the frequency or intensity of inter- and intraspecific competition within an ecosystem may increase, with the anticipated effects growing with increasing numbers of escaped fish (Naylor et al. 2005, Baskett et al. 2013, Glover et al. 2017, Atalah and Sanchez-Jerez 2020). Competition for resources (including food, habitat, and spawning mates) has primarily been studied for escaped salmonids (McGinnity et al. 2003, Naylor et al. 2005, Jonsson and Jonsson 2006), and the impacts were not limited to the conspecific species (Soto et al. 2001).

1.2.4.2 Predation

Predation pressures may also shift in the natural environment, either due to predatory behaviors of the escaped fish themselves (Valero-Rodriguez et al. 2015) or shifts in the responses of other predators in the environment because of the escaped fish (Naylor et al. 2005).

1.2.4.3 Disease

The spread of diseases or parasites from escaped fish to conspecifics and to other species is another ecological risk (Naylor et al. 2005, Baskett et al. 2013). Cultured fish may transmit novel pathogens to an environment (although farming of native or naturalized species reduces, but does not eliminate this risk), pathogens that have evolved under culture conditions (e.g., more virulent, more contagious than the wild-strain), or introduce cultured fish into the environment that have a lowered resistance to pathogens (and thus higher pathogen load and increased infectiousness when encountering other fish) (Lorenzen et al. 2012, Arechavala-Lopez et al. 2013). Escaped fish may also alter the distribution (spatially or temporally) of pathogens; the extent of this will depend on post-escape survival and behavior (Atalah and Sanchez-Jerez 2020).

1.3 Assessing Risks of Escape using Modeling Methods

The NOAA National Marine Fisheries Service (NMFS) aided in the development of a scientific decision-support tool called the Offshore Mariculture Escapes Genetics Assessment (OMEGA) model to assess the potential risks of farmed escapees to their wild counterparts and to aid in the design of management strategies to address the potential risks of escapees to marine resources. OMEGA is intended to: 1) provide insights about factors affecting risks associated with escapes from aquaculture operations, 2) simulate the scale, frequency, and dispersal of escapes into the wild population and potential impacts to wild population fitness, genetic diversity, and long-term viability, and 3) aid in the assessment of proposed aquaculture projects and the development of management strategies to address potential escape risk, including evaluating the effects of regulatory and technical advances on fish containment. Models like OMEGA are useful to understand and predict the consequences of different management alternatives and are an important tool to support environmental regulatory decisions (National Research Council 2007).

1.3.1 OMEGA Model for Assessment of Finfish Escapes

OMEGA was developed jointly by ICF and NMFS in 2012 to evaluate the relative risks of escaped cultured fish in a wild population of conspecifics. The concepts used in OMEGA are an extension of the All-H-Analyzer (AHA) tool which was used successfully in the U.S. Pacific Northwest to evaluate genetic and ecological interactions between hatchery and wild salmon and Steelhead Trout. A user guide for OMEGA containing model background and user instructions was produced the same year (ICF 2012 available at: https://www.fisheries.noaa.gov/offshore-aquaculture-escapes-genetics-assessment-omega-model). Version 2.0, developed in 2019, used for this assessment includes a Monte Carlo simulation frontend for conducting multiple iterations of a randomized simulation with the ability to vary one or more parameters based on user-specified distributions (ICF 2018). This feature is an add-on to OMEGA and requires @Risk for Excel, available from Palisade Software. @RISK operates by modifying one or more input parameter values using specified distributions of values for each iteration of a simulation. The user also selects which output model response variables to evaluate from the simulation. Model inputs and results are recorded for each iteration.

The OMEGA model is organized around three components (Figure 1.2):

1) The biology of the cultured population and details of the aquaculture operation, including the frequency and magnitude of fish escaping from the pens.

2) Factors affecting the potential for interaction between escapees and the wild population, including survival of escapees, location of the aquaculture operation relative to the wild population, and reproductive success of escapees in the wild.

3) The biology and population dynamics of the wild population, including abundance, distribution, survival, age and size at maturity, spawning characteristics, and age-specific harvest rates.

Figure 1.2. The three components of the OMEGA model.

OMEGA model input parameters describe size and growth characteristics of cultured fish, frequency and magnitude of escape events, mechanism of escape, survival of escapees in the wild, probability of escapees encountering a conspecific natural population and interbreeding, and population dynamics of the natural population. Model results describe the influence of aquaculture escapes on spawning biomass, juvenile production, and fitness of the composite population. Effects of interactions on fitness and abundance are based on the frequency and relative abundance of cultured fish that escape and survive to encounter a natural population, the difference in survival characteristics between the artificial and the natural environments, and the genetic characteristics (e.g., spatial genetic structure, selective breeding, etc.) of the cultured and natural populations. More recent model developments also evaluate potential impacts on effective population size and consequences for genetic diversity in the mixed population from escaped cultured fish.

OMEGA scenarios are modeled to assume a rate of survival of escapees based on size at escape relative to wild conspecifics. The survival rate may be adjusted to model a lower rate relative to wild conspecifics using a shaping function that is based on assumptions of predator avoidance, foraging behavior after escape, and time from escape. OMEGA also includes a parameter to describe the probability of escapees encountering the wild population. The probability of encounter is based on an understanding of the distribution of wild juveniles and spawners and the distance from a farm location. A third parameter is reproductive competency of escaped fish. At one extreme, cultured fish may be sterilized prior to stocking in cages and would have zero reproductive potential. At the other extreme, cultured fish from wild sourced broodstock may be equivalently competent as spawners as the wild conspecifics.

For fitness predictions and effects on wild population viability and abundance, OMEGA includes a model of stabilizing selection for a hypothetical trait which describes the survivorship of offspring of naturally spawning wild and culture-origin individuals as described in Ford (2002). Effects on survivorship of the wild population are modeled using a relative fitness factor of the admixed wild population of conspecifics based on the modified trait value of the mixed population (Figure 1.3). Over successive generations of escapees interbreeding the mixed wild population moves away from the natural optimum and relative fitness is less than 1.0 based on assumed selection in nature for the trait.

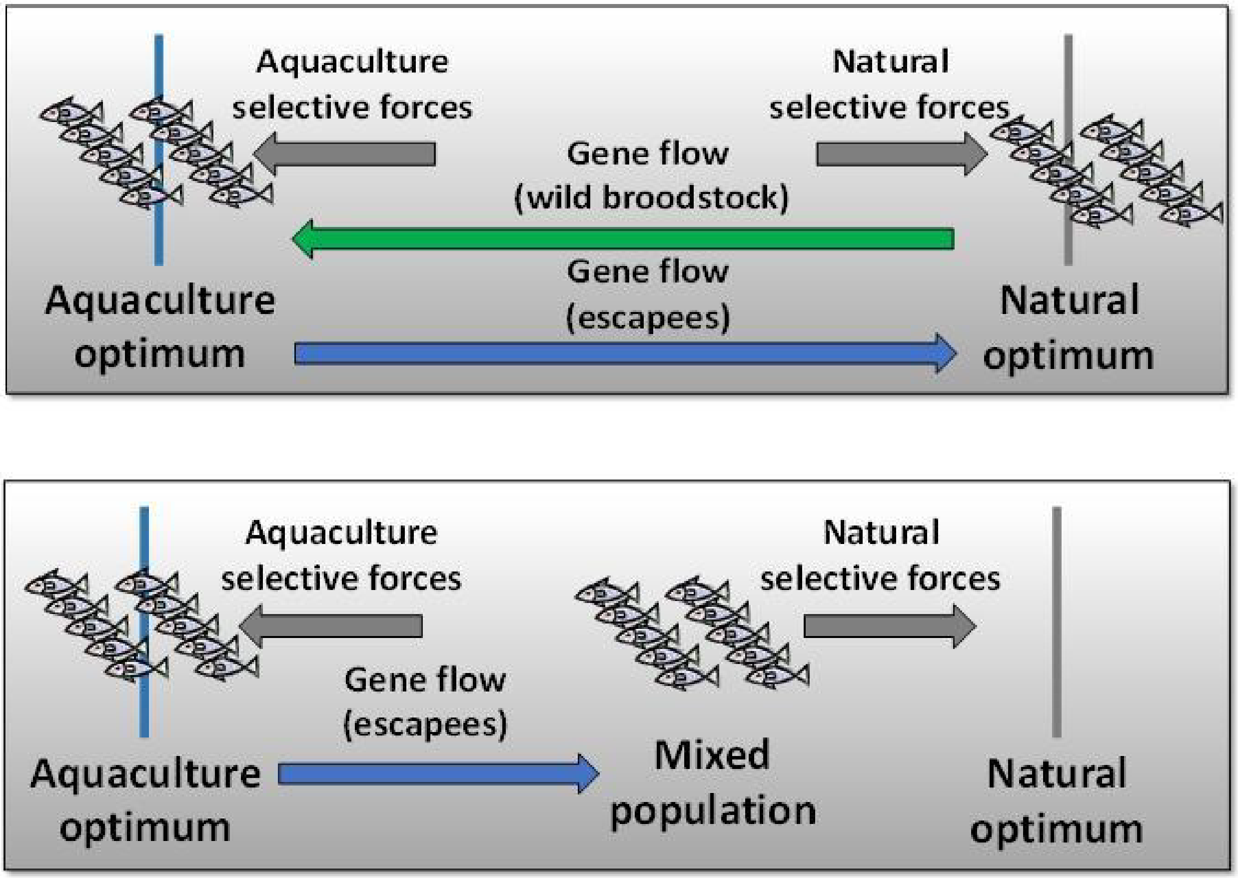

Figure 1.3. Schematic of Single Trait Fitness Model (top) and Gene flow to Wild Population with Mean Trait Value Change (bottom). Conceptual fitness model based on Ford 2002.

The potential for the wild population to experience Ryman-Laikre effects is evaluated in terms of impacts on the effective population size (N_e) and related loss of genetic diversity. Waples et al. (2016) developed a model to estimate the total effective population size (N_{eT}) of an admixed cultured–wild population and the change in effective population size (N_{eT}/N_{eW}) between wild and admixed populations. These estimates incorporate parameters such as the number of effective broodstock used in cultured fish breeding programs, the demographics of the wild population, and the predicted contribution of cultured fish to natural spawning. Calculations of these estimates were incorporated into OMEGA analyses. First, the methods outlined in Waples et al.

(2011) were integrated into OMEGA and used to estimate generation length and the effective population size in the absence of escapees (AgeNe). These metrics provided critical context for evaluating the impact of escapees on wild populations. OMEGA also used the N_e/N ratio to evaluate effective population size to census population size when considering effects from escapees with potentially low genetic diversity. Then Equation 8 from Waples et al. (2016) was applied in OMEGA to estimate N_{eT} and the reduction in N_{eT}/N_{eW} caused by breeding escapees.

Waples et al. (2012) reviewed general guidelines proposed in the scientific literature to describe the minimum effective population sizes (N_e) necessary for natural populations to maintain genetic diversity and avoid negative genetic impacts. Waples et al. (2012) described these guidelines, which are often summarized as the 50/500/5,000 rules, as follows:

1. Short-term inbreeding avoidance ($N_e \geq 50$): In domesticated populations, an N_e of 50 corresponds to an inbreeding rate of approximately 1% per generation, which can be sustained in the short term to avoid severe inbreeding effects. However, the consequences of inbreeding are thought to vary unpredictably between natural and domesticated populations.
2. Maintenance of genetic variation through mutation ($N_e \geq 500$): An N_e of 500 is suggested to balance the loss of genetic variability from drift with the gain of new additive genetic variability from mutations. This threshold, however, has been primarily tested in *Drosophila* species and remains largely unvalidated for other taxa.
3. Avoidance of fitness declines from mildly deleterious mutations ($N_e \geq 5{,}000$): An N_e of 5,000 is proposed to prevent slight reductions in population fitness caused by the accumulation of mildly deleterious mutations. These mutations, which are not strongly selected against, accumulate as genetic drift dominates in smaller populations compared to natural selection where they would be gradually removed. This estimate assumes a closed population, but even modest levels of immigration can restore genetic variability and fitness in populations affected by drift.

These thresholds provide a framework for assessing genetic risks, but their applicability may vary depending on the species, life history, and population structure. More specifically, Waples et al. (2012) suggested that large marine populations may be more susceptible to loss of genetic diversity than other species. For the case studies in this report, the OMEGA results were evaluated for potential Ryman-Laikre effects using the largest of the three estimates, the 5,000 minimum effective population sizes. Waples et al. (2012) also recommended evaluating reductions in the effective population size of wild populations (N_{eW}), specifically the ratio of total effective population size to wild effective population size (N_{eT}/N_{eW}), to assess potential Ryman-Laikre effects in large marine populations. A ratio below 0.1 may indicate potential for Ryman-Laikre effects. In OMEGA, both N_{eT}/N_{eW} and $N_e \geq 5{,}000$ were used to evaluate the potential genetic impacts of escapes and the likelihood of Ryman-Laikre effects.

1.3.1.1 Use of Case Studies

The OMEGA model was used to evaluate species-specific case studies for Southern California and the Gulf of America. The case studies are intended to provide insights into how different species' life histories, abundance, and population structure can affect estimates of introgression of cultured finfish in wild populations and the genetic impacts of escapees. Farm production scenarios developed for the case studies are hypothetical and are not intended to represent a specific farm proposal, serve as an implicit or explicit endorsement by NOAA of any species or cultivation practice, or serve as a policy recommendation or be prescriptive of any future farm proposal.

Aquaculture parameters used in the case studies (size of fish transferred to offshore pens, time in pens, and size of fish at harvest) were developed from species reviews in Richie (2021) and other sources. Species used in the case studies were selected based on industry subject matter expertise in each region. Case studies modeled a 3-Farm scenario with an annual production of 10,500 mt, and a 5-Farm scenario with an annual production of 17,500 mt, where each farm was estimated to produce 3,500 mt. All case study scenarios assumed 100% wild caught broodstock.

Each cage was assumed to contain 100,000 fish at harvest across all cases. Fish within cages were binned into three size groups to align with growth curves from culture (or wild growth curves if culture-specific data were unavailable). This categorization allowed for the assessment of escape risks at different stages during grow-out based on fish size.

Escape scenarios included fish leakage from cages and larger escapes of fish from episodic events (e.g., cage failures). Leakage rates across the production cycle were based on an assumed 0.3% escape rate across all size categories, but this rate is apportioned differently across the three size bins based on size-specific risks. This rate has been used in the Canadian and Icelandic escape modeling of total escaped farmed salmon (or 0.8 escapes per metric ton), and incorporated into that estimate is a multiplier to account for underreporting in the industry (Bradbury et al. 2020, MFRI 2020). An analysis conducted on salmon in Norway found that the actual number of escaped fish was two- to four-fold higher than the numbers reported by the industry (Skilbrei et al. 2015); this 2-4x multiplier has now been used in recent modeling of salmon escapes in Canada and Iceland to account for this under-reporting (Bradbury et al. 2020, MFRI 2020). Independently derived leakage rates, very close to the above 0.3%, have been used by the authors in other modeling efforts based on confidential conversations with the industry, which lends further confidence in this estimate.

For the smallest fish (Bin 1), the highest amount of leakage for the on-station period is expected during the time fish are held in a nursery net. This is expected due to potential size mismatches between the mesh size of the nursery net, cage mesh sizes, and the sizes of fish in the cage, both at the time of initial seeding and at the time of nursery net removal (i.e., some fish may be too small to be contained by the nursery net upon seeding, or to be contained in the regular cage once the nursery net is removed). Some loss is also expected during the seeding process and from maintenance activities related to the nursery nets (e.g., replacing the net if/when biofouling is an issue). From the total 0.3% leakage escape rate, a leakage rate of 0.2% was allocated and applied to the period during which fish are in Bin 1.

Very little loss is expected in the intermediate grow-out production pen (Bin 2), and the leakage rate apportioned to this stage is approximately 0.03% (from the total 0.3%). This low level of leakage reflects the use of superior cage construction using copper-alloy mesh or other materials which eliminates chances for small holes from chaffing, holes caused by biting predators, or holes due to general wear from fish inside the pen (Dwyer and Stillman 2009, Berillis et al. 2017, Yigit et al. 2017). It also accounts for the period fish and pens are handled the least during the grow-out process.

Leakage risk is assumed to increase with the largest fish (Bin 3), this is due to more frequent handling and activities such as size-grading for harvest, transfer of fish to harvest pens, and harvesting of fish from pens. The fraction of the leakage rate that was estimated and apportioned to this size bin was 0.07%, again from the total leakage rate of 0.3% that spanned the duration of the grow-out.

In modeling episodic escape events, parameters for both the likelihood[1] of a cage failure and the magnitude loss of fish from an episodic escape event were approximated. The highly variable pattern of escape numbers by year reported in Skilbrei et al. (2015) suggest medium to large episodic escape events occur in combination with the previously discussed leakage type escape. Norwegian studies of Atlantic Salmon suggest unreported episodic escape events occur on a regular basis (Glover et al. 2008, Glover 2010). Thus, it seems reasonable to assess episodic escapes in combination with leakage escapes to anticipate a pattern of low-level escapes (leakage) interacting with the wild population with an occasional larger influx of escapees (episodic cage failures).

It was challenging to determine the likelihood of episodic escapes for the hypothetical case study analyses. While no data were available for the case study species, escape frequencies were reviewed for aquaculture escapes of Kingfish (*S. lalandi*) from South Australia. Based on reported data from South Australia, three locations (Arno Bay, Boston Bay, and Louth Bay) were used to determine the likelihood of escapes of 1000 fish or more. The frequency of these episodic events varied among locations, with a low of one event every 10 years (10%) in Boston Bay to one event every four years (25%) in Louth Bay (Table 2.1). However, the Louth Bay site with the highest frequency of failures was also based on the fewest number of years (four) compared to the two longer running data sets with lower frequencies. While these estimates are not directly transferable for several reasons (e.g., likely different cage materials, in a bay versus

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[1] Episodic events are described as the likelihood of a cage failure occurring in a year. Likelihood is synonymous with probability in this analysis. The analysis does not evaluate the likelihood that a single cage may fail in a year. If that were the case the number of cage failures in a year would depend on the likelihood of failure and the number of cages with fish. Information used to develop likelihoods were based on the reported number of cage failures over a period of time, in other words the observed frequency of an event. Information on the number of cages with fish over the period of reported cage failures was not available to calculate likelihood of any one cage failing. This lack of information to better model the likelihood of episodic escape events is an impediment to better understanding offshore genetic risks from cage failures leading to fish escaping.

offshore, and a different species of *Seriola*), differences may offset each other and still represent the closest proxies available at the present time. Given this uncertainty, and to explore the impact that episodic loss has on the results, the frequencies from the sites were converted to an annual likelihood of a cage failure and independently simulated to explore a range of episodic events (10% to 25% annual likelihood) under the 17,500 mt production scenario. The lower production scenario used a low and high likelihood adjusted for the ratio of the low and high production assumption (10,500/17,500 = 0.60) of 6% and 15% likelihood of a cage failure. This was done to acknowledge that the lower production scenario assumes fewer farms, fewer overall cages, and a lower likelihood of cage failure.

Table 2.1. Frequency of Kingfish (*Seriola lalandi*) escapes of over 1,000 fish and corresponding likelihood of occurrence over a year based on reported escape data from three locations in South Australia.

Location	Escape frequency	Likelihood of escape occurring over course of a year
Arno Bay	Every 6.5 years	15%
Boston Bay	Every 10 years	10%
Louth Bay	Every 4 years	25%

To simulate episodic escapes more realistically, the OMEGA model was set to randomize the number of fish lost in an event between a half and a full cage of fish. The model also randomly assigned the cage loss to one of the three size bins of fish for the species.

Escaped cultured fish may survive at lower rates compared to similarly sized wild conspecifics (e.g., escaped Yellowtail Kingfish [*S. lalandi*] observed with empty stomachs or stomachs containing atypical non-food contents; see Fowler et al. 2003). However, empirical estimates of relative survival of marine fish escapees are rare. Observations that suggested lower survival, such as Fowler et al. (2003), are from fish selected for culture traits and may not reflect survival of escaped fish reared from wild caught broodstock. Hervas et al. (2010) found both short- and long-term size-dependent mortality of hatchery White Seabass released for stock enhancement. In that case, the time of year when fish were released influenced post-release mortality, with highest mortality for fish released in the winter and lowest mortality for fish released in the spring. More importantly, overall hatchery-reared White Seabass had a higher mortality in the wild compared to estimates of wild fish. However, even though available evidence suggests survival may be lower for escaped cultured fish, the case study analyses more conservatively assumed survival would be the same as the wild population's size-based survival assumed in the OMEGA.

Two additional scenarios were also modeled for each case study species to reflect a scenario that included low potential for escape of cultured fish and low survival of escapees (referred to as

"Modified" scenarios in the result figures and discussion). These two modified scenarios were modeled to recognize that the previously described assumptions may not reflect four factors affecting the number of fish escaping and their survival in the wild. They are: 1) strong measures to minimize the likelihood of episodic escapes, 2) operation plans to recapture escaped fish, 3) the placement of offshore farms that may adversely affect the survival of escapees, and 4) the effects of the culture environment (developmental effects) adversely affecting survival of escapees. The low and high production scenarios were modeled with assumptions to account for these factors. Specifically, cage failure likelihoods were modeled at 3% and 5% for low and high production scenarios, respectively, and half to three-quarters of the fish in a cage failure would be recovered (25% to 50% of the fish in a cage escape). Additionally, the two scenarios assumed escaped fish would survive at half the rate of the wild population size-based survival.

Model results were summarized in years 5 (Year 5), 10 (Year 10), and 25 (Year 25) of the simulations. The short-term results are presented to describe potential effects within a time frame applicable for environmental impact analyses and permitting applications.

OMEGA model simulations typically run for 300 simulated years to include the long-term equilibrium impacts of escaped fish. Model simulations have shown that the effect of escaped, long-lived marine fish species on fitness are slow to materialize (ref). The short-term results provide enough time, however, to understand the population trajectory with escapes. However, for two case study species, in which model results suggested a fitness impact of escaped fish, we report the long-term fitness results to help better understand long-term consequences. The long-term fitness consequences were summarized as the median loss in fitness in years 10 to 100 for each iteration.

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2.0 Southern California Candidate Species for Marine Aquaculture

2.1 Geographic range

The north, central north, south, and central south portions of the Southern California bight were considered in these evaluations.

2.2 Finfish Candidate Species for Marine Aquaculture in Southern California

2.2.1 California Yellowtail (Seriola dorsalis)

Genetic effects of culture scenarios for California Yellowtail in Southern California were evaluated using the OMEGA model. Model methods and results are reported in Section 2.3.1, Case Study: California Yellowtail. A summary of case study results is included at the end of this species profile.

2.2.1.1 Range/Description

The California Yellowtail (*Seriola dorsalis*) is a coastal pelagic species found along the eastern Pacific coast, ranging from Cabo San Lucas in Baja California Sur, Mexico, to Point Conception, California, USA (Baxter 1960, Ben-Aderet et al. 2020). This species is rarely observed north of the Southern California Bight (SCB) except in years with high water temperature anomalies (Ben-Aderet et al. 2020).

California Yellowtail is a popular sportfish throughout its range due to the angling challenge it presents and the quality of its fresh meat (Collins 1973, Huong 2020). The abundance of California Yellowtail in Southern California is believed to be dependent on ocean temperatures, with higher catches reported during years when spring water temperatures are at least three to five degrees (°F) above normal (Baxter 1960). Although a smaller number of California Yellowtail remain in the SCB year-round (Ben-Aderet 2017, Madigan et al. 2018), their abundance increases in spring and summer due to a seasonal migration of fish moving north from the more abundant populations offshore of central Baja California. Collins (1973) suggests that recreational fishing for California Yellowtail in the SCB is heavily dependent on these annual migrants from central and northern Baja California.

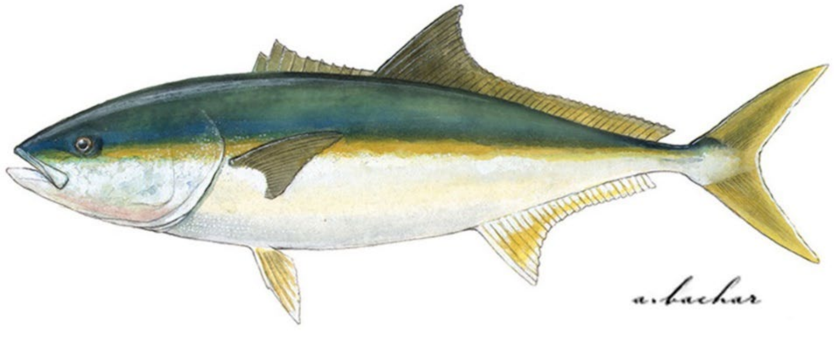

Image from California Department of Fish and Wildlife

While California Yellowtail inhabit both state and federal waters, they are managed by the California Department of Fish and Wildlife, not NOAA. Recreational bag and size limits have been established for this species; in California up to 10 fish are allowed per angler per trip, and five of those fish may be under 24 inches fork length, while in Mexico only five fish per angler, of any size, are allowed (Huang 2020). There is limited data on California Yellowtail population abundance, and no stock assessments are available. Reported catch in U.S. waters averaged 259 metric tons (range: 10 to 1,030 mt) from 2000 to 2020 (https://www.fisheries.noaa.gov/foss/). In contrast, reported catches from Mexican waters are much higher, averaging 2,038 metric tons (range: 1,175 to 2,800 mt) over the same period (Cisneros-Soberanis 2018, Enciso and Trasviña 2022). The combined average catch from U.S. and Mexican waters is 2,296 metric tons, indicating a reasonably large population across the species' entire range.

2.2.1.2 Biological Characteristics

California Yellowtail exhibit variation in habitat preference depending on their life stage. Smaller individuals (45 to 59 cm in length) are more frequently observed in pelagic offshore waters, often associated with floating kelp rafts, whereas larger individuals (83 to 98 cm in length) are more commonly found in coastal inshore areas, particularly around kelp beds (Baxter 1960, Madigan et al. 2018). However, there is limited information available on the habitat use of 1-year-old California Yellowtail (Madigan et al. 2018). California Yellowtail also display size-dependent migratory behaviors (Baxter 1960, Ben-Aderet et al. 2020). Fish measuring 61 to 90 cm were found to migrate the greatest distances, with most having moved between 200 to 300 miles in a tag-and-recapture study, while fish larger than 90 cm tended to remain near their tagging origin (Ben-Aderet 2017). This reduced movement suggests that larger fish exhibit more resident behavior (Ben-Aderet 2017).

California Yellowtail are highly fecund broadcast batch spawners that reach sexual maturity between two and three years of age and can live up to 22 years in the wild (Baxter 1960). Baxter (1960) and Sumida et al. (1985) identified the primary spawning areas for California Yellowtail in Mexican waters off Baja California, based on observations of larvae, although some spawning likely occurs in U.S. waters as suggested by the observation of larvae and large mature fish with enlarged gonads within the SCB (Madigan et al. 2018). Sumida et al. (1985) reported finding larvae from nearshore to 200 miles offshore, with only 4% of the larvae occurring in Southern California, compared to 96% off Baja California.

Spawning typically begins in July and continues until October, peaking in July (Baxter 1960; Ben-Aderet 2017). Spawning aggregations have been reported off the Coronado Islands, Baja California, Mexico, and in association with other offshore undersea features (e.g., Uncle Sam's Bank 70 nautical miles off of Baja California, Mexico; Baxter 1960). Larvae have been collected from April to October, with 83% of larvae collected in July and August from the nearshore to 200 miles off the coast of Baja California, predominately (Sumida et al. (1985). Fecundity is size-dependent with smaller females producing approximately 458,000 eggs and larger females producing up to 3,914,000 eggs (Baxter 1960). Stuart and Drawbridge (2013) found that metamorphosis occurred at 35 days post-hatching in captivity, indicating that the pelagic larval duration for this species likely extends over a month in the natural environment.

2.2.1.3 Population Structure

There has been debate regarding whether California Yellowtail in the Southern California Bight (SCB) are self-recruiting and distinct from the larger population that seasonally migrates northward from Mexico (MacCall 1996). While this possibility cannot be entirely ruled out, genetic analyses using nuclear DNA microsatellite markers and mitochondrial control region sequences have not detected significant genetic differentiation among specimens from the northeastern Pacific, including the SCB, the Pacific coast of Baja California, and the Gulf of California. These findings support the existence of a single, cohesive population over evolutionary time scales in the northeastern Pacific (Purcell et al. 2015).

2.2.1.4 Aquaculture

The genus *Seriola* is among the most widely cultured groups of marine finfish, with five species currently being cultured or under development for culture in several countries (Sicuro and Luzanna 2016). In the United States, three *Seriola* species hold commercial interest: Almaco Jack (*S. rivioliana*), which is being cultured offshore of Hawaii in net cages; Kingfish (*S. lalandi*), which is being developed for land-based recirculating aquaculture systems (RAS) following successful implementations in other countries; and California Yellowtail (*S. dorsalis*), for which permitting is being pursued for offshore aquaculture in Southern California (https://poaquafarms.com/).

California Yellowtail is of particular interest for aquaculture due to its rapid growth. It reaches market size within one to two years and has a high market value, especially as a sashimi-grade fish (Purcell et al. 2015, Rotman et al. 2021). The Hubbs-SeaWorld Research Institute (HSWRI) began culturing this species in 2003 and has made significant advancements in broodstock conditioning, larval rearing, and juvenile grow-out techniques (Rotman et al. 2021).

According to Rotman et al. (2021), captive-bred California Yellowtail spawn continuously for six months. They spawn volitionally without the need for hormone treatments when ambient water temperatures reach 16°C and ceasing when temperatures exceed 22°C (Stuart and Drawbridge 2013). More recently, Stuart and Drawbridge (2024) reported successful photothermal manipulation to induce off-season spawning in F1 California Yellowtail without compromising egg quality or quantity.

Courtship behavior in captivity in this species involves one or more males following and nudging the abdomen of a female (Stuart and Drawbridge 2013). Genetic parentage analyses by Schmidt et al. (2021) revealed sex-specific spawning dynamics, with most eggs produced by one, and to a lesser extent, a second female during each spawn. Entire spawning seasons were sometimes dominated by a few females, with only three contributing 46.4%, 29%, and 23.2% of the offspring in one season. In contrast, an average of 5.87 males contributed more evenly across spawns, with greater variation in male participation between spawning events. These dynamics suggest that maintaining genetic diversity in hatchery-raised fish could be challenging due to the lower effective number of breeders, particularly females.

Following metamorphosis (35 days after hatching) (Stuart and Drawbridge 2013), California Yellowtail exhibit high survival rates from 45 to 75 days post-hatch (>90%) but require significant oxygen and space in tank settings (Rotman et al. 2021). While commercial-scale grow-out has yet to occur, it is anticipated that California Yellowtail could reach a market size of 3 to 4 kg in under two years (Rotman et al. 2021).

2.2.1.5 Considerations on genetic risk to wild conspecifics

Data on the abundance of California Yellowtail in the wild remain limited, making natural population abundance a difficult to estimate when assessing the potential effects of aquaculture escapes. The species' transboundary movements between California and Baja California support the notion of a shared population that migrates seasonally, and catch data from California and Baja California, Mexico, suggest a robust population across the species' range (U.S. catch - https://www.fisheries.noaa.gov/foss/; Mexico catch - Cisneros-Soberanis, 2018, Enciso and Trasviña 2022). Despite historical catch data indicating a potentially abundant population, uncertainty persists due to the lack of a formal stock assessment.

California Yellowtail are distributed in both nearshore and offshore habitats, with extensive north-south migrations that increase the likelihood of interactions between escaped cultured fish and wild spawners. To mitigate potential genetic impacts on wild populations, maintaining genetic diversity through the collection of local broodstock and breeding practices designed to maximize the number of brood fish reproductively contributing to offspring is essential, particularly given the observed spawning dynamics in captivity.

The anticipated market size for California Yellowtail is 4 kg (Rotman et al. 2021). While wild individuals mature around this size (Baxter 1960, Ben-Aderet et al. 2020), cultured fish attain this size at a younger age. Although the risk of spawning in cages, and the subsequent release of gametes or fertilized eggs, is a concern, this likelihood is anticipated to be low prior to harvest of cultured fish (HSWRI, personal communication). Once this species is in offshore culture, it will be important to provide careful observation to detect any potential spawning behavior in net pens during grow-out, and if spawning is found to occur, then it will become necessary to evaluate the genetic risks from the release of gametes and larvae.

Overall, the available data suggest a low-to-moderate genetic risk to wild populations from escaped cultured *S. dorsalis*. Conducting a stock assessment coupled with an evaluation of juvenile-to-adult survival rates would provide critical information on wild stock abundance and the reproductive resilience of the population. Additionally, a fine-scale genetic study using modern methods could offer insights into the effective population size, a key indicator of genetic diversity. Potential mitigation strategies might include the production of sterile lines which could eliminate the genetic risk to wild California Yellowtail populations.

2.2.1.6 OMEGA case study to evaluate genetic risks of farm scenarios

A case study was performed using the OMEGA model to quantify population dynamics of a hypothetical California Yellowtail farm program sited in Southern California. The OMEGA model was used to simulate the response of a wild population of California Yellowtail to varying levels of culture-origin fish escapes from a farm system, resulting in a mixed cultured-wild population where some proportion of the population contains genetics of cultured fish.

Assuming an individual farm harvest production of 3,500 mt, two different production levels were modeled: the equivalent of three farms (hereafter 3-farm) with a total harvest production of 10,500 mt and the equivalent of five farms (hereafter 5-farm) with a total harvest production of 17,500 mt. The captive breeding program was assumed to use local, wild-origin fish and did not employ intentional selection for traits. Detailed modeling of California Yellowtail farm systems under a range of escape scenarios is presented in Section 2.3.1. Conclusions of OMEGA modeling in regard to potential for genetic risk are discussed in Section 2.3.4.1.

The evaluation of California Yellowtail aquaculture relied on assumed levels of wild population abundance inferred from catch data. as a formal stock assessment has not been conducted for this species. The model results for both the 3-farm and 5-farm production scenarios demonstrated a negligible loss in wild population fitness using the most conservative assumptions of low population abundance (female spawning biomass of 8,000 mt), high rate of episodic escape (25% likelihood of loss of one cage in any given year) and an assumed escape rate from program leakage of 0.3% per year. In regard to genetic diversity effects, OMEGA results indicated that while the effective population size (ratio N_{eT}/N_{eW}) would likely be reduced under both production scenarios, the large effective size of the mixed population is sufficiently large to suggest a low potential for deleterious effects of low N_e. Deleterious Ryman-Laikre effects were only found to occur for a small proportion (~<10%) of simulations using the most pessimistic assumptions for the 5-farm system. As discussed above, a stock assessment and fine-scale genetic study of the wild population would be important resources to definitively parameterize the OMEGA model for California Yellowtail and enable a more precise assessment of genetic risks to help define a sustainable scale of aquaculture production in the Southern California region.

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2.2.2 White Seabass (Atractoscion nobilis)

Genetic effects of culture scenarios for White Seabass in Southern California were evaluated using the OMEGA model. Model methods and results are in Section 2.3.2, *Case Study: White Seabass*. A summary of case study results is included at the end of this species profile in Section 2.2.2.6, *OMEGA case study to evaluate genetic risks of farm scenarios.*

2.2.2.1 Range/Description

White Seabass (*Atractoscion nobilis*) is a highly prized recreational fish in California that is primarily found from Point Conception, to Southern Baja California, Mexico, although it has been caught as far north as Juneau, Alaska (Thomas 1968). Within California, this species has been an important target for both commercial and recreational fisheries due to its high-quality flesh and the challenge it presents to anglers (Vojkovich and Reed 1983). However, overfishing led to a decline in the commercial catch of White Seabass beginning in the early 1900s, followed by a decline in the recreational catch starting in 1949 despite various management regulations that have been in place since 1931 (Vojkovich and Reed 1983, Williams et al. 2007, and references therein). Continued declines in the 1950s and 1960s sparked interest in both stock enhancement and commercial aquaculture leading to the initiation of a stock enhancement program in 1986 (CDFW 2002).

Image from California Department of Fish and Wildlife

A stock assessment for White Seabass was completed in 2016 by the Center for Advanced Population Assessment Methodology and Scripps Institution of Oceanography (Valero and Waterhouse 2016). The assessment estimated a female spawning stock biomass of 569 metric tons (mt) in 2015, compared to an unfished virgin spawning stock biomass of 2,092 mt. However, this assessment did not include fish from Baja California, Mexico. Research by Aalbers et al. (2022) and Reiber (2022) demonstrated White Seabass movements between Baja California and California, which suggested that White Seabass have a transboundary stock. Reiber also documented the capture of cultured adult White Seabass in Baja California that were originally released through stock enhancement programs in California. A comprehensive assessment of the stock structure across the species' entire range has yet to be completed. The U.S. fishery is currently managed under the California Department of Fish and Wildlife's White Seabass Fishery Management Plan (CDFW 2002).

2.2.2.2 Biological Characteristics

White Seabass are a long-lived fish species, with a maximum reported age of 28 years (Williams et al. 2007, Romo-Curiel et al. 2015). However, fish older than 21 years are rare in the population (Romo-Curiel et al. 2015). This species can reach a length of 1.5 meters and a weight of 41 kilograms, though the average weight of a commercially caught White Seabass typically ranges from 9 to 18 kilograms (Valero and Waterhouse 2016). *A. nobilis* generally exhibit rapid growth during the first eight years of life, after which growth rates tend to decline (Romo-Curiel et al. 2015).

Males reach 50% maturity at around 60 cm total length (TL), while females do not reach 50% maturity until they exceed 70 cm TL. However, it is believed that all White Seabass are mature by 80 cm TL (Vojkovich and Reed 1983, and references therein). According to Clark (1930, as cited in CDFW 2020), these sizes correspond to males maturing at around 2 years of age and females at about 3 years, with all individuals reaching maturity by 4 years.

White Seabass inhabit coastal waters and typically move closer to the surface as water temperatures warm during late spring making them more accessible to anglers. This movement coincides with their spawning season (Aalbers and Sepulveda 2015). *A. nobilis* are broadcast batch spawners, where females can release between 0.76 million and 1.5 million eggs depending on their size. However, the specific spawning intervals and the number of spawning events per season in the wild are not well understood (CDFW 2002, Aalbers and Drawbridge 2008). In a net pen placed off of Catalina Island, California, Aalbers and Drawbridge (2008) observed that spawning groups typically involved multiple males—up to nine—surrounding a gravid female. In Southern California, spawning occurs from March to September, peaking in June (Williams et al. 2007, and references therein).

After fertilization, the buoyant eggs hatch in approximately two days and the larvae remain planktonic for around 30 days (Moser et al. 1983, Allen and Franklin 1988, 1992). Moser et al. (1983) found White Seabass larvae from May to August, with a peak in July. These larvae were distributed from Santa Rosa Island, California, to Santa Maria Bay, Baja California, with only 15% found in Southern California and the remaining 85% along Baja California, Mexico. Within Baja California, 50% of the larvae were located north and 35% south of Punta Eugenia (Moser et al. 1983). Recruitment success is closely linked to the abundance of larvae and their settlement success rather than environmental factors (Allen and Franklin 1992).

Larvae and small juvenile White Seabass measuring 7 to 10 mm in length are commonly associated with algal debris rafts in shallow areas just outside of the surf zone (Moser et al. 1983, Allen and Franklin 1988). As they grow, juvenile White Seabass, which are relatively demersal and euryhaline, become associated with benthic habitats and kelp beds and may also settle into bays (Allen and Franklin 1988, 1992; CDFW 2002). Mature White Seabass typically inhabit kelp beds and rocky reefs up to 120 meters deep but have also been found schooling offshore in the upper water column during warmer periods (Allen and Franklin 1988, 1992, Aalbers and Sepulveda 2015). Adult movement of White Seabass can vary widely among individuals.

Aalbers and Sepulveda (2015) reported a mean displacement of 229 km between points of release and recapture for tagged White Seabass with a range between 2 and 624 km.

2.2.2.3 Population Structure

There has been ongoing debate about whether White Seabass populations in California and Baja California, Mexico are part of the same breeding population or if they are genetically distinct populations (Aalbers et al. 2022). Franklin et al. (2016) identified genetic structure among samples collected in Southern California, Pacific Baja California, Mexico, and the Gulf of California, Mexico. However, an earlier study by Coykendall (2005) did not detect spatial genetic structure within the Southern California Bight (SCB) or between the SCB and Baja California, Mexico. More recently, Fajardo Yamamoto (2023) reported connectivity among White Seabass populations from California and the west coast of the Baja California peninsula based on electronic tagging data, aligning with Coykendall's (2005) findings. Reiber (2022) reported a 7.4% contribution of U.S. hatchery-origin White Seabass to the adult population in Mexico based on genetic tagging studies of enhancement fish released in California. This, coupled with movement studies of tagged White Seabass showing transboundary movement between Baja California, Mexico and California, suggests that there may be a shared White Seabass stock that seasonally migrates between these regions (Aalbers et al. 2022).

Romo-Curiel et al. (2016) conducted an otolith isotope study that found significant differences in isotope signals between populations north and south of Punta Eugenia in Baja California. However, Franklin et al. (2016) grouped sampling sites north and south of Punta Eugenia into a single larger "Pacific Baja" collection for their genetic analyses potentially masking any finer-scale genetic differentiation. Romo-Curiel et al. (2016) suggested that Punta Eugenia, along with the circulation patterns around it, might serve as a barrier to connectivity between populations north and south of that point. The findings among these studies might reflect that White Seabass exhibit mixing in the Southern California Bight and Baja California, Mexico north of Punta Eugenia, but limited movements across the Punta Eugenia break. However, there is a need for more research to resolve the stock structure of White Seabass to fully understand their population dynamics and management needs.

2.2.2.4 Aquaculture

Offshore aquaculture for the replenishment of White Seabass has been ongoing since 1986, supported by multiple grow-out facilities operated by volunteers and the Hubbs SeaWorld Research Institute (HSWRI). The program releases approximately 100,000 White Seabass annually, each measuring around 20 cm in length or weighing 75 to 250 g, into the Southern California region (California Sea Grant 2017). As this is a captive breeding program aimed at restoring a depressed population, maintaining and maximizing genetic diversity is a critical component of the culture management plan.

Gruenthal and Drawbridge (2012) recommended maintaining a broodstock population size of 140 to 200 adult fish with a target of 60% females in a free-spawning mating system to ensure that the genetic representation in offspring is adequate. They found that employing sex-specific mating strategies improved the ratio of effective number to census number in the captive breeding program which is essential for maintaining genetic diversity.

Drawbridge et al. (2021) provided a summary of key parameters for captive breeding that could inform potential White Seabass aquaculture operations. In hatcheries, White Seabass can produce up to 10 batches of eggs per season with spawning occurring every 1 to 5 weeks. The species is highly fecund and is capable of producing up to 5.8 million eggs per spawn. Egg production is temperature-dependent and can be managed year-round by manipulating the photothermal conditions in broodstock tanks.

Survival rate at 50 days post-hatch ranges between 20% and 40% when using wild brood fish. Juveniles are typically transferred to outdoor rearing tanks at 90 days post-hatch where survival rates increase to 95% or more. Growth rates are highly dependent on temperature, and this is more effectively controlled in recirculating systems. A harvest weight of 0.6 to 1.0 kg can be achieved within 18 months (Drawbridge et al. 2021). There is an establish market demand for *A. nobilis*, however, the market, has been based on wild fish which are at least 2 kg, due to fishing regulations on the species. In market testing, while the smaller cultured fish were more difficult for restauranteurs to fillet, this was less of an issue for fish processors, and consumer ratings based on texture, taste, and freshness of cultured White Seabass were high (Drawbridge et al. 2021).

2.2.2.5 Considerations on genetic risk to wild conspecifics

The transboundary movement of White Seabass between California and Baja California (Aalbers et al. 2022) underscores the need for ongoing assessments of stock structure across their entire range. The current stock assessment model, which estimated a relatively small spawning biomass in California, does not account for fish from Baja California, Mexico (Valero and Waterhouse 2015). Given the evidence from recent studies, it is plausible that regions north of Punta Eugenia, Baja California, may represent a substantial portion of the same White Seabass stock found in the Southern California Bight. Further research could enhance our understanding of the population's resilience to fishing pressures, the impact of the stock enhancement program, and the potential consequences of escaped White Seabass from commercial aquaculture.

Continued genetic studies are crucial to further investigate the contribution of enhancement fish to the overall population and to assess the effective population size of the mixed population. This information is vital for evaluating the sustainability of ongoing culture under both replenishment and potential commercial aquaculture scenarios. Hervas et al. (2010) estimated that White Seabass released at 200 mm had a 1.5% survival rate to the legal minimum length of 600 mm SL, while those released at 400 mm experienced a 13.8% survival rate under optimal conditions. However, the genetic study by Reiber (2022) suggested that 46% of juvenile White Seabass sampled in Southern California originated from the stock enhancement program—a surprisingly high percentage. The Scientific Advisory Committee of the Ocean Resources Enhancement and Hatchery Program (OREHP), which runs the White Seabass stock enhancement program, has recommended further investigation into this estimate to determine whether it was upwardly biased due to challenges in the analyses (OREHP SAC Minutes 2023).

The California Department of Fish and Wildlife (CDFW) has only allowed the release of 125,000 to 350,000 fish per year by OREHP, although releases of around 100,000 fish have been more common. The broodstock for this program are wild-caught within the Southern California Bight with a replacement rate of 25% per year (Gruenthal and Drawbridge 2012, Supplemental Material). According to Bartley et al. (1995, as described in Gruenthal and Drawbridge 2012), 74 effectively breeding fish are required to capture 99% of the wild genetic diversity. Gruenthal and Drawbridge (2012) further determined, based on genetic analyses of spawning dynamics, that 140 to 200 White Seabass broodfish are needed to ultimately result in this targeted number of breeders and capture the proportion of wild genetic diversity estimated by Bartley et al. (1995). It was acknowledged, however, that rare alleles present in the wild population may be lost in hatchery fish and eventually reduced in the wild population due to supplementation (Gruenthal and Drawbridge 2012). If hatchery fish do indeed constitute 46% of juveniles in the Southern California Bight, then some of these low-frequency alleles may have been reduced or lost in the wild population. To ensure the sustainable genetic diversity of White Seabass from commercial operations, it is recommended that commercial broodstock populations be similar in size to those in the current enhancement program.

Although commercial escapes may not pose a greatly different genetic risk from stock enhancement releases, the cumulative number of fish escaping from commercial operations, in addition to intentional releases, could potentially exceed a tipping point for a relatively small wild population. If this occurs, introgression of cultured fish into wild populations could lead to losses in genetic fitness and diversity within the mixed population. However, there remains considerable uncertainty regarding the biomass and genetic stock structure of the wild population(s), and much uncertainty over the proportion of hatchery fish within the natural population, particularly in light of the recent Reiber (2022) study. This makes it challenging to assess the resilience or vulnerability of White Seabass in Southern California to introgression from commercially produced escapees. Further, with the species' long life-span, introgression may be difficult to detect initially due to sexual maturity occurring 1.5 to 2 years after escape. However, given the time it takes for White Seabass to reach maturity (3 to 4 years), if production cycles (to the point of harvest) remain around 18 months in duration (Drawbridge et al. 2021) then spawning in culture is unlikely to pose a genetic risk to wild populations.

Based on the available information, there may be a high genetic risk to wild populations from escaped cultured *A. nobilis*, but there is also high uncertainty due to the stock status of the Southern California population. Adopting practices similar to current stock enhancement efforts will help to mitigate risks to wild conspecifics by utilizing wild-caught broodstock and by maximizing genetic diversity in the hatchery produced fish. If future stock assessments increase the estimated biomass of this stock—such as by including the Baja California, Mexico population—the genetic risks to wild conspecifics may be reduced.

2.2.2.6 OMEGA case study to evaluate genetic risks of farm scenarios

A case study was performed using the OMEGA model to quantify population dynamics of a hypothetical White Seabass farm program sited in Southern California. The OMEGA model was used to simulate the response of a wild population of White Seabass to varying levels of culture-origin fish escapes from a farm system, resulting in a mixed cultured-wild population where some proportion of the population contains genetics of cultured fish.

Assuming an individual farm harvest production of 3,500 mt, two different production levels were modeled: the equivalent of three farms (hereafter 3-farm) with a total harvest production of 10,500 mt and the equivalent of five farms (hereafter 5-farm) with a total harvest production of 17,500 mt. The captive breeding program was assumed to use local, wild-origin fish and did not employ intentional selection for traits. Detailed modeling of White Seabass farm systems under a range of escape scenarios is presented in Section 2.3.2. Conclusions of OMEGA modeling in regard to potential for genetic risk are discussed in Section 2.3.4.2.

The evaluation of White Seabass aquaculture used two different ranges of abundance for the wild population based on the differing hypotheses about the species population structure. The first assumed strong genetic differentiation between Southern California and Baja California, Mexico, and the population abundance only accounted for fish in the SCB (this became the “low abundance” range), while the second assumed that the population in Southern California extends through the Baja portion of the species range, and the population abundance accounted for fish throughout that entire range (this became the “high abundance” range).

The model results for both the 3-farm and 5-farm production scenarios demonstrated a substantial loss in wild population fitness using the most conservative assumptions of low population abundance (female spawning biomass within an assumed range of 400 to 1,200 mt), high rate of episodic escape (25% likelihood of loss of one cage in any given year) and an assumed escape rate from program leakage of 0.3% per year. The results suggested that the cumulative effect of escaped fish on fitness over multiple generations would be substantial assuming a low wild abundance. In regard to genetic diversity effects, OMEGA results demonstrated that substantial reductions in effective population size were likely for both production scenarios under both low and high abundance assumptions although only a small proportion (~<10%) of simulations indicated potential for Ryman-Laikre effects for the 3-farm scenario.

The model results demonstrated that wild population abundance is a vital consideration in evaluating population response from contribution of escapes, and as such a definitive fine-scale genetic study of the Southern California and Baja California, Mexico populations is a key missing element in the evaluation of genetic risks to both wild population fitness and genetic diversity. A present-day stock assessment is also an important need to evaluate the proportional contribution of escapes and subsequent genetic effects.

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2.2.3 Striped Bass (Morone saxatilis)

Striped Bass in Southern California were evaluated using the OMEGA model. Model methods and results are in Section 2.3.3, *Case Study: Striped Bass*. A summary of case study results is included at the end of this species profile in Section 2.2.3.6, *OMEGA case study to evaluate genetic risks of farm scenarios.*

2.2.3.1 Range/Description

Striped Bass (*Morone saxatilis*) is a euryhaline coastal species with a native range along the Atlantic states and the Gulf of America. This species was introduced to many large lakes and reservoirs throughout the U.S. (Gauthier et al. 2013) and were introduced to the San Francisco Bay in the 19th Century (Smith 1895). Striped Bass subsequently became naturalized and historically were highly abundant in the San Francisco Bay and Sacramento-San Joaquin Delta partly due to the high fecundity of the species (Dill and Cordone 1997).

M. saxatilis initially thrived in its introduced range in California and experienced a rapid population explosion. By 1900, and within just 20 years of its introduction, commercial and recreational fisheries had developed for the species (Stevens et al. 1985). In response to political pressure from recreational fishers, commercial harvest of wild Striped Bass was banned in 1935 (Stevens et al. 1985). Although the population abundance declined over the decades following its peak, it hit a historic low of fewer than 580,000 legal-sized fish in 1994 (Kohlhorst 1999) before rebounding to approximately 1.3 million adults by 2000 (Moyle 2002). Attempts were made to supplement regions in California with hatchery-produced Striped Bass, but these efforts ceased due to increased predation on native winter-run Chinook salmon (*Oncorhynchus tshawytscha*) (Lindley and Mohr 2003).

Striped Bass range widely across marine areas in the Atlantic and Gulf of America (NEFSC 2019), but their ocean distribution in the Pacific is more limited. In both the eastern U.S. and the Pacific Coast, Striped Bass populations include both migratory and resident groups. However, the Pacific Coast population is less migratory, with a center around the San Francisco Bay and Sacramento-San Joaquin Delta Estuary (Boughton 2020). Within this region, Striped Bass inhabit the entire estuary and delta, as well as major rivers such as the Sacramento, Feather, Mokelumne, and San Joaquin rivers (Sabal et al. 2019, and references therein). In the San Francisco Bay region, Boughton (2020) found that their abundance decreases with distance from the mouth of the bay, and they are most likely to be found in coastal estuaries and rivers within a zone flanked by the Russian River to the north and Morro Bay to the south.

Striped Bass is managed by the California Department of Fish and Wildlife. Today, the sport fishery for this species is an important recreational activity along some regions of the Pacific Coast that is primarily concentrated in the inland areas of the San Francisco Bay region (Boughton 2020). However, due to ongoing population declines in the area, catch size limits have been imposed to help manage and protect the species (e.g., California Department of Fish and Wildlife Striped Bass; https://wildlife.ca.gov/Fishing/Inland/Striped-Bass#biology).

Image from California Department of Fish and Wildlife

2.2.3.2 Biological Characteristics

The life cycle of Striped Bass on the Pacific Coast mirrors that of its native counterparts on the Atlantic Coast. As an anadromous and iteroparous species, Striped Bass migrate between freshwater and saltwater throughout their life cycle although they primarily inhabit estuaries. This long-lived species can exceed 30 years of age (Moyle 2002). Male Striped Bass reach maturity at around 25 cm FL (fork length), which corresponds to about 4 years of age. Females reach maturity at approximately 45 cm FL, or between 4 to 6 years of age (NEFSC 2019). Historical data from Scoffield (1931) suggest slightly different maturity estimates. Based on Scoffield (1931) a portion of male fish spawn in their 3rd year, and all males spawn by their 5th year. Scoffield also reported that 35% of female Striped Bass matured and spawned in their 4th year, 87% in their 5th year, 98% in their 6th year, and 100% at older ages. While it remains uncertain whether females spawn annually, it is established that they do not spawn more than once per year (Scoffield 1931).

Fecundity in Striped Bass increases with size. For instance, a four-year-old female may produce an average of 243,000 eggs in one season, while an older female can produce an average of 1.4 million eggs (Moyle 2002). Scoffield (1931) reported an annual fecundity range for this species of between 500,000 and 2.5 million eggs.

Striped Bass spawn during the spring from March to mid-July with peak activity occurring when water temperatures range between 60 and 67°F. They prefer to spawn in large rivers with sufficient flow to keep embryos and larvae suspended in the water column until they become free-swimming (Scoffield 1931, Chadwick 1964, Stevens et al. 1985, Boughton 2020). In California, the San Francisco Bay and Sacramento-San Joaquin Delta Estuary offer more suitable conditions for Striped Bass spawning than other rivers and estuaries in the state (Moyle 2002).

As a result, breeding populations in rivers north and south of San Francisco Bay are likely small or non-existent (Boughton 2020).

Striped Bass eggs hatch in about 48 hours and the yolk sac is absorbed within 7 days (Scoffield 1931). The larvae are then carried downstream to deltas and bays (Sabal et al. 2019). The nursery areas for young Striped Bass are typically located in zones where fresh and saltwater mix in estuarine environments, with the exact location of these zones varying annually depending on river flow (Turner and Chadwick 1972). In years with low runoff, juvenile Striped Bass tend to move further upstream (Turner and Chadwick 1972). After spawning, mature fish migrate downstream to bays or the ocean during the summer and fall and move back into the delta during the winter (Sabal et al. 2019, Le Doux-Bloom et al. 2022).

Despite these general patterns, tagging data indicates that individual behaviors can vary widely (Sabal et al. 2019) and that they may also fluctuate from year to year (Le Doux-Bloom et al. 2022). Notably, a smaller proportion of Striped Bass on the Pacific Coast enter the marine environment compared to their East Coast counterparts. Sabal et al. (2019) suggested that individuals may need to reach larger sizes before venturing into the coastal ocean.

Striped Bass subadults and adults are opportunistic pelagic predators and feed on a wide range of fish species they encounter. In the Sacramento-San Joaquin Delta their diet includes juvenile salmon (Moyle 2002). However, the diet of Striped Bass in marine areas along the California coast remains largely unknown. It is likely that they exhibit similar opportunistic feeding behavior as their Atlantic counterparts and prey on a variety of fish species (Walters and Austin 2003).

2.2.3.3 Population Structure

On the Pacific Coast, little is known about the population structure of Striped Bass. However, based on their specific habitat requirements for spawning, embryo development, and larval growth it is likely that successful Striped Bass reproduction is rare outside of the freshwater areas of the Sacramento-San Joaquin Delta (Boughton 2020). While genetic studies on Striped Bass along the Pacific Coast have not been conducted, extensive research has been done on their genetic structure along the Atlantic Coast. Significant genetic differentiation has been observed at various scales across watersheds and among coastal regions of the Atlantic (e.g., Gauthier et al. 2013; Anderson et al. 2014; Harris et al. 2020; LeBlanc et al. 2020; Wirgin et al. 2020).

Anderson et al. (2014) found evidence of reduced genetic diversity and structure in some locations due to the transfer and stocking of fish. However, they also identified a site (Santee-Cooper) where stock enhancement helped maintain genetic diversity. Harris et al. (2020) similarly reported a loss of genetic variation and estimated very low effective numbers of breeders within the Roanoke River drainage. In the Roanoke basin, the effective number of breeders was likely in the tens to hundreds, while in Kerr Reservoir (the source of broodstock) the estimated number was between 75 and 125 fish. These studies demonstrate that this species is prone to impacts from breeding practices within hatcheries.

Given that fewer than 500 fish founded the California Striped Bass population (https://wildlife.ca.gov/Fishing/Inland/Striped-Bass#35540374-history) and the population declines since their introduction, it is reasonable to suspect that naturalized populations in California may have reduced genetic diversity compared to those on the East Coast. This reduction could result from founder effects and subsequent genetic drift in these greatly reduced populations. While it is possible that the initial founder populations purged some of the fitness effects associated with low genetic variation and small effective population sizes over generations, these populations may still be more susceptible to future environmental or biological challenges. Additionally, they could be at greater risk of genetic impacts from escaped cultured conspecifics.

2.2.3.4 Aquaculture

Striped Bass is considered an easy species to raise in captivity and can be cultured in various systems including ponds, recirculating systems, and offshore cages. There is a long history of Striped Bass aquaculture, with extensive research conducted on nearly every aspect of both Striped Bass and hybrid Striped Bass aquaculture (see Anderson et al. 2020 for a comprehensive review). The hybrids, a cross between *Morone saxatilis* and *M. chrysops* (White Bass), are bred to combine the ease of culture of White Bass with the growth characteristics of Striped Bass (Anderson et al. 2020).

Domestic Striped Bass breeding lines have been developed for at least17 years, and have achieved growth gains between generations ranging from 24% (F5 to F6) to 33.8% in earlier generations (F3 to F4). The time required to reach market size (defined as 1.36 kg or 3 lbs), has been reduced from 32 months in the F3 generation to 24 months in the F6 generation (Anderson et al. 2020). In culture, reproduction can occur through both hormone-induced and non-hormone-induced volitional spawning in tanks (Hodson and Sullivan 1993, Anderson et al. 2021).

While most aquaculture efforts have focused on culturing Striped Bass or hybrid Striped Bass in ponds or recirculating systems, there are ongoing efforts to develop Striped Bass strains that grow efficiently in offshore conditions (e.g., Kenter and Berlinsky 2023). These authors found that using production cycles and photothermal profiles simulated based on conditions in the Gulf of America and Atlantic Ocean, fish reached market size in approximately two years.

Off the coast of Ensenada, Baja California, Mexico, Pacifico Aquaculture currently cultures Striped Bass commercially in offshore cages. Juvenile fish are stocked into net pens after 60 to 90 days of shore-based rearing when they weigh between 1 and 10 grams. The operation reports that a size of 2 kg is achieved within 24 months.

2.2.3.5 Considerations on genetic risk to wild conspecifics

Natural spawning of Striped Bass in California is largely limited to the Sacramento-San Joaquin Delta and it is possible that low natural production occurs in other rivers (Boughton 2020). Males reach sexual maturity at a younger age and smaller size compared to females, suggesting that males are more likely to mature during the time period that fish are kept in culture. However, the location of offshore pens is typically far from natural spawning sites which reduces the risk of culture-based gamete release.

Based on known maturity schedules, escaped males are more likely to contribute to spawning with natural Striped Bass populations as they mature earlier, while escaped females would need to survive and mature for an additional two years before spawning with wild conspecifics (Scoffield 1931, NEFSC 2019). However, for escapes from Southern California farms, fish of both sexes would need to migrate north to the Sacramento-San Joaquin Delta to encounter wild, naturally spawning fish. The location of offshore net pen sites located far south of the San Francisco Bay may therefore reduce the potential of escaped Striped Bass encountering primary spawning areas.

The decline in Striped Bass abundance in the Sacramento-San Joaquin Delta (Moyle 2002) suggests that if a large number of larger-sized fish escape, there could be a fitness impact on the wild population, as these escaped fish may have a greater chance of surviving to spawn in the Delta. Additionally, a population already experiencing reduced genetic diversity due to its small size and from a limited number of founding individuals may be particularly vulnerable to further losses of genetic diversity through introgression of cultured fish.

A significant data gap exists regarding the potential movement of escaped Striped Bass to the Sacramento-San Joaquin Delta for spawning. Given the longevity of Striped Bass, it is plausible that some escaped individuals could eventually migrate north and encounter the naturalized population in the Delta. Striped Bass used in aquaculture may be genetically distinct from the wild population, and the selection for faster growth in cages, as reported by Anderson et al. (2021), suggests that escaped fish could impact the fitness of the natural population.

The available information suggests a low-to-moderate genetic risk to wild populations from escaped cultured *M. saxatilis*. The use of non-domesticated broodstock, where maintenance of genetic diversity has been prioritized, or sterile lines, would further reduce the genetic risk to natural Striped Bass populations.

2.2.3.6 OMEGA case study to evaluate genetic risks of farm scenarios

A case study was performed using the OMEGA model to quantify population dynamics of a hypothetical Striped Bass farm program sited in Southern California. The OMEGA model was used to simulate the population response of a naturalized population of Striped Bass where varying levels of culture-origin fish have escaped from the farm system, resulting in a mixed population where some proportion of the population contains genetics of culture-origin fish.

Assuming an individual farm harvest production of 3,500 mt, two different production levels were modeled: the equivalent of three farms (hereafter 3-farm) with a total harvest production of 10,500 mt and the equivalent of five farms (hereafter 5-farm) with a total harvest production of 17,500 mt. The captive breeding program was assumed to use local, wild-origin fish and did not employ intentional selection for traits. Detailed modeling of Striped Bass farm systems under a range of escape scenarios is presented in Section 2.3.3. Conclusions of OMEGA modeling in regard to potential for genetic risk are discussed in Section 2.3.4.3.

There were too many unknowns regarding the species population dynamics and genetics of naturalized populations of Striped Bass in the region and as such the evaluation of Striped Bass aquaculture focused on the number of escaped fish that would potentially survive to maturity. Culture-wild interactions may be unlikely due to the distance between Southern California and the Sacramento-San Joaquin Delta, where there is a well-known naturally spawning population. In the context of the Southern California region, escaped fish would potentially add to the abundance of Striped Bass in estuaries, bays, and marine waters of Southern California. However, while not well-documented, the possibility of smaller localized populations in larger Southern California drainages could suggest a high potential for escaped cultured fish to affect fitness and genetic diversity within California. A genetic study of Striped Bass populations throughout California waters would provide information about locally-adapted populations and potential effects of escapes surviving to maturity.

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2.2.4 Sablefish (*Anoplopoma fimbria*)

2.2.4.1 Range/Description

Sablefish, *Anoplopoma fimbria*, also known as black cod, are a commercially valuable deep-sea species found at depths between 200 and 1500 meters in the North Pacific Ocean. Their range in the northeast Pacific Ocean extends from the Aleutian Islands and the Bering Sea to Baja California, Mexico, and in the northwest Pacific Ocean from Kamchatka, Russia to Japan (Morita et al. 2012, Head et al. 2014, and references therein).

Throughout their life stages, Sablefish occupy different depths within their distribution. Juveniles are found in relatively shallow nearshore waters at depths less than 200 meters. As they grow, they gradually move offshore, with both juveniles and mature fish occupying the continental shelf slope at depths between 100 and 300 meters (Mason et al. 1983). Larger adults are found at greater depths beyond the shelf-slope, although their abundance decreases beyond 1500 meters (Mason et al. 1983, Head et al. 2014, and references therein).

In the northeast Pacific Ocean, Sablefish are managed as three populations that exhibit variations in growth rate and size at first maturity. The first population extends from Alaska to northern British Columbia, the second population occurs off British Columbia, and the third population ranges from British Columbia to Southern California (Head et al. 2014). Fish in the northern regions are reported to reach larger maximum lengths and larger sizes at maturity than those in southern regions (Head et al. 2014).

Image from NOAA Fisheries

The wild Sablefish population has recently experienced periods of decline, possibly due to low recruitment in early life stages during unfavorable environmental conditions (Krieger et al. 2019). Consequently, commercial fishery landings have also declined despite intensive population management. The fishery along the contiguous U.S. west coast is managed by the Pacific Fishery Management Council and extensive information on life history and population dynamics is available in stock assessments (PFMC 2023). In 2020, the Pacific coast female spawning stock biomass was estimated to be 90,756 metric tons (NOAA Fisheries 2022).

Although the Sablefish commercial fishery is not large, the species has high market value due to its firm white flesh which is reported to have excellent flavor and is high in omega-3 fatty acids

(Hartley et al. 2020, Goetz et al. 2021). Due to its high value, there are ongoing efforts to improve culture methods for Sablefish in Canada and to develop commercial aquaculture for the species in the U.S.

2.2.4.2 Biological Characteristics

Sablefish are an incredibly long-lived fish species with reported maximum ages exceeding 100 years (Morita et al. 2012, Head et al. 2014). They exhibit sexually dimorphic growth with females growing larger (90 to 100 cm) than males (70+ cm) (Morita et al. 2012, and references therein). Although this species grows quickly up to the point of sexual maturity, Sablefish take longer than many marine fish to reach this stage. The age of 50 percent maturity is reported to be 6.86 years, though this parameter varies with geography: fish north of Cape Mendocino, California, take 4.86 years, while those south of Cape Mendocino take 8.8 years (Morita et al. 2012, Head et al. 2014). The length at 50 percent maturity is reported to be 54 to 55 cm (Macewicz and Hunter 1994, Head et al. 2014). Average dispersal distances also differ between sexes with an average of 712 +/- 800 km for males and 877 +/- 920 km for females (Morita et al. 2012).

Sablefish spawn along the continental shelf at depths greater than 300 meters from December to March (Tolimieri et al. 2018). Females are batch spawners, and release eggs 3 to 4 times during a spawning season. Fecundity for a 2.5 kg female is estimated to be approximately 276,000 oocytes (Macewicz and Hunter 1994).

After spawning, fertilized eggs become buoyant and rise to 200 to 300 meters in the water column and hatch between 12- and 17-days post-fertilization (Tolimieri et al. 2018). Post-hatch, yolk sac larvae sink to 1,000 to 1,200 meters of depth. By approximately 40 days post-hatch, when yolk sac reserves are depleted, the larvae rise to surface waters and can be found from the nearshore to more than 200 nautical miles offshore (Moser et al. 1994, Tolimieri et al. 2018). For these broadly dispersed larvae, it is not well understood how they reach the coast for settlement, but dynamic hydrographic processes are thought to be involved (Moser et al. 1994). There is relatively little known about pelagic juvenile Sablefish, but they may also be found in surface waters nearshore, eventually settling in shelf habitats located at 250 meters or shallower (Moser et al. 1994, Tolimieri et al. 2018).

Spawning is reported to occur throughout most of the species' range (Head et al. 2014). However, although Sablefish reach sexual maturity and develop reproductive gonads in Southern California and Baja California, Mexico, it is thought that these fish do not contribute a large amount to recruitment in these regions. Instead, it has been proposed that more recruitment results from larger pelagic juveniles moving into those areas (Moser et al. 1994). It has been suggested that drifting macroalgal assemblages transport juvenile Sablefish into the southern portion of their range (i.e., Southern California and Baja California). For example, juvenile Sablefish were found in 15% of offshore drifting macroalgal assemblages in offshore areas (Hunter and Mitchell 1970 in Moser et al. 1994).

2.2.4.3 Population Structure

Signals of population structure in Sablefish across their range in the northeastern Pacific have varied by study, but generally show evidence of limited genetic structure across broad geographic regions. Trip-Valdez et al. (2012) detected pairwise genetic structure between specimens collected in the Bering Sea and Gulf of Alaska and those collected in San Quintin, Baja California, Mexico using a small number of microsatellite markers but did not detect signals of differentiation with mitochondrial COI sequences.

A study by Jasonowicz et al. (2017) used restriction site-associated DNA sequencing to evaluate thousands of genome-wide single nucleotide polymorphisms (SNPs) to assess population genetic structure in 441 mature fish collected in 2012 from the Northern and Southern Bering Sea, Aleutian Islands, Gulf of Alaska, Washington, Oregon, and California. Analyses indicated only low and insignificant levels of differentiation which suggested that fish sampled across this broad range constituted a single population. This single population concept is supported by tag recoveries showing that Sablefish move across currently designated management regions (Johnson et al. 2023, and references therein).

More recently, Orozco-Ruiz et al. (2023) investigated genetic structure in 252 specimens with 11 microsatellites and 121 specimens with mitochondrial D-loop sequences from a geographic range extending from Kamchatka, Russia, the Bering Sea, Gulf of Alaska, British Columbia, Washington, California, and Baja California, Mexico although not every site was available for both marker types. Similar to Trip-Valdez et al. (2012), the two marker types resulted in somewhat different pictures of genetic structure with mitochondrial data supporting genetic differentiation between the western and eastern Pacific, while the microsatellite markers found the greatest differentiation between Baja California, Mexico and other portions of the Sablefish's range. However, the microsatellites in one analysis (DAPC), detected geographic differentiation among males but not females from Gulf of Alaska, Aleutian Islands, and Bering Sea.

Discrepancies between the two most recent studies (i.e., Jasonowicz et al. 2017 and Orozco-Ruiz et al. 2023) may be attributable, in part, to different sampling ranges. In Orozco-Ruiz et al. (2023), the significant pair-wise comparisons differentiated Commander, Aleutian Islands, Shirshov, Russia, and the West Bering Sea, Russia, from other populations. The microsatellite data indicated the Baja California site was genetically differentiated from the other locations. These regions were not sampled in the Jasonowicz et al. (2017) study making direct comparisons impossible. Additionally, the time period over which specimens were collected could be a confounding factor. While Jasonowicz et al. (2017) collected all samples in 2012, Orozco-Ruiz et al. (2023) collected samples over a 10-year period with specimens in some locations collected in single years (e.g., 2008 or 2012), whereas other sites had samples collected over numerous years (e.g., 2012-2018). Although the life span of Sablefish extends beyond this sampling period, Sablefish recruitment is estimated to be quite variable, with years of low or negative recruitment followed by years of above average or strong recruitment. Recent modeling indicates that 2008, 2013, 2015, 2016, 2020, and 2021 were particularly large recruitment years and cohorts (Johnson et al. 2023). Variable recruitment preceding and during the Orozco-Ruiz et al. (2023) sampling period could have potentially impacted signals of genetic differentiation due to cohort recruitment signals.

Collectively, these studies indicate that along the west coast of the U.S., no genetic differentiation is present among sites ranging from California to Washington, although Sablefish in Baja California may have some degree of genetic isolation. The lack of genetic population structure throughout much of their range may be attributable to the long planktonic larval durations in this species and the long distances mature Sablefish disperse over their lifespans (Goetz et al. 2021).

2.2.4.4 Aquaculture

Grow-out of wild-caught Sablefish juveniles began in the 1960s, but culture involving spawning induction, egg hatching, and larval and juvenile rearing did not commence until the 1980s in Canada. Sablefish are now commercially cultured by several small companies in Canada (Hartley et al. 2020, Goetz et al. 2021). In the U.S., several companies have attempted to culture Sablefish, but commercial aquaculture efforts were hindered by the lack of established broodstock populations and the high cost and duration of larval rearing (Hartley et al. 2020). Most of the ongoing work in the U.S. focuses on developing culture and husbandry techniques at the NOAA Manchester Research Station in Washington state (Goetz et al. 2021). There has also been interest in culturing Sablefish in Mexico and South Korea, but no known commercial culture exists in these countries. Similarly, China has shown interest in Sablefish aquaculture but there is limited information beyond experimental work in a few research institutions (Hartley et al. 2020).

Detailed descriptions of Sablefish aquaculture techniques are provided in Hartley et al. (2020) and Goetz et al. (2021) and these approaches are summarized below. Currently, most Sablefish broodstock are collected from the wild several months ahead of planned spawning attempts, often coinciding with naturally occurring spawning periods. To maintain the broodstock in spawning condition, the fish are kept in low-light conditions and in chilled water between 5 and 6°C, simulating natural conditions (Hartley et al. 2020, Goetz et al. 2021). Hatchery-reared broodstock populations (F1s) have been developed by a few companies in Canada and cultured females are capable of producing eggs between 3 and 4 years of age (Rubi et al. 2022).

This species does not spawn volitionally in culture but gamete production can be hormonally induced followed by strip spawning where 250,000 to 500,000 eggs may be obtained from a single fish (Hartley et al. 2020). Fertilization protocols and sperm cryopreservation methods have been developed for this species (Goetz et al. 2021, and references therein). In a commercial operation in Canada, 10 to 15 females and 5 to 10 males in a brood population are hormonally induced to spawn. Fertilization is achieved by combining eggs from each female with the milt of 1 to 2 male fish to generate approximately 30 pairwise crosses (Rubi et al. 2022). Even with this crossing approach, parentage analyses revealed high variation among brood fish contributions in pooled juvenile offspring with the majority of juveniles produced by less than half of the participating brood fish (Rubi et al. 2022).

Sablefish eggs are exceedingly fragile and are vulnerable to handling and to tank parameters including temperature and salinity. Due to the depths where natural spawning occurs, only red light may be used during the egg incubation period which lasts between 12- and 14-days post-fertilization (dpf) (Hartley et al. 2020). Post-hatch, yolk-sac larvae, which are also fragile, are held in upwelling tanks where they incubate until approximately 45 dpf at 5 to 6°C. After this period, they are switched to ambient flow-through water and light is gradually introduced. By this point, the yolk sac has been reabsorbed and the larvae begin consuming live feed cultures (e.g., rotifers and *Artemia*). The larvae grow more quickly at this stage but are not considered metamorphosed until they can digest dry feeds, possess all fins, and feed and swim without additional turbidity in the tanks (Goetz et al. 2021, and references therein). Mortality is high during these early culture periods (Rubi et al. 2022).

Early juveniles may be transferred to outdoor nursery tanks at 100 dpf and a size of approximately 0.3 to 0.5 g. Cannibalism is problematic until fish reach 20 to 30 g but can be reduced by size sorting and sorting according to feeding and agonistic behaviors (Goetz et al. 2021). The Sablefish may remain in the nursery tanks for another 100 days or until they reach 75 g, at which point they can be placed in net pens although they may be transferred for grow-out at smaller sizes between 10 and 20 g (Hartley et al. 2020). At one facility in Canada, it is estimated that offspring are kept in the hatchery for approximately a year prior to outplanting in net pens (Rubi et al. 2022). The grow-out period may last another 22 to 30 months (Hartley et al. 2020), with cultured Sablefish reaching a harvestable size of 2.5 kg in a 2-year grow-out period; similar growth in the wild would take 5 to 6 years (Goetz et al. 2021).

Interestingly, the NOAA Manchester Research Facility has developed an all-female monosex broodstock through the generation of neomales (phenotypic male fish with a female XX genotype) by masculinization treatment during early development. When neomale fish (XX) are bred with female fish (XX), all XX female offspring are produced. Based on grow-out experimentation with stocking at 75 g, monosex female populations reach 2.5 kg in 667 days compared to 760 days in mixed-sex populations thus reducing the time to market size by over 12 percent (Goetz et al. 2021).

2.2.4.5 Considerations on genetic risk to conspecifics

Juvenile and adult Sablefish are distributed along the West Coast, and offshore Sablefish culture operations would likely be situated within or immediately adjacent to coastal juvenile and subadult habitats. Sablefish spawn in waters deeper than 300 meters (Mason et al. 1983), and depending on the location of the continental slope, this could be only several miles offshore and thus, much closer to potential culture operation sites.

The likelihood of escaped Sablefish encountering the West Coast population is unknown but likely high due to the species' distribution along the continental shelf. Juvenile Sablefish move into coastal areas during their first summer and remain for 1 to 2 years before migrating to deeper waters as subadults and eventually residing along the continental slope as adults (Mason et al. 1983, Beamish and McFarlane 1988, Maloney and Sigler 2008). Escapees from offshore culture would be likely to encounter juvenile Sablefish and would only need to migrate to the continental slope to encounter mature adults. However, no information is currently available regarding the behavior of Sablefish post-escape (Sumaila et al. 2005). This is a topic that should be studied to determine survival and movements following escape (e.g., transition to live food, predation, dispersal) and to identify successful approaches for recapturing escaped fish.

The harvest size of 2.5 kg would be achieved before individuals reach maturity. Additionally, Sablefish do not spawn volitionally in culture and must be hormonally induced and manually stripped. Natural spawning events occur at depths of hundreds of meters, a habitat vastly different from a net pen. As such, there is a very low risk of spawning and gamete release in net pens.

While there may be many reasons to locally source brood fish, genetic analyses and tagging studies suggest it is unlikely that escaped fish will disrupt existing population structure or locally adapted variation along the U.S. west coast. However, given the reduced genetic variation likely reflected in a broodstock population (compared to existing variation in the wild population) and high variation in parental contribution among hatchery offspring noted in at least one hatchery, there is a genetic risk to wild conspecifics due to a loss of genetic variation if large numbers of escaped fish successfully recruit to the wild population.

While breeding programs currently utilize wild-caught or F1 broodstock, domesticated broodstock could potentially lead to fitness impacts in wild conspecifics. OMEGA modeling of a hypothetical commercial Sablefish operation using domesticated broodstock and producing 10,000 mt of Sablefish annually indicated negative fitness impacts for the wild population when high levels of leakage and frequent episodic losses were simulated (Gruenthal et al. 2017). However, the modeled scenarios were used for model demonstration and actual production scenarios would differ from the parameters used in that modeling effort.

While the spawning biomass of this species appears to be increasing, there are high levels of uncertainty in estimates of spawning biomass which range between 49,643 mt and 185,395 mt (Johnson et al. 2023). Potential genetic impacts of escaped Sablefish will vary greatly depending on the wild stock abundance and spawning biomass, ranging from low (at the highest estimated biomass) to moderate (at the lowest estimated biomass). Genetic risks will be greater at high production levels and if domesticated broodstock are used. Conversely, genetic risks may be reduced if hatchery practices maximize genetic diversity in offspring and frequently rotate wild-caught broodstock.

Careful consideration of genetic impacts to wild conspecifics is warranted in this species. The broad dispersal capacity and long lifespan of Sablefish may allow the population to withstand some level of incursions of escaped cultured fish. However, impacts on genetic diversity and population fitness may be long-lasting and could be further amplified by periods of low natural recruitment.

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2.2.5 California Halibut (Paralichthys californicus)

2.2.5.1 Range/Description

The California Halibut (*Paralichthys californicus*) is a large benthic fish distributed along the west coast of the U.S. from the Quillayute River in Washington down to Magdalena Bay on the Baja California peninsula in Mexico (Allen 1990, MacNamara et al. 2024). Historically, the greatest numbers of California Halibut in the U.S. were found from Morro Bay to San Diego, California (Allen 1990, and references therein).

P. californicus is the largest paralichthyid in this region (MacNamara et al. 2024) and one of the largest bony fish in the nearshore area (Allen 1990). The preferred habitat of this species varies by life stage with mature fish found in nearshore coastal waters up to 100 meters in depth, though the majority of mature fish are found at depths less than 30 meters (Kramer 1990, Fodrie and Mendoza 2006). While mature fish may be found in coastal waters, young *P. californicus* rely on estuaries and embayments as important nursery grounds, and juvenile fish often concentrate at the mouths of estuaries and avoid deeper waters in these habitats (Kramer 1990, Fodrie and Mendoza 2006).

Due to its large size and high meat quality, the California Halibut is highly valued in both commercial and recreational fisheries (Vargas-Peralta et al. 2020, MacNamara et al. 2023). These fisheries are managed by the California Fish and Game Commission and the California Department of Fish and Wildlife (CDFW). While the California Halibut is considered one of the most important flatfishes for both commercial and recreational fisheries in central and southern California (Allen 1990, Kramer 1990, CDFW 2011), catches have been gradually declining since the 1930s (Love and Brooks 1990).

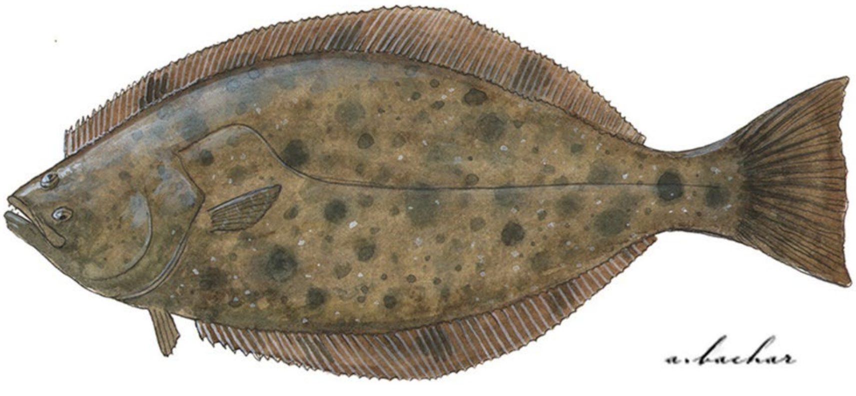

Image from the California Department of Fish and Wildlife

From 1930 to 1960, the majority of landings came from Southern California, but since then, landings in Northern California have been consistently higher. This shift is likely due to early exploitation in the south and various regulatory and environmental factors (CDFW 2022). Despite the implementation of various regulatory measures, such as bag and size limits (Love and Brooks 1990), no stock status reference points have been developed for *P. californicus* on which to base management measures (CDFW 2011). Additionally, there are no estimates of absolute abundance for this species (CDFW 2022).

In the most recent stock assessment from 2020, California Halibut were treated as separate northern and southern stocks with the boundary at Point Conception. While CDFW (2022) acknowledges some degree of connectivity between the two stocks, they argue that regional differences in biology, fishery regulations, and data availability justify the use of two separate stocks in assessments. However, data deficiencies regarding the two stocks have prevented their use in management decisions. A review recommended the collection of additional data, improvements to models, and the estimation of the abundance of initial unfished populations to better support these stocks, particularly the northern stock (CDFW 2022).

In addition to their importance in commercial and recreational fisheries, California Halibut are also being considered as a potential aquaculture species for both commercial food production and stock enhancement purposes (Stuart et al. 2021, MacNamara et al. 2022). Stock enhancement efforts for this species aim to support depleted fisheries for California Halibut in the Southern California Bight (MacNamara et al., 2022).

2.2.5.2 Biological Characteristics

P. californicus is a broadcast spawning species that spawns multiple times throughout the season (Allen 1990, Barnes and Starr 2018). Mature fish may spawn year-round from Rosario Bay, Baja California, Mexico, to Point Conception, California, with spawning peaks from February to March and again between July and October, though these times can vary by location (Moser and Watson 1990, CDFW 2011). Adults typically move from offshore to inshore coastal areas, usually at depths between 6 and 20 meters, to spawn (Allen 1990). In Southern California, this inshore movement for spawning generally occurs from April through May (CDFW 2011).

As with most fish species, fecundity in *P. californicus* is size-dependent (CDFW 2011). Annual fecundity estimates range between 5.2 and 81 million eggs per year, while batch fecundity averages around 600,000 eggs per spawn ± 318,419 eggs (Barnes and Starr 2018). The eggs are buoyant and planktonic, and larvae hatch in approximately two days at a size of 2.0 mm (Allen 1990). Planktonic larvae exhibit diel migrations and occupy the upper 30 meters of the water column (CDFW 2011). While most larvae are found over the continental shelf within 6 km of shore, the oldest larvae are located very near shore prior to settling (Kramer 1990, Moser and Watson 1990). The larvae undergo metamorphosis after 20 to 29 days at a size between 7.5- and 9.4-mm standard length (Allen 1990) and settle in protected areas such as bays and estuaries or in shallow coastal waters (Allen 1990, Kramer 1990, CDFW 2011, Barnes et al. 2015).

Because of the low abundance of *P. californicus* eggs and larvae found within bays and estuaries, it is believed that small juveniles move into these protected areas after metamorphosis (CDFW 2022). Juvenile California Halibut appear to use bays, lagoons, and estuaries as nursery habitats (Fodrie and Mendoza 2006) and it is rare to find young-of-the-year California Halibut in exposed coastal regions (Allen et al.1990). Semi-protected areas (harbors and leeward sides of islands or points) have between one-half and one-quarter of the density of juvenile fish compared to protected habitats (Allen et al. 1990).

After settling in protected habitats, juveniles remain in the bays and estuaries for two years before migrating out to the open coast. Juveniles (<150 mm) are rarely found in open coastal habitat (Allen 1990). Males make this migration to the coast as mature fish at 2 to 3 years (or between 200- and 230-mm SL), while females migrate out to the open coastal habitat at 4 to 5 years (or between 380- and 430-mm SL) (Allen 1990).

While the habitat and distribution of California Halibut larvae and juveniles have been well characterized, less is known about the dispersal of mature fish other than their shoreward movements for spawning (CDFW 2011). Limited data suggest that older fish are capable of dispersing over great distances (up to 224 km), but may not frequently move over such distances (Allen 1990).

Age-length relationships and von Bertalanffy growth curves have been established for California Halibut taking into account differences in sex and stock origin (CDFW 2022). Female halibut generally exhibit faster growth rates and reach larger sizes compared to males indicating sexual dimorphism (Barnes et al. 2015). Moreover, regional variations in growth have been observed. California Halibut from central California grow faster but attain smaller maximum sizes compared to those from Southern California (Barnes et al. 2015).

In Southern California, male California Halibut reach sexual maturity between 190 and 320 mm (1 to 3 years of age), with 50% maturity at 230 mm, while females mature at larger sizes between 360 and 590 mm (2 to 7 years of age) with 50% maturity at 470 mm (4 years of age) (Love and Brooks, 1990). In contrast, in Central California males mature between 257 and 290 mm (1 to 3 years of age) with 50% mature at 270 mm and females mature between 466 and 513 mm (2 to 4 years of age) with 50% mature at 473 mm (2.6 years) (Lesyna and Barnes 2016). According to CDFW (2022), the legal size-limit of 559 mm provides male fish with significantly more spawning opportunities than females in wild populations (by one or more years) before they become susceptible to harvest in the fishery. Additionally, females are more frequently landed than males in these fisheries (MacNamara et al. 2024).

The natural mortality rate for *P. californicus* is estimated at 0.3, similar to other flatfish species. Males may experience slightly higher natural mortality as compared to females (CDFW 2011, CDFW 2022). While there are reports of a few individuals living up to 30 years, recent estimates suggest lifespans of 19 years for females and 16 years for males (CDFW 2011, and references therein). The largest recorded individuals reach lengths of up to 1520 mm and weights of up to 33 kg (Allen 1990).

2.2.5.3 Population Structure

There is little information available regarding the genetic spatial structure of California Halibut across its geographical range (CDFW 2011). Early studies using restriction fragment length polymorphism (RFLP) analyses of genomic DNA found no significant geographic differentiation among California Halibut collected from San Diego to Monterey, California (Woonick 1993). Similarly, Morgan (1997) detected no clear patterns of geographic structure among specimens sampled along the California coast and Baja California, Mexico, using RFLPs.

A more recent study by Craig et al. (2011) utilized mitochondrial cytochrome *b* sequences from specimens spanning from Half Moon Bay, California, to Bahia Magdalena, Mexico. Their findings indicated genetic homogeneity among populations including those across proposed biogeographic boundaries at Point Conception and Los Angeles, California. Although some pairwise comparisons revealed significant genetic differentiation, no distinct geographic pattern was evident.

While these studies on California Halibut suggest high gene flow among populations throughout California and Baja California, Mexico, these conclusions are tempered by the limited sample sizes or the markers used in early investigations. That is, mtDNA and RFLPs are suitable for estimating geneflow over long time periods and there is therefore the possibility that genetic structure is present but has been undetected. The resolution of these studies may not have been sufficient to detect subtle signals of population differentiation which are now more easily identified through genomic approaches, or through studies where larger numbers of genetic markers are utilized (e.g., microsatellites or single nucleotide polymorphism (SNP) markers).

While Vargas-Peralta et al. (2020) sequenced the mitochondrial genome of *P. californicus*, comprehensive nuclear genomic sequencing and the development of extensive genetic marker sets have yet to be undertaken for this species. Given the proposed two-stock model, historical declines in abundance, and interest in stock enhancement strategies for California Halibut, there is a pressing need to identify patterns of population connectivity and local adaptation more definitively.

2.2.5.4 Aquaculture

While numerous flatfish species such as the Olive Flounder (*Paralichthys olivaceus*), Common Sole (*Solea vulgaris*), and Turbot (*Scophthalmus maximus*) are commercially cultured worldwide, the cultivation of California Halibut has remained experimental (Conklin et al. 2004). Research on cultivation techniques for this species has been ongoing since the 1980s with a predominant focus on stock replenishment rather than large-scale commercial food production (Stuart et al. 2021).

As outlined by Stuart et al. (2021), current practices involve using wild-caught broodstock fish acclimated to captive conditions. These brood fish are able to spawn volitionally through manipulation in light levels and water temperature or under ambient seasonal conditions. Eggs are collected from brood tanks and sorted to select only viable fertilized eggs which are considered sensitive to handling stress at this stage (Conklin et al. 2004). Larval hatching and developmental rates are influenced by water temperature and larvae typically emerge from their eggs within 48 hours. Newly hatched larvae possess a yolk sac and undeveloped mouths (Gadomski et al. 1990) and they begin feeding approximately 4 to 5 days post hatch (dph), with yolk sac depletion typically occurring by 6 dph. After about a month, larvae start to undergo metamorphosis and settle on the tank bottom (Gadomski et al. 1990). Stuart et al. (2021) reported survival rates from egg to 50 dph juveniles can reach up to 30 percent.

According to Stuart et al. (2021), while cultured California Halibut may have the potential to satisfy the lucrative live-fish market demand in the U.S. (currently dominated by imported Olive Flounder), significant progress in grow-out to market size has been limited. Stuart et al. (2021) noted that achieving the market size of 1 kg may take up to 3 years, in contrast to other paralichthyid species that reach market size within 14 to 16 months. To improve the economic viability of commercial California Halibut culture, research is needed in several areas: optimizing growth rates, managing or preventing skewed sex ratios, enhancing feed formulations, and addressing mal-pigmentation issues in culture settings (Stuart et al. 202, MacNamara et al. 2022, 2023).

While there is currently no information available on offshore culture of California Halibut, experiences with sea-based culture of other flatfish species, such as Atlantic Halibut (*Hippoglossus hippoglossus*) and to a lesser extent Turbot (*Scophthalmus maximus*), in the Atlantic Ocean provide insights into unique challenges faced in flatfish grow-out pens (Brown 2002). Pens for flatfish are typically based on modified designs of salmon cages and can be either surface cages, which are more common, or newer submersible cages. A critical difference is the need for a rigid base in the pen that does not sag under the weight of the benthic flatfish aggregating on the bottom (Brown 2002).

Other aspects of flatfish culture differ from offshore culture of other fish species. These include challenges such as handling mortalities (deceased fish may be obscured by live fish at the bottom of the pen), crowding since all fish occupy the same horizontal space of the cage, and the complexity of changing and cleaning nets, when needed, on the pen's bottom (Brown 2002). However, as highlighted in Brown's review (2002), methods and techniques to address these challenges are continually evolving.

2.2.5.5 Considerations on genetic risk to wild conspecifics

There is significant uncertainty in assessing the genetic risk posed by escaped or released cultured California Halibut to wild populations. This uncertainty arises from several key areas where information is lacking, including stock abundance, genetic structure, and adult dispersal patterns. The proposed southern stock has experienced a notable population decline, making these populations potentially more susceptible to genetic impacts from the introgression of cultured fish due to their reduced numbers. A better understanding of current and historical stock abundance would aid in evaluating the susceptibility of these populations. Additionally, a comprehensive assessment of population structure and genetic diversity is crucial for understanding gene flow levels between northern and southern stocks, identifying patterns of connectivity on a smaller scale, and guiding broodstock sourcing with regard to the potential for the existence of locally adapted populations. Although the limited genetic data currently available suggest that structure may only occur on very broad scales, research utilizing more genetic markers or genomic approaches and analyzing larger numbers of specimens may reveal finer resolution than earlier studies. Furthermore, greater knowledge of dispersal patterns in mature fish is essential to understand the scale over which escaped fish may move and to anticipate the potential spread of cultured genotypes among wild populations. While tracking data exists for juvenile California Halibut, little research has been conducted on mature fish. Although regional movements may be more common in these long-lived fish, they are also capable of moving hundreds of kilometers. Over a lifespan, this could represent significant dispersal of cultured fish genotypes for any escaped or released fish that successfully recruits into wild populations.

In commercial aquaculture efforts, the anticipated grow-out duration of three years to market size would likely result in most male and at least some female fish becoming sexually mature and spawning in the pens. The 20-plus day pelagic larval duration suggests that cultured eggs and larvae could disperse over distances greater than those between offshore pens and the nearshore coastline. It is not known if newly settled cultured juveniles would move into protected nursery habitats like their wild conspecifics do. However, if these are offspring of wild-caught broodstock, environmental or behavioral cues may still influence that migration. If, on the other hand, this behavior varies between cultured and wild-origin fish, then the survival of escaped fish may be reduced as juvenile survival is thought to be lower in open habitats compared to protected ones (Allen et al. 1990, Kramer 1990).

Due to the high level of uncertainty in several key factors, the depressed population abundances of the southern stock, the high potential for spawning in sea pens, and the long life-spans of the fish, the genetic risk from escaped cultured California Halibut on wild populations is considered to be high. However, acquiring additional information about these key factors or implementing mitigating strategies could significantly reduce this risk to a lower level.

There are several strategies to mitigate the potential genetic impacts of escaped or released fish on wild conspecifics. General approaches include collecting broodstock from regions closest to the planned operations to minimize impacts on genetic structure , considering prevailing ocean currents between grow-out sites and coastal habitats to anticipate regions that may receive the most escaped larvae and fish, and designing broodstock and hatchery practices to optimize and preserve genetic diversity in hatchery-reared fish (e.g., frequent rotation of broodstock, maximizing parental cross combinations, parentage analyses of cohorts). This last approach is particularly important for operations focused on stock replenishment. However, greater knowledge of the genetic structure and diversity in the wild population and genetic monitoring of the cultured populations will be needed based on the currently described spawning methods. If domesticated lines are used in commercial culture, sterilization approaches may be the best method to prevent genetic impacts on wild populations from escaped fish and larvae.

Given the life-history of this California Halibut, another mitigation strategy is selecting grow-out sites away from coastal embayments or protected areas to reduce the number of escaped fish that survive and recruit into natural populations, although this strategy mainly applies to larvae and smaller juvenile escapees. Producing all phenotypically male fish (if they remain masculinized in a pen system) could reduce the likelihood of fertilized eggs or larvae escaping from pens. However, female fish may be favored for their faster growth rates and larger sizes. This approach may be worth exploring if other benefits can offset the additional expense of the longer grow-out period required for male fish. Additionally, identifying escaped cultured *P. californicus* in natural habitats may be feasible through pigmentation changes common in cultured California Halibut which could be used to identify and potentially target escaped cultured fish in natural settings (MacNamara et al. 2023, and references therein). However, intentionally generating these pigmentation changes in culture settings may be unattractive due to the decreased market value of the mal-pigmented fish.

2.2.5.6 References

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2.2.6 Olive Flounder (Paralichthys olivaceus)

2.2.6.1 Range/Description

The Olive Flounder (*Paralichthys olivaceus*), also known as Hirame in Japan and Nopchi in Korea, is a benthic, carnivorous flatfish endemic to the temperate and subtropical coastal range around Japan, the Korean Peninsula, and parts of the Chinese coasts along the Yellow Sea and East China Sea (Koshiishi et al. 1991, Matsuoka 1995, Kim et al. 2010). While this species may be found as far south as Northern Borneo and the Philippines, its primary distribution is in the waters around southern Japan and South Korea (Hamidoghli et al. 2020). There are no Olive Flounder populations in Southern California, or along the U.S. West Coast.


Image from Global Seafood Alliance

Throughout its range, it inhabits coastal waters up to 200 m deep, with preferred depths between 10 and 100 m. It tolerates thermal ranges between 5.8°C and 28.5°C, with a narrower preferred range of 20°C to 25°C (Hamidoghli et al. 2020, Kurita et al. 2021).

The Olive Flounder is the only paralichthyid species along the coast of Asia (Sun et al. 2022) and is highly valued commercially throughout this region (Hamidoghli et al. 2020), including in Japan, where it is one of the most important species for the coastal fishery (Koshiishi et al. 1991, Kurita et al. 2021). Stock declines in Japan led to the cultivation of this species for both stock enhancement purposes and commercial food production (Koshiishi et al. 1991). Aquaculture production of Olive Flounder has expanded significantly in Korea, making it one of the country's leading marine finfish species, with additional growth in China as well (Kikuchi and Takeda 2001, Stieglitz et al. 2021).

This species can grow up to 100 cm in length and up to 9.1 kg in weight but is considered market sized at weights between 0.5 kg and 1.5 kg (Koshiishi et al. 1991, Matsuoka 1995, Hamidoghli et al. 2020, Froese and Pauly 2023).

2.2.6.2 Biological Characteristics

This species exhibits sexually dimorphic growth patterns with females growing larger than males (Stieglitz et al. 2021). Additionally, there are regional differences in size and growth rates that may influence the timing of sexual maturation (Yoneda et al. 2007). Olive Flounder are thought to become sexually mature in the third spring for males and the fourth spring for females (Koshiishi et al. 1991) which typically occurs around 45 cm in total length (Hamidoghli et al. 2021).

Both temperature and photoperiod are believed to influence spawning, but the timing of the spawning seasons varies by region (Kurita et al. 2021). This species is a batch spawner with spawning durations lasting for 2 months and migration to deeper waters during spawning periods. (Koshiishi et al. 1991). As with most fish species, fecundity increases with size. According to a review by Sun et al. (2022), a 480 mm female fish may produce up to 200,000 eggs while a 600 mm female may produce up to 400,000 eggs.

After hatching, Olive Flounder larvae are planktonic for a month or more (Koshiishi et al. 1991, Kim et al. 2010, Kurita et al. 2021). Initially, the larvae do not feed and are sustained by a yolk sac that is reabsorbed by approximately 4 days post-hatch (dph) (Geng et al. 2019). This species starts to metamorphose around 30 to 32 dph at approximately 15 mm in size, at which point they move towards shallower nursery grounds between 10 and 20 m in depth (Koshiishi et al. 1991). They remain in the nursery grounds for 2 months until they reach approximately 100 to 120 mm in total length and then move towards deeper waters (Koshiishi et al. 1991). Males and females grow quickly from 0 to 3 years of age with growth slowing at 4 years for males and 5 years for females. Individuals reach maximum size at 7 to 8 years (Masubuchi et al. 2024).

2.2.6.3 Population Structure

There are no populations of Olive Flounder in natural environments in the U.S., and the genetic studies presented here focus on its range in the western Pacific.

Genetic studies based on *P. olivaceus'* endemic range have not provided a straightforward picture of geographic population structure which may be partly due to the species' long larval duration, and due to the resolution of genetic markers used in these studies. A study focused on the South Korean peninsula did not find significant genetic differentiation between populations on the western and southern coastlines but did find significant variation between those pooled sites (i.e., the western and southern coastlines) and the eastern coast (Kim et al. 2010) using 9 microsatellite markers. Another study investigating populations along the Pacific coast of Japan did not detect genetic population structure using F-statistics, but did find heterogeneity between sites when investigating mitochondrial nucleotide substitutions between northern and southern regions (Shigenobu et al. 2013). More recently, a larger-scale study of specimens collected from six locations along the Chinese coastline and four locations across Japan revealed no clear signals of geographically based genetic structure using mitochondrial control region sequencing.

However, specific locations (e.g., the Fuqing population) exhibited varying patterns of genetic isolation and variation that could not be attributed to geographic isolation (Sun et al. 2022).

Several genetic studies have also investigated genetic variation and differentiation between hatchery and wild populations. Kim et al. (2010) found that Korean hatchery populations did not exhibit significantly different genetic variation compared to wild populations. Conversely, microsatellite and mitochondrial DNA sequencing analyses found that hatchery populations in Japan had significantly reduced genetic variability compared to wild populations both in the number of alleles and levels of genetic diversity. These hatchery populations exhibited high genetic differentiation among the hatchery strains and between hatchery strains and wild populations likely due to founder broodstock effects and/or husbandry practices (Sekino et al. 2002). Based on these results, the authors suggested that continued releases of hatchery-reared fish into the wild may result in a loss of genetic diversity in wild populations or the loss of locally adapted gene pools (Sekino et al. 2002).

2.2.6.4 Aquaculture

In Japan, aquaculture of the Olive Flounder has been conducted since the late 1970s (Koshiishi et al. 1991, Matsuoka 1995, Kikuchi and Takeda 2001). Production technology developed in Japan was used to establish *P. olivaceus* aquaculture in South Korea in the 1990s and within a few years, production in Korea surpassed that of Japan (Hamidoghli et al. 2020). As reviewed in Hamidoghli et al. (2020), as of 2017, production of Olive Flounder in South Korea was 17 times greater than in Japan. As mentioned above, significant production of cultured Olive Flounder in Japan has also been directed towards stock enhancement purposes leading to millions of juvenile fish being released annually (e.g., 18 million juveniles released in 1992) (Matsuoka 1995).

For commercial production, broodstock fish are able to spawn volitionally in captivity at only two years of age when provided with the appropriate water temperature and photoperiod profiles to initiate spawning (Stieglitz et al. 2021). Following hatching and metamorphosis, frequent size grading is required to reduce high mortality due to cannibalism although this becomes less of an issue as the fish grow (Matsuoka 1995). Extensive domestication has occurred in commercial hatchery lines for this species (Stieglitz et al. 2021).

Grow-out to a harvestable size is conducted both in land-based tanks and net pens, although land-based tanks are the most prevalent strategy used for Olive Flounder (Kikuchi and Takeda 2001, Stieglitz et al. 2021). This species does not tolerate high wave activity, so net pens need to be placed in protected areas such as bays and inlets (Matsuoka 1995). Fish also need to be 10 cm or larger before being placed into net pens to withstand wave action even in protected sites (Matsuoka 1995). Olive Flounder in net pens are prone to developing abrasions from the nets, which lowers market value, and they experience higher mortality rates compared to those in land-based systems (Koshiishi et al. 1991). While land-based tanks are more commonly utilized they incur higher infrastructure expenses (Matsuoka 1995). Additionally, many farms still use older flow-through configurations instead of more advanced closed recirculating aquaculture systems (RAS) which pose a threat to the biosecurity of hatchery populations (Hamidoghli et al. 2020).

In a culture setting, fish can grow to 0.5 kg in 9 to 10 months and to 1 kg in 14 to 16 months, with survival rates of 60 to 80 percent (Kikuchi and Takeda 2001). Stieglitz et al. (2021) report a slightly faster time to harvest, with Olive Flounder reaching market size (0.8 to 1.2 kg) in 12 to 18 months under optimal culture conditions (e.g., water temperature, feeding regime, stocking density, etc.). In addition to the short period to market size, highly efficient feed conversion ratios in this species increase the economic viability of their production (Kikuchi and Takeda 2001).

Growth differences based on sexual dimorphism in this species can also be utilized for faster grow-out to harvest size. Since phenotypic sexual development is linked to water temperature, monosex culture of females can be achieved by maintaining rearing temperatures between 15°C and 19°C; above those temperatures, larvae develop into males (Stieglitz et al. 2021).

As this species is not native to the U.S., there are no plans for offshore culture of the Olive Flounder. However, experimental aquaculture research on Olive Flounder is ongoing at the University of Miami. This research focuses on developing more efficient and cost-effective RAS production techniques and improving hatchery populations through continued selective breeding (Stieglitz et al. 2021). Broodstock currently held at the University of Miami have been selectively bred for several generations overseas and are able to reach a 1 kg market size in a year or less. This research program aims to develop land-based RAS aquaculture for this species across the U.S., and may try to position itself in the role of supplying Olive Flounder fingerlings to other commercial RAS grow-out facilities in the country (Stieglitz et al. 2021). According to Stieglitz et al. (2021), Olive Flounder produced overseas currently supply a valuable live market in the U.S. and domestically produced Olive Flounder could take advantage of this market opportunity. There may also be an opportunity to utilize smaller fish (0.4 to 0.6 kg) for whole fish entrees in restaurants (Stieglitz et al. 2021).

2.2.6.5 Considerations on genetic risk to wild conspecifics

As there are no plans for offshore culture of this species and no wild *P. olivaceus* populations in the U.S., there is no genetic risk of cultured escapes impacting conspecific populations. If land-based facilities were to pose a minimal risk of escapement due to their physical proximity to the marine environment, this risk would likely be minimal in terms of non-native species establishment.

However, if offshore aquaculture were explored for this species in the future, there could be potential for the species to become established. As a top predator in its home range (Yasuda et al. 2010), the Olive Flounder could pose serious ecological risks to native species in U.S. waters. Mitigation strategies could include using highly domesticated lines with traits such as albinism on the ocular side which has been shown to result in up to 100% mortality due to increased predation (Koshiishi et al. 1991). Additionally, Koshiishi et al. (1991) found that released juvenile flounder had a reduced ability to feed and escape from predators compared to wild fish resulting in lower survivability of hatchery fish. While U.S. waters would represent a novel environment, it is reasonable to consider that similar feeding and predation pressures would exist, potentially leading to similar outcomes.

2.2.6.6 References

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2.3 OMEGA Genetic Risk Modeling Case Studies for Finfish in Southern California

Case studies were modeled using the OMEGA model described in Section 1.1.3, *OMEGA Model for Assessment of Finfish Escapes*. The case studies are intended to help with understanding how species population structure, life history, and abundance can influence potential effects of escaped fish on the genetics of wild populations of conspecifics. The case studies also highlight the level of certainty when assessing the risks for a data-rich or data-poor species. The case studies are not intended to describe a particular proposed aquaculture operation. Farm assumptions in the case study assessments are generalized based on published literature for each case study species. Specifics of operations such as size when fish are transferred to offshore cages, time in cages, and harvest methods are important to fully evaluate the potential of fish escaping from cages and their survival in nature and to spawning.

The three case study species for Southern California are California Yellowtail (*S. dorsalis*), White Seabass (*Atractoscion nobilis*), and Striped Bass (*Morone saxatilis*). California Yellowtail and White Seabass are endemic species present in marine areas of Southern California and Baja California, Mexico. Tagging studies have shown both species make northerly and southerly movements between Southern California and Baja California. In contrast, Striped Bass are a non-native species introduced from the Atlantic coast.

Baxter (1960) and Ben-Aderet et al. (2020) are the primary source information for California Yellowtail life history in this assessment. A stock assessment has not been conducted for this species thus the population dynamics could only be inferred from California Yellowtail catch data from California and Baja California, Mexico and from *Seriola* stock assessments in the Gulf of America.

The case study assessment for White Seabass draws on multiple sources of information. In Southern California, the White Seabass population is supplemented with hatchery fry, and research has documented several aspects of hatchery efforts, including reproductive success in captivity (Gruenthal and Drawbridge 2012), post-release dispersal, growth, and survival of released fry (Hervas et al. 2010), and long-term movement patterns of hatchery-reared fish (MacNamara et al. 2022).Valero and Waterhouse (2016) completed a stock assessment and a 2016 abundance estimate within California. The White Seabass range extends into Baja California, Mexico, and the Gulf of California, Mexico. There is evidence of three subpopulations across the range (Franklin et al. 2016) and tagging studies provide evidence of fish migrating between Southern California and Baja California (Aalbers et al. 2022). The case study assessment considered a low abundance population limited only to the California abundance, and a higher abundance population based on both the California and Baja California population abundance that also included catch data from Baja California.

Striped Bass is a euryhaline coastal species with a native range along the Atlantic states and the Gulf of America. Striped Bass were introduced to the San Francisco Bay in the 19th Century (Smith 1895). The species subsequently became naturalized and historically was highly abundant in the San Francisco Bay and Sacramento-San Joaquin Delta. Abundance levels declined to a historic low of less than 580,000 legal size fish in 1994 (Kohlhorst 1999). Abundance increased to about 1.3 million adults by the late 1990s (Moyle 2002).

Striped Bass range widely in marine areas of the Atlantic and Gulf of America (NEFSC 2019) but seem to have a limited ocean distribution in the Pacific. Boughton (2020) concluded that the Striped Bass distribution in the ocean "declines in abundance with distance from the Golden Gate and would most likely use coastal estuaries and rivers in the zone directly flanking the Golden Gate, encompassed by the Russian River on the north and Morro Bay on the south." In contrast to the other two species, the case study evaluation of Striped Bass using OMEGA does not attempt to model effects of escapees on the genetics of the species. There are too many unknowns regarding the population dynamics of Striped Bass in California, the species population structure and population genetics, and the migration of escaped Striped Bass to encounter spawning Striped Bass. The case study assessment for Striped Bass references life history studies from Atlantic coast stocks as similar studies are not available for the Pacific coast. The survival and subsequent movement of escaped Striped Bass to encounter spawning fish in the freshwater portion of the Sacramento-San Joaquin Delta is a significant unknown.

2.3.1 Case Study: California Yellowtail

California Yellowtail is a coastal pelagic species found along the eastern Pacific coast with a primary distribution from Cabo San Lucas in Baja California Sur, Mexico, north to Point Conception, California (Ben-Aderet et al. 2020). Southern California is effectively the northern edge of the California Yellowtail distribution (Figure 2.1) and it is seldom observed north of the Southern California Bight (SCB) except in years with high water temperature anomalies (Ben-Aderet et al. 2020). The abundance of California Yellowtail in Southern California is believed to be dependent on ocean temperatures, and higher catches are reported in years when water temperatures are at least three to five degrees (°F) above normal in the spring (Baxter 1960). Although a smaller number of California Yellowtail are present in the SCB year-round (Ben-Aderet 2017, Madigan et al. 2018), in spring and summer abundance increases with a seasonal migration of fish moving north from the greater abundance of fish offshore of central Baja California (Baxter 1960).

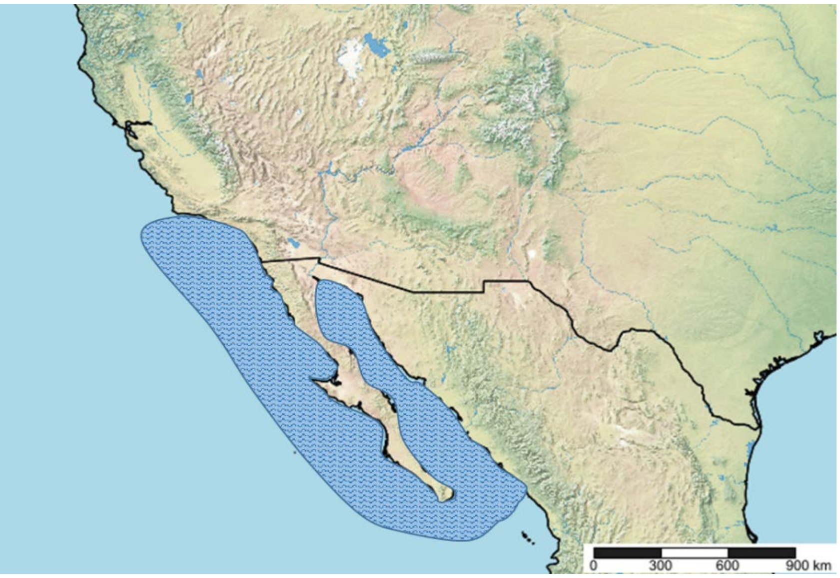

Figure 2.1. California Yellowtail Population Range.

There has been some debate as to whether California Yellowtail in the SCB may be self-recruiting and distinct from the larger population that seasonally shifts northward from Mexico (MacCall 1996). While this possibility cannot be excluded, population genetic studies support a single population in the NE Pacific, with no significant genetic structure detected between fish sampled in Southern California and Baja California, Mexico (Purcell et al. 2015). This evidence of lack of genetic structure supports the case study analysis that assumes a single population of California Yellowtail.

The absence of a population assessment for this species required modeling escape risk for a range of possible population abundances. Female spawning biomass varied between 8,000 mt and 18,000 mt for the case study analysis to describe a possible range of abundances. This range was chosen based on a review of catch data from California and Baja California, Mexico (Figure 2.2). Total catch (~80% from Mexico waters) ranged from 2,000 to 3,000 mt in recent years.

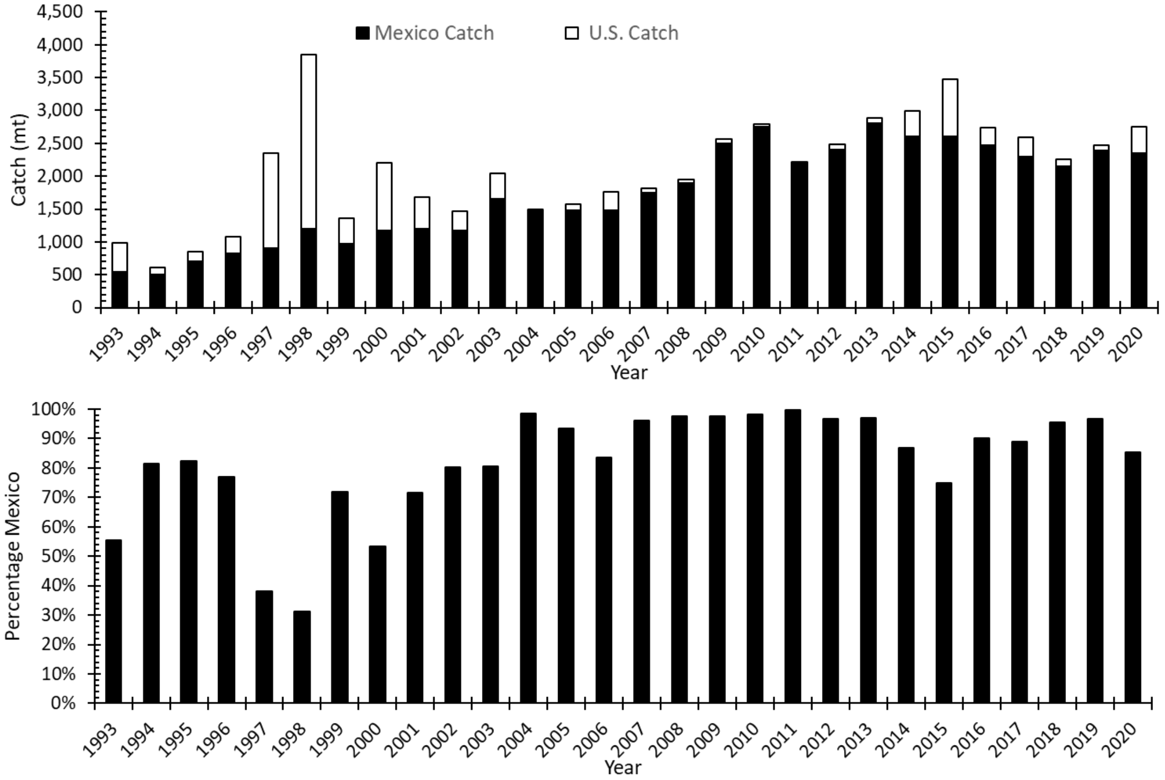

Figure 2.2. California Yellowtail Landings Sources: U.S. catch - https://www.fisheries.noaa.gov/foss/, Mexico catch - Cisneros-Soberanis, 2018 and Enciso and Trasviña 2022)

Estimates of N_e and the ratio of N_e/N_T and N_e/N_A were made assuming over-dispersed variation in reproductive success at age (i.e., a Poisson scaling factor of 3) using the AgeNe program (Waples et al. 2011). Results are summarized in Table 2.2 for the low and high population abundance assumptions. The ratio of N_e to total N was estimated to be 0.274. The ratio of N_e to adult N (N_A) was estimated to be 0.406. The number of breeders in a year (N_b) was estimated to vary between 1,907,650 and 3,838,284 adults. The total number of fish age 1 and older using the AgeNe model for the low abundance assumption was estimated to be 5,569,338 fish and for the high abundance assumption 11,194,899 fish. The estimated number of adults for low and high abundance assumptions was estimated to be 3,753,789 and 7,552,804 fish, respectively. These estimates of abundance are based on the life table model framework of Waples et al. (2011) and results differ slightly from total abundance estimates in OMEGA using a life cycle simulation model framework with varying survival and fishery exploitation rates.

Table 2.2. California Yellowtail calculated values of effective population size (N_e) with over-dispersed variation in reproductive success (Poisson factor = 3.0) using equations in Waples et al. 2011 and AgeNe program.

Scenario	Max Age	Generation Length	N_T	N_A	N_b	N_e	N_e / N_T	N_e / N_A
Low Population Abundance	22 yrs	7.7 yrs	5,569,338	3,753,789	1,907,650	1,710,971	0.27	0.41
High Population Abundance	22 yrs	7.7 yrs	11,194,899	7,552,804	3,838,284	3,442,555	0.27	0.41

Notes:
NT = Total number of individuals age 1 and older
NA = Total number of adults
Nb = Effective number of breeders in a year
Ne = Effective population size

Model simulations in OMEGA for the low (3-Farm, 10,500 mt annual production) and high production (5-Farm, 17,500 mt annual production) scenarios are presented in Table 2.3. Fish size was estimated as weight in kilograms at the end of each phase of grow-out in cages. Fish size at harvest was estimated as the midpoint of the market weight range (3.5 to 4.0 kg) as described in Rotman et al. (2021). The number of fish transferred to cages was calculated based on the midpoint market weight and a harvest goal of 10,500 mt and 17,500 mt. The number of cages assumes 100,000 fish per cage at market size. Modeled size of fish when transferred to offshore cages was 30 grams (0.03 kg) and time from transfer to harvest was assumed to be 85 to 92 weeks.

As described in Section 1.3.1.1, *Use of Case Studies*, leakage assume a total loss of 0.3% of fish in a cage over the entire period fish are in cages with 65% of the total leakage occurring in the smallest bin, 10% in the mid-sized bin, and 25% in the largest bin. The total number of fish escaping under the low and high production scenarios was 8,739 and 14,564 fish, respectively (Table 2.3).

As described in Section 1.3.1.1, *Use of Case Studies*, episodic escapes are defined as cage failures, where escape losses ranged from half to all of the fish within a given cage. Two rates of episodic escape frequencies were modeled for the high production scenario: 1) one event every 10 years (10% annual likelihood of an episodic escape event), and 2) 2.5 events every 10 years (25% annual likelihood of an episodic escape event). In the low production scenario, the modeled episodic escape likelihoods were adjusted downward using the same ratio as the high production assumptions to account for the reduced number of cages with fish and, consequently, the lower likelihood of episodic escapes. Thus, the episodic escape frequencies for the low production scenario were: 1) 0.6 events every 10 years (6% annual likelihood of an episodic escape event), and 2) 1.5 events every 10 years (15% annual likelihood of an episodic escape event). In the "modified" escape scenarios, the low escape likelihoods were halved to 3% and 5% annual likelihood under the low and high production scenarios, respectively. The number of

fish escaping was reduced to between a quarter and half of the fish in a cage to account for partial fish escape recovery.

Table 2.3. California Yellowtail production scenarios modeled for the case study.

Scenario	*Fish Size at Harvest (kg)*	*# Fish at Harvest*	*# Cages*	*0.5 kg Escaping via Leakage Annually*	*3.5 kg Escaping via Leakage Annually*	*3.95 kg Escaping via Leakage Annually*	*Total*
3-Farm, 10,500 mt	3.75	2,658,228	27	5,895	819	2,025	8,739
5-Farm, 17,500 mt	3.75	4,430,380	45	9,825	1,364	3,375	14,564

The various model scenarios and the predicted cumulative number of fish from leakage and episodic losses at the three time points of the simulations are presented in Table 2.4. The results presented are the median, 5th percentile, and 95th percentile values across the 1,000 simulations at Year 5, Year 10, and Year 25. The median number of cumulative escaped fish in the wild population increases with the higher escape likelihoods and over time for all scenarios. The increase in number of cultured fish over time is most pronounced (approximately 50% increase between Year 5 and Year 25) with the 15% episodic likelihood assumption under the 3-Farm scenario and with the 10% episodic likelihood assumption under the 5-Farm scenario. The lower end (5th percentile) and higher end (95th percentile) number of escaped fish in the population vary much less across the time steps. The lower end reflects the few model iterations (out of 1,000) that include only annual leakage—where, by chance, no episodic escapes occurred—and any fish surviving from previous years. In contrast, the higher end represents iterations with both leakage and multiple episodic escapes occurring within the three time-steps.

Modeled survival rates of escaped cultured fish to enter the population varied between 40% for the smallest sized fish and 56% for the mid-sized and largest fish in Table 2.3. Modeled survival of escaped cultured fish to survive to spawn with wild California Yellowtail varied between 27% for the smallest sized fish and 55% for the mid-sized and largest sized fish. Escaped California Yellowtail of the smallest size class began contributing to spawning after 3.5 years in the wild, while mid-sized and largest individuals contributed after 1.5 years. At harvest, cultured California Yellowtail were approaching the size at which wild fish reach 100% sexual maturity, which is between 55 cm and 70 cm, and approximately 2.2 kg to 4.3 kg (Baxter 1960).

The median number of cultured fish in the wild population under the low and high production scenarios varied between 28,560 and 79,858 fish across all time steps and production scenarios (Table 2.4). These results in the context of the estimated total number of age 1 and older California Yellowtail using the model framework in Waples et al. (2011) of 5.6 to 11.2 million fish (Table 2.3) predict that the abundance of escaped California Yellowtail in the wild population would be approximately 0.5% to 1.5% of the combined population of cultured and wild California Yellowtail in Year 25.

In Year 5, under the 3-Farm simulations, the predicted cumulative median number of escaped fish in the population ranged between 16,396 (at the 6% likelihood) and 28,560 fish (with the 15% likelihood) (Table 2.4). Simulations with the highest escape outcomes (95th percentile) indicated that a maximum of between 70,256 (with the 6% likelihood) and 93,425 (with the 15% likelihood) escaped fish may accumulate in the wild population. The results were skewed with most simulations resulting in numbers well below the 95th percentile amounts.

In Year 25, under the 3-Farm simulations, the predicted cumulative median number of escaped fish in the population ranged between 22,973 (with the 6% likelihood) and 42,745 fish (with the 15% likelihood) (Table 2.4). Simulations with the highest escape outcomes (95th percentile) indicated that a maximum of between 78,997 (with the 6% likelihood) and 106,922 (with the 15% likelihood) escaped fish may accumulate in the wild population. The results were moderately skewed with median values closer to the low end of the 5th and 95th percentile range.

In Year 5, under the 5-Farm simulations, the predicted cumulative median number of escaped fish in the population ranged between 27,818 (with the 10% likelihood) and 62,443 fish (with the 25% likelihood) (Table 2.4). Simulations with the highest escape outcomes (95th percentile) indicated that a maximum of between 90,934 (with the 10% likelihood) and 129,304 (with the 25% likelihood) escaped fish may accumulate in the wild population. In contrast to results for the 3-Farm scenarios with lower episodic likelihoods, results for the 5-Farm scenarios with the 10% likelihood were moderately skewed and not skewed with the 25% likelihood.

In Year 25, under the 5-Farm simulations, the predicted cumulative median number of escaped fish in the population ranged between 43,130 (with the 10% likelihood) and 79,858 fish (with the 25% likelihood) (Table 2.4). Simulations with the highest escape outcomes (95th percentile) indicated that a maximum of between 101,842 (with the 10% likelihood) and 151,880 (with the 25% likelihood) escaped fish may accumulate in the wild population. The results for the 5-Farm scenarios with the 10% likelihood were moderately skewed and not skewed with the 25% likelihood.

Table 2.4. The cumulative number of cultured California Yellowtail in the wild population resulting from leakage and episodic losses under the 3-Farm and 5-Farm case study scenarios. Shown are the median, and 5th and 95th percentiles.

Case Study Scenario:	Cumulative number escaped cultured fish in population		
3-Farm, 10,500 mt	**Median**	**5th**	**95th**
Number of Cultured Fish in Year 5			
Leakage + Episodic (15% annual likelihood)	28,560	15,261	93,425
Leakage + Episodic (6% annual likelihood)	16,396	15,091	70,256
Number of Cultured Fish in Year 10			
Leakage + Episodic (15% annual likelihood)	38,689	18,689	104,570
Leakage + Episodic (6% annual likelihood)	20,696	18,208	70,742
Number of Cultured Fish in Year 25			
Leakage + Episodic (15% annual likelihood)	42,745	20,720	106,922
Leakage + Episodic (6% annual likelihood)	22,973	19,214	78,997
5-Farm, 17,500 mt			
Number of Cultured Fish in Year 5			
Leakage + Episodic (25% annual likelihood)	62,443	25,916	129,304
Leakage + Episodic (10% annual likelihood)	27,818	25,248	90,934
Number of Cultured Fish in Year 10			
Leakage + Episodic (25% annual likelihood)	75,926	34,381	144,093
Leakage + Episodic (10% annual likelihood)	41,622	30,660	100,808
Number of Cultured Fish in Year 25			
Leakage + Episodic (25% annual likelihood)	79,858	37,130	151,880
Leakage + Episodic (10% annual likelihood)	43,130	32,260	101,842

The simulation results are displayed graphically in Figure 2.3. The number of cultured fish in the wild population are shown in the top figures and the number of cultured fish surviving to spawn are shown in the middle figures. The percentage of escaped fish as a proportion of population spawning abundance is shown in the bottom figures. The high episodic likelihood results are shown in Figure 2.3A 15% and 25%) and the low episodic likelihoods in Figure 2.3B (6% and 10%). The low and high production scenarios are grouped within Year 5, Year 10, and Year 25 time steps in the figures. The lower and upper whiskers in the figures reflect the 5th and 95th percentiles predicted across all 1,000 simulations and the horizontal bars are the median values.

In Year 25, under the 3-Farm simulations with the high 15% episodic likelihood assumption, the predicted cumulative median number of escaped fish surviving to spawn was approximately

35,000 fish (Figure 2.3A, middle). The predicted cumulative 95th percentile number of cultured fish surviving to spawn was approximately 90,000. Under the 5-Farm simulations with the 25% episodic likelihood assumption, the predicted cumulative median number of escaped fish surviving to spawn exceeded 60,000 (Figure 2.3A, middle). The predicted cumulative 95th percentile number of cultured fish surviving to spawn was approximately 130,000.

In Year 25, under the 3-Farm simulations with the low 6% episodic likelihood assumption, the predicted cumulative median number of escaped fish surviving to spawn was approximately 20,000 (Figure 2.3B, middle). The predicted cumulative 95th percentile number of cultured fish surviving to spawn was approximately 60,000. In Year 25, under the 5-Farm simulations with the low 10% episodic likelihood assumption the predicted cumulative median number of escaped fish surviving to spawn was approximately 35,000 (Figure 2.3A, middle). The predicted cumulative 95th percentile number of cultured fish surviving to spawn was approximately 90,000.

The number of escaped fish as a proportion of the combined wild and escaped fish spawning abundance is shown in the bottom figures in Figure 2.3. Note the 5th and 95th percentiles in these figures include the previously described range of escaped fish surviving to spawn plus they include the range of female spawning biomass assumed in the simulations (8,000 mt to 18,000 mt). This reflects the simulated stochastic variability associated with the episodic escape events and the uncertainty in the population abundance of California Yellowtail. Combining these two sources of variation expanded the predicted range of the proportion of escaped California Yellowtail spawning with wild counterparts (5th to 95th percentiles), and encompassed the full range of potential modeled outcomes.

Across all time steps and production scenarios, the median proportion of cultured fish in the wild spawning population under the low and high production scenarios, with high episodic likelihoods assumed, ranged from approximately 0.001 to 0.03 (Figure 2.3A, bottom). In Year 25, under the 3-Farm simulations with the high 15% episodic likelihood assumption, the predicted proportion of cultured fish ranged from approximately 0.003 (5th percentile) to approximately 0.021 (95th percentile) with a median of approximately 0.0075 (Figure 2.3A, bottom). In Year 25, under the 5-Farm simulations with the 25% episodic likelihood assumption, the predicted proportion of cultured fish ranged from approximately 0.006 (5th percentile) to approximately 0.029 (95th percentile) with a median of approximately 0.014 (Figure 2.3A, bottom).

In Year 25, under the 3-Farm simulations with the low 6% episodic likelihood assumption, the proportion of cultured fish in the wild spawning population ranged from approximately 0.003 (5th percentile) to approximately 0.013 (95th percentile) with a median of approximately 0.005 (Figure 2.3B, bottom). In Year 25, under the 5-Farm simulations with the low 10% episodic likelihood assumption, the proportion of cultured fish in the wild spawning population ranged from approximately 0.005 (5th percentile) to approximately 0.02 (95th percentile) with a median of approximately 0.0075 (Figure 2.3B, bottom).

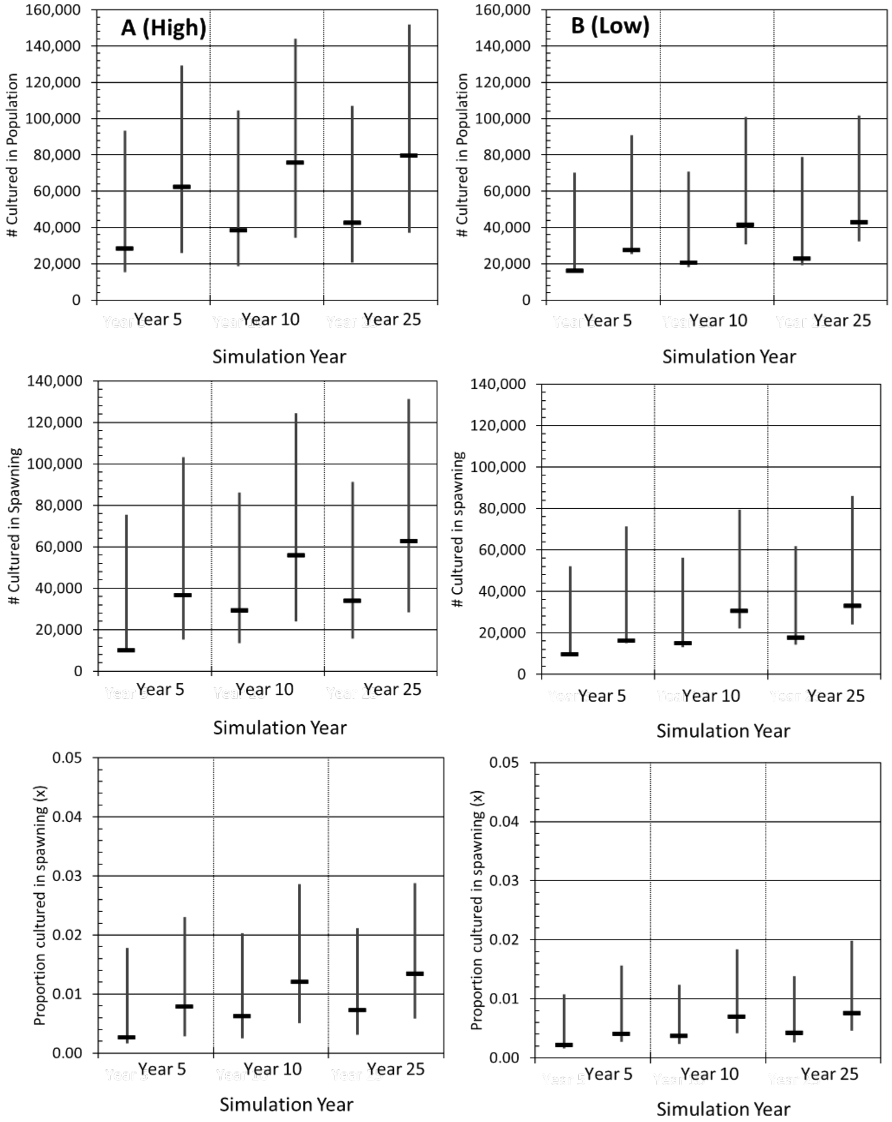

Figure 2.3. The number of cultured California Yellowtail under low (10,500 mt) and high (17,500 mt) production scenarios in the population (top), population spawning abundance (middle), and the percentage of cultured fish in spawning (bottom). A) Model results with high episodic cage failure assumptions. B) Model results with low episodic cage failure assumptions. In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year. Shown are the median (horizontal line), and 5th and 95th percentiles ("whiskers").

Under the low and high production scenarios with modified model assumptions to represent lower escape potential and reduced survival of California Yellowtail escapees, the median number of cultured fish in the wild population was approximately one-quarter of that in the high escape scenarios (Table 2.5). Recall these two scenarios assumed: 1) low likelihood of episodic escapes (3% and 5% for low and high production scenarios, respectively); 2) recovery of escaped fish (half to three-quarters of fish recaptured following an episodic escape); and 3) lower survival of escaped fish entering the population and surviving to spawn (relative survival was halved).

Table 2.5. The cumulative number of cultured California Yellowtail in the wild population resulting from leakage and episodic losses under the 3-Farm and 5-Farm case study scenarios with modified assumptions: low escape likelihood, recovery of escaped fish, and low survival of escaped fish. Shown are the median, and 5th and 95th percentiles.

Case Study Scenario:	Cumulative number escaped cultured fish in population		
3-Farm, 10,500 mt	**Median**	**5th**	**95th**
Number of Cultured Fish in Year 5			
Leakage + Episodic (3% annual likelihood) +Recovery+ Low escape survival	8,068	7,511	17,857
Number of Cultured Fish in Year 10			
Leakage + Episodic (3% annual likelihood) + Low escape survival	9,962	9,004	20,825
Number of Cultured Fish in Year 25			
Leakage + Episodic (3% annual likelihood) + Low escape survival	10,497	9,433	20,760
5-Farm, 17,500 mt			
Number of Cultured Fish in Year 5			
Leakage + Episodic (5% annual likelihood) + Recovery + Low escape survival	13,601	12,535	26,666
Number of Cultured Fish in Year 10			
Leakage + Episodic (5% annual likelihood) + Recovery + Low escape survival	16,884	15,094	28,751
Number of Cultured Fish in Year 25			
Leakage + Episodic (5% annual likelihood) + Recovery + Low escape survival	17,800	15,797	29,177

Under modified assumptions, the median number of cultured fish in the wild population ranged from 8,068 to 17,800 across all time steps and production scenarios. Given an estimated total of 5.6 to 11.2 million age-1 and older California Yellowtail (Table 2.1), these results predict that escaped California Yellowtail would constitute only 0.1% to 0.3% of the combined cultured-wild population.

Figure 2.4 graphically displays escape scenarios with reduced escape potential and low survival rates for California Yellowtail escapes. In Year 25, under the 3-Farm simulations with a 3% episodic escape likelihood, the predicted cumulative median number of escaped fish surviving to spawn was approximately 9,000 fish (Figure 2.4, middle). In the 5-Farm simulations with a 5% episodic likelihood, this number increased to about 14,000 fish. The bottom panel in Figure 2.4 shows the proportion of escaped fish in the combined wild and escaped spawning population. The median proportion of cultured fish in the wild spawning population under both low and high production scenarios remained extremely low (<0.001).

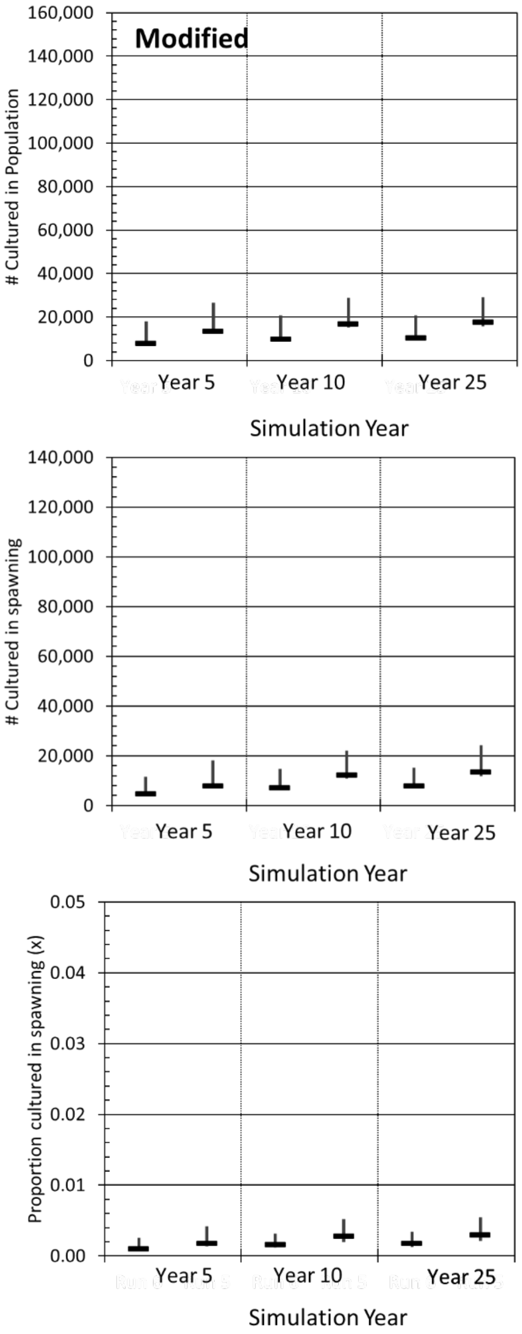

Figure 2.4. The number of cultured California Yellowtail under low (10,500 mt) and high (17,500 mt) production scenarios in the population (top), population spawning abundance (middle), and the percentage of cultured fish in spawning (bottom) with modified assumptions (low escape likelihood, recovery of escaped fish, and low survival of escaped fish). In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year. Shown are the median (horizontal line), and 5th and 95th percentiles ("whiskers").

Results suggest no effect on population fitness, even at the 95th percentile, under the high production scenario and high episodic escape assumption (with cultured fish comprising less than 3% of mixed population, as shown in Figure 2.3). Simulations incorporating leakage, a low likelihood of cage failures, partial recovery of escaped fish, and low survival of escaped California Yellowtail predicted a maximum of less than 0.5% cultured fish in the mixed population (Figure 2.4). Across the entire range of wild population abundances modeled, the potential for fitness loss remained undetectable in simulations.

The potential for reduction in N_e is presented in Figure 2.5 under high and low cage failure likelihoods. The potential for reduction in N_e is presented in Figure 2.6 under a modified scenario that assumes low and high production scenarios with low likelihood of escapes, recovery of escaped fish, and low survival of escaped fish. The results in Figure 2.5 (middle) do not indicate a substantial loss of genetic diversity when comparing N_{eT} against the general rule-of-thumb that N_e greater than 5,000 fish is sufficient to avoid deleterious effects of small N_e. It is important to note that across all cage failure frequencies, the cultured fish spawning with wild California Yellowtail in Year 25 were from multiple years of cultured fish escaping and thus the calculated N_{eT} may be a low estimate as parents of these fish would include wild broodstock collected over multiple years (i.e., have a higher N_{eC} than calculated in the modified Ryman-Laikre model). However, Waples et al. (2012) also recommended that a reduction in N_{eW} (i.e., ratio N_{eT}/N_{eW}) be considered in large marine populations and values less than 0.1 may have Ryman-Laikre effects. The reduction in N_{eW} at the highest likelihood of cage failure approached a level where potential Ryman-Laikre effects may occur in the mixed population (Figure 2.5A, bottom). The median value calculated was above 0.25 and a small proportion of model iterations resulted in values of <0.10.

The results for all modified scenarios in Figure 2.6 (middle) with low likelihood of escapes, recovery of escaped fish, and low survival of escaped fish do not suggest a loss of genetic diversity when comparing N_{eT} against the general rule-of-thumb that N_e greater than 5,000 fish is sufficient to avoid deleterious effects of small N_e. Additionally, the predicted reduction in N_{eW} (i.e., ratio N_{eT}/N_{eW}) (Figure 2.6 bottom) was well above the 0.1 threshold suggested by Waples et al. (2012).

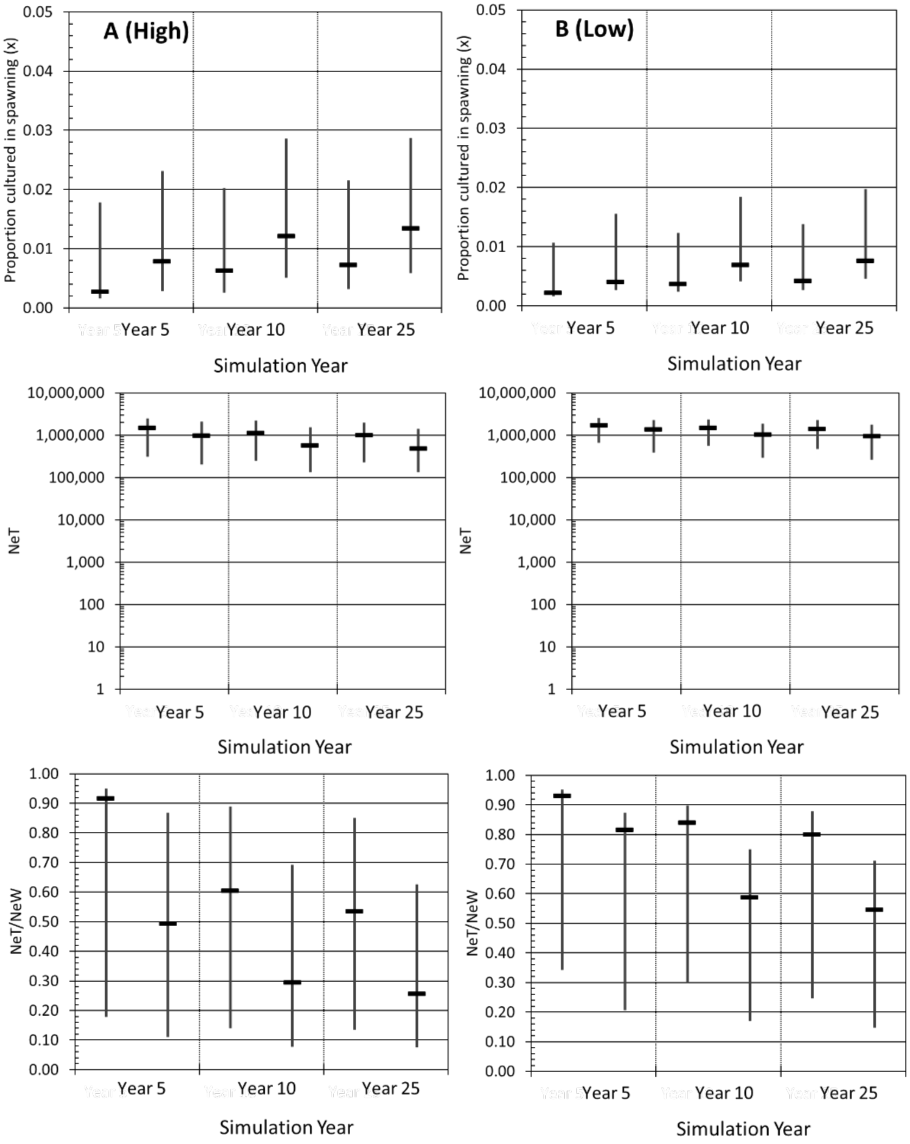

Figure 2.5. Predicted potential reduction in effective population size (N_{eT}) of California Yellowtail with high cage failure likelihood (A) and low cage failure likelihood (B). In each figure the 10,500 and 17,500 mt production scenarios are shown by simulation year. Shown are the median (horizontal line), and 5th and 95th percentiles ("whiskers").

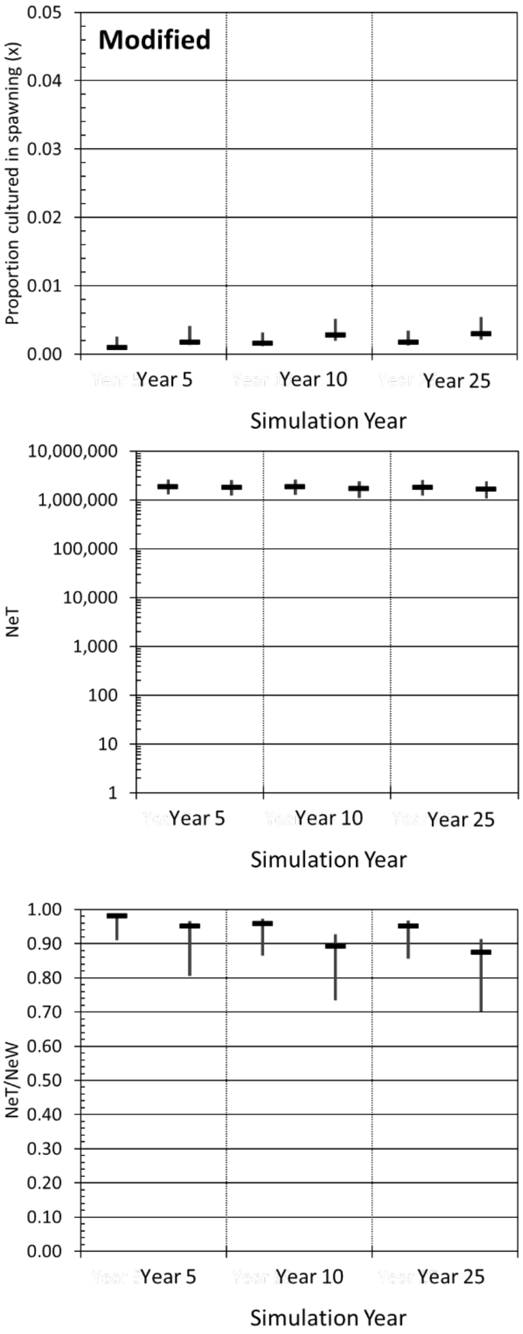

Figure 2.6. Predicted potential reduction in effective population size (N_{eT}) of California Yellowtail with low cage failure likelihood, recovery of escaped fish, and low survival of escaped fish. In each figure the 10,500 and 17,500 mt production scenarios are shown by simulation year. Shown are the median (horizontal line), and 5th and 95th percentiles ("whiskers").

2.3.2 Case Study: White Seabass

As described in Section 2.2.2, *White Seabass*, a stock assessment for White Seabass was completed in 2016 (Valero and Waterhouse 2016). The stock assessment model estimated a female spawning stock biomass of 569 mt and an unfished spawning stock biomass of 2,092 mt. The stock assessment in Valero and Waterhouse did not include biomass estimates from Baja California, Mexico. Aalbers et al. (2022) reported White Seabass movements between Baja California and California and suggested that this supports "the transboundary nature of this stock." However, they also acknowledged conflicting sources that reported different stocks or spawning areas for this species. Transboundary movement was also suggested by Rieber (2022). Reiber (2022) reported the occurrence of adult, cultured White Seabass originating from stock enhancement releases in California captured from Baja California. However, Franklin et al. (2016) present data demonstrating genetic structure of three "sub-groups/populations": a northern group within the Southern California Bight, a southern group including Pacific Baja California, and a Gulf of California group.

This case study analysis of White Seabass was completed for two scenarios, a U.S. population simulation (low abundance simulation) consistent with the assessment by Valero and Waterhouse (2016) and an extended population (high abundance simulation) that includes the Baja California portion of the species range. The low abundance scenario was based on the 2015 estimated biomass in Valero and Waterhouse (2016) of 569 mt in 2015 (~95% asymptotic interval: 241- 896 mt). While the range of input values for the low abundance scenario followed Valero and Waterhouse (2016), simulations used a wider range than they reported as a means to consider a more abundant contemporary population in California. The high abundance scenario was modeled to consider the possible distribution of escaped White Seabass south into Baja California to spawn which would dilute the contribution of escaped fish to spawning aggregations in California.

The low and high abundance simulations modeled escape risk across a range of possible population abundances. The low abundance case study simulation modeled a spawning biomass of 400 mt to 1,200 mt and the high abundance case study simulation modeled a spawning biomass of 1,600 mt to 5,100 mt. The high abundance model was approximated based on catch data from California and Baja California, Mexico (Figure 2.7). Total catch ranged from 743 to 1,249 mt from 2005 to 2019, with an average of 80% of the catch from Baja California.

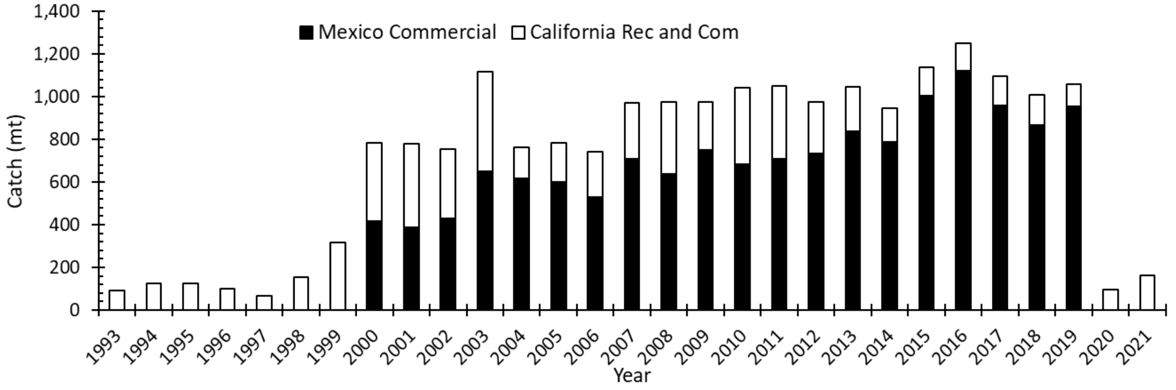

Figure 2.7. White Seabass Landings, Sources: U.S. catch - https://www.fisheries.noaa.gov/foss/, Mexico catch - Fajardo-Yamamoto et al 2022, catch not reported prior to 2000 and 2020-2021)

Estimates of N_e and the ratio of N_e/N_T and N_e/N_A were made assuming over-dispersed variation in reproductive success at age (i.e., a Poisson scaling factor of 3) using the AgeNe program (Waples et al. 2011) for the low and high abundance simulations (Table 2.6). Generation length was estimated to be 8.9 years using the AgeNe program (Waples et al. 2011).

The estimated number of breeders in a year (N_b) ranged from 54,779 to 93,907 adults for the low abundance scenario and from 228,246 to 418,450 adults for the high abundance scenario. Effective population size (N_e), as estimated by the AgeNe model, ranged from 69,253 to 118,719 fish in the low abundance scenario and from 288,553 to 529,013 fish in the high abundance scenario. Total fish aged one year or older were estimated at 265,428 to 455,019 for the low abundance scenario and 1,105,949 to 2,207,521 for the high abundance scenario. The estimated adult population ranged from 103,348 to 177,168 fish for the low abundance scenario and from 430,617 to 789,463 fish for the high abundance scenario.

The estimated ratio of N_e to total N was 0.26. The estimated ratio of N_e to adult N (N_A) was 0.67. These estimates of abundance were based on the life table framework of Waples et al. (2011) and differed from total abundance estimates in OMEGA using a life cycle population simulation framework with varying survival and fishery exploitation rates.

Model simulations in OMEGA for the low (3-Farm, 10,500 mt annual production) and high production (5-Farm, 17,500 mt annual production) scenarios are presented in Table 2.7. Fish size is reported as weight in kilograms at the end of that each phase of grow-out in cages. Fish size at harvest is reported as the midpoint of the market weight range (0.9 to 1.1 kg) as reported in Drawbridge et al. (2021). The number of fish transferred to cages was calculated based on the midpoint market weight and a harvest goal of 10,500 mt and 17,500 mt. The number of cages assumed 100,000 fish per cage at market size. Modeled size of fish when transferred to offshore cages was 6 grams (0.006 kg, 10 cm[2]) and time from transfer to harvest was assumed to be 70 to

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[2] Length – weight conversion from Velero and Waterhouse 2016

77 weeks. The calculated number of fish in net pens was over 10 million fish assuming a 1.0 kg size to market in the low production scenario and over 17 million fish in the high production scenario.

Table 2.6. White Seabass calculated values of effective population size (N_e) with over-dispersed variation in reproductive success (Poisson factor = 3.0) using equations in Waples et al. 2011 and AgeNe program.

Scenario	Max Age	Generation Length	N_T	N_A	N_b	N_e	N_e / N_T	N_e / N_A
Low Abundance	27 yrs	8.9 yrs	265,428 – 455,019	103,348 – 177,168	54,779 – 93,907	69,253 – 118,719	0.26	0.67
High Abundance			1,105,949 – 2,027,521	430,617 – 789,463	228,246 - 418,450	288,553 – 529,013		

Notes:
N_T = Total number of individuals age 1 and older
N_A = Total number of adults
N_b = Effective number of breeders
N_e = Effective population size

As described in Section 1.3.1.1, *Use of Case Studies*, leakage assumes a loss of 0.3% of fish in a cage over the entire period fish are in cages with 65% of the total leakage occurring in the smallest bin, 10% in the mid-sized bin, and 25% in the largest bin. The total number of fish escaping under the low and high production scenarios were 33,955 and 56,592, respectively (Table 2.7). This reflects a higher number of escaped fish from leakage compared to other case study species. This is due to the smaller anticipated market size of White Seabass, more individuals are required to produce 10,500 mt and 17,500 mt, as modeled production is based on the annual weight of fish held to reach market size.

As described in Section 1.3.1.1, *Use of Case Studies*, episodic escapes are defined as cage failures, where escape losses ranged from half to all of the fish within a given cage. Two rates of episodic escape frequencies were modeled for the high production scenario: 1) one event every 10 years (10% annual likelihood of an episodic escape event), and 2) 2.5 events every 10 years (25% annual likelihood of an episodic escape event). In the low production scenario, the modeled episodic escape likelihoods were adjusted downward using the same ratio as the high production assumptions to account for the reduced number of cages with fish and, consequently, the lower likelihood of episodic escapes. Thus, the episodic escape frequencies for the low production scenario were: 1) 0.6 events every 10 years (6% annual likelihood of an episodic escape event), and 2) 1.5 events every 10 years (15% annual likelihood of an episodic escape event). In the "modified" escape scenarios, the low escape likelihoods were halved to 3% and 5% annual likelihood under the low and high production scenarios, respectively. The number of fish escaping was reduced to between a quarter and half of the fish in a cage to account for partial fish escape recovery.

Modeled survival rates of escaped cultured fish entering the wild population were the same across all three size categories of escaped White Seabass, with a 37% survival rate to enter the population and a 17% survival rate to spawn in the wild population. Escaped White Seabass of all sizes were predicted to begin contributing to spawning after approximately 5.5 years in the wild. In natural settings, White Seabass reach sexual maturity at around 75 cm (3.6 kg) for males and 80 cm (4.4 kg) for females, according to Valero and Waterhouse (2016). Assuming that all cultured White Seabass are harvested at around 1.0 kg, escaped fish would have a comparable survival profile to wild one-year-old White Seabass, supporting the assumption of similar survival rates across all size categories in natural conditions.

Table 2.7. White Seabass production scenarios modeled for the case study.

Scenario	*Fish Size at Harvest (kg)*	*# Fish*	*# Cages*	*Annual # Escaping via Leakage*			*-*
				0.3 kg	***0.95 kg***	***1.0 kg***	***Total***
3-Farm, 10,500 mt	1	10,500,000	105	22,892	3,188	7,875	33,955
5-Farm, 17,500 mt	1	17,500,000	175	38,153	5,314	13,125	56,592

The various model scenarios and the predicted cumulative number of fish from leakage and episodic losses at the three time points of the simulations are presented in Table 2.8. The results presented are the median, 5th percentile, and 95th percentile values across the 1,000 simulations at Year 5, Year 10, and Year 25. The median number of cumulative escaped fish in the wild population increases with the higher escape likelihoods and over longer time periods for all scenarios. The number of escaped cultured fish in the population increases over time for all production scenarios, with median values rising by 30% to 40% between Year 5 and Year 25 under both the 3-Farm and 5-Farm scenarios (Table 2.8). Between Year 10 and Year 25, this increase was more modest, at approximately 6% to 9%. The range between the lower (5th percentile) and higher (95th percentile) numbers of escaped fish showed less variation across time steps. The lower end reflects the few model iterations (out of 1,000) that include only annual leakage—where no episodic escapes occurred by chance—and any surviving fish from previous years. Despite representing low production scenarios, levels of escaped fish remain relatively high with an assumed harvest size of 1.0 kg per fish. In contrast, the higher end captures iterations with both leakage and multiple episodic escapes occurring within the three time-steps.

The median number of cultured fish in the wild population under the low and high production scenarios varied between 53,105 and 152,520 fish across all time steps and production scenarios, excluding the modified scenario (Table 2.8). The projected percentages of cultured white seabass in the wild population, based on the estimated number of age-1 and older wild white seabass (using the Waples et al. 2011 model framework) for both low abundance (0.3 to 0.5 million fish) and high abundance (1.1 to 2.0 million fish) scenarios under high episodic cage failure likelihood, were as follows:

- Low Production Scenario - By Year 25, cultured white seabass are expected to make up approximately 16% to 25% of the combined population in the low abundance scenario and approximately 4% to 7% in the high abundance scenario.
- High Production Scenario - By Year 25, cultured white seabass are projected to constitute about 25% to 36% of the combined population in the low abundance scenario and approximately 7% to 12% in the high abundance scenario.

The percentages of cultured White Seabass in the wild population under the low episodic cage failure likelihood condition are as follows:

- Low Production Scenario - By Year 25, cultured White Seabass are expected to make up approximately 14% to 22% of the combined population in the low abundance scenario and approximately 4% to 6% in the high abundance scenario.
- High Production Scenario - By Year 25, cultured White Seabass are expected to make up approximately 22% to 32% of the combined population in the low abundance scenario and approximately 6% to 10% in the high abundance scenario.

In Year 5, under the 3-Farm simulations, the median predicted cumulative number of escaped fish in the population ranged from 53,105 (with a 6% likelihood) to 65,572 fish (with a 15% likelihood) (Table 2.8). Simulations with the highest escape outcomes (95th percentile) suggested a maximum accumulation of between 87,819 (6% likelihood) and 112,420 fish (15% likelihood) in the wild population. Median values were slightly skewed towards the lower end of this range.

In Year 25, under the 3-Farm simulations, the median predicted cumulative number of escaped fish in the population ranged from 74,827 (6% likelihood) to 89,369 fish (15% likelihood) (Table 2.8). Simulations with the highest escape outcomes (95th percentile) suggested a maximum accumulation of between 111,156 (6% likelihood) and 138,547 fish (15% likelihood) in the wild population. Median values were again slightly skewed towards the lower end of the range.

In Year 5, under the 5-Farm simulations, the median predicted cumulative number of escaped fish in the population ranged from 90,157 (10% likelihood) to 116,417 fish (25% likelihood) (Table 2.8). Simulations with the highest escape outcomes (95th percentile) indicated that a maximum of 136,929 (10% likelihood) to 169,619 fish (25% likelihood) could accumulate in the wild population. Overall, and unlike the 3-Farm scenarios with lower episodic likelihoods, results for the 5-Farm scenarios with 10% and 25% likelihoods were evenly distributed within the 5th and 95th percentiles.

In Year 25, under the 5-Farm simulations, the median predicted cumulative number of escaped fish in the population ranged from 127,081 (10% likelihood) to 152,520 fish (25% likelihood) (Table 2.8). Simulations with the highest escape outcomes (95th percentile) indicated a maximum accumulation of 173,708 (10% likelihood) to 210,670 fish (25% likelihood) in the wild population. Overall, the results for the 5-Farm scenarios with 10% and 25% likelihoods were evenly distributed between the 5th and 95th percentiles.

Table 2.8. The cumulative number of cultured White Seabass in the wild population resulting from leakage and episodic losses from current year escapes and surviving fish from previous years under the 3-Farm and 5-Farm case study scenarios simulation results. Shown are the median, and 5th and 95th percentiles.

Case Study Scenario:	Cumulative number escaped cultured fish in population		
3-Farm, 10,500 mt	**Median**	**5th**	**95th**
Number of Cultured Fish in Year 5			
.Leakage + Episodic (15% annual likelihood)	65,572	49,407	112,420
Leakage + Episodic (6% annual likelihood)	53,105	48,901	87,819
Number of Cultured Fish in Year 10			
Leakage + Episodic (15% annual likelihood)	83,071	63,154	129,848
Leakage + Episodic (6% annual likelihood)	68,877	61,189	108,989
Number of Cultured Fish in Year 25			
Leakage + Episodic (15% annual likelihood)	89,369	68,986	138,547
Leakage + Episodic (6% annual likelihood)	74,827	65,007	111,156
5-Farm, 17,500 mt			
Number of Cultured Fish in Year 5			
Leakage + Episodic (25% annual likelihood)	116,417	84,558	169,619
Leakage + Episodic (10% annual likelihood)	90,157	81,818	136,929
Number of Cultured Fish in Year 10			
Leakage + Episodic (25% annual likelihood)	144,075	108,949	194,302
Leakage + Episodic (10% annual likelihood)	118,726	101,991	168,923
Number of Cultured Fish in Year 25			
Leakage + Episodic (25% annual likelihood)	152,520	118,242	210,670
Leakage + Episodic (10% annual likelihood)	127,081	110,143	173,708

The simulation results presented in Table 2.8 are displayed graphically in Figure 2.8 (top figures) and the number of cultured fish surviving to spawn are displayed in the bottom figures. The high episodic likelihood results are shown in Figure 2.8A (left) (15% and 25% for the low and high production scenarios, respectively) and the low episodic likelihoods in Figure 2.8B (right) (6% and 10% for the low and high production scenarios, respectively). The low and high production scenarios are grouped within Year 5, Year 10, and Year 25 time-steps in the figures. The lower and upper whiskers in the figures reflect the 5th and 95th percentiles predicted across all 1,000 simulations and the horizontal bars are the median values.

In Year 25, under the 3-Farm simulations with the high 15% episodic likelihood assumption, the median cumulative number of escaped fish surviving to spawn was approximately 36,000, with a 95th percentile estimate of around 55,000 fish (Figure 2.8A, bottom). For the 5-Farm simulations with a 25% episodic likelihood, the median cumulative number of escaped fish surviving to spawn was approximately 60,000, with a 95th percentile of about 85,000 fish.

In Year 25, under the 3-Farm simulations with the low 6% episodic likelihood assumption, the median cumulative number of escaped fish surviving to spawn was approximately 30,000, with a 95th percentile estimate of around 46,000 fish (Figure 2.8B, bottom). For the 5-Farm simulations with a low 10% episodic likelihood, the median cumulative number of escaped fish surviving to spawn was approximately 50,000, with a 95th percentile of about 69,000 fish.

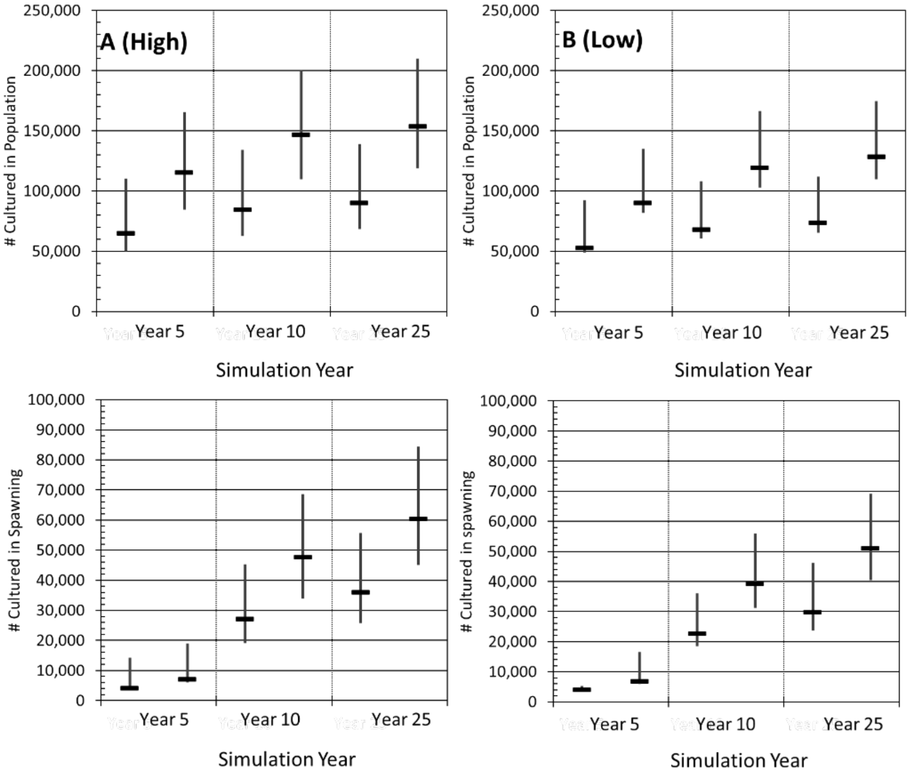

Figure 2.8. The number of cultured White Seabass under low (10,500 mt) and high (17,500 mt) production scenarios in the population (top) and population spawning abundance (bottom). A) Model results with high episodic cage failure assumptions (figures on left). B)

Model results with low episodic cage failure assumptions (figures on right). In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year. Shown are the median (horizontal line), and 5th and 95th percentiles ("whiskers").

The proportion of cultured White Seabass spawning in the mixed cultured-wild population, as simulated in the OMEGA model, is shown in Figure 2.9. The top figure illustrates the proportion of cultured fish spawning under the low White Seabass abundance scenario, while the bottom figure shows the proportion under the high abundance scenario. The 5th and 95th percentiles in these figures account for the previously described range of escaped fish surviving to spawn (i.e., Figure 2.8), along with the variation in female spawning biomass assumed in the simulations. These figures, therefore, represent the modeled stochastic variability due to episodic escape events and the uncertainties surrounding White Seabass population abundance.

Under the low White Seabass abundance scenario, with both low and high production scenarios and high episodic cage failure likelihoods, the median proportion of cultured fish in the mixed cultured-wild spawning population ranged from approximately 0.04 to 0.34 across all time steps and production scenarios (Figure 2.9A, top). In Year 25, for the 3-Farm simulations with the 15% episodic likelihood assumption, the predicted proportion ranged from about 0.16 (5th percentile) to approximately 0.31 (95th percentile), with a median of around 0.22. Under the 5-Farm simulations with the 25% episodic likelihood assumption, the predicted proportion of cultured fish ranged from just over 0.25 (5th percentile) to approximately 0.43 (95th percentile), with a median of about 0.34.

Under the low White Seabass abundance scenario, with both low and high production scenarios and low episodic cage failure likelihoods, the median proportion of cultured fish in the mixed cultured-wild spawning population ranged from approximately 0.03 to 0.29 across all time steps and production scenarios (Figure 2.9B, top). In Year 25, for the 3-Farm simulations with the 6% episodic likelihood assumption, the predicted proportion ranged from around 0.15 (5th percentile) to 0.28 (95th percentile), with a median of approximately 0.20. For the 5-Farm simulations with the 10% episodic likelihood assumption, the predicted proportion ranged from about 0.24 (5th percentile) to 0.37 (95th percentile), with a median of 0.29.

For the high White Seabass abundance scenario, with both low and high production scenarios and high episodic cage failure likelihoods, the median proportion of cultured fish in the mixed cultured-wild spawning population ranged from approximately 0.01 to 0.10 across all time steps and scenarios (Figure 2.9A, bottom). In Year 25, under the 3-Farm simulations with the 15% episodic likelihood assumption, the predicted proportion ranged from about 0.04 (5th percentile) to 0.10 (95th percentile), with a median of approximately 0.06. For the 5-Farm simulations with the 25% episodic likelihood assumption, the predicted proportion ranged from around 0.07 (5th percentile) to 0.15 (95th percentile), with a median of 0.10.

For the high White Seabass abundance scenario, with both low and high production scenarios and low episodic cage failure likelihoods, the median proportion of cultured fish in the mixed cultured-wild spawning population ranged from less than 0.01 to 0.09 across all time steps and scenarios (Figure 2.9B, bottom). In Year 25, under the 3-Farm simulations with the 6% episodic likelihood assumption, the predicted proportion ranged from about 0.04 (5th percentile) to 0.08 (95th percentile), with a median of approximately 0.05. In the 5-Farm simulations with the 10% episodic likelihood assumption, the predicted proportion ranged from around 0.07 (5th percentile) to 0.12 (95th percentile), with a median of 0.09.

Model results for the high and low likelihood scenarios in Year 5 are highly skewed, with the median values close to the low end of the range. The higher proportions of cultured fish in the wild population occur in simulations where occasional episodic events happen during the first five years of the simulation. As time progresses, the median values shift closer to the middle of the range. This change is attributed to the accumulation of escaped fish from leakage, which gradually contributes a significant portion of the cultured fish in the mixed population over the course of the simulation.

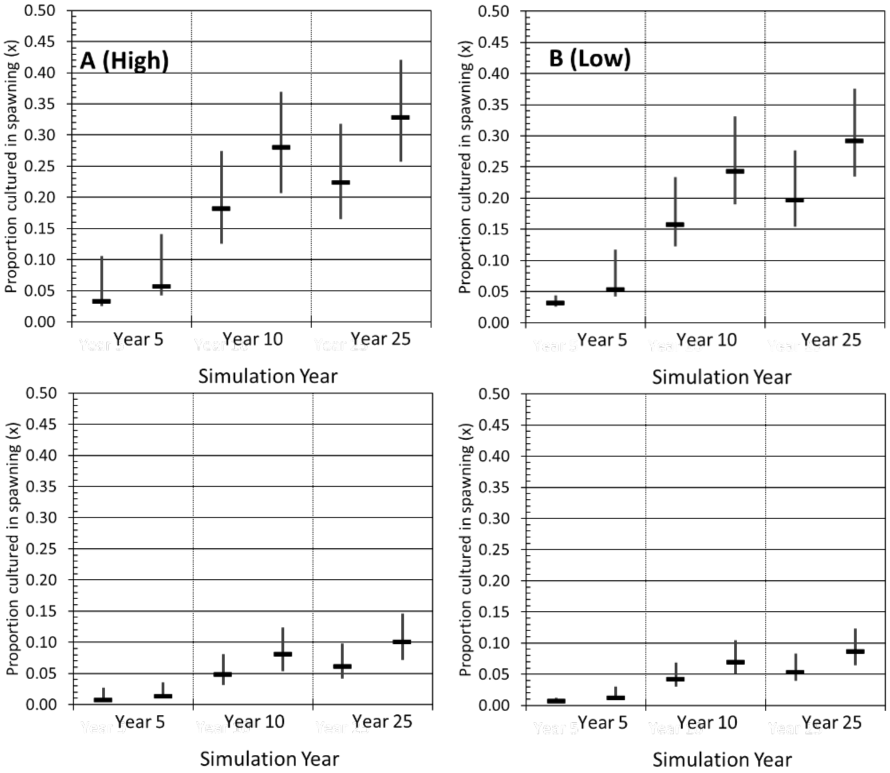

Figure 2.9. The proportion cultured white seabass in spawning under low (10,500 mt) and high (17,500 mt) production scenarios with low (top) and high (bottom) population abundance assumptions. A) Model results with high episodic cage failure assumptions. B) Model results with low episodic cage failure assumptions. In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year. Shown are the median (horizontal line), and 5th and 95th percentiles ("whiskers").

Table 2.9 presents the number of cultured fish in the wild population under the low and high production scenarios with modified model assumptions to describe a lower potential for White Seabass escapes and lower survival of escapees. These simulations assumed low likelihood of episodic escapes (3% and 5% for low and high production scenarios, respectively), fewer fish escaping in an episodic escape (half to three-quarters of fish in a cage retained or recaptured following a cage failure), and modeled survival of escaped fish to enter the population and survive to spawn was halved.

Table 2.9 presents the number of cultured White Seabass in the wild population under the low and high production scenarios, incorporating modified model assumptions that reflect a lower potential for escapes and lower survival of escapees. These simulations assumed: 1) a low likelihood of episodic escapes (3% for the low production scenario and 5% for the high production scenario); 2) fewer fish escaping during an episodic event (half to three-quarters of the fish in a cage retained or recaptured following a cage failure); 3) survival rates for escaped fish to both enter the population and survive to spawn were reduced by half.

The number of fish escaping from leakage was not modified in the simulations, so while the results for the modified scenario simulations were substantially lower due to the reduced survival of escapees and fewer fish escaping from cage failure, they were not as low as those predicted for California Yellowtail. This difference was primarily due to the significant role of leakage in the number of escaped fish for White Seabass, which was not as substantial for California Yellowtail. The higher number of White Seabass held in cages for annual harvest under the 3-Farm and 5-Farm model scenarios compared to California Yellowtail contributed to the greater impact of leakage on the overall number of escaped White Seabass.

The median number of cultured fish in the wild population varied between 26,303 and 59,944 fish across all time steps and production scenarios (Table 2.9). The results from these simulations are further illustrated in Figure 2.10, with the top figures displaying the number of cultured fish in the wild population. The bottom figures show the number of cultured fish surviving to spawn.

In Year 25, under the 3-Farm simulations with the 3% episodic likelihood assumption, the median predicted cumulative number of escaped fish surviving to spawn was approximately 15,000 fish (Figure 2.9, middle). The low and high production scenarios are grouped within the Year 5, Year 10, and Year 25 time-steps in the figures. The lower and upper whiskers in the figures represent the 5th and 95th percentiles, respectively, reflecting the range predicted across all 1,000 simulations. The horizontal bars indicate the median values for each scenario at each time step. These results help visualize the variation in the number of escaped fish and their survival to spawning within the different production conditions.

In Year 25, under the 3-Farm simulations, the median predicted cumulative number of escaped fish surviving to spawn was approximately 14,000 fish (Figure 2.10, bottom). The predicted cumulative 95th percentile number of cultured fish surviving to spawn was approximately 17,000 fish. Under the 5-Farm simulations, the median predicted cumulative number of escaped fish surviving to spawn was approximately 23,000 fish, with the predicted cumulative 95th percentile number of cultured fish surviving to spawn reaching approximately 29,000 fish.

Table 2.9. The cumulative number of cultured White Seabass in the wild population resulting from leakage and episodic losses under the 3-Farm and 5-Farm case study scenarios with modified assumptions: low escape likelihood, recovery of escaped fish, and low survival of escaped fish. Shown are the median, and 5th and 95th percentiles.

Case Study Scenario:	**Cumulative number escaped cultured fish in population**		
3-Farm, 10,500 mt	**Median**	**5th**	**95th**
Number of Cultured Fish in Year 5			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	26,303	24,431	34,436
Number of Cultured Fish in Year 10			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	33,256	30,397	40,614
Number of Cultured Fish in Year 25			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	35,660	32,044	42,832
5-Farm, 17,500 mt			
Number of Cultured Fish in Year 5			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	44,194	40,550	53,407
Number of Cultured Fish in Year 10			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	55,850	50,611	66,362
Number of Cultured Fish in Year 25			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	59,944	53,775	69,517

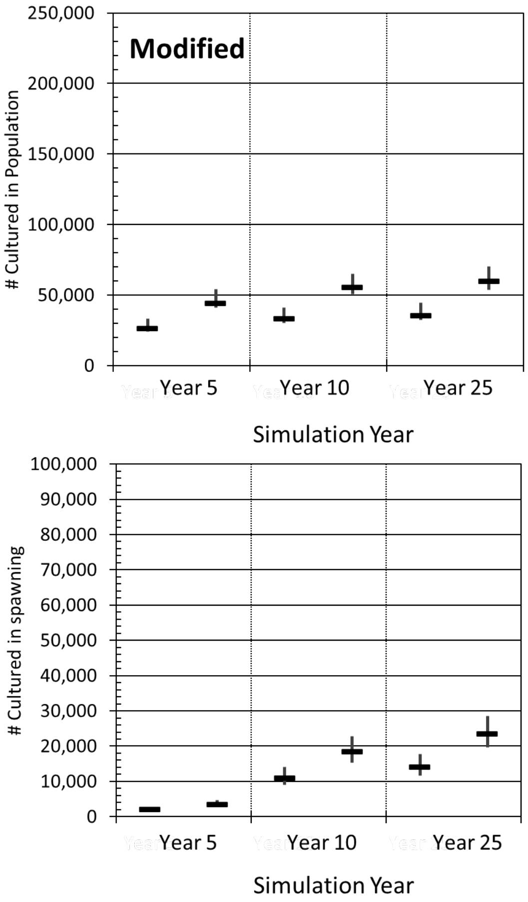

Figure 2.10. The number of cultured White Seabass under low (10,500 mt) and high (17,500 mt) production scenarios in the population (top) and spawning (bottom) with modified escape assumptions (low escape likelihood, recovery of escaped fish, and low survival of escaped fish). In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year. Shown are the median (horizontal line), and 5th and 95th percentiles ("whiskers").

The proportion of cultured White Seabass spawning in the mixed cultured-wild spawning population, based on the OMEGA model simulations with modified escape assumptions, is displayed in Figure 2.11. The top figure represents the proportion of cultured fish spawning under the low White Seabass abundance scenario, while the bottom figure shows the same for the high abundance scenario. The 5th and 95th percentiles in these figures reflect the range of escaped fish surviving to spawn (from Figure 2.9), along with the variability in the range of female spawning biomass assumed in the simulations. These figures capture the stochastic variability related to episodic escape events and the uncertainty in the wild population abundance of White Seabass, illustrating the range of potential outcomes under different assumptions.

The median proportion of cultured fish in the mixed cultured-wild spawning population under the low White Seabass abundance scenario, across both low and high production scenarios, varied between approximately 0.02 and 0.16 over all time steps and production scenarios (Figure

2.11, top). In Year 25, under the 3-Farm simulations, the predicted proportion ranged from about 0.08 (5th percentile) to approximately 0.13 (95th percentile), with a median of approximately 0.10. Under the 5-Farm simulations in Year 25, the predicted proportion of cultured fish ranged from about 0.13 (5th percentile) to approximately 0.20 (95th percentile), with a median of approximately 0.16.

The median proportion of cultured fish in the admixed cultured-wild spawning population under the high white seabass abundance scenario, across both low and high production scenarios, varied between less than 0.01 and 0.04 over all time steps and production scenarios (Figure 2.11, bottom). In Year 25, under the 3-Farm simulations, the predicted proportion ranged from approximately 0.02 (5th percentile) to approximately 0.03 (95th percentile), with a median of approximately 0.03. Under the 5-Farm simulations in Year 25, the predicted proportion of cultured fish ranged from 0.03 (5th percentile) to approximately 0.06 (95th percentile), with a median of approximately 0.04.

Model results with modified escape assumptions predicted an increasing trend in the proportion of escaped fish in the wild population over time. By Year 25, this proportion was projected to reach a median of approximately 0.10 under the 3-Farm production scenario with the low abundance assumption and 0.16 under the 5-Farm production scenario with the same low abundance assumption. In contrast, under the high abundance assumption, the proportion of cultured fish in the population remains below 0.05 in nearly all simulations, reflecting lower relative impacts of escape events at higher wild population levels.

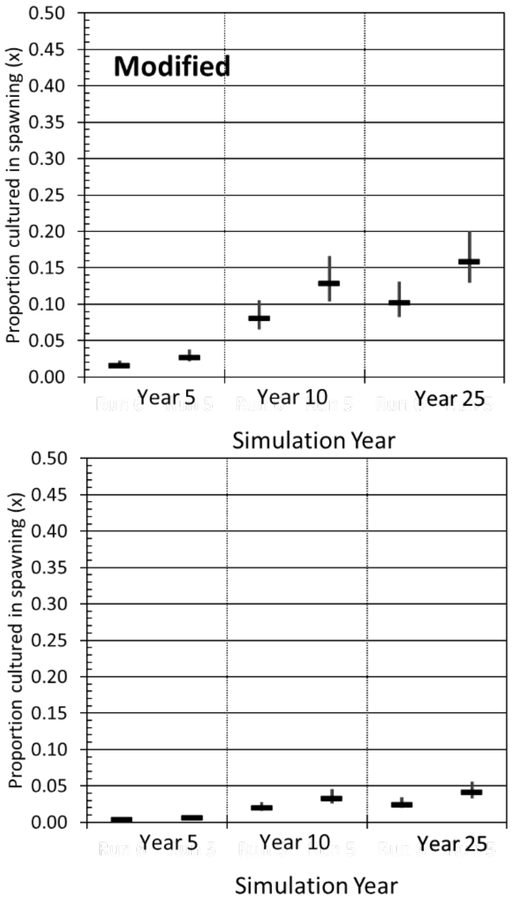

Figure 2.11. The proportion cultured White Seabass in spawning under low (10,500 mt) and high (17,500 mt) production scenarios with low (top) and high (bottom) population abundance assumptions and modified escape assumptions (low escape likelihood, recovery of escaped fish, and low survival of escaped fish). In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year. Shown are the median (horizontal line), and 5th and 95th percentiles ("whiskers").

Model simulations indicated a predicted decline in relative fitness of the wild White Seabass population due to the presence of escaped cultured fish, with the most pronounced losses occurring under the low abundance scenario. By Year 25, under the low White Seabass abundance scenario and high episodic cage failure likelihoods, the median relative fitness was projected at 0.985 for the low production scenario and 0.971 for the high production scenario (Figure 2.12a, top). For simulations assuming low episodic cage failure likelihoods, the Year 25 median relative fitness was slightly higher, estimated at 0.988 for the low production scenario and 0.978 for the high production scenario (Figure 2.12b, top), indicating a smaller relative fitness loss with fewer escape events.

Under the White Seabass high abundance scenario, predicted losses in relative fitness were minimal, with fitness declines remaining under 0.005. By Year 25, with high episodic cage failure likelihoods, the predicted median relative fitness was 0.999 for the low production scenario and 0.996 for the high production scenario (Figure 2.12a, bottom). For low episodic cage failure likelihoods, the predicted fitness impact was negligible, with a median fitness value of essentially 1.0 (indicating no fitness effect) for the low production scenario and 0.997 for the high production scenario (Figure 2.12b, bottom).

In Year 25, with modified escape assumptions under the low White Seabass abundance scenario, the predicted median relative fitness was 0.996 for the low production scenario and 0.991 for the high production scenario (Figure 2.12c, top). Under the high White Seabass abundance scenario, the predicted median relative fitness was essentially 1.0 for both low and high production scenarios, indicating no significant effect on fitness (Figure 2.12c, bottom).

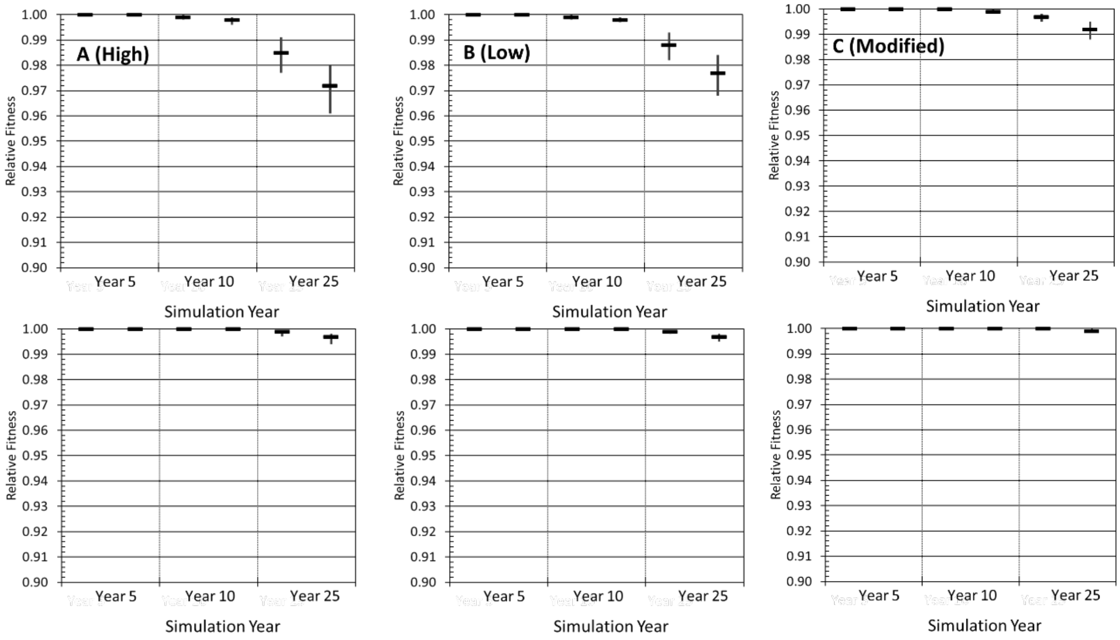

Figure 2.12. Predicted short-term relative fitness effects under low (10,500 mt) and high (17,500 mt) production scenarios with low (top) and high (bottom) population abundance assumptions. A) Model results with high episodic cage failure assumptions. B) Model results with low episodic cage failure assumptions, and C) Model results with modified escape assumptions. In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year. Shown are the median (horizontal line), and 5th and 95th percentiles ("whiskers").

Effects of escaped fish on fitness are a long-term consequence in a relatively long-lived species like White Seabass. Model simulation results were also generated for a long-term, 90-year period (years 10 – 100). Median values were calculated for each simulation iteration to capture the midpoint outcome over the period. The estimated median value and the 5th and 95th percentile values are the median of the 1,000 iteration medians and the range of median values across all model iterations. In summary, the relative fitness results presented in Figure 2.13 are not the most extreme fitness loss from the model simulations, but rather they are intended to approximate potential outcomes of long-term escapes on population fitness.

The long-term potential loss in fitness, as shown in Figure 2.13, was substantial under the low White Seabass abundance scenario. Under high episodic cage failure assumptions, the median predicted relative fitness loss was 0.10, with a range from 0.01 to 0.17 (Figure 2.13, top). Fitness loss was less severe with low episodic cage failure, showing a median of 0.05 and a range between 0.006 and 0.08. Under the high White Seabass abundance scenario, the potential loss in fitness was not as significant. Here, the median predicted loss was 0.016, with a range from 0.001 to 0.021 under high episodic cage failure assumptions (Figure 2.13, top). The modified scenario also indicated a long-term fitness loss under the low abundance scenario, with a median of 0.03 and a range of 0.002 to 0.05. However, fitness loss was negligible under the high White Seabass abundance scenario with modified escape assumptions (Figure 2.13, bottom).

Loss in fitness can be reduced using wild-caught broodstock but not avoided. Escaped fish did not differ substantially from wild fish early in simulations as the wild population traits affecting fitness would largely be unaffected by escaped fish. The greater loss of relative fitness reported for the long-term results compared to the short-term results reflects a cumulative effect over multiple generations of escaped fish and a change in mean trait value in wild fish collected for broodstock. Model simulations included feedback over multiple generations with repeated escapes and spawning of escaped fish resulting in a shift in the mean trait value of the combined admixed wild population of white seabass. Unintended domestication selection in the culture environment would result in the admixed population slowly shifting towards the hatchery optimum trait value. The long-term effects of escaped fish on fitness of the wild population are potentially substantial under the low population abundance scenario and would affect survival and abundance of the wild population.

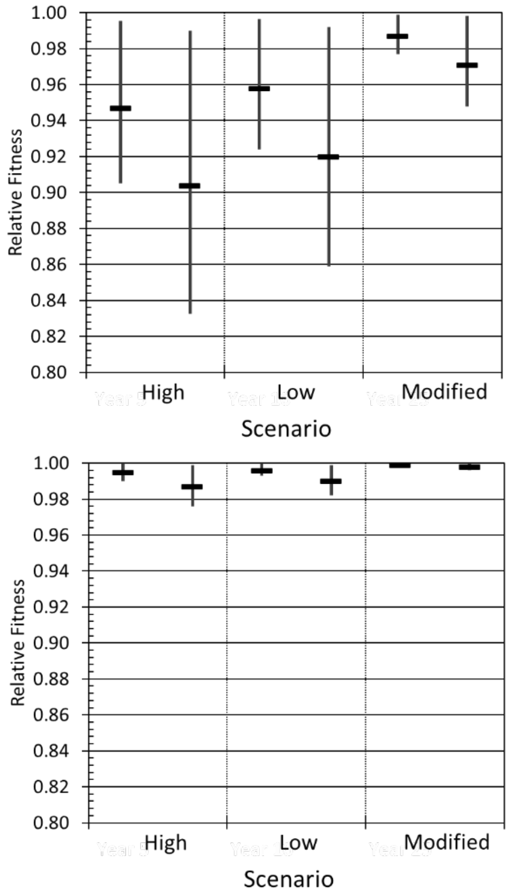

Figure 2.13. Relative fitness effects in years 10 to 100 under the low production (10,500 mt) and high production (17,500 mt) scenarios for White Seabass under previously described model assumptions for high, low, and modified escape assumptions. Shown are results for the low (top) and high (bottom) population abundance assumptions. The box-whisker plots show the range of median predicted loss in fitness (5th and 95th percentiles) across the 1000 model iterations over a 90-year period. The median predicted loss in fitness is the median of the 1000 model iterations.

Figures 2.14 through 2.16 illustrate the potential for reductions in effective population size (N_e) due to escaped White Seabass, across varying abundance scenarios and escape likelihoods. Specifically, Figure 2.14 shows reductions in N_e under the low White Seabass abundance scenario with high and low episodic cage failure likelihoods, while Figure 2.15 displays similar projections under the high abundance scenario. Figure 2.16 provides results with modified escape assumptions for both low and high abundance scenarios. In each figure, the top graph represents the proportion of escaped fish in the spawning population, the middle graph displays the calculated total effective population size (N_{eT}), and the bottom graph indicates reductions in wild effective population size (N_{eW}), expressed as the N_{eT}/N_{eW} ratio. These figures collectively highlight the relationship between escape events and genetic diversity loss in wild populations, with notable implications under different population abundances and escape frequencies.

Figure 2.14 (middle) indicates that the total effective population size (N_{eT}) in Year 25 could fall substantially below the recommended threshold of 5,000, a level below which small effective population sizes may lead to deleterious genetic consequences. This reduction reflects the cumulative effect of multiple years of cultured White Seabass escaping and subsequently spawning with wild populations. The N_{eT} calculated here may be an underestimation, as these escapees were derived from broodstock collected across multiple years, potentially yielding a higher cumulative effective population size (N_{eC}) than indicated by the modified Ryman-Laikre model. Waples et al. (2012) also recommended that the ratio of N_{eT} to wild N_e (N_{eW}) be monitored in large marine populations, with reductions below a 0.1 threshold potentially indicating significant Ryman-Laikre effects. In Year 25, under the low abundance scenario, the N_{eW} ratio was well below this 0.1 threshold, suggesting a considerable likelihood of Ryman-Laikre effects in the mixed cultured-wild white seabass population (Figure 2.14, bottom). This result emphasizes the potential for substantial reductions in genetic diversity, especially under conditions of low wild population abundance and continued escapement from aquaculture operations.

Results in Figure 2.15 demonstrate that, under the high White Seabass abundance scenario, the reduction in N_e and potential genetic impacts are less pronounced than in the low abundance scenario. However, even with high population abundance, there remains a risk of Ryman-Laikre effects in Year 25 under conditions of high episodic cage failure likelihood. This suggests that, despite the buffering effect of a larger wild population, episodic escapes can still lead to a notable reduction in genetic diversity within the mixed cultured-wild spawning population.

The results presented in Figure 2.16 (left) indicate that, under the low abundance scenario with modified escape assumptions (i.e., low likelihood of escapes, recovery of escaped fish, and low survival of escaped fish) there remained a potential risk of genetic diversity loss. This is evidenced by the comparison of N_{eT} against the 5,000-fish rule-of-thumb threshold and the observed reduction in N_{eW} (N_{eT}/N_{eW} ratio), both of which suggested possible genetic impacts in the mixed population. In contrast, the high abundance scenario shown in Figure 2.16 (right) revealed no significant risk of genetic diversity loss. Here, N_{eT} remained above the 5,000-fish guideline, and there is no substantial reduction in N_{eW}, suggesting that under high abundance conditions, genetic diversity in the mixed population was less vulnerable to the impacts of cultured fish escapes.

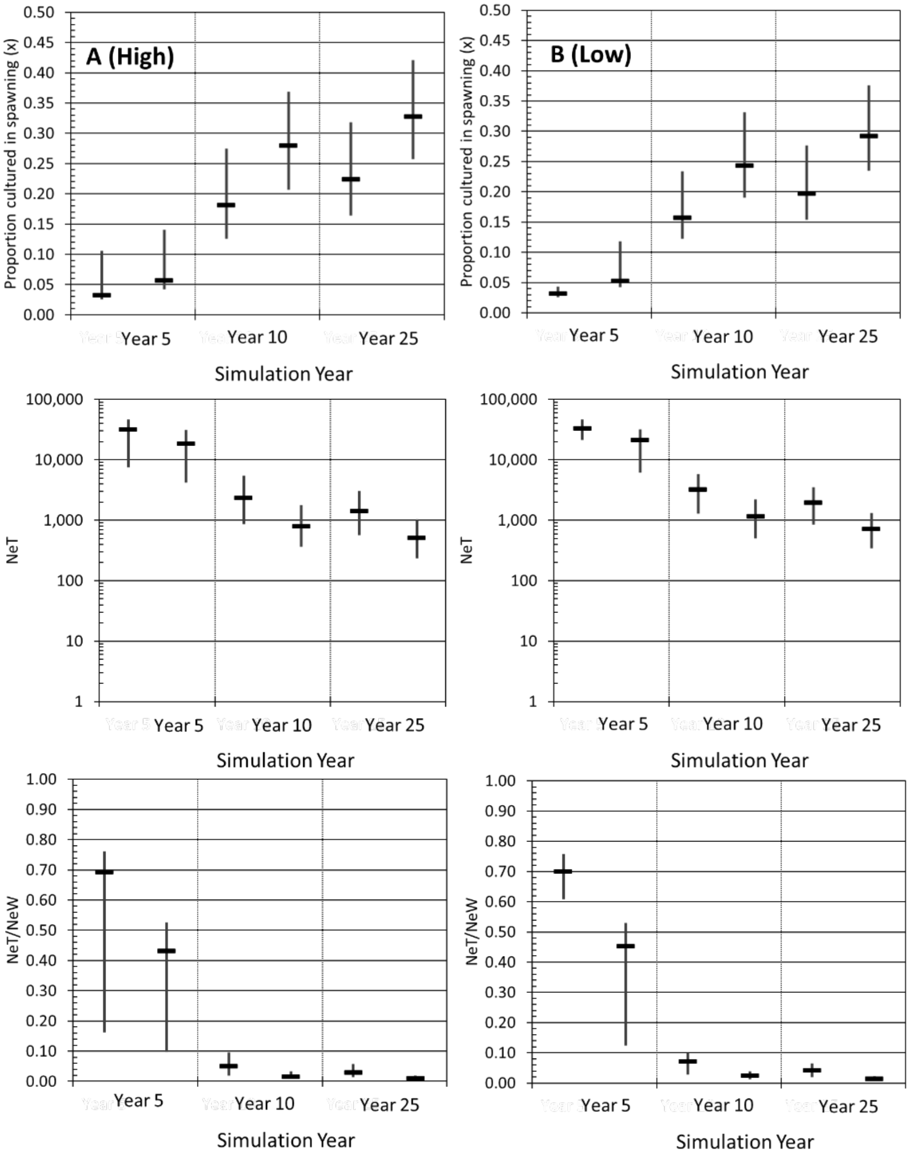

Figure 2.14. Predicted potential reduction in effective population size (*N_{eT}*) of White Seabass under the low abundance scenario with high cage failure frequency (A) and low cage failure frequency (B). In each figure the 10,500 and 17,500 mt production scenarios are shown by simulation year.

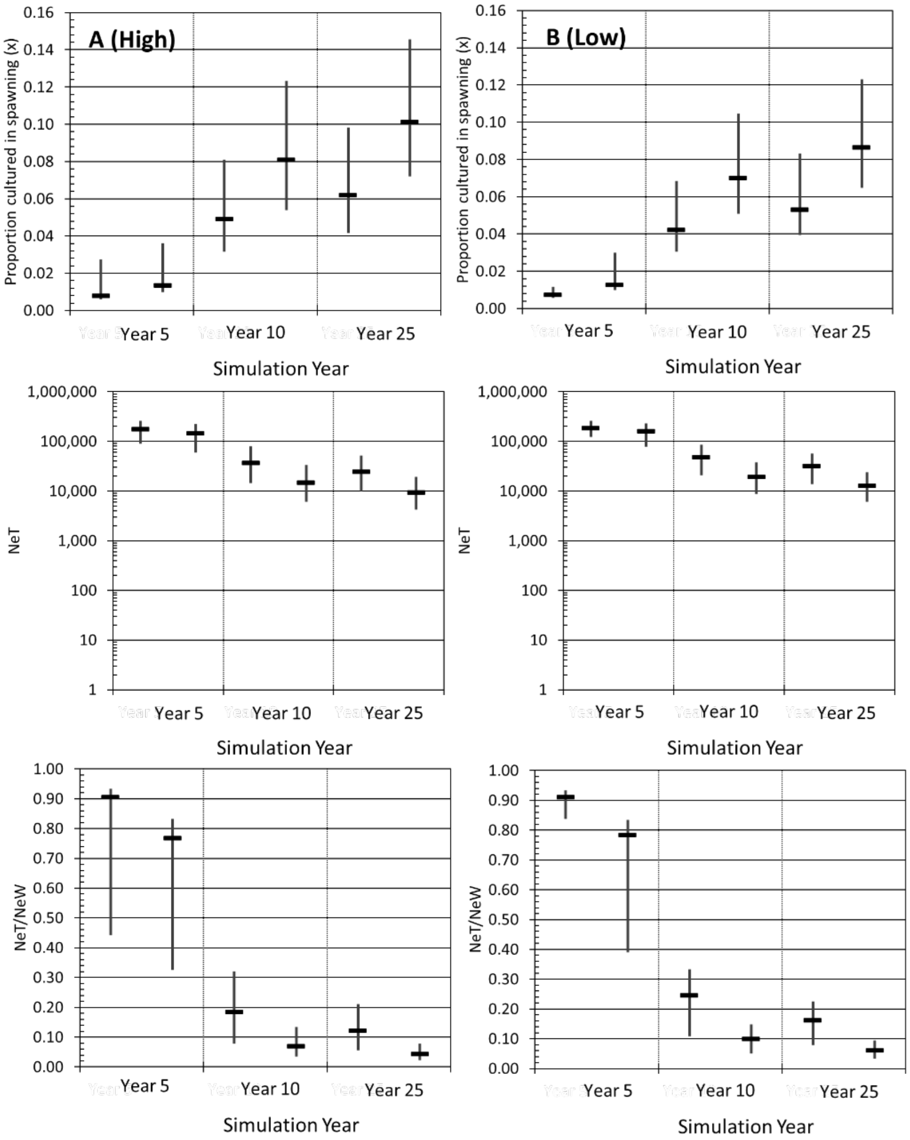

Figure 2.15. Predicted potential reduction in effective population size (N_{eT}) of White Seabass under the high abundance scenario with high cage failure frequency (A) and low cage failure frequency (B). In each figure the 10,500 and 17,500 mt production scenarios are shown by simulation year.

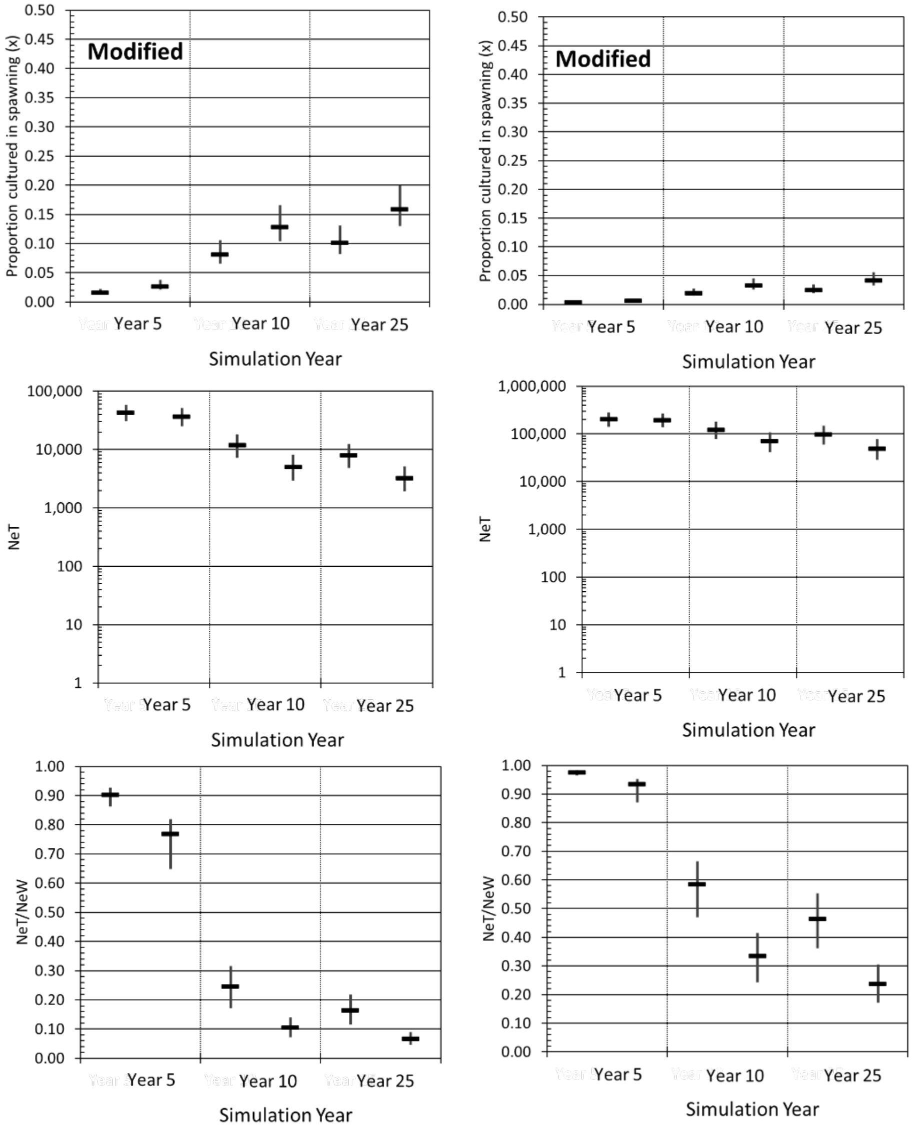

Figure 2.16. Predicted potential reduction in effective population size (N_{eT}) of White Seabass under the low (left) and high (right) abundance scenarios with modified escape assumptions: low cage failure frequency, recovery of escaped fish, and low survival of escaped fish. In each figure the 10,500 and 17,500 mt production scenarios are shown by simulation year.

2.3.3 Case Study: Striped Bass

Striped Bass is a native fish of the Atlantic and Gulf Coast that was transplanted into California's San Francisco Bay estuary in 1879 and since then has become naturalized (Smith 1895, reviewed in Boughton 2020). Little is known about its distribution and ecology in estuaries and rivers of the California coast outside of the San Francisco Bay/Sacramento-San Joaquin Delta system. Moyle (2002) described Striped Bass as needing "three basic requirements to complete their life cycle: (1) a large cool river for spawning, with sufficient flow to keep embryos and larvae suspended off the bottom until they reach the estuary and become free-swimming; 2) a large body of water with large populations of small fishes for forage; and 3) a productive estuary where larval and juvenile Striped Bass can take advantage of large invertebrate populations." Boughton (2020) concluded, based on a review of literature of Striped Bass presence in rivers, estuaries, and marine waters of California and habitat requirements of the species, that most fish observed in coastal estuaries originated in the San Francisco Bay/Delta system and use local systems opportunistically for foraging. However, because of a lack of information from smaller estuaries adjacent to the San Francisco Bay/Delta Boughton could not rule out the possibility of local reproduction.

The case study evaluation of Striped Bass using OMEGA did not attempt to model effects of escapees on the genetics of the species. There were too many unknowns related to the species population genetics, distribution of mature fish relative to potential locations of offshore cages, and population dynamics of the species. However, the possibility of smaller, localized populations in larger Southern California drainages suggests a potential for escaped cultured Striped Bass to affect fitness and genetic diversity within California. Boughton (2020) described observations of adults in the Salinas River and Carmel River, "but no evidence of eggs or larvae has been found—perhaps due to a lack of ichthyoplankton surveys anywhere except in Elkhorn Slough". Alternatively, escaped cultured fish would need to survive and seek out favorable spawning habitat in the freshwater portion of the Sacramento-Joaquin Delta to encounter reproducing Striped Bass.

The evaluation in OMEGA focused on the number of fish that may escape and survive to subadult and adult life stages in marine waters. These escapees may add to the abundance of piscivorous Striped Bass in estuaries, bays, and marine waters of Southern California. The analysis did not attempt to evaluate the contribution of escaped Striped Bass to spawning and fitness effects.

Striped Bass are considered easy to raise. A domestic stock of Striped Bass has been developed for Striped Bass aquaculture and recreational fishery stock enhancement (Anderson et al. 2021). Selective breeding of Striped Bass over six generations has demonstrated substantial improvements in growth. Third generation Striped Bass required three years to achieve market size (1.36 kg to 2.27 kg [3.0 to 5.0 lb.]) while sixth generation Striped Bass achieved market size after two years. Currently, Pacifico Aquaculture cultures Striped Bass commercially in offshore cages in Ensenada, Baja California Mexico and a 2 kg size is achieved in eighteen to twenty-four months (Pacifico Aquaculture 2024).

Model simulations in OMEGA for the low (3-Farm, 10,500 mt annual production) and high production (5-Farm, 17,500 mt annual production) scenarios are presented in Table 2.10. Fish size is weight in kilograms at the end of each phase of grow-out in cages. Fish size at harvest is the midpoint of the market weight range (1.36 to 2.27 kg; 3.0 to 5.0 lbs) in Anderson et al. (2021). The number of fish transferred to cages was calculated based on the midpoint market weight and a harvest goal of 10,500 mt and 17,500 mt. The number of cages assumes 100,000 fish per cage at market size. Modeled size of fish when transferred to offshore cages was 10 grams (0.01 kg) and time from transfer to harvest was assumed to be three years (156 weeks) based on growth data for F3 Striped Bass reported by Anderson et al. (2021). However, grow-out time may be shorter as Pacifico Aquaculture (2024) reports using selectively bred captive broodstock to obtain a 2.0 kg market size fish after approximately two years in marine cages. The calculated number of fish in net pens was over 5.8 million with the 1.8 kg size assumption with the low production scenario and over 9.7 million with the high production scenario.

As described in Section 1.3.1.1, *Use of Case Studies*, leakage assume a loss of 0.3% of fish in a cage over the entire period fish are in cages with 65% of the total leakage occurring in the smallest bin, 10% in the mid-sized bin, and 25% in the largest bin. The total number of fish escaping under the low and high production scenarios were 19,924 and 33,094 fish, respectively (Table 2.10).

As described in Section 1.3.1.1, *Use of Case Studies*, episodic escapes are defined as cage failures, where escape losses ranged from half to all of the fish within a given cage. Two rates of episodic escape frequencies were modeled for the high production scenario: 1) one event every 10 years (10% annual likelihood of an episodic escape event), and 2) 2.5 events every 10 years (25% annual likelihood of an episodic escape event). In the low production scenario, the modeled episodic escape likelihoods were adjusted downward using the same ratio as the high production assumptions to account for the reduced number of cages with fish and, consequently, the lower likelihood of episodic escapes. Thus, the episodic escape frequencies for the low production scenario were: 1) 0.6 events every 10 years (6% annual likelihood of an episodic escape event), and 2) 1.5 events every 10 years (15% annual likelihood of an episodic escape event). In the "modified" escape scenarios, the low escape likelihoods were halved to 3% and 5% annual likelihood under the low and high production scenarios, respectively. The number of fish escaping was reduced to between a quarter and half of the fish in a cage to account for partial fish escape recovery.

Table 2.10. Striped Bass production scenarios modeled for the case study.

Scenario	*Fish Size at Harvest (kg)*	*# Fish*	*# Cages*	*Annual # Escaping via Leakage*			*-*
				0.1 kg	***0.7 kg***	***1.8 kg***	***Total***
3-Farm, 10,500 mt	1.8	5,833,333	59	13,582	1,918	4,425	19,924
5-Farm, 17,500 mt	1.8	9,722,222	98	22,559	3,185	7,350	33,094

The various model scenarios and predicted cumulative number of fish from leakage and episodic losses at the three time points of the simulations are presented in Table 2.11. The median number of cumulative escaped fish in the wild population increases with the higher escape likelihoods and over time for all scenarios. The number of cultured fish over time increased for all scenarios (median values increased by 30% to 40% between Year 5 and Year 25) under both the 3-Farm and 5-Farm scenarios (Table 2.11).

The estimated survival rates of escaped fish in marine waters varied by size class, with the smallest fish surviving at a rate of 38%, mid-sized fish at 60%, and the largest fish at 62% (Table 2.10). Modeled survival rates to reproductive maturity were lower, with 10% for the smallest fish, 20% for mid-sized fish, and 27% for the largest fish. The time to reach 100% maturity also varied by size, with the smallest escaped Striped Bass requiring over 7.5 years in marine waters to reach 100% maturity, while the largest fish required approximately 5.5 years. For comparison, wild female Striped Bass on the Atlantic coast reach 50% sexual maturity by age 6 (at around 2.7 kg) and reach 100% maturity by age 8 (approximately 5.0 kg) (NEFSC 2019). This assessment did not assume that escaped fish surviving to maturity would encounter spawning Striped Bass in the wild.

The median number of cultured fish in marine waters under the low and high production scenarios varied between 38,739 and 151,529 fish across all time steps and production scenarios, excluding the modified scenario (Table 2.11). In Year 5, the 3-Farm simulations predicted a median cumulative number of escaped fish in marine waters ranging from approximately 38,739 fish under the 6% episodic escape likelihood assumption to 56,212 fish under the 15% likelihood assumption (Table 2.11). In simulations with the highest escape outcomes (95th percentile), the number of escaped fish in the wild could reach up to 94,248 with the 6% likelihood and up to 117,104 with the 15% likelihood. Notably, the median values for these scenarios are skewed toward the lower end of the range, with distributions leaning closer to the 5th percentile values.

In Year 25, under the 3-Farm simulations, the predicted median cumulative number of escaped fish in marine waters ranged from 62,822 fish with a 6% episodic escape likelihood to 87,198 fish with a 15% likelihood (Table 2.11). Simulations with the highest escape outcomes (95th percentile) indicated a potential maximum accumulation of escaped fish between 120,875 (with the 6% likelihood) and 158,176 (with the 15% likelihood). This reflects an approximate 35% increase in the number of escaped fish in marine waters compared to Year 5. Median values for the 3-Farm scenarios were skewed toward the lower end of the 5th to 95th percentile range, though the skewness was less than it was in Year 5.

In Year 5, under the 5-Farm simulations, the predicted median cumulative number of escaped fish in marine waters ranged from 65,898 fish with a 10% episodic escape likelihood to 101,160 fish with a 25% likelihood (Table 2.11). Simulations reflecting the highest escape outcomes (95th percentile) indicated potential maximum accumulations between 136,448 fish (with the 10% likelihood) and 168,686 fish (with the 25% likelihood). The median value for the 5-Farm scenario with a 25% escape likelihood was evenly distributed within the 5th and 95th percentile range, whereas under the 10% likelihood scenario, it was skewed toward the lower end of this range.

In Year 25, the 5-Farm simulations predicted that the median cumulative number of escaped fish in marine waters would range from 109,450 fish with a 10% escape likelihood to 151,529 fish with a 25% likelihood (Table 2.11). For simulations with the highest escape outcomes (95th percentile), the maximum accumulation was predicted to range from 173,620 fish (10% likelihood) to 227,864 fish (25% likelihood). The distributions for the 5-Farm scenarios with both the 10% and 25% likelihoods were generally even across the 5th to 95th percentiles, indicating a balanced distribution of outcomes in these scenarios.

Table 2.11. The cumulative number of cultured Striped Bass free swimming in marine waters resulting from leakage and episodic losses from current year escapes and surviving fish from previous years under the 3-Farm and 5-Farm case study scenarios. Shown are the median, and 5th and 95th percentiles.

Case Study Scenario:	Cumulative number escaped cultured fish in marine waters		
3-Farm, 10,500 mt	**Median**	**5th**	**95th**
Number of Cultured Fish in Year 5			
Leakage + Episodic (15% annual likelihood)	56,212	36,281	117,104
Leakage + Episodic (6% annual likelihood)	38,739	35,580	94,248
Number of Cultured Fish in Year 10			
Leakage + Episodic (15% annual likelihood)	78,280	48,290	147,845
Leakage + Episodic (6% annual likelihood)	53,695	46,227	112,654
Number of Cultured Fish in Year 25			
Leakage + Episodic (15% annual likelihood)	87,198	55,241	158,176
Leakage + Episodic (6% annual likelihood)	62,822	52,002	120,875
5-Farm, 17,500 mt			
Number of Cultured Fish in Year 5			
Leakage + Episodic (25% annual likelihood)	101,160	61,072	168,686
Leakage + Episodic (10% annual likelihood)	65,898	59,400	136,448
Number of Cultured Fish in Year 10			
Leakage + Episodic (25% annual likelihood)	135,996	86,765	213,421
Leakage + Episodic (10% annual likelihood)	97,453	78,710	165,778
Number of Cultured Fish in Year 25			
Leakage + Episodic (25% annual likelihood)	151,529	100,659	227,864
Leakage + Episodic (10% annual likelihood)	109,450	87,712	173,620

The simulation results in Figure 2.14 graphically depict the number of escaped cultured fish in marine waters in the top figures, and the number of cultured fish that survive to reach an age and size consistent with sexually mature Striped Bass (maturity) in the bottom figures. It is important to note that under this scenario the count of fish surviving to maturity does not imply the actual number of escaped fish that may encounter spawning wild Striped Bass.

Figure 2.14 displays results from high and low episodic escape likelihood scenarios, with high likelihoods (15% and 25% for the low and high production scenarios, respectively) shown in Figure 2.14A (left) and low likelihoods (6% and 10% for the low and high production scenarios, respectively) shown in Figure 2.14B (right). Both production scenarios are grouped by time steps at Year 5, Year 10, and Year 25. In each figure, the lower and upper whiskers represent the 5th and 95th percentiles across all 1,000 simulations, and the horizontal bars denote the median values.

In Year 25, the 3-Farm simulations with a high 15% episodic likelihood assumption predicted a median cumulative number of approximately 30,000 escaped fish surviving to maturity (Figure 2.14A, bottom). The cumulative 95th percentile for cultured fish surviving to spawn was approximately 57,000 fish. Under the 5-Farm simulations with a 25% episodic likelihood assumption, the median cumulative number of escaped fish surviving to spawn reached approximately 55,000 fish, while the cumulative 95th percentile was approximately 84,000 fish.

In Year 25, the 3-Farm simulations with a low 6% episodic likelihood assumption predicted a median cumulative number of approximately 24,000 escaped fish surviving to maturity (Figure 2.14B, bottom). The cumulative 95th percentile for fish surviving to maturity was approximately 42,000 fish. For the 5-Farm simulations with a 10% episodic likelihood assumption, the median cumulative number of escaped fish surviving to maturity reached approximately 40,000 fish, while the cumulative 95th percentile for fish surviving to spawn was approximately 60,000 fish.

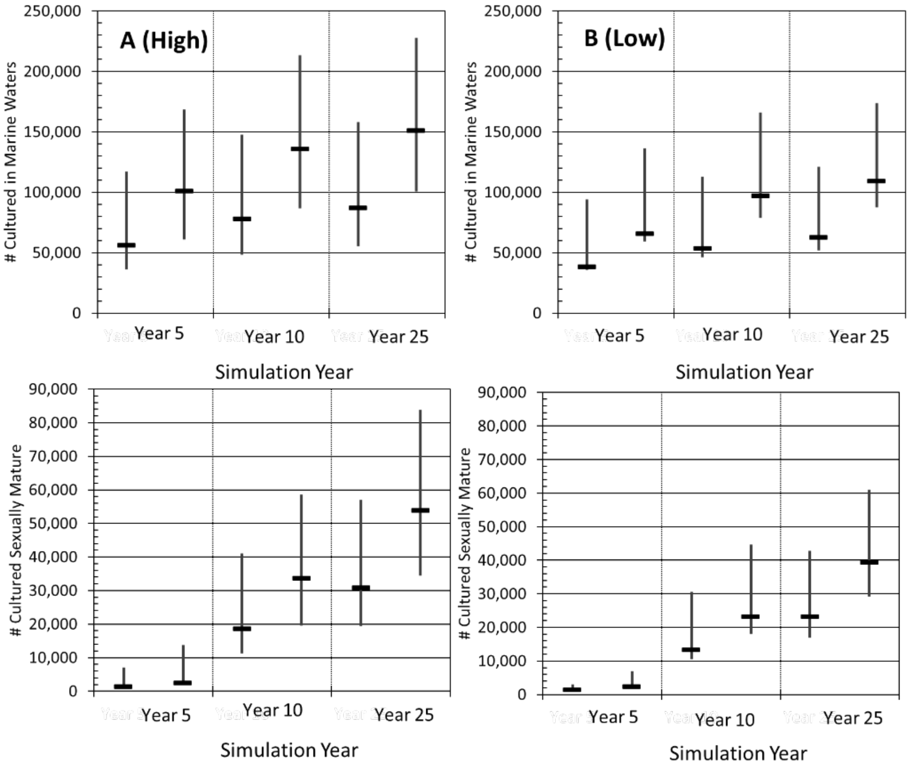

Figure 2.14. The number of cultured Striped Bass under low (10,500 mt) and high (17,500 mt) production scenarios in marine waters (top) and the number that are sexually mature in marine waters (bottom). A) Model results with high episodic cage failure assumptions. B) Model results with low episodic cage failure assumptions. In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year.

Under modified model assumptions that reflect a lower likelihood of Striped Bass escape and reduced survival of escapees, the median number of escaped fish in marine waters was slightly over one-third of the high escape scenarios (Table 2.12). These scenarios assumed: 1) a low likelihood of episodic escapes (3% for the low production scenario and 5% for the high production scenario); 2) partial recapture of the escaped fish (with half to three-quarters of the escaped fish being recovered after an escape event); and 3) low survival rates among the escaped fish. The median number of escaped fish in marine waters varied between 19,156 fand 48,235 fish across all time steps and production scenarios.

Table 2.12. The cumulative number of cultured Striped Bass free swimming in marine waters resulting from leakage and episodic losses under the 3-Farm and 5-Farm case study scenarios with modified assumptions (low escape likelihood, recovery of escaped fish, and low survival of escaped fish). Shown are the median, and 5th and 95th percentiles.

Case Study Scenario:	**Cumulative number escaped cultured fish in marine waters**		
3-Farm, 10,500 mt	**Median**	**5th**	**95th**
Number of Cultured Fish in Year 5			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	19,156	17,698	29,157
Number of Cultured Fish in Year 10			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	25,800	23,036	36,790
Number of Cultured Fish in Year 25			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	28,846	25,474	39,907
5-Farm, 17,500 mt			
Number of Cultured Fish in Year 5			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	32,047	29,393	44,902
Number of Cultured Fish in Year 10			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	43,238	38,568	56,270
Number of Cultured Fish in Year 25			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	48,235	42,650	61,197

Figure 2.15 illustrates the escape scenarios with lower escape potential and reduced survival for escaped Striped Bass. In Year 25, under the 3-Farm simulations with a 3% episodic likelihood of escape, the predicted median cumulative number of escaped fish surviving to maturity was approximately 10,000 fish (Figure 2.15, bottom). For the 5-Farm simulations with a 5% episodic escape likelihood, the median cumulative number of escaped fish reaching maturity was approximately18,000 fish by Year 25.

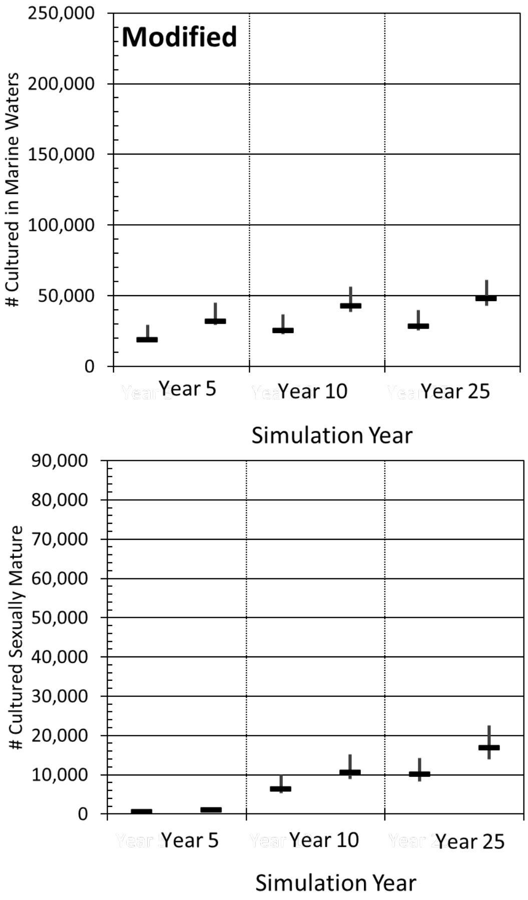

Figure 2.15. The number of escaped cultured Striped Bass under low (10,500 mt) and high (17,500 mt) production scenarios in marine waters (top) and the number that are sexually mature in marine waters (bottom) with modified assumptions (low escape likelihood, recovery of escaped fish, and low survival of escaped fish). In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year.

2.3.4 Southern California Case Study Conclusions

The OMEGA model was used to evaluate potential genetic impacts from escaped California Yellowtail and White Seabass on wild conspecifics. The Striped Bass case study did not model the potential genetic impacts of escaped fish on wild conspecific populations. This decision stemmed from Striped Bass being a naturalized species in California, originally introduced from the Atlantic coast, and significant uncertainties regarding the likelihood of escaped fish encountering naturalized populations. These unique circumstances did not align with the available knowledge and methodologies for assessing genetic impacts.

The potential impacts of cultured fish escaping include genetic effects from introgression of cultured fish with the wild populations leading to a loss of fitness. This loss of fitness is from the unintended selection of traits during captive rearing that are maladapted in the natural environment. Another potential impact of cultured fish escaping into nature is a reduction in the effective population size and subsequent loss of genetic diversity within the wild population.

The focus of this case study exercise for the Southern California species was to evaluate the potential genetic impacts of escaped fish. Ecological effects from escaped fish were not analyzed but could occur and may include predation, competition, or disease transfer to wild conspecifics or to other species within the marine ecosystem. The case study analyses reported the number of fish escaping from leakage and cage failure which could be used to further evaluate potential ecological effects from escaped fish.

2.3.4.1 California Yellowtail Conclusions

For California Yellowtail, simulation results under the high production scenario with high escape likelihood predict negligible effects on population fitness. Important factors that minimize the potential for loss of fitness in the wild population include: the use of locally sourced, wild broodstock in the captive breeding program, the absence of intentional selection for specific traits in the captive breeding program, and the existence of a single population of California Yellowtail that appears abundant relative to the case study production scenarios and modeled escape scenarios. However, there is some uncertainty as to the latter as a formal stock assessment has not been completed for the population. Historical catch data from Southern California and Baja California, Mexico were evaluated which suggested that the population is abundant across the entire range of the species. The case study evaluated a range of wild population abundances to acknowledge this uncertainty and to assess the impacts of escaped fish over a range of abundance estimates; result conclusions are based on a female spawning biomass of between 8,000 mt and 18,000 mt that is stable over the 25-year simulation period.

Simulation results suggest no effect on population fitness even at the 95th percentile under the high production, high episodic escape rate, and low population abundance assumptions. Unintentional selection during captive breeding (of F1 fish) was accounted for in the model following the first year of production. The mixed population moved very slightly away from the wild fitness optimum and towards the cultured fitness optimum in subsequent years of the simulations (see Section 1.3.1, *OMEGA Model for assessment of finfish escapes* for an explanation of fitness optimums), but this shift was insufficient to result in a loss of fitness in the mixed population.

The escape scenarios that reflected a lower potential for California Yellowtail escape and low survival of escaped fish (i.e., modified scenarios) predicted no loss in fitness across the entire range of wild population abundances modeled.

The predicted effective size of the mixed population (N_{eT}) exceeded 100,000 fish, indicating that, overall, risks of deleterious effects due to small N_e were minimal. However, under the high production scenario with frequent episodic cage failures and low population abundance, the reduction in effective population size (N_{eT}/N_{eW} ratio) suggested potential genetic diversity loss by Year 25. Simulations nearing the the 95th percentile approached the 0.10 N_{eT}/N_{eW} threshold, indicating possibly Ryman-Laikre effects that could reduce genetic diversity in the wild population. In contrast, California Yellowtail scenarios that modeled lower escape likelihoods and reduced survival rates for escaped fish, predicted a much lower risk of genetic diversity reduction across all modeled population sizes.

Conclusions from this case study evaluation would be better supported with a stock assessment coupled with an analysis of optimum yield and transboundary fisheries management policies. The importance of this data need is also made timelier by the trends in catch data that suggest increasing exploitation of California Yellowtail across its range.

2.3.4.2 White Seabass Conclusions

For White Seabass, model simulations considered two distinct population abundance scenarios to account for geographic and demographic variability. The low population abundance scenario was based on a population range limited to California, with a modeled female spawning biomass ranging from 400 mt to 1,200 mt. In contrast, the high population abundance scenario expanded the population range to include Baja California, Mexico, and modeled a female spawning biomass ranging from 1,600 mt to 5,100 mt. Similar to the California Yellowtail, these simulations included a range of potential population abundances to account for uncertainty in the assumed population size.

A notable difference in the White Seabass case study, compared to other species evaluated, is the smaller modeled market size of 1.0 kg. This smaller size necessitated a significantly higher number of fish to achieve the same target harvest levels of 10,500 mt for the 3-Farm scenario and 17,500 mt for the 5-Farm scenario. Specifically, the model required between 10.5 million and 17.5 million fish to be held in cages, respectively. In practice, this increase in fish numbers would necessitate more cages, leading to a higher potential for episodic cage failures. However, the case study did not adjust the likelihood of episodic escapes, maintaining the same leakage and episodic escape frequencies as those used for other species.

Due to the large numbers of fish modeled in cages during grow-out, the leakage-based escapes in the White Seabass case study were substantially higher than for other species. As a result, this increased the impact from this type of escape relative to episodic escapes (particularly as the episodic frequency was not upwardly adjusted). By Year 25, under low population abundance, high production, and high episodic escape frequency, the median proportion of escaped fish in the wild population surpassed 0.30 (i.e., 30%), indicating that cultured fish made up a substantial part of the mixed population. Under the high population abundance scenario, this proportion was reduced but remained high relative to California Yellowtail. By Year 25, under high population abundance, high production, and either episodic escape frequency, the median proportion of cultured fish in the wild population was approximately 0.10 (i.e., 10%).

While fitness was not greatly impacted over the first 25 years of production, long term loss of fitness (90 years) was more substantial under the low abundance, high episodic loss scenario, 0.10 (i.e., 10% fitness loss in mixed population relative to wild population), but impacts were less severe with low episodic frequencies (0.05), and even less with the higher abundance or modified scenarios. The greater loss of relative fitness reported for the long-term results compared to the short-term results reflects a cumulative effect over multiple generations of escaped fish and a change in mean trait value in wild fish collected for broodstock. Under most scenarios, results indicated a reduction in effective population size and a reduction in the genetic diversity, with potential for Ryman-Laikre effects, in the mixed cultured-wild population. Even under the modified scenario with low abundance, there remained a risk for potential genetic impacts in the mixed population. In contrast, under the high abundance scenario, N_{eT} remained above the 5,000-fish guideline, indicated less risk of genetic diversity loss in the mixed population.

Given the difference in predicted impacts based on the low and high abundance scenarios, an updated stock assessment, combined with a range-wide assessment of population genetics, is needed. Furthermore, the case study did not evaluate the risk to loss of genetic diversity among subpopulations reported in Franklin et al. (2016). Transboundary movement of escaped White Seabass and subsequent spawning would reduce genetic diversity among those subpopulations and impact locally adapted variation (if any exists).

2.3.4.3 Striped Bass Conclusions

The case study evaluation of Striped Bass using OMEGA did not attempt to model effects of escapees on the genetics of the species. The model results are instead intended to provide an assessment of potential introgression of Striped Bass with naturalized populations of Striped Bass in California. Escaped fish from farm sites closer to the primary natural population in the San Francisco Bay/Delta system would likely have a higher potential to interbreed with natural spawners. It is likely that the introgression of cultured Striped Bass into the naturalized population is likely to mirror impacts observed in other species, with the same potential to reduce fitness and effective population size of the naturalized mixed population.

The estimate of abundance in Moyle (2002) of 1.3 million adults in 2000 suggests that the potential for fitness and Ryman-Laikre effects is low. The predicted median number of escaped Striped Bass under the 5-Farm scenario and high episodic cage failure assumption exceeded 150,000 fish in Year 25. The predicted number of escaped Striped Bass that survived to reach sexually maturity was approximately 55,000 fish. The extent that these fish may survive in marine waters and migrate into the San Francisco Bay/Delta system to spawn is probably very low compared to the potential for escaped California Yellowtail and White Seabass to encounter breeding adults in marine waters.

2.3.4.4 Additional Conclusions Specific to Effective Population Size (N_e) Predictions in Southern California Case Study Species

Model simulations predicted a reduction in effective population size and a potential loss of genetic diversity in both California Yellowtail and White Seabass using the modified Ryman-Laikre effect model framework in Waples et al. (2016). The potential for loss of genetic diversity is most severe for White Seabass under the low population abundance scenario.

The impact of escaped or released fish on effective population size (N_e) in a mixed population, the effect of N_e on the genetic diversity in that population, and the consequences of genetic diversity on adaptive potential for a species are important questions that garner great interest but also have high levels of uncertainty. The realization that the ratio of N_e to total population size (N) may be orders of magnitude higher than previous estimates for many marine fish with high fecundity and high early mortality rates (Waples et al. 2018, Jones et al. 2019, Tringali and Lowerre-Barbierri 2023) has led to a rethinking of how early-life stages in fish are characterized (Tringali and Lowerre-Barbieri 2023), and a paradigm shift in recruitment dynamics theory for these species (Lowerre-Barbieri et al. 2017, Árnason et al. 2023).

With some low level of escapement on a regular basis, or possibly infrequent larger incursions of escaped fish into the wild population from episodic cage failures, the mixed populations of California Yellowtail and White Seabass may be resilient to some reduction in N_e, in part due to their intermediate generation lengths and assumed high lifetime variance in reproductive success. Resilience in a population is thought to arise from variable selective pressures acting across all life-stages in an ever-changing environment, from the egg and larval stages through spawning, reproductively mature fish, which helps shape the genetic diversity in the population (Lowerre-Barbieri et al. 2017, Tringali and Lowerre-Barbieri 2023).

Accidental release of California Yellowtail and White Seabass from cages results in fish entering the population at a size where they have avoided the natural environment's selective forces acting (perhaps most strongly) on the earliest life stages with the highest mortality (Tringali 2023). While this could give those escaped fish a greater advantage in contributing offspring to subsequent generations, and hence lowering N_e and genetic diversity in the mixed population, the larger and more fecund wild individuals may have the more important advantage of having survived that selective gauntlet which could lead to a greater lifetime reproductive success for those individuals and provide an important buffer for the mixed population. However, the efficacy of that buffer and the potential for the population to maintain its resiliency will vary over time (e.g., temporal stochasticity), by environmental conditions (e.g., water temperatures impacting spawning events), and with external pressures (e.g., fishing pressure, frequency of escapes).

Quantifying or trying to weigh the outcomes between these opposing impacts is not possible with the current state of knowledge. However, avoidance of reductions in N_e and losses of genetic diversity will only be improved by reducing the number of escaped fish (e.g., operational designs and plans to minimize escape events), ensuring that escaped fish have genetic backgrounds that capture a large portion of the existing genetic diversity in the region of the commercial operation (e.g., regional broodstock selection with a sufficient brood size and breeding design to maximize culture-based N_e), and/or generating fish that will not survive in the wild environment or produce offspring in subsequent generations (e.g., sterilization). Further reduction of risk is possible by using more adults for broodstock and parentage analysis of captive breeders to monitor and maximize breeding effective (N_b) to census size (N) ratio, as is done for white seabass stock enhancement (Gruenthal and Drawbridge 2012). One possible approach would be to develop broodstock to supply multiple farms and distribute fry to the farms that include offspring from the entire pool of broodstock. That would increase genetic diversity of fish in a cage as a hedge if the fish were to escape.

3.0 Gulf of America Candidate Species for Marine Aquaculture

3.1 Geographic Range

Regions considered in this analysis were in the west, central, east, and southeast of the Gulf of America (hereafter, 'Gulf').

3.2 Finfish Candidate Species for Marine Aquaculture in the Gulf of America

3.2.1 Red Drum (Sciaenops ocellatus)

Genetic effects of culture scenarios for Red Drum in the Gulf were evaluated using the OMEGA model. Model methods and results are in Section 3.3.1 *Case Study: Red Drum*. A summary of case study results is included at the end of this species profile in Section 3.2.1.6, *OMEGA case study to evaluate genetic risks of farm scenarios.*

3.2.1.1 Range/Description

The Red Drum (*Sciaenops ocellatus*) is a member of the family Sciaenidae which includes drums and croakers. This estuarine-dependent species is euryhaline, meaning it can tolerate a wide range of salinities (Peters and McMichael 1987). *S. ocellatus* is found along the nearshore Atlantic coast north to New England and throughout the Gulf. Within the Gulf, it ranges from the Rio Grande in Texas to Florida Bay, with particularly high prevalence in Texas, Louisiana, and Mississippi (Patillo et al. 1997, and references therein). Red Drum in the Gulf are managed as a single stock, with recreational harvest regulated by the Gulf States (GSFMC 2023). The species is popular among anglers and historically was important for commercial fisheries. However, severe overfishing in the 1980s led to the implementation of regulatory measures for both commercial and recreational catches as well as the closure of the Gulf Exclusive Economic Zone (EEZ) to all Red Drum fishing (Patillo et al. 1997; GSFMC 2023). Inshore fisheries are now primarily managed by individual states for recreational harvest with Mississippi being the only state that maintains a commercial quota for Red Drum in state waters.

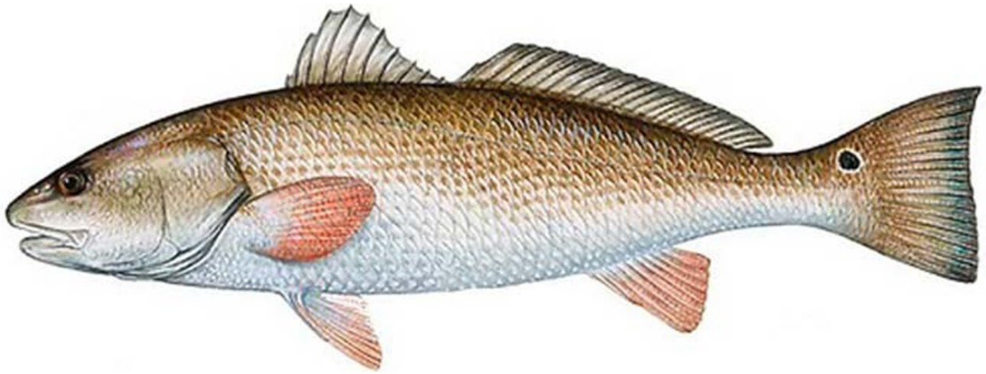

Image from the Florida Fish and Wildlife Conservation Commission

3.2.1.2 Biological Characteristics

Red Drum can live up to 37 years (Beckman et al. 1989). Both sexes reach 50% sexual maturity by age 4, with all fish mature by age 6 (Wilson and Nieland 1994). Wilson and Nieland (1994) reported that at 50% maturity, males are approximately 66 cm (3.4 kg) and females about 69 cm (4.0 kg). However, Bennetts et al. (2019) suggested that males are not spawning-capable until 4.5 years (703 mm TL) and females until 5.8 years (840 mm TL). The largest recorded Red Drum in the Gulf weighed 59 pounds (TPWD 2023).

Spawning peaks in the Gulf during late summer and early fall, and occurs in inlets, estuaries, and nearshore shelf waters (Peters and McMichael 1987). Red Drum are batch spawners. Bennetts et al. (2019) reported an average of 3.7 days between spawns and 10.5 spawning events per female each season. Bennetts et al. (2019) also noted that up to 20% of fish in a spawning season were sexually mature but did not spawn, suggesting that Red Drum may not spawn every year. Mature females are highly fecund, producing between 160,000 and 3,270,000 eggs per batch, with an annual potential of up to 60 million eggs (Wilson and Nieland 1994). Fecundity increases with size, and females can continue spawning throughout their lives without cessation (Wilson and Nieland 1994).

After spawning in nearshore and inshore regions, the buoyant pelagic eggs and larvae are carried into bays and estuaries by tidal currents (Pattillo et al. 1997, and references therein). Although the larvae are pelagic, they seek vegetated areas, such as seagrass beds for settlement which occurs at around 8 mm in size, and stay there during their early juvenile stages (Holt et al. 1983; Stunz et al. 2002). Juveniles are found in various habitats, including open estuary areas, back bays, coves, shallow shorelines, marshes, tidal pools, reefs, and river mouths, but generally move further into the estuary to grow (Pattillo et al. 1997, and references therein). Once they reach 40 to 120 mm TL, Red Drum migrate back into primary bays and deeper waters. In the Gulf, Red Drum usually remain in bays for their first three years before moving into the Gulf for the rest of their lives (TPWD 2023). Adults are more frequently found in marine environments, particularly in shallow nearshore waters up to 25 km offshore at depths between 40 and 70 meters (Pattillo et al. 1997, and references therein).

Dispersal varies within the species but has been characterized as largely non-migratory with the exception of less frequent broadscale movements and seasonal offshore migrations for spawning (Pattillo et al. 1997). Some individuals move only a few kilometers over several months, while others migrate 24 to 63 km in a similar period. Some fish, tracked for over a year, have migrated hundreds of kilometers (e.g., 778 km, 316 km) from their release point (Overstreet 1983). Aggregations of Red Drum have been observed in spring (Overstreet 1983), and in the fall, adults gather in large numbers at bay passes, where they are commonly caught by anglers (TPWD 2023).

3.2.1.3 Population Structure

Gold et al. (1993, 1994, 1999) and Seyoum et al. (2000) reported weak genetic divergence between Atlantic and Gulf populations of Red Drum. Within the northern Gulf, Gold et al. (1999) found evidence of isolation by distance, where genetic differentiation increases with geographic distance, and suggested this pattern might be influenced by sex-specific behaviors. Their analysis indicated a geographic neighborhood size relative to genetic migration of 500-600 km. The neighborhood concept in the Gold et al. (1999) related to the scale (kms) over which there are positive correlations in genetic relatedness between adjacent localities, with decreasing correlation as distance between localities increases. Further supporting this isolation-by-distance pattern, Gold et al. (2001) proposed a stepping-stone model of gene flow across the northern Gulf and Gold and Turner (2002) identified a similar neighborhood size of 700-900 km.

A tagging study by Lowerre-Barbieri et al. (2019) also revealed the potential for restricted movements across regions in the Gulf. In this acoustic tagging study of adult Red Drum from known spawning aggregations off Tampa Bay and Charlotte Harbor, strong annual spawning site fidelity was revealed along with low straying rates between spawning aggregations (Lowerre-Barbieri et al. 2019). However, the authors acknowledged the potential for longer-distance movement given the species' reproductive lifespan of at least 30 years and the study's relatively short duration of four years.

A more recent genomic study utilizing restriction-site associated DNA (RAD) sequencing examined genetic differentiation patterns in both neutral and outlier loci, the latter of which may be under selection pressure. The neutral loci suggested a gradual genetic change consistent with an isolation-by-distance pattern, however, significant differentiation was found between the northwest Gulf (Biloxi Bay, Mississippi, through the Lower Laguna Madre, Texas) and the northeast Gulf (Apalachicola, Florida, southeast to Charlotte Harbor, Florida). This genetic signal was an order of magnitude stronger when the outlier loci were analyzed (Hollenbeck et al. 2019).

Stock enhancement programs have been initiated in various locations within the Gulf. The Texas Parks and Wildlife Department (TPWD) has been releasing hatchery-bred fingerlings since 1983, with 15 to 30 million fingerlings released annually into eight different bays and estuaries along the Texas coast (Vega et al. 2003). Karlsson et al. (2008) demonstrated that hatchery fish exhibit reduced allelic richness and genetic diversity compared to wild fish. O'Leary et al. (2022) found similar reductions in genetic diversity among hatchery fish due to the limited number of effective breeders resulting from current breeding practices and logistical constraints. Based on estimated genetic effective population sizes in the hatchery fish compared to the wild population, Gold et al. (2008) indicated that there was reasonable potential for a Ryman-Laikre effect on the wild population which could lead to a decrease in the effective size and to losses in fitness and genetic diversity in the mixed population. Despite these concerns, Carson et al. (2009) did not detect negative impacts on genetic diversity or long-term effective population size in supplemented wild populations, suggesting that the TPWD stock enhancement program has not genetically compromised wild Red Drum populations in the areas studied. This may be due, in part, to the low survival rates of hatchery fish. Carson et al. (2014) recaptured hatchery-released fish to assess survival rates, finding that the majority of recovered hatchery fish were in the 0-1 age class (158 out of 208 fish), with the remaining 50 fish in the 1-2 or 2-3 age classes. This suggests that genetic impacts on wild populations may be limited by the low survival of hatchery fish to sexual maturity.

The South Carolina Department of Natural Resources also implemented a stock enhancement program, releasing 6 million juveniles and 260 million larvae into the Charleston Harbor estuary between 1999 and 2011 (Katalinas et al. 2018). Katalinas et al. (2018) reported much higher rates of hatchery fish in the wild population, with up to 49.6% of a sub-adult year class and up to 12% of the spatially separated spawning population consisting of hatchery fish. Despite this, genetic diversity in the spawning population did not show signs of negative impacts over the course of the stocking program. However, it remains unclear how much the hatchery fish contribute to spawning populations. As these sub-adult fish reach reproductive maturity and increase in fecundity with larger sizes, their impact on the genetic diversity of the wild population could increase making continued monitoring an important consideration.

3.2.1.4 Aquaculture

Current aquaculture efforts for Red Drum in the Gulf primarily focuses on stock enhancement programs (GSFMC 2023). The largest of these programs is in Texas, where 15 million fingerlings have been released annually since 2010. Before 2010, annual releases varied between 15 and 30 million fingerlings (Vega et al. 2003, GSMFC 2023). Broodstock fish are sourced from the wild, and in captivity they can have long production periods of 10 years or more. To maximize genetic diversity, 25% of the broodstock are replaced annually, and broodfish are rotated among tanks (McEachron et al. 1995, as reported in O'Leary et al. 2022).

Red Drum are released for enhancement purposes when they reach a target size of 30-35 mm in length (Vega et al. 2011). Developing a captive broodstock from cultured offspring has proven challenging and is generally not practiced (Sink et al. 2018). The species can spawn volitionally in tanks, and to extend the spawning period broodfish are kept in indoor tanks where environmental conditions are manipulated to promote longer spawning periods (Sink et al. 2018). The desired market size for Red Drum is approximately 1.4 kg at harvest, which requires a production cycle of 16 to 24 months depending on the mean temperature at the culture location (Sink et al. 2019).

In the United States, 95% of Red Drum production occurs in Texas, primarily near Matagorda Bay (Sink et al. 2019). On a global scale, Red Drum is produced extensively throughout Asia, particularly in China and Taiwan, with marine cage culture being practiced in China and Israel (Lutz 2022).

3.2.1.5 Considerations on genetic risk to wild conspecifics

Genetic studies of Red Drum stock enhancement programs, such as the Texas Parks and Wildlife Department (TPWD) program, indicate that effective population size remained stable and genetic diversity was not compromised after 20 years of releases (Carson et al. 2009). However, significant uncertainties remain regarding the survival rates of hatchery fish to sexual maturity (e.g., in Texas) and the proportion of hatchery fish that contribute to spawning (e.g., in South Carolina). The survival rates of escaped, larger, commercially cultured fish are likely to differ considerably from those of released larvae and fingerlings.

The reproductive resilience and longevity of Red Drum may buffer some level of genetic introgression from cultured fish (Tringali and Lowerre-Barbieri 2023), but the lack of comprehensive data on Red Drum abundance in the Gulf adds uncertainty to the potential effects of escapes (SEDAR 2016). A stock assessment of Gulf Red Drum in Florida waters (Addis 2020) provides some insight, but across the species' entire range, Red Drum is considered data-limited due to the absence of data on the offshore population (SEDAR 2016). Recommendations for model parameters to represent stock dynamics were made in 2016 with calls for additional research into the distribution of large adults in state waters that may be susceptible to recreational fishing (Skyler et al. 2016, Hightower et al. 2016). Such research could improve models assessing the abundance of the adult population and help to evaluate the genetic risks of escaped Red Drum.

The potentially complex metapopulation structure of Red Drum, and the wide range of unique environmental conditions within inlets, estuaries, and bays this species may adapt to across their distribution in Gulf, highlight the importance of careful monitoring of adult spawning migrations. To minimize genetic risks, it is important that broodstock for aquaculture be sourced from within their "home" range, which in some areas of the Gulf may span hundreds of kilometers. Escaped Red Drum that stray and spawn with populations outside their “home” range could contribute to genetic homogenization across populations, and potentially reduce genetic diversity or erode local adaptations (if any exist).

Given the uncertainties in stock dynamics and abundance, there is a moderate genetic risk to wild populations from escaped cultured *Sciaenops ocellatus*. To minimize this risk, steps should include sourcing local broodstock and maximizing genetic diversity in hatchery fish using the available information on spawning dynamics in culture. These measures will help reduce the potential for the loss of locally adapted genetic variation and preserve genetic diversity in wild populations.

3.2.1.6 OMEGA case study to evaluate genetic risks of farm scenarios

A case study was performed using the OMEGA model to quantify population dynamics of a hypothetical Red Drum farm program sited within the Gulf. The OMEGA model was used to simulate the population response of a wild population of Red Drum where varying levels of culture-origin fish escaped from the farm system, resulting in a mixed cultured-wild population where some proportion of the population contains genetics of cultured fish.

Assuming an individual farm harvest production of 3,500 mt, two different production levels were modeled: the equivalent of three farms (hereafter 3-farm) with a total harvest production of 10,500 mt and the equivalent of five farms (hereafter 5-farm) with a total harvest production of 17,500 mt. The captive breeding program was assumed to use local, wild-origin fish and did not employ intentional selection for traits. Detailed modeling of Red Drum farm systems under a range of escape scenarios is presented in Section 3.3.1. Conclusions of OMEGA modeling in regard to potential for genetic risk are discussed in Section 3.3.4.1.

As discussed above, Red Drum are a data-limited species in the Gulf. There is stock assessment data for nearshore spawning aggregations in Florida but there is no data on the abundance of the offshore population. Notably, this species has been undergoing stock enhancement since the 1980s, which presents an ongoing pressure on genetic diversity, however genetic studies have thus far indicated a stable population with a healthy effective population size. The evaluation of Red Drum aquaculture relied on an estimate of wild population abundance using the AgeNe model, which estimated adult abundance at about 8.9 million fish. The model results for both 3-farm and 5-farm production scenarios demonstrated a negligible loss in wild population fitness assuming high rate of episodic escape (25% likelihood of loss of one cage in any given year) and an assumed escape rate from program leakage of 0.3% per year. In regard to genetic diversity effects, OMEGA results suggest that while the effective population size (ratio N_{eT}/N_{eW}) would likely be reduced under both production scenarios, the large effective size of the mixed population would be sufficiently large to suggest a low potential for deleterious effects of low N_e under most scenarios, however, deleterious Ryman-Laikre effects may occur under a 5-farm scenario with either low or high episodic escape rates. For a 3-farm system, Ryman-Laikre effects were found to occur for only small proportion (~<10%) of simulations using the high episodic escape rate assumption.

A stock assessment covering the Gulf region would be an important resource to definitively parameterize the OMEGA model for Red Drum, considering the migratory behavior of this species. Ongoing genetic monitoring on a subregional scale, including offshore areas and locations of stock enhancement would inform understanding of population structure, effects on genetic diversity from stock enhancement, and the buffering effects of reproductive resilience in Red Drum.

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3.2.2 Almaco Jack (Seriola rivoliana)

Genetic effects of culture scenarios for Almaco Jack in the Gulf were evaluated using the OMEGA model. Model methods and results are in Section 3.3.2. A summary of case study results is included at the end of this species profile in Section 3.2.2.6, *OMEGA case study to evaluate genetic risks of farm scenarios.*

Almaco Jack are a data-limited species in the Gulf. SEDAR 49 (2016) authors concluded that information is generally not available for Almaco Jack. The following information on range/description, behavior, and population structure is incomplete.

3.2.2.1 Range/Description

Almaco Jack, *Seriola rivoliana*, is a commercially and recreationally fished pelagic species found across the globe in tropical areas, including in: the western Atlantic Ocean, Gulf, Caribbean Sea, eastern Atlantic Ocean along west Africa and the Canary Islands, the Philippines, Australia, Hawaiian Islands, Peru, and Mexico (Smith Vaniz et al. 2015, Mendoza-Portillo et al. 2020).

In the Gulf, there is no information on stock structure for the Almaco Jack so it is managed as a single unit stock (SEDAR 2016). The most recent catch data were reported in 2014 with a total of 19,061 fish landed at a cumulative weight of 131,227 lb. (SEDAR 2016). The Gulf Fishery Management Council determined overfishing of Almaco Jack was occurring as of 2020 (https://gulfcouncil.org/species/jack-almaco/).

3.2.2.2 Biological Characteristics

The life history data for Almaco Jack are generally considered incomplete, and further research has been recommended to gather information on age, reproduction, and growth parameters (SEDAR 2016). *Seriola rivoliana* is a fast-growing species found in waters with temperatures above 22°C. Growth rates for this species increases as water temperatures rise, even past 30°C (Blanco et al. 2022). Smith-Vaniz et al. (2015) reported that Almaco Jack can grow up to 80 cm fork length (FL), although individuals around 55 cm FL are more common. The Florida Fish and Wildlife Conservation Commission noted that along the Florida coast, *S. rivoliana* can reach up to 88 cm FL (GSMFC 2023).

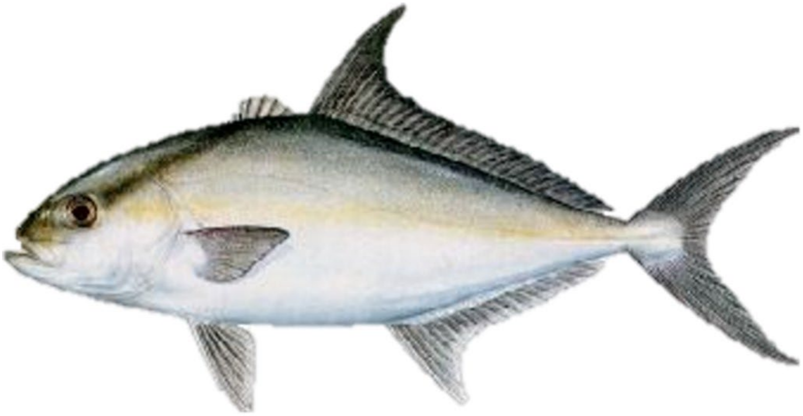

Image from the Gulf of Mexico Fishery Management Council

Like other *Seriola* species, juveniles often associate with floating objects and algae such as *Sargassum* (Bacheler et al. 2022), while adults tend to be more associated with benthic structures, residing at depths of 3 to 250 meters (Smith-Vaniz et al. 2015). Bacheler et al. (2022) observed that of the four *Seriola* species found along the southeastern U.S. coast, *S. rivoliana* has the least tendency to aggregate, and is often observed either solitarily or in small groups. However, they are sometimes seen in mixed groups with *S. dumerili* (Bacheler et al. 2022). Both species exhibit similar responses to environmental conditions, habitat preferences, schooling behavior, and body sizes (Bacheler et al. 2022), contributing to frequent misidentification between these species (Renshaw and Gold 2009). *S. rivoliana* is more abundant near high-relief hard-bottom substrates and is frequently found around artificial reef structures such as oil platforms (Garner et al. 2019).

Spawning for *S. rivoliana* occurs from April to November, with timing likely dependent on water temperature (Blanco 2022, UWI 2016, Sims 2019). Almaco Jack are pelagic spawners, and certain populations, such as those in Belize, form spawning groups. Males reach sexual maturity at approximately 22 months and females at 24 months (UWI 2016). Females can produce between 300,000 and 1 million eggs two to three times per week during a spawning season (Sims 2019).

3.2.2.3 Population Structure

There are no studies on the population genetic structure of Almaco Jack in the Gulf and they are currently managed as a single stock (SEDAR 2016). The only available study addressing genetic differentiation in this species was published by Mendozo-Portillo et al. (2020). This study examined population genetic structure across the Pacific and Atlantic Oceans, including the southern Gulf, using 25 variable mitochondrial cytochrome c oxidase sub-unit 1 sites and 3,678 nuclear single nucleotide polymorphism (SNP) loci. Their analyses identified three distinct genetic groups: the western Atlantic, central Pacific, and eastern Pacific. Additionally, the SNP loci identified a fourth group off Baja California Sur, Mexico, though this differentiation was not supported by the mitochondrial data.

Pairwise estimates of genetic differentiation using both mitochondrial and nuclear markers showed no significant differences among samples from the western Atlantic populations (Florida/Cuba vs. Veracruz-Tamaulipas/Tuxpan Veracruz/Veracruz vs. Yucatán) (Mendozo-Portillo et al. 2020). To better inform management decisions, further fine-scale genetic or genomic analyses are necessary across the U.S. Atlantic, Gulf coasts, and the broader Gulf range of *S. rivoliana*.

3.2.2.4 Aquaculture

Seriola rivoliana is considered a strong candidate for aquaculture development due to its fast growth, high-quality flesh, and high market value (Roo et al. 2014, Sicuro and Luzzana 2016, Viader-Guerrero et al. 2021). It also adapts well to commercial feeds and rearing conditions (Sicuro and Luzzana 2016). Aquaculture of Almaco Jack has been explored in several regions, including Mexico, Japan, Ecuador, Spain (Canary Islands), and the U.S. (Blacio 2004, Roo et al. 2014, Sicuro and Luzzana 2016).

In the U.S., Almaco Jack aquaculture has primarily been developed in Hawaii, though some research has also been conducted in the Gulf, including a small offshore demonstration project off the coast of Florida (Verner-Jeffreys et al. 2006, Sicuro and Luzzana 2016). Aquaculture focused research began on this species in Hawaii in the mid-1990s, and through this work, volitional spawning was achieved using wild-collected broodfish (Laidley et al. 2004, Verner-Jeffreys et al. 2006). Further studies closed the species' life cycle by achieving maturation and spawning in hatchery-raised fish. Pilot-scale offshore cage production started in 2004, with fish reaching 1.8 kg in 8 months and 3 kg in 18 months (Laidley et al. 2004, Sims 2019). Commercial offshore production is now operational off Kona-Kailua, Hawaii (Blue Ocean Mariculture; https://bofish.com/).

Spawning techniques for Almaco Jack vary by region. In Hawaii, Mexico, and Ecuador, captive broodstock undergo natural volitional spawning in tanks (Blacio 2004, Verner-Jeffreys et al. 2006), while in other regions (e.g., Canary Islands), hormonal induction is used (Roo et al. 2014). In Ecuador, the spawning period lasts three months (Blacio 2004), but in Hawaii, photoperiod manipulation extends spawning year-round (Laidley et al. 2004).

Roo et al. (2014) noted that females in captivity for three years (weighing 4.08 ± 2.2 kg and measuring 57.19 ± 7.28 cm SL) remained sexually immature, while all males were capable of producing milt. Blacio (2004) observed that volitional spawning in Ecuador was temperature-dependent, occurring when water temperatures reached 26°C. One female weighing 20 kg produced approximately 12 million eggs in a season (Blacio 2004).

3.2.2.5 Considerations on genetic risk to wild conspecifics

There is limited biological information and no stock structure assessment for Almaco Jack in the Gulf. Further research is required to better understand the species' life history, reproduction, maturity, and growth parameters (SEDAR 2016). Additionally, studies on Almaco Jack abundance in the Gulf are necessary to assess its vulnerability to genetic diversity loss and fitness decline due to interactions with escaped cultured fish. These data gaps create significant uncertainty in evaluating the genetic risks posed by escapees. Based on available information and the current overfishing status in the Gulf, escaped fish may present a moderate-to-high genetic risk to wild populations.

To mitigate potential genetic risks from offshore aquaculture in the Gulf, broodstock should be regularly replenished from wild populations to maintain genetic diversity and minimize the loss of effective population size in the wild due to interbreeding with cultured fish. The likelihood of interactions between cultured and wild Almaco Jack may be lower for an offshore program in the Exclusive Economic Zone (EEZ) where most catch occurs along the continental shelf. However, an aquaculture site near the shelf would likely be in closer proximity to wild conspecifics, increasing the chances of interactions between escaped and wild fish.

3.2.2.6 OMEGA case study to evaluate genetic risks of farm scenarios

A case study was performed using the OMEGA model to quantify population dynamics of a hypothetical Almaco Jack farm program sited in the Gulf. The OMEGA model was used to simulate the population response of a wild population of Almaco Jack where varying levels of culture-origin fish have escaped from the farm system, resulting in a mixed cultured-wild population where some proportion of the population contains genetics of cultured fish.

Assuming an individual farm harvest production of 3,500 mt, two different production levels were modeled: the equivalent of three farms (hereafter 3-farm) with a total harvest production of 10,500 mt and the equivalent of five farms (hereafter 5-farm) with a total harvest production of 17,500 mt. The captive breeding program was assumed to use local, wild-origin fish and did not employ intentional selection for traits. Detailed modeling of Almaco Jack operations under a range of escape scenarios is presented in Section 3.3.2. Conclusions of OMEGA modeling in regard to potential for genetic risk are discussed in Section 3.3.4.2.

Almaco Jack is a data-limited species in the Gulf, and no stock assessment has been conducted for this species, and as such abundance of this species in the Gulf is unknown. The evaluation of Almaco Jack aquaculture relied on assumed levels of wild population abundance inferred from catch data for Greater Amberjack (*Seriola dumerili*) which was identified as an appropriate proxy species given similar life history characteristics and ecology. Almaco Jack are caught at a rate of about 10% of catch of Greater Amberjack, equating to a female spawning biomass of 338 to 750 mt. OMEGA results for both 3-farm and 5-farm production scenarios demonstrated a small loss in wild population fitness in the near term, but over 100 years, a cumulative effect occurs where the trait value shifts toward the culture optimum over time in the admixed population. This is also due to the increasing proportion of cultured fish in the spawning population over time, assuming escape rates continue at the assumed levels of episodic escape and leakage. As such, deleterious effects of fitness loss are more likely for Almaco Jack than for the other two candidate species studies for the Gulf. In regard to genetic diversity effects, OMEGA results suggest that the effective population size (ratio N_{eT}/N_{eW}) would likely be reduced under both production scenarios, and the effective size of the mixed population would be near or slightly below sustainable levels of N_e. However, deleterious Ryman-Laikre effects were only found to occur for a small proportion (~<10%) of simulations using the most pessimistic assumptions for the 3-farm simulation, assuming a high level of episodic events. For the 5-farm simulation, Ryman-Laikre effects occur in approximately half of the simulations.

There is considerable uncertainty about this species and further studies are needed regarding stock abundance and population structure to predict the response of wild populations in the Gulf more accurately due to potential genetic effects from escapes.

3.2.2.7 References

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3.2.3 Cobia (Rachycentron canadum)

Genetic effects of culture scenarios for Cobia in the Gulf were evaluated using the OMEGA model. Model methods and results are in Section 3.3.3. A summary of case study results is included at the end of this species profile in Section 3.2.3.6, *OMEGA case study to evaluate genetic risks of farm scenarios.*

3.2.3.1 Range/Description

Cobia (*Rachycentron canadum*) is a highly migratory marine finfish found in tropical and subtropical waters with a near-global distribution (Shaffer and Nakamura 1989). In the U.S., Cobia ranges along the Atlantic coast from Massachusetts to southern Florida and throughout the Gulf, extending from Key West, Florida, to Campeche, Mexico (Dawson 1971, Shaffer and Nakamura 1989). This species grows rapidly during its first two years, with individuals exceeding 2 kg within the first year (Franks et al. 1999). Cobia can be found in both offshore and nearshore environments and are known to be attracted to buoys, piers, and artificial structures (Biesiot et al. 1994, Franks et al. 1999, GSMFC 2019).

Cobia is an important species for recreational fisheries in the Gulf, with approximately 90% of catches attributed to recreational landings, primarily in Florida and Louisiana (Williams 2001). While Cobia is also landed in commercial fisheries, these catches are largely incidental (Williams 2001). Total catches (landed plus discards) in the Gulf have fluctuated between 1,700 and 3,000 metric tons from 2000 to 2018, and the modeled spawning stock biomass estimates varied between approximately 3,200 mt and 4,900 mt, with an average of 4,020 mt (SEDAR 2020). Cobia in the Atlantic and Gulf are managed as separate stocks. In the Gulf, they are managed federally under the Coastal Migratory Pelagic (CMP) Resources Fishery Management Plan by the Gulf and South Atlantic Fishery Management Councils which also includes King Mackerel and Spanish Mackerel (GSMFC 2019).

Image from NOAA Fisheries

3.2.3.2 Biological Characteristics

Cobia have a lifespan of up to 15 years, and reach a weight of up to 68 kg (the largest recorded catch weight as of 2019). However, in the Gulf the maximum observed age is 11 years (GSMFC 2019). Sexual dimorphism in size has been noted, with females reaching an average fork length (FL) of 1,050 mm and a maximum age of 11 years, while males have an average FL of 952 mm and a maximum age of 9 years (Franks et al. 1999). Both sexes are believed to reach 50% sexual maturity by age 2 and 100% maturity by age 3, at which point they are approximately 100 cm in length and weigh about 13.0 kg (SEDAR 2020). Growth rates are fastest in water temperatures exceeding 28°C (GSMFC 2019).

Cobia spawn in the Gulf from April to September and females are batch spawners with batch fecundity estimates ranging from 377,000 to 1,980,500 eggs (Biesiot et al. 1994). Mean relative fecundity is reported to be between 29.1 ± 4.8 and 53.1 ± 9.4 eggs/g ovary-free body weight (Brown-Peterson et al. 2000). Spawning intervals vary, with females in the north-central Gulf spawning every 5 days, and those in the western Gulf spawning once every 9 to 12 days (Brown-Peterson et al. 2000). Individual females may only spawn for a portion of the overall spawning season (Brown-Peterson et al. 2000). Spawning occurs both in nearshore regions and along the continental shelf 50 to 90 km offshore (Ditty and Shaw 1992, Brown-Peterson et al. 2000).

Cobia eggs hatch in approximately 24 hours at 29°C, with eggs and larvae typically found in the upper meter of the water column (Ditty and Shaw 1992). The pelagic larval phase lasts about 30 days, after which larvae transition to the juvenile stage at around 20 mm SL (Ditty and Shaw 1992). Juveniles are mainly found in inshore coastal areas such as beaches, river mouths, barrier islands, and bays (GSMFC 2019). Adults are commonly found in shallow coastal waters, but they are also known to associate with floating debris like *Sargassum* and artificial structures such as oil and gas platforms (Shaffer and Nakamura 1989, Ditty and Shaw 1992, Gallaway et al. 2021). They can be solitary or occur in small groups and are often seen in the presence of larger fish, sharks, and sea turtles (GSMFC 2019, Gallaway et al. 2021).

Cobia migrate to southern Florida in late fall and early winter, and return to the northern Gulf coast spawning and feeding grounds in the spring and summer. From March to October, they are commonly found in northwest Florida, Alabama, Mississippi, and southeast Louisiana (Biesiot et al. 1994, Franks et al. 1999). It is suggested that mixing between Atlantic and Gulf Cobia may occur in the Florida Keys during the winter (Williams 2001). This is supported by tagging studies that show 1% of tagged fish from the Atlantic and Gulf being recaptured in the other region (Perkinson and Denson 2012).

3.2.3.3 Population Structure

The population structure of Cobia (*Rachycentron canadum*) in the Gulf and the Atlantic is complex, with evidence suggesting genetic structure between populations near the state border between Florida and Georgia (Perkinson et al. 2019, SEDAR 2020). In a study combining tagging and genetic analyses, Perkinson et al. (2019) identified two distinct stocks along the U.S. coastline using 10 microsatellite loci. One stock extended from Texas to Hobe Sound, Florida, on the east coast, while the second stock ranged from Savannah, Georgia, to the Chesapeake Bay, Virginia. The transition between these two stocks was believed to occur between Cape Canaveral and northern Georgia, although fine-scale structure within this zone has yet to be fully resolved (Perkinson et al. 2019).

Within the northern Atlantic stock, Darden et al. (2014) found low but significant genetic differentiation between inshore and offshore populations. Cobia collected offshore of South Carolina and North Carolina were genetically homogenous, while those from inshore areas in South Carolina and Virginia were distinct from each other and from the offshore group. The factors driving this genetic structure are unclear, but may be linked to migratory behaviors and site fidelity to specific spawning aggregations (Darden et al. 2014). More research is necessary to better understand these connectivity patterns.

Further investigation is also needed to clarify the migration routes of the population near the Georgia-Florida boundary and the segment that migrates south along Florida's eastern coast into the Gulf (GSMFC 2019). High-resolution genetic or genomic studies across the Cobia's Gulf range would provide valuable insights into the genetic risks posed by potential aquaculture escapes.

3.2.3.4 Aquaculture

Cobia has attracted interest for aquaculture due to its ability to spawn in tank settings with high fecundity, adapt to tank and net pen environments, grow rapidly under culture conditions, and accept commercial feed (Holt et al. 2007, Benetti et al. 2021). However, these same traits have posed challenges for the expansion of commercial Cobia aquaculture. The species requires high-energy, high-protein diets to maintain the rapid growth that makes it a commercially viable species. Commercial culture has operated for Cobia in many regions around the world including Taiwan, China, Vietnam, Belize, Mexico, Bahamas, Philippines, and Panama and has been explored in the U.S. (FAO 2009). However, growth in commercial aquaculture of this species slowed in 2012-2013. Benetti et al. (2021) attribute this decline to challenges with culturing protocols, difficulties in meeting Cobia's specific environmental and nutritional needs, and the challenges of maintaining broodstock on a commercial scale.

Cobia can be induced to spawn volitionally in tanks through photothermal manipulation, which mimics wild spawning conditions or through hormonal methods (Holt et al. 2007). Larval and early juvenile stages are typically reared in tanks or onshore ponds before being transferred to offshore cages (Liao et al. 2004, Weirich et al. 2004). Both nearshore and offshore cages are used in global grow-out production, but stocking densities must be carefully managed, and optimal water conditions (clean water, high flow rates, favorable temperatures) are essential to reduce grow-out times and minimize disease outbreaks (FAO 2009, Wu et al. 2020). Even under optimum conditions growth in Cobia is variable. Benetti et al. (2010) reported that growth varied between 3.5 and 6 kg at two sites over similar time scales. A review by Liao et al. (2004) also reports similar growth rates with harvest weights of 6–10 kg after 1 to 1.5 years. However, growth rates also vary significantly between individuals, and vary by culturing conditions with faster growth observed at lower stocking densities and higher temperatures. Despite its potential, Cobia's high nutritional and environmental demands drive up production costs (Benetti et al. 2021).

Although Cobia holds promise for aquaculture, the high production costs and the need to balance growth rates with nutritional and infrastructure requirements present challenges. As of 2019, Panama was the only commercial-scale producer of Cobia in the Americas (Benetti et al. 2021). In that program, Cobia spawn year-round, and a family-based breeding program has been implemented to improve the quality of offspring. Genotypic analyses have also been implemented to improve selection on aquaculture traits such as growth, fillet yield, and feed conversion ratios (Benetti et al. 2021). Survival in pens is not known but given requirements and disease susceptibility, it is assumed mortality in cages is higher than other species.

3.2.3.5 Considerations on genetic risk to wild conspecifics

The relatively early maturity of Cobia (50% reaching maturity by age 2) suggests that some fish in aquaculture cages may spawn before harvest, particularly males, which tend to mature earlier (Williams 2001). However, since many aquaculture operations harvest fish within a year, the number of reproductively mature fish in cages is likely to be small. The species' distribution, which includes both inshore and offshore areas, increases the likelihood that escaped Cobia may encounter wild conspecifics. Additionally, Cobia’s known tendency to aggregate around artificial structures, such as net pens, may increase this encounter risk. However, this aggregation behavior might provide an opportunity to recover escaped fish following a cage failure.

The absence of defined population structure in the Gulf and the relatively large size of the Cobia stock in this region could help buffer against genetic impacts such as reduced fitness and loss of genetic diversity from escaped cultured fish. Based on available data, the genetic risk posed to wild populations by escaped cultured *R. canadum* is likely low to moderate.

To further mitigate these risks, operations could be sited away from known spawning aggregation areas to reduce the potential for encounters between cultured and wild fish. In addition, maximizing genetic diversity in aquaculture breeding programs and selecting broodstock from regions within the Gulf could further minimize genetic impacts from escapes.

3.2.3.6 OMEGA case study to evaluate genetic risks of farm scenarios

A case study was performed using the OMEGA model to quantify population dynamics of a hypothetical Cobia farm program sited in the Gulf. The OMEGA model was used to simulate the population response of a wild population of Cobia where varying levels of culture-origin fish have escaped from the farm system, resulting in a mixed cultured-wild population where some proportion of the population contains genetics of cultured fish.

Assuming an individual farm harvest production of 3,500 mt, two different production levels were modeled: the equivalent of three farms (hereafter 3-farm) with a total harvest production of 10,500 mt and the equivalent of five farms (hereafter 5-farm) with a total harvest production of 17,500 mt. The captive breeding program was assumed to use local, wild-origin fish and did not employ intentional selection for traits. Detailed modeling of Cobia farm systems under a range of escape scenarios is presented in Section 3.3.3. Conclusions of OMEGA modeling in regard to potential for genetic risk are discussed in Section 3.3.4.3.

The evaluation of Cobia aquaculture relied on an estimate of wild population abundance using the AgeNe model, which estimated adult abundance at about 1.02 million fish. The model results for both 3-farm and 5-farm production scenarios demonstrated a negligible loss in wild population fitness assuming high rate of episodic escape (25% likelihood of loss of one cage in any given year) and an assumed escape rate from program leakage of 0.3% per year. In regard to genetic diversity effects, OMEGA results suggest a low potential for deleterious effects of low N_e. Deleterious genetic diversity loss or Ryman-Laikre effects were not detected in any of the simulations.

To reduce model uncertainty, a stock assessment and genetic study of the wild population are needed to inform natural population dynamics in OMEGA scenarios.

3.2.3.7 References

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3.2.4 Greater Amberjack (Seriola dumerili)

3.2.4.1 Range/Description

The Greater Amberjack, *Seriola dumerili*, is a reef-associated species with a global distribution in subtropical and temperate waters (Manooch and Potts 1997, Main et al. 2019). These fish are found from the coastal pelagic zone to deep reef drop-offs, ranging from the surface to depths of up to 355 meters (Gallaway et al. 2021, and references therein). In the United States, *S. dumerili* inhabits waters from North Carolina to the Gulf. The South Atlantic Fishery Management Council divides Greater Amberjack into two management regions: Atlantic and Gulf, with a boundary between the two stocks running through the Dry Tortugas and the Florida Keys to the coast of Florida (SEDAR 2014).

Greater Amberjack are important to both recreational and commercial fisheries in the Gulf (Thompson et al. 1999). However, fishing pressure has led to declining estimates of total and spawning stock biomasses of *S. dumerili* since the 1950s. In 1989, Greater Amberjack, along with Almaco Jack, Lesser Amberjack, and Banded Rudderfish, were added to the Gulf Reef Fish Fishery Management Plan (SEDAR 2020). The most recent stock assessment estimates (2018) indicate a total biomass of 4,850 mt and an abundance of 1.385 million fish, with a spawning stock biomass of 2,432 mt, which are among the lowest estimates on record. Average recruitment from 2009 to 2018 was also the lowest since the dataset began in 1970 (SEDAR 2020). Based on the conclusions from the recent stock assessment, the Gulf Greater Amberjack stock remains overfished and is undergoing overfishing (SEDAR 2020).

Interestingly, a recent study found that a significant number of Greater Amberjack are associated with offshore oil platforms in the Gulf which act as aggregation structures for various fish species (Gallaway et al. 2021, and references therein). The abundance of Greater Amberjack varied by platform depth, with fish found at platforms between 30 and 300 meters deep. The majority of these fish were located in the Louisiana state management zone where deep platforms are common (Gallaway et al. 2021). The number of *S. dumerili* associated with these platforms potentially constituted up to 45% of the known stock, with approximately 336,210 fish (age 2+ years) identified around the platforms in 2017, and 313,602 fish (age 2+ years) in 2018; the decrease in 2018 was due to the removal of 89 platforms (Gallaway et al. 2021). It is uncertain whether

Image from NOAA Fisheries

these fish are accounted for in current stock models and it was recommended in the most recent stock assessment that these fish be incorporated into future models (SEDAR 2020). If they are not currently accounted for, then the abundance of *S. dumerili* may be considerably greater than current estimates.

3.2.4.2 Biological Characteristics

Greater Amberjack exhibits rapid growth, and reach maturation between 2-3 years. They also have high market value for fillet products (Nakada 2008, Main et al. 2019, Zupa et al. 2017). The maximum lifespan of this species was estimated to be 15 years (Murie and Parkyn 2008), and reach a maximum weight at 81 kg (SEDAR 2014). Females grow slightly larger than males, reaching a maximum length of 1,940 mm FL, compared to a maximum length of 1,814 mm for males (SEDAR 2014). This sexual dimorphism results in size-specific sex ratios. (Harris et al. 2007).

In the Gulf, female fish reach 50% sexual maturity at around 900 mm FL. By age class, 4.2% of female amberjack are sexually mature by age 2, 8.6% by age 3, 85.7% by age 4, and 100% by age 6 and older (Murie and Parkyn 2008). There are also data to suggest that a small number of 1-year-old fish can become sexually mature (Murie and Parkyn 2008). Generally, the age and size at maturity for Gulf fish are older and larger than those for female *S. dumerili* in the South Atlantic (SEDAR 2014) where 50% maturity is attained between 719- and 745-mm FL (Harris et al. 2007).

Greater Amberjack are broadcast batch spawners with an annual fecundity of between 18 and 59 million eggs which may be spread out over as many as 14 spawning events during a season (Harris et al. 2007, SEDAR 2014). Spawning is believed to occur offshore and at two known spawning locations: 1) off the Louisiana coast (for the Gulf stock) and 2) off the Florida Keys (for the Atlantic stock) (Hargrove et al. 2018). The spawning season extends from March to May, although peak spawning periods may vary between these sites (Gulf) (Wells and Rooker 2004, Murie and Parkyn 2008, SEDAR 2014). Spawning behaviors vary in this species, with some individuals migrating to spawning aggregations, while others spawn within their smaller home range (Gallaway et al. 2021).

Following spawning, eggs hatch in approximately 35 hours at water temperatures between 23.1 and 23.7°C (Masuma et al. 1990). While not well characterized, the pelagic larval duration is estimated to last 30 days (Hasegawa et al. 2020). Juveniles between 3 and 210mm SL are found in association with *Sargassum* drifting offshore. When juveniles are between 5 and 6 months of age, or between 200 and 300mm TL, they start to transition from the *Sargassum* to demersal habitats such as reefs and rocky areas (Wells and Rooker 2004, Harris et al. 2007). Subadults become associated with various structures at sizes greater than 400 mm SL (Manooch and Potts 1997, Wells and Rooker 2004, SEDAR 2014). Wells and Rooker (2004) found a greater abundance of *S. dumerili* offshore compared to inshore areas.

Based on tagging studies, Greater Amberjack generally exhibit limited dispersal, although individual fish are capable of moving over 1,000 km. McClellan and Cummings (1997) found that out of 569 recaptured tagged fish in the Gulf, 54% were taken within 46.3 km of the release site, and 92.7% were taken within 185.2 km (or 100 nautical miles). Additionally, 31% of the Gulf fish were recaptured within 90 days, with the time at liberty extending up to 6 years (McClellan and Cummings 1997). This study also detected low levels of movement from the Atlantic to the Gulf (1.3% out the tagged fish in the Atlantic) and from the Gulf to the Atlantic (1.6% of the tagged fish). Murie et al. (2011) found that recaptured tagged *S. dumerili* (n=169) moved an average of 69.54 km with a median distance of 8.0 km. While most fish stayed within a smaller range, a few dispersed over much longer distances, for example, up to 1,500.6 km (Murie et al. 2011).

3.2.4.3 Population Structure

Several population genetic studies on Greater Amberjack in the Gulf have raised more questions than answers regarding the connectivity between the Gulf and Atlantic stocks and among locations within the Gulf. Gold and Richardson (1998) used mitochondrial restriction sites to examine Greater Amberjack from 11 locations in the Gulf and the U.S. South Atlantic coast. They found low but significant heterogeneity when comparing pooled samples from the Florida Keys and South Atlantic to those from the Gulf. However, they did not detect significant spatial haplotype patterns among locations in the northern Gulf.

Murie et al. (2011) found low but significant overall differentiation among *S. dumerili* populations in the Gulf using 15 microsatellite markers. They observed significant but low levels of genetic structure between reported spawning populations in the northwest Gulf (off Louisiana) and the Florida Keys. The authors suggested that while their results indicate a low degree of differentiation within the Gulf and between the Gulf and Atlantic, the data do not strongly support independent demographic populations in the Gulf and Florida Keys. They also noted that traditional population genetic approaches may have limitations in estimating connectivity among these populations.

Crandall et al. (2013) used a non-genetic approach and detected significant differences in otolith shape between age-3 fish in Louisiana and Florida. While they suggested some differentiation between these locations, their overall analysis supported the existence of one stock within the Gulf. More recently, Hargrove et al. (2018) examined connectivity among populations in the Gulf and Florida Keys using 11 microsatellite markers. They found very low but significant levels of genetic differentiation, with pairwise F_{ST} estimates ranging from 0.002 (between fish sampled in Louisiana and spawning fish in the Florida Keys, Atlantic) to 0.016 (between spawning fish in Louisiana and western Florida). Like Murie et al. (2011), Hargrove et al. (2018) concluded that genetic data did not support independent demographic populations between the Gulf and Florida Keys, nor did it support broad panmixia. Instead, the results suggested modest levels of genetic exchange (few individuals per generation), consistent with tagging data.

Studies utilizing a larger number of markers, such as SNPs or genomic data, might better resolve connectivity patterns between the Gulf and Atlantic stocks and among regions in the Gulf. A 2024 study by Katirtzoglou et al. using three types of genetic markers (mitochondrial control region sequences, microsatellites [n=10], and SNPs [n=1051]) identified three genetically distinct groups (one in the Mediterranean and two in the Atlantic) not detected in earlier studies. A similar approach may effectively resolve populations along the U.S. Gulf and Southeast Atlantic coasts.

3.2.4.4 Aquaculture

Commercial aquaculture of *S. dumerili* is well-established in Japan, where it, along with *S. quinqueradiata*, represents a significant portion of finfish aquaculture (Nakada 2008). The species is also widely cultured in the Mediterranean (Sicuro and Luzzana 2016) and is being considered for further aquaculture expansion across Europe (https://www.diversifyfish.eu). However, in the United States, there is currently no active research or commercial production of Greater Amberjack (Main et al. 2019).

Greater Amberjack is regarded as a promising candidate for aquaculture due to its fast growth rate, high survival during grow-out, efficient feed conversion, high-quality flesh, and established market demand (FAO 2016, Main et al. 2019). However, aquaculture of this species poses significant challenges compared to other *Seriola* species, primarily due to inconsistent reproduction and the unreliable or low availability of juveniles for grow-out (Sarih et al. 2018, Fakriadis et al. 2020). Even in regions where Greater Amberjack aquaculture is more established, such as Japan and the Mediterranean, closed life-cycle fingerling production is still limited and not yet widely practiced on a commercial scale (Hamasaki et al. 2009; FAO 2016). Instead, operations often rely on capture-based aquaculture, where wild-caught juveniles are raised to harvest size. Efforts continue to improve culture-based reproduction to reduce reliance on wild populations (Hamasaki et al. 2009; FAO 2016).

Hormonal treatments are frequently employed to induce spawning in *S. dumerili* (Zupa et al. 2017), although some locations have reported success with volitional spawning in broodstock fish. Spontaneous spawning has been observed in Japan (Kawabe et al. 1998) and the Canary Islands (Jerez et al. 2006), but not yet in the Mediterranean region (Sarih et al. 2018). A study by Fakriadis et al. (2020) in the Mediterranean found that females reared in sea cages exhibited a higher potential for reproductive success than those reared in tanks, where fertilization success was nearly 0%. Males reared under both conditions showed reduced sperm production compared to wild males, but tank rearing did not further negatively affect sperm quality parameters compared to sea cage rearing (Fakriadis et al. 2020).

Grow-out durations for *S. dumerili* vary depending on the desired market size and the water temperature where the fish are cultured. In Japan, *S. dumerili* reach 6.0 kg in 2.5 years, while in the Mediterranean, they reach 1 kg after 1 year, 3 kg after 2 years, and 6 kg after 3 years (FAO 2016).

3.2.4.5 Considerations on genetic risk to wild conspecifics

When evaluating the genetic risk posed by cultured *S. dumerili* escapes on wild populations, several critical considerations must be addressed, including the depressed size of the stock in the Gulf and the species' tendency to aggregate around structures. The size and health of the wild population are essential components to assessing the risk from aquaculture escapes. The Gulf stock is currently considered overfished and undergoing overfishing, with its abundance and spawning stock biomass low relative to other species.

If current stock estimates are accurate, the genetic diversity of this stock may already be reduced, thereby decreasing the natural population's capacity to withstand or buffer further losses of genetic fitness and diversity through the introgression of cultured fish. However, there is a degree of uncertainty in these stock assessment estimates due to the large numbers of Greater Amberjack estimated to occur around Gulf oil platforms and whether these fish have been accounted for in current stock models. If stock assessments have underestimated the population size by not including these platform-associated fish, the next stock assessment may estimate a larger Gulf stock, which could potentially better withstand a greater level of introgression from cultured fish.

The tendency of *S. dumerili* to aggregate around structures increases the likelihood of wild fish encountering escaped cultured fish, as pen cages may act as additional aggregation sites for wild populations. Importantly, the tendency of larger fish to aggregate around structures could lead to escaped fish staying in close proximity to the net pens. This behavior might provide an opportunity for the recapture of escaped fish, provided they can be distinguished from wild individuals.

Given the age and sizes at which this species reaches sexual maturity, it is likely that some fish will be sexually mature prior to harvest. If volitional spawning occurs in net pens, gametes and larvae could be transported away from offshore cages in association with drifting *Sargassum* mats, which would provide another habitat to potentially mix with wild larval *S. dumerili*.

Another important consideration is the pattern of connectivity among stocks (Gulf and Atlantic) and within the Gulf, where some questions remain. Gene flow between the Gulf and the Atlantic may provide a mechanism for restoring genetic diversity and offer additional buffering capacity against detrimental genetic impacts from escaped cultured fish. However, if dispersal between stocks is occurring at rates of only a few individuals per generation, this mechanism may not operate on a timescale relevant for mitigating impacts from aquaculture escapes. On a regional level, if future studies resolve and identify spatially-based genetic structure in the Gulf, individual populations may be more susceptible to losses of local adaptation and genetic diversity from aquaculture escapes.

While uncertainties remain regarding stock abundance and population structure, the available information suggests a high genetic risk to wild populations from escaped cultured *S. dumerili*. Using wild-caught broodstock from the Gulf, ideally collected near planned offshore operations, may help reduce potential impacts. Maintaining high genetic diversity in hatchery-produced juveniles will also be particularly important. Controlling reproduction in captivity is key to preventing hatchery gametes and larvae from entering the natural population. Additionally, developing approaches to confer sterility in hatchery-produced fish would mitigate genetic risks to natural populations.

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3.2.5 Florida Pompano (Trachinotus carolinus)

3.2.5.1 Range/Description

The Florida Pompano (*Trachinotus carolinus*) is a subtropical coastal pelagic species inhabiting waters between 17°C and 32°C (Finucane 1969). It has a broad distribution ranging from Massachusetts to Brazil (Gilbert 1986, Main et al. 2007, FAO 2016). Despite its wide range along the eastern U.S. coast and into the Gulf (including seasonal presence along the Mississippi, Alabama, Louisiana, and Texas coasts; Gunter 1958, Bellinger and Avault 1970, Wheeler et al. 2002), over 90% of U.S. landings for this species occur in Florida (Murphy et al. 2008, Weirich 2021).

T. carolinus is highly valued in both commercial and recreational fisheries, with market demand exceeding the wild-caught supply, leading to a high market value (Main et al. 2007, Murphy et al. 2008). Managed at the state level, the Florida Fish and Wildlife Conservation Commission has implemented minimum size and bag limits for recreational fisheries and vessel limits for the commercial fishery (Murphy 2008). A stock assessment for the Gulf population in 2008 indicated a stable population abundance of about 500,000 to 600,000 fish from the 1990s to early 2000s. Associated biomass estimates from that time suggested that abundance exceeded the minimum size threshold for maintaining both Atlantic and Gulf stocks (Murphy et al. 2008).

This species inhabits both nearshore zones along sandy beaches with high salinities and bays and estuarine zones with lower salinities (Murphy et al. 2008). Juvenile fish are found in greater densities along the coastal surf zone or in unvegetated areas of estuaries (Gunter 1958, Solomon and Tremain 2009).

3.2.5.2 Biological Characteristics

Florida Pompano are known to exhibit schooling behavior (Schrandt 2015). While they inhabit zones with a wide range of salinities, inshore, these fish prefer turbid places and avoid clear waters (Seyoum 2017). This species is cold intolerant and avoids areas where water temperatures fall below 20°C (Weirich 2021).

Image from Texas Parks and Wildlife Department

Male and female *T. carolinus* become sexually mature between one and three years of age, and generally grow to maximum weights ranging from 0.7 to 2.3 kg (Gilbert 1986). Murphy (2008) reported that females grow faster and reach larger sizes than males. In a sampling survey, maximum female age of 7 years was reported, with maximum female length of 481 mm FL (in a 4-year-old female), while maximum male age of 6 years was reported, with maximum male length of 410 mm FL (in a 5-year-old male fish) (Murphy 2008).

Florida Pompano grow rapidly, reaching up to 280 mm FL in a year. Female fish reach 50% maturity around age 1 (between 300- and 325-mm FL), and it is suspected that males likely mature within their first year (Murphy 2008). Fecundity estimates range between 133,000 and 800,000 eggs per season (Murphy 2008, and references therein), and this species appears capable of batch spawning every 3 to 4 days (Hoff et al. 1978).

Although information on spawning in the wild is limited (Weirich 2021), it is thought that *T. carolinus* spawn offshore (Gunter 1958). This is inferred from the presence of larvae < 2 weeks old sampled 8 to 24 km offshore (Finucane 1969 and references therein). Spawning and larval growth favor temperatures between 25 and 30°C in the Gulf (Weirich 2021). Florida Pompano are believed to have prolonged spawning seasons in this region, as evidenced by juveniles (approximately 15 mm in length) detected from June to October (Finucane 1969). Additionally, *T. carolinus* may spawn year-round in the warmer regions of the Gulf and Caribbean Sea (Berry and Iversen 1967).

Hatching time for eggs varies with temperature, ranging from 25 to 38 hours (Hoff et al. 1978). Newly hatched larvae possess a yolk sac, which is quickly reabsorbed, and feeding begins three days post-hatching (dph) (Hoff et al. 1978). While the pelagic larval duration was not explicitly stated, Hoff et al. (1978) found that at 24 dph, fish had obtained the complete coloration of juvenile Florida Pompano. This finding aligns with Finucane (1969), who estimated that there was probably a month or less between spawning and the appearance of juveniles off beaches in the surf zone. Early in post-settlement, Pompano (under 20 mm standard length) recruit to coastal beach zones, and then leave when they reach 80 to 120 mm SL and/or when the water cools below 19°C (Solomon and Tremain 2009, and references therein).

Dispersal in this species is not well understood, but a limited study by Berry and Iversen (1967) found that *T. carolinus* tagged in Florida were capable of moving up to 164 miles from the point of tagging.

3.2.5.3 Population Structure

There are very few studies to date on the population structure of Florida Pompano in the Gulf. Murphy (2008) reviewed results from a study conducted by Fish and Wildlife Conservation Commission-Fish and Wildlife Research Institute (FWC-FWRI) scientists that examined the genetic structure of *T. carolinus* collected from Brownsville, TX (and nearby waters of Mexico), Apalachicola, FL, Tampa Bay, FL, Stuart, FL, and Bogue Sound, NC. Results based on 13 microsatellite markers indicated that Florida Pompano comprised a single genetic stock within coastal U.S. waters and showed no isolation-by-distance pattern or differentiation between Gulf and Atlantic populations. However, the study did detect significant divergence between the above locations and specimens collected from Puerto Rico. This strong divergence between samples in Florida (Tampa Bay) and Puerto Rico was also detected by Seyoum et al. (2017).

The statistical power of the work described by Murphy (2008) is difficult to assess, and no manuscript detailing the approaches and sample size of that study was found. Further study to identify more subtle signals of genetic structure or local adaptation may be warranted but will depend on greater detail being provided from the FWC-FWRI study.

3.2.5.4 Aquaculture

There has been longstanding interest in culturing Florida Pompano due to their high growth rate, acceptance of commercially prepared diets, and adaptability to a broad range of culturing approaches (Riley et al. 2009). Aquaculture efforts date back to the 1950s with the grow-out of wild-caught individuals in ponds, impoundments, and tanks (Finucane 1969, Smith 1973, and references therein). Early efforts also included attempts to culture this species in cages (Smith 1973). After initial efforts encountered challenges in developing reliable and commercially feasible culture practices, there was renewed interest in *T. carolinus* culture following advancements in culturing other species (Weirich et al. 2021). Currently, commercial offshore net pens are being used for culture of this species in a few locations (e.g., Panama), and culture research is ongoing in Florida, Alabama, and Texas (Weirich et al. 2019).


Image from Ken Riley, NOAA Fisheries

Broodstock can be acquired from the wild or grown on-site (F1 or F2 broodstock) and have consistent year-round egg production, spawning volitionally in tanks following temperature and photoperiod conditioning and hormone implantation (Riley et al. 2009, Wills et al. 2023). Strip spawning of conditioned and hormonally implanted fish may also be used (Riley et al. 2009). For approximately half of the hormonally induced fish spawned (11 out of 20 fish). Within that group, 3 female and 2 male fish contributed to 95.8% and 94.7% of the 45-day post-hatching offspring, respectively. This suggests that reduced effective brood fish population sizes could lead to a significant loss of genetic diversity in hatchery offspring under volitional spawning approaches.

Under laboratory conditions, eggs hatched approximately 30 to 36 hours post-fertilization when held between 24 to 26°C. While no cannibalism was reported by Riley et al. (2009), they noted that aggressive larvae reached metamorphosis earlier than non-aggressive larvae, which may be an example of, or may lead to, unintended selective processes for this species in a hatchery setting.

Grow-out of Florida Pompano has been accomplished in both recirculating systems and net cages. Smith (1973) reported stocking juveniles at 7 g in cages, while Weirich et al. (2021) mentioned initial stocking sizes of 10 to 15 g. After the initial stocking, size grading may be needed when the fish reach 100 to 150 g prior to the remaining grow-out duration (Weirich et al. 2021). Survival from this point to harvest is reported as good (Weirich et al. 2021).

Smith (1973) noted that grow-out duration was influenced by stocking density, with fish seeded at 7 g reaching 454 g within a year, taking between 46.8 and 50.8 weeks to harvest. Finucane (1969) had earlier reached a similar conclusion about *T. carolinus* in ponds, finding that they reached market size in approximately a year. Likewise, Weirich et al. (2019) reported that these fish reach market size in under a year (~275 days).

This species has remarkably quick sexual maturation, with significant proportions of males (nearly all) and females (approximately 50%) reaching reproductive maturity in under a year (Murphy et al. 2008). As such, spawning maturity coincides closely with harvest timing. There is market potential for smaller, "pan-size" Florida Pompano that may be harvested earlier (Smith 1973), or across multiple size categories (e.g., 350-450 g, 450-600 g, 600-800 g) to account for growth variation in the cultured fish (Weirich et al. 2021). Harvesting fish at smaller sizes may reduce the proportion reaching sexual maturity prior to harvest.

Interestingly, Smith (1973) reported that Florida Pompano released after cage-conditioning remained and fed in the area of the cages. Small fish that escaped stayed near the cages until they were preyed upon by the large assemblage of wild fish that were also found in proximity to the cages, which included both those feeding on excess pellets and predators feeding on the smaller fish. Even when the cages were removed, the released Florida Pompano stayed in proximity to the dock near where the cages had been placed, although the fish were reported to be very thin. This phenomenon was also detected in escaped *T. carolinus* off the Atlantic coast, near Plantation Key, Florida (Smith 1973). While behaviors may vary in offshore grow-out sites, it is possible that escaped Florida Pompano may initially remain near the pen structure in some situations, which could help recapture escaped fish during grow-out.

Based on research to date, NOAA Fisheries has determined that Florida Pompano is ready for commercial aquaculture, and that culture of this species would promote the expansion of a domestic aquaculture industry (https://coastalscience.noaa.gov/news/noaa-identifies-florida-pompano-as-commercially-ready-for-u-s-marine-aquaculture/, accessed 04-2024). However, significant challenges to commercial feasibility remain, particularly concerning growth rates, feed conversion, and maturation timing. Additionally, the market potential for a farmed product needs to be determined (Weirich 2021, Wills 2023).

3.2.5.5 Considerations on genetic risk to wild conspecifics

Considering the early maturation of this species, its distribution along the coast, and probable offshore spawning, it is likely that any escapes from culture would encounter wild conspecifics and have opportunities to interbreed. While the presence of a large, homogenous population in the Gulf may help buffer genetic impacts from escaped cultured *T. carolinus*, there is uncertainty in these stock characteristics. More research is needed regarding stock abundance and distribution to determine if biomass levels for this species have been maintained over time. Additionally, fine-scale genetic studies would provide more evidence to support the hypothesis that Florida Pompano are a randomly mating species throughout its range or demonstrate regional-level structure. These indicators of population health are critical to determine if escape events may result in genetic effects from encounters with wild populations.

Based on the above information, there is a moderate genetic risk to wild populations from escaped cultured *T. carolinus*, with a high degree of uncertainty based on available information on stock characteristics. However, the use of wild-caught broodstock may help reduce these impacts to a lower-moderate level, particularly if the broodstock program can maintain high genetic diversity levels in hatchery-produced fish. This may be challenging using volitional spawning approaches, based on the genetic parentage results mentioned in the *Aquaculture* section.

For aquaculture of Florida Pompano, selective breeding for growth and other factors may ultimately be necessary for a commercially feasible program. Methods to delay maturation or create sterile lines would also support improved growth rates while reducing the risk for maturation and gamete releases before harvest, and reduce the risk of genetic impacts from escaped fish on wild populations. Further, it will be important to determine if the reported Florida Pompano behavior of remaining near the pen structure following escape similarly applies to offshore operations. This tendency may provide a way for escapes to be recaptured or fished and removed, which could be an important mitigation strategy under some situations.

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3.2.6 Black Sea Bass (Centropristis striata)

3.2.6.1 Range/Description

Black Sea Bass (*Centropristis striata*) are a commercially valuable warm temperate Serranid species, with a range extending from Maine to the Florida Keys and into the Gulf (Drohan et al. 2007, Musick and Mercer 1977). In the Gulf, this species has been reported from northern Florida to Texas (Bowen and Avise 1990), though they are most commonly found between Tampa and Apalachee Bays in Florida (Hood et al. 1994, and references therein). There are few reports of Black Sea Bass in the western or central Gulf. While Finucane et al. (1978) reported *Centropristis* larvae off the coast of Texas, those samples were not identified to species. This species can live up to 12 years but more commonly has a maximum lifespan of 9 years, with most individuals in a population being much younger (Watanabe 2021, SEDAR 2023). A 2023 stock assessment indicated that the South Atlantic stock, which extends into the Florida Keys, had experienced a significant decline in abundance and is currently overfished and undergoing overfishing, with an estimated total biomass of about 3,000 mt in 2021. This marked a change in status compared to the 2018 assessment, which indicated the stock was not overfished (SEDAR 2023). No specific stock data for the Gulf were identified.

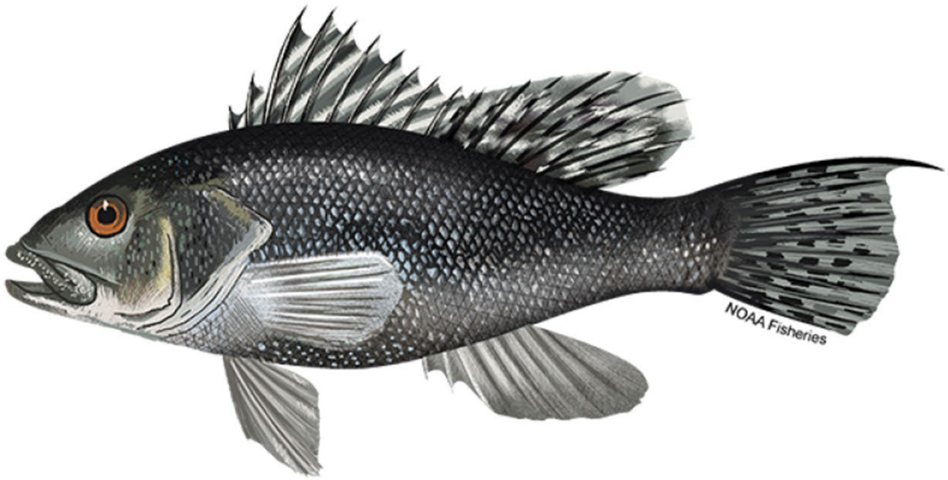

Image from NOAA Fisheries

In the Atlantic, the Black Sea Bass fishery is managed in both state and federal waters by fishing councils (e.g., Mid-Atlantic Fishery Management Council, Atlantic States Marine Fisheries Commission) while NOAA implements rules and regulations for this fishery (NOAA Fisheries; https://www.fisheries.noaa.gov/species/black-sea-bass/management). In the Gulf, the fishery is managed at the state level, where bag limits and rules on minimum sizes have been implemented, for example, in Florida (Florida Fish and Wildlife Conservation Commission; https://myfwc.com/fishing/saltwater/recreational/black-sea-bass/).

3.2.6.2 Biological Characteristics

As reviewed in Hood et al. (1994), Black Sea Bass are considered non-migratory and become residential once established on a particular reef. Adult fish aggregate near limestone and coral outcroppings or submerged reefs at depths of 7.3 to 18.3 meters, while juvenile and subadult fish are found along the deeper areas of estuaries along the Florida Gulf coast (Hood et al. 1994, and references therein, Drohan et al. 2007). This species does exhibit some seasonal inshore/offshore movements thought to be associated with different life stages and spawning behavior. As water temperatures cool, Black Sea Bass move from estuaries to offshore locations along the continental shelf (Drohan et al. 2007).

This species broadcast spawns in the Gulf from December to April (Hood et al. 1994), and fertilized eggs and pelagic larvae drift offshore to develop. Early aquaculture research indicated that eggs hatch approximately 8 to 12 hours post-fertilization (Roberts et al. 1976). In the same study, the larval duration to metamorphosis and settlement was found to be 24 days (Roberts et al. 1976). However, Edwards et al. (2008) used a pelagic larval duration of 20 to 35 days in a study modeling early dispersal patterns for this species. Juveniles settle nearshore at sizes greater than 0.5 inches, and then move into bays, sounds, and estuaries (Watanabe et al. 2021).

Black Sea Bass are protogynous hermaphrodites, with females becoming sexually mature between 1 and 3 years of age and then transitioning to males, often between 2 and 4 years of age when they are larger. Hood et al. (1994) found that males became more common than females once fish were larger than 210 mm, corresponding to an age of 4 years. Within the Gulf, Black Sea Bass may grow quickly in their first year, reaching an average of 122 mm. The maximum size of this species within the Gulf is 330 mm and a maximum age of 7 years (Hood et al. 1994). The authors also reported that females outnumbered males in their study by a ratio of 1.5:1 (Hood et al. 1994).

3.2.6.3 Population Structure

Currently, this species is managed as three separate stocks: two stocks along the U.S. Atlantic coast (*Centropristis striata striata*), and one in the Gulf, with the Gulf stock being considered a separate subspecies (*C. striata melana*) (Roy et al. 2012). The subspecific classification was supported based on several morphometric, meristic, and osteological studies (Drohan et al. 2007, and references therein). This designation was further supported by Bowen and Avise (1990), who reported a phylogenetic distinction between the Gulf and the Atlantic populations based on a restriction enzyme analysis of mitochondrial DNA, and by Roy et al. (2012), who also found deep differentiation between the Gulf and Atlantic samples using mitochondrial sequence data. Interestingly, Black Sea Bass in the Gulf were reported to be smaller (maximum length of 330 mm) and shorter-lived (maximum age of 7 years) than the Atlantic populations (340-430 mm, and 9–10 years, respectively) (Hood et al. 1994, and references therein).

3.2.6.4 Aquaculture

Black Sea Bass aquaculture research has primarily focused on land-based recirculation aquaculture systems (RAS) (Watanabe et al. 2021), making the near-term consideration of this species for offshore cage culture uncertain. Market potential does exist, with aquaculture products targeting the fresh or live markets for a range of fish sizes, from 0.5 lbs. to over 2 lbs. (Watanabe et al. 2021). Based on experimental grow-out in RAS, Black Sea Bass were able to grow to an average size of 568 g (range of 270 to 1,100 g) in 20 months, aligning with marketable size for this species. It is unknown how this time to harvest would vary if fish were placed in net pens in the Gulf.

Most aquaculture studies report on the capture and subsequent spawning of wild-caught broodstock, which requires hormonal induction for females to spawn or physical strip spawning of the animals (Roberts et al. 1976, Howell 2003, Watanabe et al. 2021). While some manipulations may accelerate spawning by a couple of months (Howell et al. 2003), no studies have suggested that sexual maturation in captive fish differs from the wild population range of sexual maturation.

3.2.6.5 Considerations on genetic risk to wild conspecifics

The lack of information about Black Sea Bass across numerous aspects, including stock health and abundance, population structure, biology (particularly regarding hermaphroditic transitions under culture settings), and net pen culture methods, leads to a high degree of uncertainty in evaluating the genetic risk posed by escaped cultured Black Sea Bass on wild populations.

Stock abundance and health of Black Sea Bass are not well known within the Gulf, but the neighboring South Atlantic stock has seen a significant decline in recent years. Region-specific direct methods of abundance and age-sampling would provide more information about population structure in the Gulf and the size of the population(s), which is crucial for evaluating genetic risk to wild populations.

Genetic studies have not identified structuring among locations within the Gulf, but the resolution may have been insufficient to detect subtle genetic variation within the sampled range due to the methodologies available at the time. While non-migratory species associated with inshore areas, such as Black Sea Bass, could potentially exhibit a high degree of spatial genetic structure, the relatively long offshore pelagic dispersal of eggs and larvae (20 to 35 days) in this species may prevent genetic structure at smaller spatial scales. Future studies will be important to explore spatial genetic structure among Black Sea Bass populations in the Gulf and to define their distribution in this region, particularly in the central and western portions of the Gulf.

It is also important to better understand the impact of hermaphroditism on recruitment and how the timing may shift under culture settings. If escaped fish are primarily female, as might be expected if grow-out occurs in under 2 years, they may have a better chance of spawning with wild territorial males than if the sexes were reversed. If escaped fish are males (or are close to transitioning to males), behavioral differences between cultured and wild fish may benefit wild males in establishing territorial areas in benthic habitats, leading to lower recruitment of cultured male fish in the wild. However, it would be expected that after some time in the wild, cultured fish may eventually succeed at a rate similar to wild fish. Importantly, if cultured fish retain any trait (e.g., higher growth rate or increased aggression) that might confer an advantage over wild fish, then cultured fish may eventually disproportionately contribute as large males (given the skewed sex ratio with fewer males) to successive generations.

Because offshore culture has not been explored in this species, it is unknown whether the fish would reach maturity prior to harvest in net pens under ambient water temperatures. It is also unknown if fish would be induced to spawn volitionally in the net pens, and thus no conclusion can be made on the risk of gamete or larval escape in a net pen setting. If hormonal treatment and/or strip spawning is still required, there is likely little-to-no risk from these types of escape. However, if sexually mature fish do spawn in the net pens, there is potential for larvae to encounter pelagically distributed wild larvae during portions of the year.

Fish escaping from offshore pens may have an increased likelihood of encountering wild Black Sea Bass during portions of the year when wild juveniles and adults move offshore along the edge of the continental shelf. However, when natural populations shift inshore, and the wild fish become more strongly associated and territorial in the benthic habitat (Gwak 2003), the likelihood of encounters with escaped Black Sea Bass may be lessened with the increased distance.

Based on the above information, if the stock is healthy and not diminished, and if there is low risk of spawning in net pens (based upon currently used spawning approaches and time to maturity), then the genetic risk to wild populations from escaped fish may be moderate-to-low. This is in part because specific habitats and behaviors of wild fish (e.g., use of estuaries for juveniles, territorial behavior in adult males) may favor wild fish over cultured fish. If, alternatively, the stock is not healthy or has been significantly diminished, or if cultured fish develop traits that provide an advantage under natural conditions (e.g., increased growth rate, high level of aggression), then the genetic risk to wild conspecifics may be high from escaped Black Sea Bass.

In either scenario, risk may be reduced if operations source broodstock from the subspecies of Black Sea Bass found in the Gulf, ideally from populations nearby the planned operations, since population structure is not currently characterized. Additionally, maximizing genetic diversity through spawning cross design or broodstock rotation is important for reducing genetic impacts on wild populations from escaped fish, particularly for populations where wild biomass has been reduced or is low.

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3.2.7 Spotted Seatrout (Cynoscion nebulosus)

3.2.7.1 Range/Description

Spotted Seatrout (*Cynoscion nebulosus*) are marine fish commonly found in estuarine habitats, with a range extending from Massachusetts in the Atlantic to the Bay of Campeche in Mexico in the Gulf (Blanchet et al. 2001). Within the Gulf, this species is most densely distributed from the west coast of Florida through Texas (Blanchet et al. 2001). Spotted Seatrout is the most frequently caught recreational fish in the U.S. and the fourth most frequently harvested fish by the recreational fishery (NMFS 2022). Although the Spotted Seatrout supports a small commercial fishery in a few states (Leaf et al. 2017), recreational catches account for 98% of the total harvest (Blaylock et al. 2021).

Management of the Spotted Seatrout occurs at the state level, with states setting varying limits on the number and size of fish that can be retained, with the aim of reducing fishing pressure on this species. These regulations are based on state stock assessments, which have shown varying levels of decline and recovery across different states (Murphy et al. 2011, Leaf et al. 2017, Bohaboy et al. 2018, Jermain 2019, West et al. 2021).

3.2.7.2 Biological Characteristics

Spotted Seatrout often remain within their natal estuaries throughout their 3 to 5 years of life (Lowerre-Barbieri et al. 2013, Seyoum et al. 2018, Blaylock et al. 2021), with few fish recaptured more than 50 km from their tagging locations (Blanchet et al. 2001). Juveniles and adults are associated with various estuarine habitats, including seagrasses, sand, mud, oil platforms, and shell reefs, and are considered omnivorous predators, feeding on crustaceans and fish in their environment (Blanchet et al. 2001). Spotted Seatrout do exhibit sexual dimorphism with larger females than males; this species generally shows a 1:1 sex ratio, although sex biases within individual bays and sounds have been observed (Johnson et al. 2011).

C. nebulosus are batch spawners, with spawning season peaking May to July, though the length of the spawning season can range from five months in Mississippi to seven months in Florida (Brown-Peterson et al. 2002). Males spawn more frequently than females, spawning every 2.2 days compared to every 9.3 days for females (Lowerre-Barbieri et al. 2013). There is also variation in spawning frequency across their geographic range, possibly associated with salinity profiles within different estuaries (Brown-Peterson et al.

Image from South Carolina Department of Natural Resources

2002). Size at sexual maturation varies by estuary location, with 50% sexual maturation occurring between 260 and 295 mm in total length (Brown-Peterson et al. 2002). In some Gulf locations, this can occur by Age-1 (Blanchet et al. 2001), although this ranges between 1 and 3 years of age (Ramsey and Wakeman 1987). Fecundity increases with fish size; for a 1 kg female, annual fecundity may range from 15 to 20 million eggs (Brown-Peterson 2002).

While there is no consensus on preferred spawning habitats for this species, Spotted Seatrout may shift locations to select environmental conditions conducive to spawning success, such as salinities between 7.0‰ and 25.8‰ and temperatures between 24.5°C and 33.5°C. These conditions may occur within bays, nearshore Gulf, offshore, or in open water channels between barrier islands, with the majority of spawning aggregations occurring at depths of 2-10 m (Blanchet et al. 2001).

Following spawning, pelagic eggs hatch between 12 and 24 hours (Fable et al. 1978, Alshuth and Gilmore 1995). Early larval stages (2-6 mm) have been found in both marine and estuarine areas, while larger larvae (6-18 mm) are typically demersal (Blanchet et al. 2001). This demersal period may begin earlier, with Spotted Seatrout eggs and early larvae reported to sink within 48 hours of fertilization, which is thought to increase local recruitment (Gilmore 2002).

3.2.7.3 Population Structure

There have been numerous studies on the population genetic structure of Spotted Seatrout, which have found varying levels of genetic differentiation among locations but are generally consistent with an isolation-by-distance pattern, with some biogeographic breaks where genetic dispersal may be more limited (Gold et al. 1999, Gold et al. 2002, Ward et al. 2007); this has been further supported by tagging studies (Blanchet et al. 2001 and references therein). Using microsatellites and mitochondrial data, Anderson and Karel (2010) found genetic subdivision across three regions (upper-, middle-, and lower-coast) of Texas, with areas of limited abundance generally mirroring the genetic patterns detected.

In a microsatellite study of Spotted Seatrout collected from Grand Isle, Louisiana (westernmost site), four bays in Mississippi, Pensacola, Florida, and Apalachicola, Florida (easternmost site), no significant divergence was detected between Louisiana and the Mississippi-Alabama border (Grand Bay, MS). However, the easternmost site (Apalachicola) was significantly different from all sampled locations, and Pensacola was also significantly different from all sites other than the neighboring Grand Bay, MS (Somerset and Saillant 2014). While no obvious barriers exist between these locations, the authors believed that the greater abundance of Spotted Seatrout across the Louisiana-Alabama region, compared to western Florida, may increase genetic homogenization across that area (Somerset and Saillant 2014).

Seyoum et al. (2018) conducted a study using mitochondrial sequences and 38 microsatellite loci to analyze samples collected across 18 locations from Texas to North Carolina (Atlantic coast), representing most of the species' range. Their results indicated the presence of a western Gulf stock (South Padre Island, Texas to Fort Walton, Florida), an eastern Gulf stock (Apalachicola

Bay, Florida to Biscayne Bay, Florida), and an east coast Atlantic stock (Sebastian Inlet, Florida to Morehead, North Carolina—the most northerly sampled site), with additional patterns of isolation by distance within those three stocks (Seyoum et al. 2018). The authors suggested that Apalachicola Bay is a region marked by intense changes in various environmental conditions within the estuaries (e.g., annual changes to salinity ranging between near freshwater to marine conditions) and has been identified as a region of genetic break in other demersal fish and invertebrates (Seyoum et al. 2018 and references therein).

Genomic analyses may further resolve adaptive variation among these populations (Blaylock et al. 2021). For example, physical and physiological differences exist among Spotted Seatrout populations (Brown-Peterson et al. 2002, Johnson et al. 2011), but it is not known at this time whether those differences may have a genetic basis.

Although there are discrepancies in the genetic studies, the species is managed as a single stock within each state with the exception of Florida, which is divided into a northern and southern stock (Murphy et al. 2011), and Texas, where a regional management approach is being considered (e.g., Lower Laguna Madre; https://tpwd.texas.gov/fishboat/fish/didyouknow/coastal/troutinllm1.phtml), accessed 9-13-23).

3.2.7.4 Aquaculture

Aquaculture programs for Spotted Seatrout are primarily focused on stock supplementation, where juveniles are released to support natural populations, benefiting recreational fisheries. These efforts are led by the University of Southern Mississippi and the Texas Parks and Wildlife Department. In Texas alone, over 133 million juveniles have been produced and released into coastal regions (Blaylock et al. 2021). No domestication efforts are known, and supplementation programs utilize wild-caught broodstock, with 25% of the broodstock exchanged annually to minimize genetic impacts on wild populations (Blaylock et al. 2021).

Two established aquaculture methods, outdoor rearing ponds and recirculating aquaculture systems (RAS), are used to rear Spotted Seatrout larvae and juveniles prior to release (Colura et al. 1976, Blaylock et al. 2005). Spawning broodstock, weighing between 0.5 to 1.5 kg, are kept in groups of 15 to 30 fish with a 1:1 sex ratio (Blaylock et al. 2021). Although hormonal induction of spawning has been developed and used successfully in this species (e.g., Colura et al. 1990), more often broodfish are subjected to photoperiod-temperature cycles to induce gamete maturation and volitional spawning in tanks. This method is used by the Texas Parks and Wildlife Department in their stock supplementation hatchery (Blaylock et al. 2021).

Cannibalism and aggression are significant issues in Spotted Seatrout culture, mostly during the larval stages (Manley et al. 2014, 2015). In culture settings, Spotted Seatrout can reach market size (approximately 450 g and 35-38 cm TL) in 10 months (Blaylock et al. 2021), although growth rates and times to harvest may differ in net pen culture.

3.2.7.5 Considerations on genetic risk to wild conspecifics

The residency of Spotted Seatrout in their natal estuaries is crucial in evaluating the genetic risks posed to wild populations from escaped cultured conspecifics. At a minimum, aquaculture operations in the Gulf should select broodstock from either the western or eastern Gulf stocks described in Seyoum et al. (2018). This means choosing broodstock west of Apalachicola Bay or from the remainder of Florida, depending on the location of the aquaculture operation. To account for more fine-scale genetic structuring among populations, operations should also select broodstock from the closest population while considering prevailing ocean current patterns, which could help predict the estuarine locations most likely to receive the majority of escaped fish.

Although it is difficult to predict survival rates for escaped fish, Hendon and Rakocinski (2016) reported outcomes from experimental releases of late juvenile hatchery-reared Spotted Seatrout across three habitat settings within a caged structure. Their study indicated that hatchery juveniles were able to transition successfully to expected wild prey items, although juveniles released in the open water habitat (most similar to a net pen) experienced significantly lower relative growth compared to juveniles released in submerged aquatic vegetation or non-vegetative shoreline habitats (Hendon and Rakocinski 2016). Based on these results, escaped Spotted Seatrout would likely transition to wild prey relatively successfully, but there may be a survival cost (due to slower growth) associated with the offshore location. If offshore operations are miles from the coastline, there is a low likelihood that escaped fish would immediately encounter wild conspecifics. However, if the escaped fish survive and move towards the coastline, they would likely encounter Spotted Seatrout populations.

Early maturation and spawning in the net pens cannot be excluded since volitional spawning mimics natural conditions, grow-out is to 10 months, and at least some fish are reproductively active by Age-1. While most natural spawning locations are closer to shore, there is potential for eggs and larvae to drift to suitable settlement areas. Without a 'natal' estuarine habitat, escaped fish may be less likely to reproductively contribute to the spawning population, as seen in escaped Atlantic Salmon. However, releases of juveniles may lead to greater reproductive potential as some degree of natal imprinting may still occur (Hansen 2006).

Other considerations for Spotted Seatrout include population and habitat health. This species has experienced historic population declines across the Gulf since the 1970s (e.g., Vega et al. 2009), and recovery varies by state, with some regions still undergoing overfishing (e.g., West et al. 2021). As mentioned above, stock supplementation programs have been used to assist population recovery and enhance recreational fisheries. While genetic management has been taken into account in these hatchery programs to minimize impacts on wild populations, no information is available on the potential genetic diversity loss in mixed populations following stocking. This species is also particularly vulnerable to the degradation and destruction of estuaries, which directly impact population abundance (Blanchet et al. 2001).

Taken together, the resiliency of Spotted Seatrout populations to resist or recover from large incursions of escaped fish may be lower than other species. Conversely, there may be greater capacity within regions to accommodate additional escaped fish due to lower population abundance if fitness and genetic diversity impacts to wild populations were minimized. The genetic risk of escaped cultured fish to wild Spotted Seatrout populations may be moderate-to-low when compared to potential impacts from continued releases of juvenile fish from stock enhancement efforts. If commercial production utilizes locally-sourced, wild-caught broodstock, then additional impacts may be minimal.

However, there are some key uncertainties for this species, which does increase risk in trying to evaluate genetic impacts on wild populations. No information was found to provide insight into how reproductively successful escaped Spotted Seatrout might be if released from an offshore location. While juveniles released within estuarine habitats as part of stock supplementation efforts may imprint to the location of release, it is not known whether fish escaping from an offshore commercial pen will remain reproductively “homeless” (Hansen 2006) or successfully integrate reproductively once conspecifics are found. Another area of uncertainty is that despite evaluations of genetic population structure, the impacts from stock supplementation on wild populations in terms of loss of genetic diversity or reduction in the mixed population effective breeding size are unknown but important considerations.

Blaylock et al. (2021) also pointed out that additional studies investigating genomic variation may help identify patterns of local adaptation for this species, which could be an important consideration in preserving variation in such a heterogeneous environment and crucial to selecting broodstock best adapted to a region. Lastly, varying metrics on the status of the populations based on spawning potential ratios (SPR) across the states (Blanchet et al. 2001) make it challenging to make clear comparisons on the health of the stocks across the Gulf.

Addressing these uncertainties is essential for the responsible management of Spotted Seatrout populations and the implementation of effective aquaculture and stock supplementation programs.

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3.2.8 Tripletail (Lobotes surinamensis)

3.2.8.1 Range/Description

Tripletail (*Lobotes surinamensis*) are migratory fish found worldwide in tropical and temperate waters. In the western Atlantic, their range extends from Cape Cod, Massachusetts, to Argentina, including the Gulf and the Caribbean (Strelcheck et al. 2004, VanderKooy 2016, Jefferson et al. 2021). Within the Gulf, they are most common in the northern Gulf waters and estuaries from April to October, moving southward as water temperatures cool in the fall and winter (Strelcheck et al. 2004, Jefferson et al. 2021).

Adult Tripletail are often associated with rocky bottoms, channel markers, jetties, sea buoys, pilings, and wrecks (Brown-Peterson and Franks 2001, Strelcheck et al. 2004). Juveniles are typically found near floating macroalgal assemblages, particularly *Sargassum* (Brown-Peterson and Franks 2001). Both adults and juveniles can be found in shallow waters, estuaries, bays, inlets, and in deeper waters up to 160 km offshore (Brown-Peterson and Franks 2001, Ushakow et al. 2024).

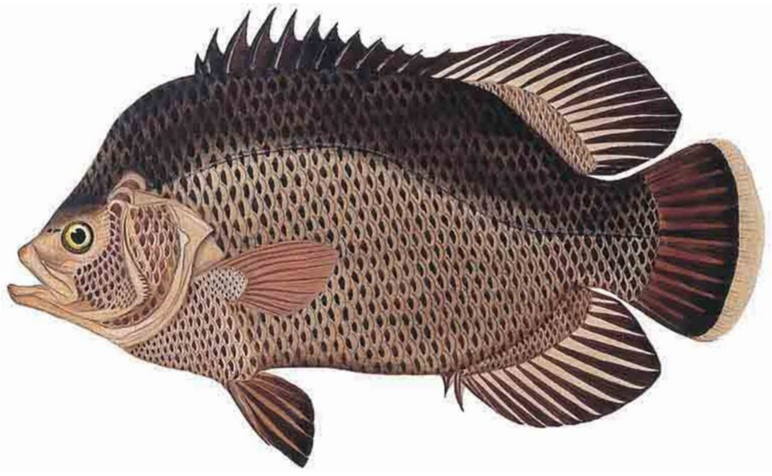

Image from Texas Parks and Wildlife Department

Recreationally, Tripletail are popular, with recreational landings surpassing commercial landings (Strelcheck et al. 2004). Due to their low densities, it is difficult for commercial fisheries to target them, and instead they catch Tripletail opportunistically (VanderKooy 2016). Both recreational and commercial fisheries are managed at the state level, with bag and size limits varying by state (Ushakow et al. 2024).

There is growing demand for Tripletail in the U.S. market, which is currently met by imports from regions where the species is more abundant (e.g., Guyana, Brazil, Venezuela; VanderKooy, 2016). Establishing aquaculture for Tripletail could provide a domestic supply and create a new market opportunity (Adams 2022).

3.2.8.2 Biological Characteristics

There is some debate about the maximum age of Tripletail, but generally, they are considered to grow and mature rapidly, with a relatively short lifespan of 4 to 7 years (Strelcheck et al. 2004, Jefferson et al. 2021). Tripletail may grow over 400 mm in their first year and reach sexual maturity by age 1. About 50% of females reach sexual maturity at 494 to 594 mm TL (1 to 2 years of age), and all males larger than 380 mm are sexually mature (Strelcheck et al. 2004).

Brown-Peterson and Franks (2001) also found that female Tripletail in the north-central Gulf reach 50% sexual maturity at 485 mm TL and 1 year of age.

Spawning in Tripletail is thought to occur offshore along the outer continental shelf in the northern Gulf from June to August, with some variations in timing based on location (Ditty and Shaw 1994, Brown-Peterson and Franks 2001, Strelcheck et al. 2004). Females are batch spawners, capable of spawning every 3 to 5 days with a mean batch fecundity of 444,743 ± 201,139 eggs per female, or a relative batch fecundity of 47.6 ± 18.1 eggs/gram ovary-free body weight (Brown-Peterson and Franks 2001). For a 61 cm TL female, this translates to an annual fecundity of 4.5 to 8 million eggs (VanderKooy, 2016).

There is limited information about wild eggs and larvae of Tripletail (Fagundes et al. 2021). Ditty and Shaw (1994) collected larvae offshore in surface tows, with the smallest larvae (under 5.0 mm) collected at stations over 110 m deep. Under culture conditions, eggs hatch approximately 24 hours post-fertilization, and larvae begin feeding at 3 to 4 days post-hatching after the yolk sac is reabsorbed (Saillant et al. 2014).

Seasonal shifts in the prevalence of Tripletail in the Gulf and Southern Atlantic indicate migratory behaviors. Adults and juveniles arrive in spring and may reside in passes, inlets, bays, and coastal waters from St. Marks, Florida, to St. Bernard River, Texas, throughout the summer (Ditty and Shaw 1994). They depart in the fall when water temperatures cool, and possibly overwinter near South Florida/Florida Keys (VanderKooy 2016). Tagging information, particularly for the Gulf, is limited, but tagging off Georgia indicates fish may disperse up to 200 to 500 miles, though most are recaptured near their release point if recaptured within 100 days of tagging, suggesting some site or region fidelity (VanderKooy 2016).

3.2.8.3 Population Structure

According to VanderKooy (2016), while Tripletail are found globally in tropical and temperate waters, sequencing data from the Fish Barcode Information System indicates significant divergence between Tripletail populations in the Atlantic and Indo/Pacific regions. Specimens from the Mediterranean suggest this region might have historically been a migratory route between these ocean basins. Mitochondrial COI sequences revealed shared haplotypes between six out of seven sequenced specimens from Brazil and the one specimen from the Gulf (Alabama). However, these methods are not designed to detect subtle population structures or contemporary connectivity patterns. Since no genetic studies addressing population structure have been conducted, Tripletail in the western Central Atlantic Ocean, Gulf, and Caribbean are managed as a single stock. Conducting population genetic studies on Tripletail should be a high priority to determine the connectivity among these regions.

3.2.8.4 Aquaculture

Aquaculture efforts for Tripletail are relatively recent, with research into culture methods spanning just over two decades. Franks et al. (2001) conducted a grow-out trial on wild Tripletail juveniles in a culture setting and found high growth rates in recirculating aquaculture systems

(RAS). Saillant et al. (2014) investigated captive reproduction and early larval culture, discovering that Tripletail do not spawn naturally under simulated photothermal cycles. They initially explored hormonal induction to achieve gamete maturation and spawning, which was further advanced by Saillant et al. (2021) and Adams (2022).

Larval rearing studies indicated that eggs hatch approximately 24 hours post-fertilization, with a switch to exogenous feeding by 4 days post-hatching (dph) and a transition to prepared feeds at 25 dph (Saillant et al. 2014, 2021). Initial grow-out trials in RAS showed average growth rates of 170 grams per month until reaching market size (1 kg or larger) (Saillant et al. 2021). There is currently no information available on the offshore grow-out of Tripletail.


Image from the Gulf States Marine Fisheries Commission

Ongoing culturing and husbandry research by Franks (2001), Saillant et al. (2014, 2021), and Adams (2022) demonstrates the potential for Tripletail aquaculture due to their fast growth and the feasibility of closing their life cycle in captivity. However, continued optimization is needed to achieve consistent gamete maturation, spawning, and fertilization, and to improve survival during the early larval stages. If the U.S. market for Tripletail expands, the initial culturing results suggest that aquaculture of this species could become viable (Saillant et al. 2021).

3.2.8.5 Considerations on genetic risk to wild conspecifics

Based on descriptions of where adult and juvenile Tripletail occur, it is likely that wild fish may occasionally overlap spatially with offshore net pens. This species is known to aggregate around floating objects, which could include net pen structures, increasing the likelihood of encounters between escaped Tripletail and their wild conspecifics.

While Tripletail do not spawn volitionally in RAS culture, it is unknown whether they would spawn naturally in offshore pens. This remains a key uncertainty regarding their culture, as their growth rates and early maturity suggest the potential to reach sexual maturity in under a year, possibly before reaching a marketable harvest size. This could lead to the release of gametes and larvae into regions inhabited by wild conspecifics, though the limited data on Tripletail reproduction and grow-out approaches makes this speculative.

The lack of information on the genetic structure, migratory behaviors, grow-out and harvesting approaches, and natural reproduction of Tripletail leads to high uncertainty about the potential genetic effects of escaped fish on wild conspecifics. If populations are large and connected through migratory behaviors, moderate amounts of culture may pose little genetic risk to the wild population. However, until more is known about this species, particularly its genetic population connectivity and offshore culturing approaches, there is too much uncertainty for a meaningful assessment of genetic risk from offshore aquaculture of Tripletail.

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3.2.9 Southern Flounder (Paralichthys lethostigma)

3.2.9.1 Range/Description

Southern Flounder (*Paralichthys lethostigma*) are distributed throughout most of the Gulf, including Texas, Louisiana, Mississippi, Alabama, and Florida, but are most prevalent in the western portion of the Gulf (Enge and Mulholland 1985, Gilbert 1986). On the Gulf-side of Florida, they are only found north of Tampa Bay, Florida with the exception of Caloosahatchee River Estuary, and on the Atlantic coast, they are found north of Loxahatchee River, Florida up to North Carolina (Gilbert 1986). This species may be found in muddy benthic habitats in shallow estuaries, nearshore areas, and offshore waters up to depths of 120 m (Stokes 1977).

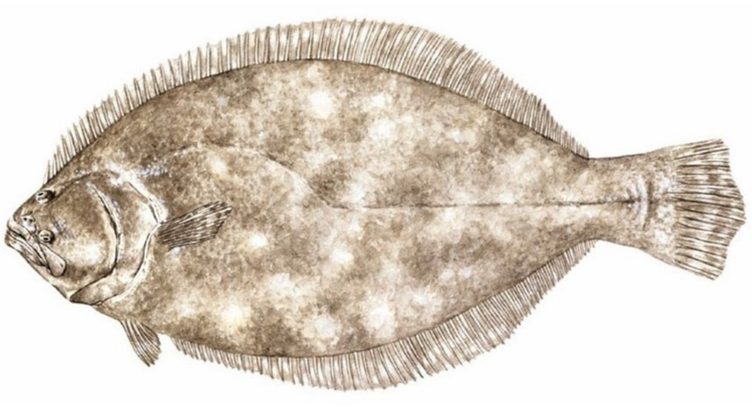
Image from Texas Parks and Wildlife Department

Southern Flounder are an important recreational and commercial species within the Gulf due primarily to their highly desirable flesh quality (VanderKooy 2015). This species is managed at the state level with each state implementing varying regulations (if any) for those fisheries (VanderKooy 2000). Over the last decade, overall landings have decreased, and the majority of the catch is now from recreational fisheries (Powers et al. 2018, West et al. 2020). Declining *P. lethostigma* populations have been reported across their range in the Gulf and the Atlantic coast (Fischer and Thompson 2004, Froeschke et al. 2011, Flowers et al. 2019, West et al. 2020, Erickson et al. 2021), which may be due, in part, to long-term fishing pressure on these populations and highly variable annual recruitment success (Beeken et al. 2023). To slow or reverse these declines, states have enacted various regulations to reduce daily bag limits, increase minimum sizes for captured fish, and implement seasonal closures (Midway et al. 2024).To assist population recovery, the Texas Parks and Wildlife Department initiated a Southern Flounder stock enhancement program in 2006; in 2022 this program released approximately 300,000 juvenile Southern Flounder along the Texas coast (https://agrilifetoday.tamu.edu/2023/11/13/stock-enhancement-program-shows-promise-in-enhancing-texas-southern-flounder-population/; accessed 7-25-2024).

3.2.9.2 Biological Characteristics

Southern Flounder exhibit a broad range of thermal and salinity tolerance, though their ability to withstand these conditions varies by life stage and season (Stokes 1977, Rogers et al. 1984). Young recruits and juveniles prefer shallow, low-salinity nursery areas in estuaries and marshes, while older fish migrate to deeper, more saline waters as they grow (Rogers et al. 1984, Fischer and Thompson 2004). Their distribution also shifts seasonally, with Southern Flounder commonly found in estuaries during the warmer summer months and moving offshore for spawning and to avoid cold temperatures during winter (Stokes 1977).

Sexual dimorphism is evident in Southern Flounder, with females growing faster and reaching larger sizes than males (Fischer and Thompson 2004, Corey et al. 2017). Growth rates also vary by location—both between broader regions such as the Atlantic and Gulf, and within smaller geographic areas such as within states—likely due to differences in environmental conditions within estuaries (Midway et al. 2015). Maximum age for Southern Flounder is reported as 4 years for males and 8 years for females. Males typically range from 127 to 414 mm total length (TL), with a mode around 280 mm, while females range from 189 to 764 mm TL, with a mode around 390 mm (Fischer and Thompson 2004).

In the north-central Gulf, Southern Flounder females typically reach sexual maturity at lengths between 245 and 368mm TL, which corresponds to ages of 1 to 2 years, with a mean length at maturity of 303 mm TL (approximately 1 year of age) (Corey et al. 2017). However, male-specific data are limited, making it challenging to provide similar estimates for males. There is some variability in these maturity estimates, with Midway et al. (2015) reporting a mean length at 50% maturity ranging from 200 to 238 mm across various locations, and Smith and Scharf (2010) noting 385 mm in North Carolina. Although some fish may reach sexual maturity in their first year, Stokes (1977) suggested that they typically do not participate in spawning until they are 2 years old.

Southern Flounder, ranging from 1 to 3 years of age, migrate offshore to spawn between October and December in Texas (Stokes 1977) or from November to January in the north-central Gulf (Corey et al. 2017). They are batch spawners and can spawn over consecutive days, producing an estimated total of 120,000 eggs (Arnold et al. 1977). After spawning, the eggs hatch offshore, and the pelagic larvae have a duration from hatching to the onset of metamorphosis of 40 to 46 days, reaching lengths of 8 to 11 mm TL (Arnold et al. 1977). Metamorphosis is typically completed by 50 to 51 days post-hatching (Arnold et al. 1977), which aligns closely with an otolith-based estimate of a mean period of 47 days for metamorphosis (Beeken et al. 2023). The larvae then gradually migrate back towards the coast and estuaries as they near the end of metamorphosis (van Maaren and Daniels 2001). Juvenile Southern Flounder remain in these inshore areas until they approach 300 mm TL, marking the end of their juvenile period (Stokes 1977). This life cycle involves considerable movement across, and utilization of, a large geographic range (van Maaren and Daniels 2001).

It is possible that older Southern Flounder males remain offshore year-round, as they have not been observed returning to estuaries after spawning (Stokes 1977). However, there is limited information about their habitat use because they are often underrepresented in sampling efforts (Midway et al. 2015). For instance, among 627 tagged fish recoveries, only 2% were male, and only a single male was found out of 180 fish examined for maturity (Smith and Scharf 2010). Similarly, Midway et al. (2015) reported a skewed sex ratio, with a considerably higher number of females compared to males, and a high percentage of females (80-90%) being landed in fisheries. The reasons for this lower male ratio are not well understood and could be due to several factors: smaller size of males which might make them less targeted by the fishing industry, possible shifts in distribution that make them less accessible for sampling and fishing, or potentially increased mortality as bycatch in other fisheries (VanderKooy et al. 2000, Midway et al. 2015).

3.2.9.3 Population Structure

Between Southern Flounder populations in the Atlantic and Gulf, several studies have detected significant divergence, which indicated extremely limited gene flow between these regions, and supported the consideration of these populations as distinct stocks (Blandon et al. 2001, Anderson and Karel 2012, Wang et al. 2015, O'Leary et al. 2021). Within the Gulf, the genetic structure of Southern Flounder is less clear. An allozyme study found statistically significant allele frequency clines in one locus across the Gulf, suggesting some level of genetic structuring (Blandon et al., 2001). This study also noted allele frequency differences between Galveston and Matagorda Bays along the Texas coast, possibly due to seasonal current patterns that limit egg and larval dispersal between these areas (Blandon et al., 2001). Anderson and Karel (2012) similarly found some evidence of isolation by distance in the Gulf although they did not detect discrete populations.

More recently, a study using 4,122 single nucleotide polymorphism (SNP) loci found significant heterogeneity among estuaries. Most pairwise comparisons within the Gulf were not significant and the heterogeneity did not follow a linear isolation-by-distance pattern, but instead, analyses indicated that environmental variables among estuaries might explain part of the genomic variation (O'Leary et al., 2021).

Collectively, these findings indicate that dynamic processes, such as currents and environmental parameters associated with estuarine habitats, may contribute to limited dispersal and potential local adaptation of Southern Flounder populations within the Gulf. However, more research is needed to fully understand these patterns.

3.2.9.4 Aquaculture

Culturing approaches for Southern Flounder have been developed since the 1970s, primarily using wild-caught broodstock conditioned to farm conditions over at least a year (Arnold et al. 1977). While volitional spawning of Southern Flounder is achievable through light and temperature manipulation (Arnold et al. 1977), hormone injections are more commonly used to induce spawning, facilitating a larger number of eggs spawned at once through strip spawning (Smith et al. 1999, Daniels et al. 2010). Eggs hatch at 55 hours when held at 17°C (Daniels et al. 2010). Newly hatched larvae possess yolk sacs that are reabsorbed by 4 to 5 days post-hatching (dph), after which the larvae are transitioned onto live food until metamorphosis, which occurs between 40 and 55 dph (Arnold et al. 1977, Daniels et al. 2010).

Because Southern Flounder exhibit environmental sex determination, where genetic females may develop as phenotypic males, culture approaches must be precise, particularly regarding water temperatures prior to sex differentiation (approximately 75 to 100 mm TL) to avoid drastically skewed sex ratios in hatchery offspring (van Maaren and Daniels 2001, Luckenbach et al. 2003, Daniels et al. 2010). If these stringent conditions to equalize sexes are not followed, hatchery offspring have been reported to be up to 99% phenotypic males (Smith et al. 1999).

Southern Flounder aquaculture is being conducted in the Gulf through stock enhancement programs in Texas and Alabama (Midway et al. 2024). Texas has been running stock enhancement programs since 2006 and has released almost a million fingerlings into Texas waters since the program began (Midway et al. 2024). In Alabama, broodstock were acquired in 2018, and releases began in 2020 with 12,000 fingerlings, followed by 34,000 in 2021, and 102,000 in 2022 (https://gulfcoastmedia.com/stories/apparent-flounder-rebound-has-gulf-coast-encouraged,166743, https://www.outdooralabama.com/mrd-fisheries-section/claude-peteet-mariculture-center; accessed July 30, 2024). According to Midway et al. (2024), current stock enhancement programs in Texas and Alabama use tags to identify broodstock fish and regularly rotate broodstock to maximize genetic diversity in the hatchery-produced fish.

For commercial aquaculture, it is likely that operations will focus on producing all-female offspring due to their faster growth rates and larger size (Daniels et al. 2010). Limited trials indicate that all-female populations can reach a harvestable size of 1.5 lbs in 14 months (Daniels et al. 2010). However, grow-out durations for offshore aquaculture operations have not yet been determined. Notably, Southern Flounder can thrive in both freshwater (or near freshwater) and marine conditions, which will likely influence decisions on the most profitable locations for growing these fish to market size.

3.2.9.5 Considerations on genetic risk to wild conspecifics

Southern Flounder exhibit a low level of genetic heterogeneity across the Gulf, with environmental factors thought to influence any patterns of differentiation more than geographic distance (O'Leary et al. 2021). Adults migrate from estuaries to offshore spawning grounds, and the larval stage lasts for 40-50 days, allowing for dispersal over considerable distances. These factors facilitate gene flow within the Gulf, although environmental conditions within estuaries may impose varying selection pressures on the dispersed larvae.

Currently, Southern Flounder are managed at the state level, which has resulted in fragmented stock data across the region. Erickson et al. (2021) reported that Southern Flounder recruitment has declined throughout their range in the Gulf and along the U.S. southeast Atlantic coast from 1978 to 2018. Similarly, declining abundances of Southern Flounder in the Gulf were noted by Froeschke et al. (2011) and West et al. (2020). A comprehensive single-species stock assessment would be beneficial to determine the overall status of the Southern Flounder population across the Gulf.

Cultivating Southern Flounder offshore minimizes the chance of escaped fish reaching estuary habitats where their conspecifics usually reside. However, given the distances wild Southern Flounder can move, it is reasonable to consider that at least some escaped fish could disperse into estuarine regions. During their offshore spawning period, escaped fish are more likely to encounter conspecifics and potentially follow them back to estuary habitats.

Based on reported ages at sexual maturation, ranging between 1 and 2 years, and the anticipated grow-out duration of 14 months (estimated for female monosex culture), there is a reasonable likelihood that Southern Flounder would reach sexual maturity and spawn before harvest. However, the estimated grow-out duration was based on RAS culture, and the duration would likely differ in offshore pens. Wild fish have a relatively narrow window where spawning leads to successful recruitment (Beeken et al. 2023). Shifting offshore production runs so that cultured fish do not mature during the 2-to-3-month natural spawning period may reduce the likelihood of successful recruitment from any larvae or gametes escaping from the cages.

While the stock enhancement efforts in Texas and Alabama must be considered when evaluating the genetic impacts on wild populations, the success of these fingerlings recruiting into the wild population and the quantification of their contributions to wild populations have not yet been assessed (Midway et al. 2024). Consequently, it is challenging to determine the impact these culturing efforts may have had on the genetic diversity of natural populations. Southern Flounder commercially cultured offshore would be considerably larger than the released fingerlings (except at pen seeding times) and would likely survive at a higher rate than released juveniles. If commercial programs pursue all-phenotypically female hatchery fish to take advantage of their higher growth rates, then escaped fish may disproportionately contribute to subsequent recruitment events.

Based on the species profile and the above information, escaped cultured Southern Flounder may have a moderate genetic impact on wild populations. The depressed abundance and spawning biomass of the species in the Gulf increases susceptibility to impacts, while the distances between offshore operations and the wild populations during most of the year, along with the narrow conditions and periods of the year dictating successful recruitment, likely act to limit potential impacts.

Sourcing broodstock from nearby populations may reduce potential genetic impacts, but given the species' complex genetic heterogeneity patterns, it may not be as effective as it would be in other species. However, maintaining genetic diversity in hatchery populations is still an important mitigation step (through maximizing spawning pairs or rotating broodstock), particularly with the possibility that natural populations may have already lost genetic diversity due to depressed abundance.

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3.3 OMEGA Genetic Risk Modeling Case Studies for Finfish in the Gulf of America

Similar to Southern California, case studies were modeled for the three Gulf candidate species using the OMEGA model described in Section 2.1.3, *OMEGA Model for Assessment of Finfish Escapes*. The case studies are intended to help with understanding how species population structure, life history, and abundance can influence potential effects of escaped fish on the genetics of the wild population of conspecifics. The case studies also highlight the level of certainty when assessing the risks for a data-rich or data- poor species. The case studies are not intended to describe a particular proposed aquaculture operation. Farm assumptions in the case study assessments are approximate based on available published literature. Specifics of operations such as size when fish are transferred to offshore cages, time in cages, and harvest methods are important to fully evaluate the potential of fish escaping from cages and their survival in nature and to spawning.

The three case study species for the Gulf are Red Drum (*Sciaenops ocellatus*), Almaco Jack (*S. rivoliana*), and Cobia (*Rachycentron canadum*). All three are native species present in marine waters of the Gulf. Research on the population structure of Almaco Jack and Cobia indicate that within the Gulf they may be single panmictic populations. The Red Drum case study focused on the NW Florida region and is based on the stock assessment in Addis (2020) for this region.

3.3.1 Case Study: Red Drum

Red Drum (*Sciaenops ocellatus*) are a member of the Sciaenidae family of fishes, which includes drums and croakers. The species can tolerate a range of water salinities (i.e., euryhaline). The population occurs along the nearshore Atlantic coast to New England and the Gulf (GSFMC 2023). Red Drum is a popular recreational species in state waters. Red Drum were severely overfished in the 1980s leading to closure of commercial harvest and fishery restrictions on recreational catch to rebuild the stock, as well as closure of marine waters between 3 miles and 200 miles (exclusive economic zone (EEZ)) to Red Drum fishing (GSFMC 2023).

Addis (2020) reported little evidence for genetic-based population structure of Red Drum along the Florida coast in the Gulf. However, Addis (2020) decided to complete a stock assessment using a finer population structure in the Gulf to address concerns that stock assessments should address a regional geographic scale. As described in Section 3.2.1, *Red Drum*, recent tagging studies in the Tampa Bay region indicated fairly high spawning site fidelity and natal homing suggesting a finer stock structure, although there was some mixing with a population 132 km to the south and a portion of tagged fish moved out of the range of monitoring (Lowerre-Barbieri et al. 2016, Lowerre-Barbieri et al. 2019). However, the authors did not discount longer distance movement of Red Drum because of the short study duration (4 years) and a reproductive life span of at least 30 years.

The Red Drum case study assessment was completed for the NW Florida population unit assessed in Addis (2020) and represented by the Panhandle and Big Bend Florida management units (Figure 3.1).

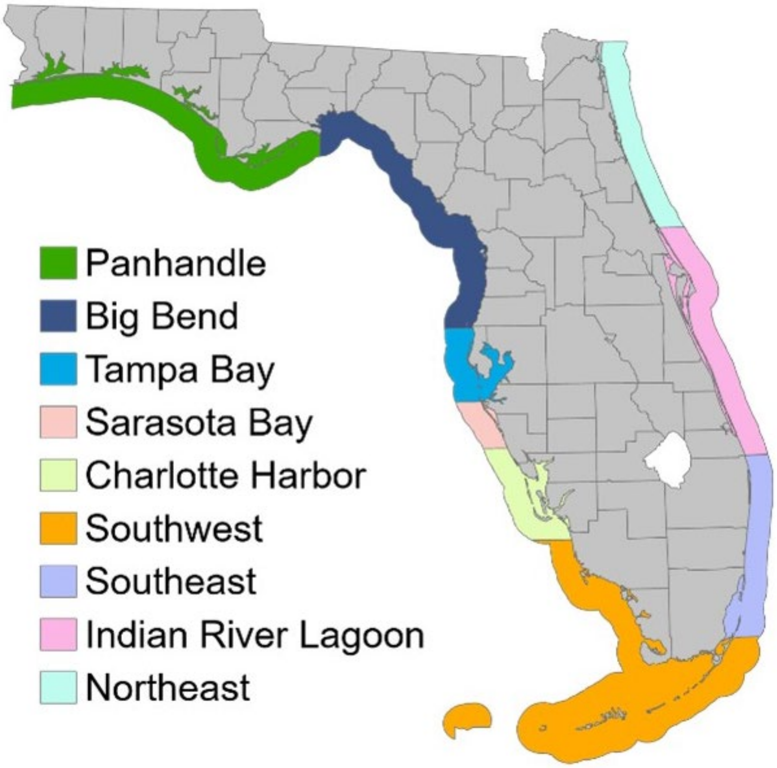

Figure 3.1. Florida Red Drum management zones defined 2022 (Florida Fish and Wildlife Conservation Commission, https://myfwc.com/fishing/saltwater/recreational/red-drum/)

Red Drum are long lived with a maximum age of 36 to 40 years (Murphy and Taylor 1990, Tringali and Lowerre-Barbieri 2023). Both sexes reach 50% sexual maturity by age 4 and 100% of Red Drum are sexually mature by age 6 (Wilson and Nieland 1994). At 50% sexual maturity Red Drum males are approximately 66 cm (3.4 kg) and females approximately 69 cm (4.0 kg). The largest recorded size of Red Drum in the Gulf is 59 pounds (TPWD 2023).

Estimates of N_e and the ratio of N_e/N_T and N_e/N_A were made assuming over-dispersed variation in reproductive success at age (i.e., a Poisson scaling factor of 3) using the AgeNe program (Waples et al. 2011). Results are summarized in Table 3.1. The estimated number of breeders in a year (N_b) was 2,409,455. The estimated effective population size (N_e) from the AgeNe model was 3,755,067. The total estimated number of fish age one and older (N_T) 10,800,422. The estimated number of adults (N_A) was 8,946,846 fish. The estimated ratio of N_e to total N was 0.35. The estimated ratio of N_e to adult N (N_A) was 0.42. These estimates of abundance are based on the life table framework of Waples et al. (2011) and will differ from total abundance estimates in OMEGA using a life cycle population simulation framework with varying survival and fishery exploitation rates. Generation length was estimated to be 11.4 years using AgNe (Waples et al. 2011), which was approximately consistent with the Tringali and Lowerre-Barbieri (2023) estimate of 12 years.

Table 3.1. Red Drum calculated values of effective population size (N_e) with over-dispersed variation in reproductive success (Poisson factor = 3.0) using equations in Waples et al. 2011 and AgeNe program.

Scenario	Max Age	Generation Length	N_T	N_A	N_b	N_e	N_e / N_T	N_e / N_A
Over dispersed (Poisson factor = 3)	40 yrs	11.4 yrs	10,800,422	8,946,846	2,409,455	3,755,067	0.35	0.42

Notes:
N_T = Total number of individuals age 1 and older
N_A = Total number of adults
N_b = Effective number of breeders
N_e = Effective population size

Model simulations in OMEGA for the low (3-Farm, 10,500 mt annual production) and high production (5-Farm, 17,500 mt annual production) scenarios are presented in Table 3.2. Fish size is weight in kilograms at the end of each phase of grow-out in cages. Fish size at harvest is the midpoint of the market weight range (1.2 to 1.6 kg) as described in Sink (2019). The number of fish transferred to cages was calculated based on the midpoint market weight and a harvest goal of 10,500 mt and 17,500 mt. The number of cages assumes 100,000 fish per cage at market size. Modeled size of fish when transferred to offshore cages was 50 grams (0.05 kg) and time from transfer to harvest was assumed to be 40 to 48 weeks. The calculated number of fish in net pens was 7,446,809 million fish with the 1.4 kg size assumption with the low production scenario and 12,411,348 fish with the high production scenario.

As described in Section 1.3.1.1, *Use of Case Studies*, leakage assume a loss of 0.3% of fish in a cage over the entire period fish are in cages with 65% of the total leakage occurring in the smallest bin, 10% in the mid-sized bin, and 25% in the largest bin. The total number of fish escaping under the low and high production scenarios were 25,298 and 42,164 fish, respectively (Table 3.2). This represents a high number of escaped fish from leakage compared to the other study species in the Gulf. The other case study species were held to a larger market size thus with a low and high production based on annual weight of fish held to market size, more Red Drum would be needed to produce 10,500 mt and 17,500 mt.

As described in Section 1.3.1.1, *Use of Case Studies*, episodic escapes are defined as cage failures, where escape losses ranged from half to all of the fish within a given cage. Two rates of episodic escape frequencies were modeled for the high production scenario: 1) one event every 10 years (10% annual likelihood of an episodic escape event), and 2) 2.5 events every 10 years (25% annual likelihood of an episodic escape event). In the low production scenario, the modeled episodic escape likelihoods were adjusted downward using the same ratio as the high production assumptions to account for the reduced number of cages with fish and, consequently, the lower likelihood of episodic escapes. Thus, the episodic escape frequencies for the low production scenario were: 1) 0.6 events every 10 years (6% annual likelihood of an episodic escape event), and 2) 1.5 events every 10 years (15% annual likelihood of an episodic escape event). In the "modified" escape scenarios, the low escape likelihoods were halved to 3% and 5% annual likelihood under the low and high production scenarios, respectively. The number of

fish escaping was reduced to between a quarter and half of the fish in a cage to account for partial fish escape recovery.

Table 3.2. Red Drum production scenarios modeled for the case study.

Scenario	***Fish Size at Harvest (kg)***	***# Fish***	***# Cages***	***Annual # Escaping via Leakage***			***-***
				0.15 kg	***1.25 kg***	***1.4 kg***	***Total***
3-Farm, 10,500 mt	1.4	7,446,809	75	17,377	2,296	5,625	25,298
5-Farm, 17,500 mt	1.4	12,411,348	125	28,962	3,827	9,375	42,164

The various model scenarios predicted the cumulative number of fish from leakage and episodic losses at three time points in the simulations (Table 3.3). The results presented are the median, 5th percentile, and 95th percentile values across the 1,000 simulations at Year 5, Year 10, and Year 25. The median number of cumulative escaped fish in the wild population increased with the higher escape likelihoods and over longer time periods for all scenarios. The increase in number of cultured fish nearly doubles between Year 5 and Year 25 with the 15% and 25% episodic likelihood assumptions under the 3-Farm and 5-Farm scenarios. The median number of escaped fish doubles over time with the lower episodic likelihood assumptions (6% and 10% for low and high production scenarios, respectively). The range between the lower (5th percentile) and higher (95th percentile) numbers of escaped fish showed less variation across time steps. The lower end reflects the few model iterations (out of 1,000) that include only annual leakage—where no episodic escapes occurred by chance—and any surviving fish from previous years. In contrast, the higher end captures iterations with both leakage and multiple episodic escapes occurring within the three time-steps.

Modeled survival of escaped cultured fish to enter the population varied between approximately 60% for the smallest and mid-sized fish, and 67% for the largest-sized fish in Table 3.2. Modeled survival of escaped cultured fish to survive to spawn with wild Red Drum varied between 37% for the smallest and mid-sized fish, and 50% for the largest sized fish. The smallest and mid-sized escaped Red Drum began contributing to spawning after 4.5 years in nature and the largest sized fish contributed after 3.5 years in nature. The estimated period before escaped fish would be ready to spawn with wild Red Drum was based on estimates of sexual maturity at approximately 70 cm (3.4 kg) using von Bertalanffy growth and maturity schedule parameters for the Northwest region of wild Red Drum in Addis (2020).

Across all time steps and production scenarios (excluding the modified scenario), the median number of cultured fish in the wild Red Drum population ranged between 88,255 and 292,658 fish (Table 3.3). Using an estimated total abundance of age 1 and older Red Drum in the NW Florida population group of 10.8 million fish, based on the model framework by Waples et al. (2011) (Table 3.1), the abundance of escaped Red Drum in the wild would represent approximately 1.5% to 2.6% of the total mixed population of Red Drum by Year 25.

In Year 5, under the 3-Farm simulations, the predicted median cumulative number of escaped fish in the wild population ranged from 66,878 (under a 6% escape likelihood) to 88,255 fish (under a 15% escape likelihood) (Table 3.3). Simulations reflecting the highest escape outcomes (95th percentile) predicted that up to 137,618 fish (6% likelihood) and 183,859 fish (15% likelihood) could accumulate in the wild. The results were moderately skewed, with median values trending toward the lower end of the predicted range.

By Year 25, under the 3-Farm simulations, the predicted median cumulative number of escaped fish in the wild population ranged from 134,901 fish (under a 6% escape likelihood) to 169,511 fish (under a 15% escape likelihood) (Table 3.3). Simulations reflecting the highest escape outcomes (95th percentile) projected that up to 206,980 fish (6% likelihood) and 255,229 fish (15% likelihood) could accumulate in the wild. The median results in Year 25 were less skewed, indicating a substantial accumulation of cultured fish in the population at this simulation endpoint.

In Year 5, under the 5-Farm simulations, the predicted median cumulative number of escaped fish in the wild population ranged from 113,253 fish (with a 10% escape likelihood) to 160,329 fish (with a 25% escape likelihood) (Table 3.3). Simulations showing the highest escape outcomes (95th percentile) suggested that up to 200,779 fish (10% likelihood) and 249,235 fish (25% likelihood) could accumulate in the wild. Results for the 5-Farm scenarios with the 10% likelihood were very skewed and not skewed with the 25% likelihood.

In Year 25, under the 5-Farm simulations, the predicted median cumulative number of escaped fish in the wild population had doubled compared to Year 5. Median values ranged from 229,301 fish (with a 10% likelihood) to 292,658 fish (with a 25% likelihood) (Table 3.3). Simulations with the highest escape outcomes (95th percentile) predicted a maximum accumulation of between 310,721 fish (10% likelihood) and 401,513 fish (25% likelihood) in the wild population. Results for the 5-Farm scenarios with both the 10% and 25% likelihoods were slightly skewed.

Table 3.3. The cumulative number of cultured Red Drum in the wild population resulting from leakage and episodic losses from current year escapes and surviving fish from previous years under the 3-Farm and 5-Farm case study scenarios simulation results. Shown are the median, and 5th and 95th percentiles.

Case Study Scenario:	**Cumulative number escaped cultured fish in population**		
3-Farm, 10,500 mt	**Median**	**5th**	**95th**
Number of Cultured Fish in Year 5			
Leakage + Episodic (15% annual likelihood)	88,255	62,289	183,859
Leakage + Episodic (6% annual likelihood)	66,878	61,573	137,618
Number of Cultured Fish in Year 10			
Leakage + Episodic (15% annual likelihood)	133,466	85,916	219,408
Leakage + Episodic (6% annual likelihood)	97,998	84,534	166,419
Number of Cultured Fish in Year 25			
Leakage + Episodic (15% annual likelihood)	169,511	124,270	255,229
Leakage + Episodic (6% annual likelihood)	134,901	110,165	206,980
5-Farm, 17,500 mt			
Number of Cultured Fish in Year 5			
Leakage + Episodic (25% annual likelihood)	160,329	105,006	249,235
Leakage + Episodic (10% annual likelihood)	113,215	102,311	200,779
Number of Cultured Fish in Year 10			
Leakage + Episodic (25% annual likelihood)	221,044	153,983	320,502
Leakage + Episodic (10% annual likelihood)	171,592	142,686	249,177
Number of Cultured Fish in Year 25			
Leakage + Episodic (25% annual likelihood)	292,658	217,652	401,513
Leakage + Episodic (10% annual likelihood)	229,301	185,712	310,721

Figure 3.2 visually represents the simulation results detailed in Table 3.3. The top figures show the cumulative number of cultured fish in the wild population, while the middle figures depict the subset of these escaped fish expected to survive to spawning age. The bottom figures display escaped fish as a proportion of the spawning population abundance. High episodic likelihood results are illustrated in Figure 3.2A (left) (15% and 25% likelihoods for the low and high production scenarios, respectively), while low episodic likelihood results are shown in Figure 3.2B (right) (6% and 10% likelihoods for the low and high production scenarios, respectively). Data are grouped within the Year 5, Year 10, and Year 25-time steps, with lower and upper whiskers reflecting the 5th and 95th percentiles across 1,000 simulations, and horizontal bars representing median values.

By Year 25, under the 3-Farm simulations with a high episodic likelihood of 15%, the model predicted a median cumulative number of approximately 120,000 escaped fish surviving to spawn (Figure 3.2A, middle). The 95th percentile projection for this group was estimated to be approximately 170,000 cultured fish potentially surviving to spawn. In the 5-Farm simulations with an even higher episodic likelihood of 25%, the median prediction for escaped fish surviving to spawn reached approximately 200,000 fish, with a 95th percentile maximum of about 265,000 fish surviving to spawning age.

In Year 25, with a low episodic likelihood of 6% under the 3-Farm simulations, the predicted median cumulative number of escaped fish surviving to spawn was approximately 95,000 fish (Figure 3.2B, middle). The 95th percentile projection predicted that up to 135,000 cultured fish could survive to spawn. Under the 5-Farm simulations with a 10% episodic likelihood, the predicted median cumulative number of escaped fish surviving to spawn was approximately 155,000 fish, with the 95th percentile reaching approximately 210,000 fish.

The bottom figures in Figure 3.2 illustrate the proportion of escaped fish relative to the combined spawning abundance of both wild and escaped fish. Notably, the 5th and 95th percentiles in these figures capture the range of escaped fish predicted to survive to spawning, as described previously. While model simulations incorporate stochastic variability in population abundance, they do not include range of possible population sizes; therefore, the range displayed largely results from the variability in escaped fish numbers. These figures capture the stochastic nature of population abundance and episodic escape events as modeled in the simulations.

The median proportion of cultured fish within the wild population's spawning abundance, under both low and high production scenarios and assuming high episodic escape likelihoods, varied from approximately 0.003 to 0.029 across all time steps and production scenarios (Figure 3.2, bottom). In Year 25 under the 3-Farm simulations with a 15% episodic likelihood, the predicted proportion of cultured fish ranged from about 0.012 (5th percentile) to 0.022 (95th percentile), with a median of approximately 0.016 (Figure 3.2A, bottom). For the 5-Farm simulations with a 25% episodic likelihood, the Year 25 predicted proportion ranged from approximately 0.022 (5th percentile) to 0.035 (95th percentile), with a median of approximately 0.027.

In Year 25, under the 3-Farm simulations with the low 6% episodic likelihood assumption, the proportion of cultured fish ranged from approximately 0.011 (5th percentile) to 0.018 (95th percentile), with a median of approximately 0.012 (Figure 3.2B, bottom). For the 5-Farm simulations with the low 10% episodic likelihood assumption, the proportion of cultured fish ranged from approximately 0.019 (5th percentile) to 0.028 (95th percentile), with a median of approximately 0.021.

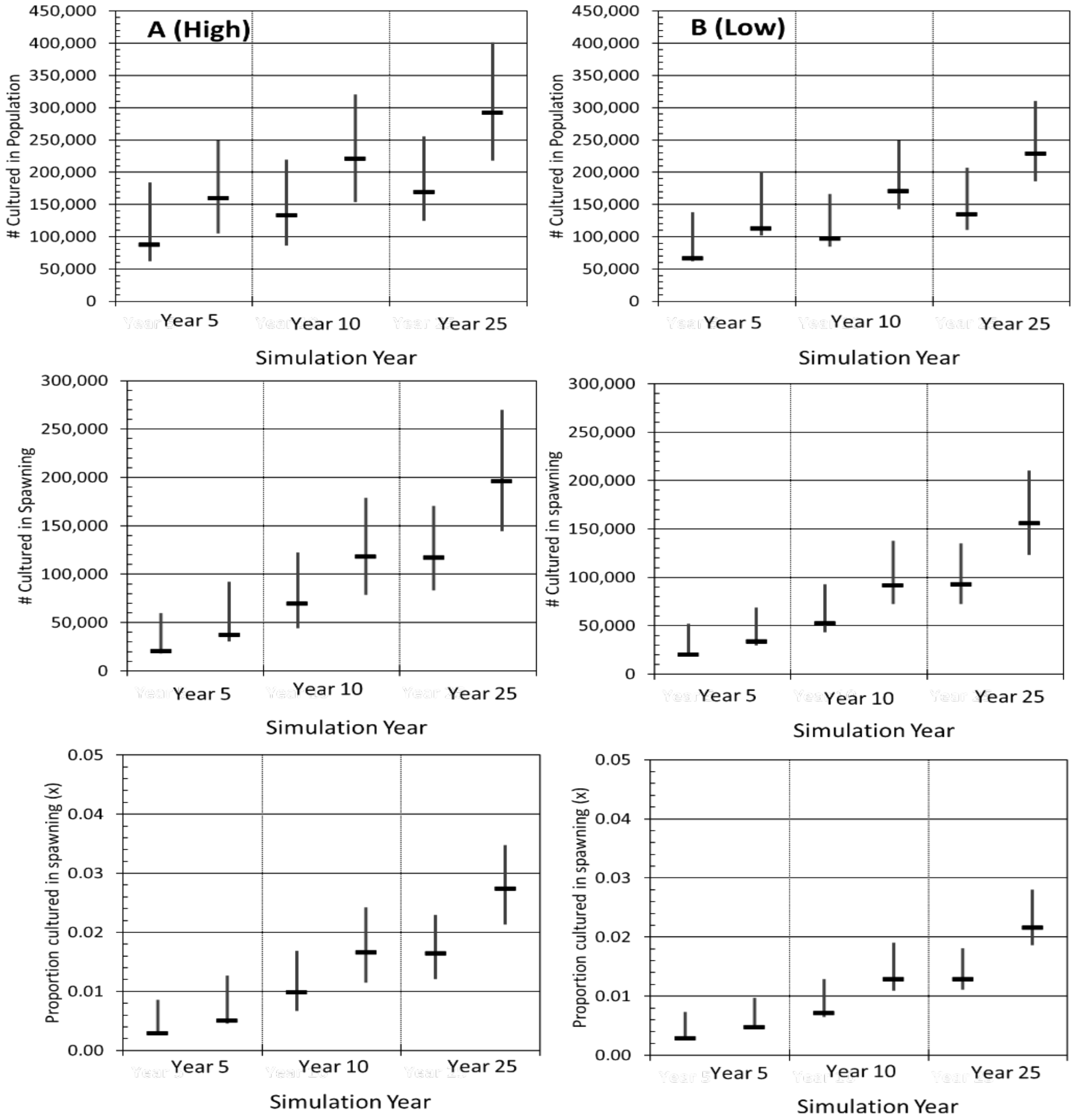

Figure 3.2. The number of cultured Red Drum under low (10,500 mt) and high (17,500 mt) production scenarios in the population (top), population spawning abundance (middle), and the proportion cultured fish in spawning (bottom). A) Model results with high episodic cage failure assumptions. B) Model results with low episodic cage failure assumptions. In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year.

The median number of cultured fish in the wild population under the low and high production scenarios, with modified model assumptions reflecting a lower potential for Red Drum escape and low survival of escapees, was approximately one-third of the high escape scenarios (Table 3.4). These modified scenarios assumed: 1) low likelihood of episodic escapes (3% for low production and 5% for high production); 2) recovery of escaped fish (with half to three-quarters recaptured following an episodic escape); 3) and reduced survival (by half) of escaped fish to enter the population and survive to spawn.

The median number of cultured fish in the wild population under modified assumptions ranged between 33,092 and 103,113 fish across all time steps and production scenarios. Considering the estimated total number of age 1 and older Red Drum in the model framework of Waples et al. (2011) (10.8 million fish; Table 3.1), the predicted abundance of escaped Red Drum in the wild NW Florida population would represent approximately 0.6% to 0.9% of the combined population of both cultured and wild Red Drum in Year 25.

The escape scenarios that reflected a lower potential for Red Drum escape and low survival of escapees are presented graphically in Figure 3.3. In Year 25, under the 3-Farm simulations with the 3% episodic likelihood assumption, the predicted median cumulative number of escaped fish surviving to spawn was approximately 45,000 fish (Figure 3.3, middle). In Year 25, under the 5-Farm simulations with the 5% episodic likelihood assumption, the predicted median cumulative number of escaped fish surviving to spawn was approximately 70,000 fish. The proportion of escaped fish in the combined wild and escaped fish spawning abundance is shown in the bottom figure of Figure 3.3. In Year 25, the median proportion of cultured fish in the wild population spawning abundance was approximately 0.006 under the low production scenario and approximately 0.01 under the high production scenario.

Table 3.4. The cumulative number of cultured Red Drum in the wild population resulting from leakage and episodic losses under the 3-Farm and 5-Farm case study scenarios with modified assumptions: low escape likelihood, recovery of escaped fish, and low survival of escaped fish.

Case Study Scenario:	Cumulative number escaped cultured fish in population		
3-Farm, 10,500 mt	**Median**	**5th**	**95th**
Number of Cultured Fish in Year 5			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	33,092	30,592	46,932
Number of Cultured Fish in Year 10			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	46,423	41,507	61,735
Number of Cultured Fish in Year 25			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	62,098	53,521	76,744
5-Farm, 17,500 mt			
Number of Cultured Fish in Year 5			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	55,398	51,021	70,868
Number of Cultured Fish in Year 10			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	78,164	69,019	96,358
Number of Cultured Fish in Year 25			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	103,113	89,067	124,139

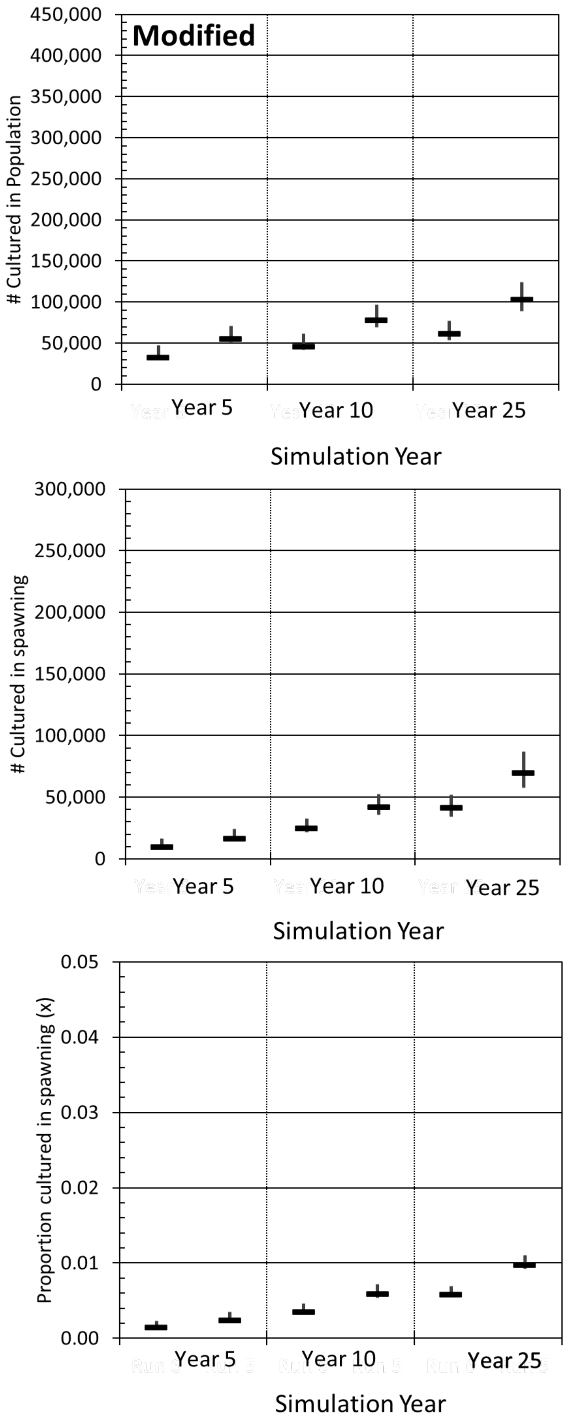

Figure 3.3. The number of cultured Red Drum under low (10,500 mt) and high (17,500 mt) production scenarios in the population (top), population spawning abundance (middle), and the proportion cultured fish in spawning (bottom) with modified assumptions: low escape likelihood, recovery of escaped fish, and low survival of escaped fish. In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year.

The results suggested that there was no effect on population fitness, even at the 95th percentile under the high production scenario and high episodic escape assumption, where the proportion of cultured fish in the mixed population is predicted to be just over 0.03 (Figure 3.2). Simulation results that incorporated leakage, low likelihood of cage failures, recovery of a portion of escaped fish, and low survival of escaped Red Drum (i.e., the "modified" scenario) predicted a maximum proportion of cultured fish in the mixed population of slightly over 0.01 (Figure 3.3). The potential for a loss of fitness was undetectable across the entire range of wild population abundances modeled in the simulations.

The potential for a reduction in effective population size (N_e) is presented in Figure 3.4, which shows results for both high and low cage failure likelihoods. Figure 3.5 presents the potential for reduction in N_e under modified escape assumptions for the low and high production scenarios.

The results in Figure 3.4 (middle) indicate that there is no substantial loss of genetic diversity when comparing N_{eT} (total effective population size) to the general guideline that an N_e greater than 5,000 fish is sufficient to avoid the deleterious effects of small N_e. However, it is important to note that across all cage failure frequencies, the cultured fish spawning with wild Red Drum in Year 25 were derived from multiple years of cultured fish escapes. As a result, the calculated N_{eT} may be a low estimate, as the parents of these fish would include wild broodstock collected over multiple years, which would likely lead to a higher N_{eC} (effective population size of cultured fish) than calculated in the modified Ryman-Laikre model.

Waples et al. (2012) also recommended considering the reduction in N_{eW} (wild effective population size), specifically the ratio of N_{eT}/N_{eW}, in large marine populations. Values less than 0.1 for this ratio may indicate that there is potential for the population to experience Ryman-Laikre effects. For both low and high cage failure rates, the reduction in N_{eW} under the 5-farm production scenario in Year 25 had a median value below 0.1 which suggested potential for Ryman-Laikre effects in the mixed population (Figure 3.4, bottom).

The results in Figure 3.5 (middle) under the low likelihood of escapes, recovery of escaped fish, and low survival of escaped fish scenario (i.e., "modified" scenario) do not suggest a loss of genetic diversity when comparing N_{eT} (total effective population size) to the general rule-of-thumb that an N_e greater than 5,000 fish is sufficient to avoid the deleterious effects of small N_e. The predicted reduction in N_{eW} (wild effective population size), represented by the ratio of N_{eT}/N_{eW} (Figure 3.5, bottom), under the modified assumptions, remained well above the 0.1 threshold suggested by Waples et al. (2012), indicating no significant risk of Ryman-Laikre effects.

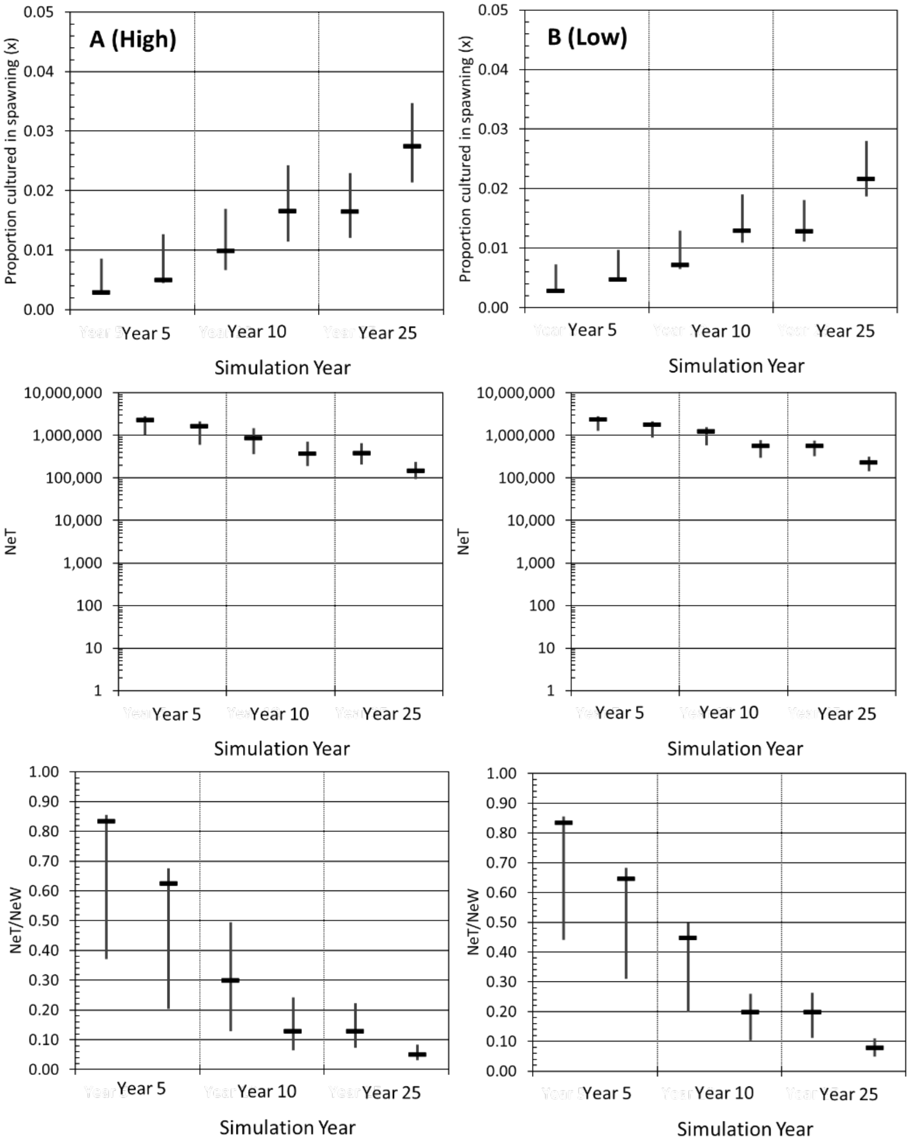

Figure 3.4. Predicted potential reduction in effective population size (N_{eT}) of Red Drum with high cage failure frequency (A) and low cage failure frequency (B). In each figure the 10,500 and 17,500 mt production scenarios are shown by simulation year.

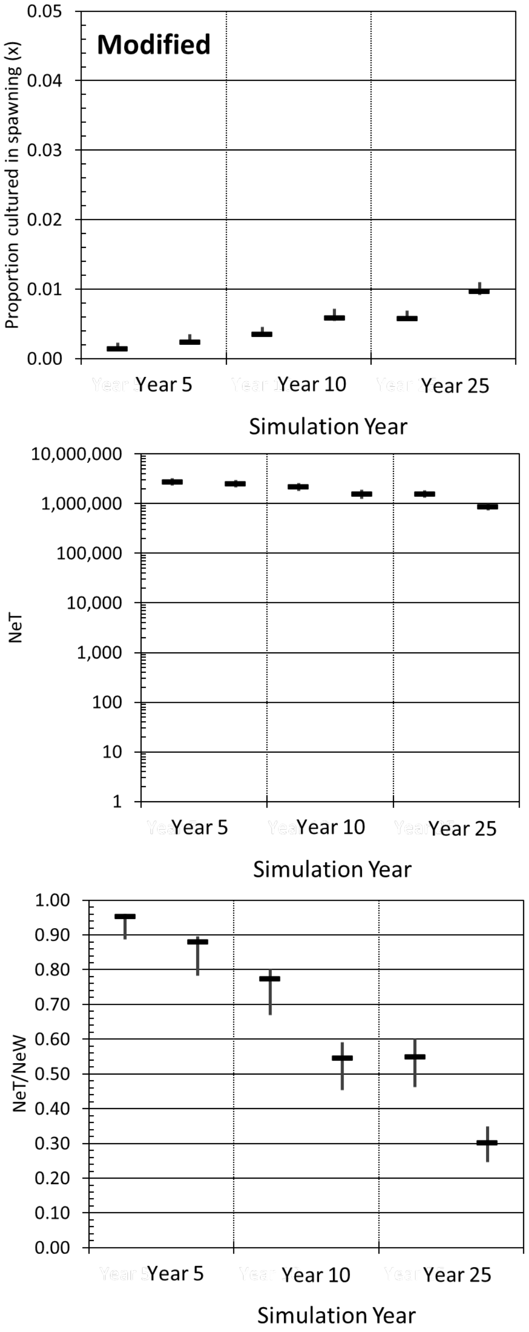

Figure 3.5. Predicted potential reduction in effective population size (N_{eT}) of Red Drum with modified assumptions: low cage failure frequency, recovery of escaped fish, and low survival of escaped fish. In each figure the 10,500 and 17,500 mt production scenarios are shown by simulation year.

3.3.2 Case Study: Almaco Jack

There are no studies of population genetic structure for Almaco Jack in the Gulf or elsewhere. Population genetic studies in seriolids show little to no divergence within water masses, like other pelagic finfish, such as tuna and billfish. For example, Gold and Richardson (1998) found evidence of two stocks of Greater Amberjack off the southeastern U.S., one in the northern Gulf and a second along the western Atlantic coast. Thus, research to date in closely related species indicates that Almaco Jack within the Gulf may be a single panmictic population.

The Greater Amberjack was identified as the most appropriate proxy species for Almaco Jack in the Gulf for developing natural population parameters in OMEGA. The species have similar life history characteristics and ecology. Although Almaco Jack may be somewhat larger, and they are known to co-localize in schools (i.e., are highly-associated with one another, as well as with Lesser Amberjack and Banded Rudderfish). In the Gulf, observed catch locations for the species appear to overlap, clustering along the edge of the shelf.

Although the SEDAR 49 Gulf Data-limited Species Data Workshop urged caution when using Greater Amberjack parameter values when assessing other jack species, the group also noted that little is known about Almaco Jack and itself proceeded to use Greater Amberjack as a proxy for Almaco Jack in SEDAR 49 (Sagarese et al. 2016). Thus, updated model parameters for Greater Amberjack in SEDAR 70 (2020) were the primary guide to modeling Almaco Jack in OMEGA in the Gulf.

The SEDAR 70 (2020) recruitment carrying capacity value of approximately 3.7 million recruits for Greater Amberjack likely does not reflect population abundance of Almaco Jack based on catch data for the two species. Gulf catch data for the two species suggest Almaco Jack are not as abundant in the Gulf (Figure 3.6). Hence, based on discussions with researchers in the Gulf, the proportion of Almaco Jack in the catch data (~10%) was used to adjust the Greater Amberjack model capacity parameter downward. This equates to a recruitment capacity of 369,500 fish compared to a Greater Amberjack recruitment capacity of 3,695,000 fish. Like California Yellowtail and White Seabass, model simulations used a range of capacity assumptions to address uncertainty in population abundance. Model simulations varied female spawning biomass between 338 mt and 750 mt.

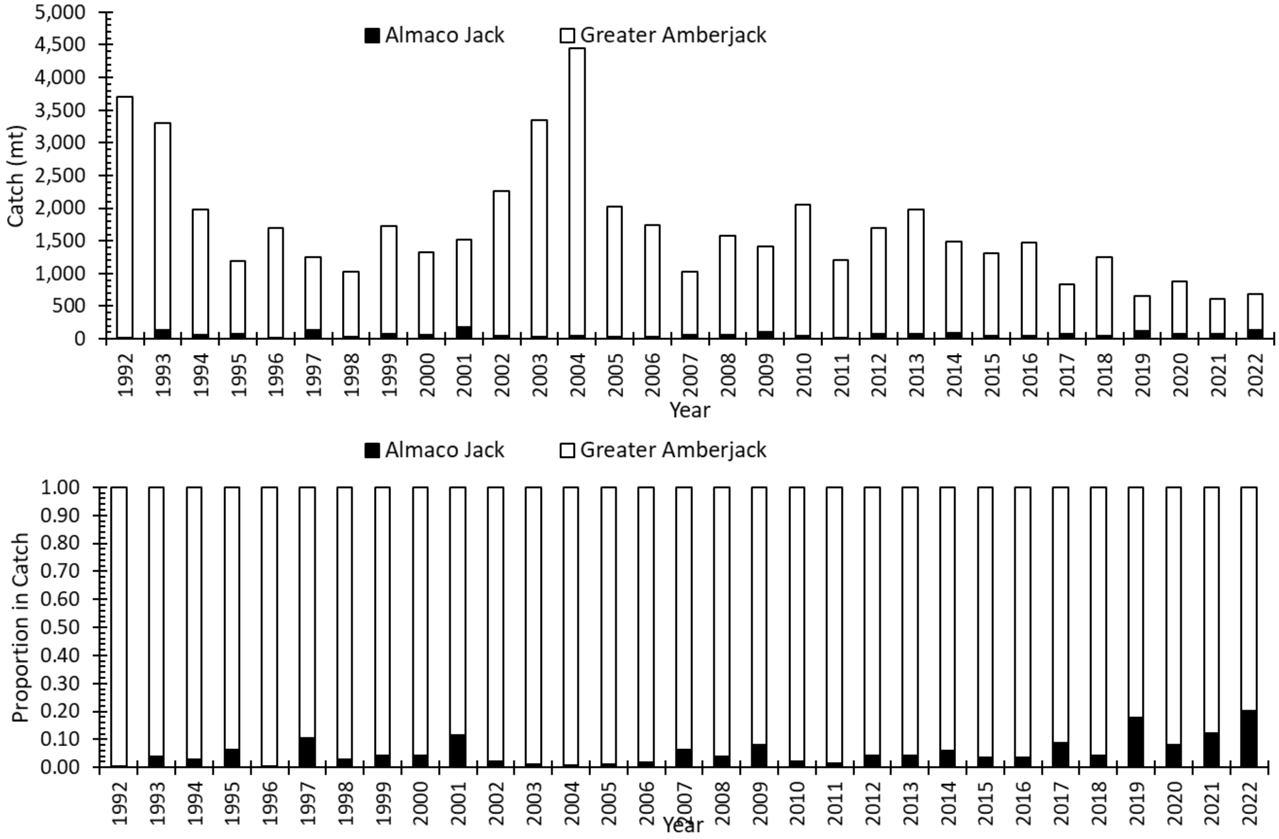

Figure 3.6. Public Catch Data for Almaco Jack and Greater Amberjack. Source: FOSS, https://www.fisheries.noaa.gov/foss

Estimates of N_e and the ratio of N_e/N_T and N_e/N_A were made assuming over-dispersed variation in reproductive success at age (i.e., a Poisson scaling factor of 3) using the AgeNe program (Waples et al. 2011). Results are summarized in Table 3.5 for the low and high population abundance assumptions. The ratio of N_e to total N was estimated to be 0.16. The ratio of N_e to adult N (N_A) was estimated to be 0.25. The number of breeders in a year (N_b) was estimated to vary between 42,014 and 93,131 adults. The total number of fish age 1 and older using the AgeNe model for the low abundance assumption was estimated to be 354,666 fish and for the high abundance assumption 786,166 fish. The estimated number of adults for low and high abundance assumptions was estimated to be 225,650 and 500,183 fish, respectively. Note these estimates of abundance are based on the life table model framework of Waples et al. (2011) and results differ slightly from total abundance estimates in OMEGA using a life cycle simulation model framework with varying survival and fishery exploitation rates.

Table 3.5. Almaco Jack calculated values of effective population size (N_e) with over-dispersed variation in reproductive success (Poisson factor = 3.0) using equations in Waples et al. 2011 and AgeNe program.

Scenario	Max Age	Generation Length	N_T	N_A	N_b	N_e	N_e / N_T	N_e / N_A
Low Population Abundance	22 yrs	8.9 yrs	354,666	225,650	42,014	55,323	0.16	0.25
High Population Abundance			786,166	500,183	93,131	122,632		

Notes:
N_T = Total number of individuals age 1 and older
N_A = Total number of adults
N_b = Effective number of breeders
N_e = Effective population size

Model simulations in OMEGA for the low (3-Farm, 10,500 mt annual production) and high production (5-Farm, 17,500 mt annual production) scenarios are presented in Table 3.6. Fish size is weight in kilograms at the end of each phase of grow-out in cages. Assumed fish size at harvest is the upper market weight range of 1.8 to 2.5 kg in reported by Blue Ocean Aquaculture in Hawaii (Blanco et al. 2022). The number of fish transferred to cages was calculated based on the market weight and a harvest goal of 10,500 mt and 17,500 mt. The number of cages assumed 100,000 fish per cage at market size. Modeled size of fish when transferred to offshore cages was 30 grams (0.03 kg). Time from transfer to harvest was assumed to be 52 weeks (Blanco et al. 2022).

As described in Section 1.3.1.1, *Use of Case Studies*, leakage assumed a loss of 0.3% of fish in a cage over the entire period fish are in cages with 65% of the total leakage occurring in the smallest bin, 10% in the mid-sized bin, and 25% in the largest bin. The total numbers of fish escaping due to leakage under the low and high production scenarios were 13,874 fish and 22,907 fish, respectively (Table 3.6).

As described in Section 1.3.1.1, *Use of Case Studies*, episodic escapes are defined as cage failures, where escape losses ranged from half to all of the fish within a given cage. Two rates of episodic escape frequencies were modeled for the high production scenario: 1) one event every 10 years (10% annual likelihood of an episodic escape event), and 2) 2.5 events every 10 years (25% annual likelihood of an episodic escape event). In the low production scenario, the modeled episodic escape likelihoods were adjusted downward using the same ratio as the high production assumptions to account for the reduced number of cages with fish and, consequently, the lower likelihood of episodic escapes. Thus, the episodic escape frequencies for the low production scenario were: 1) 0.6 events every 10 years (6% annual likelihood of an episodic escape event), and 2) 1.5 events every 10 years (15% annual likelihood of an episodic escape event). In the "modified" escape scenarios, the low escape likelihoods were halved to 3% and 5% annual likelihood under the low and high production scenarios, respectively. The number of fish escaping was reduced to between a quarter and half of the fish in a cage to account for partial fish escape recovery.

Table 3.6. Almaco Jack production scenarios modeled for the case study.

Scenario	*Fish Size at Harvest (kg)*	*# Fish*	*# Cages*	*Annual # Escaping via Leakage*			*-*
				0.5 kg	***2.25 kg***	***2.5 kg***	***Total***
3-Farm, 10,500 mt	2.5	4,216,867	43	9,345	1,304	3,225	13,874
5-Farm, 17,500 mt	2.5	7,028,112	71	15,429	2,153	5,325	22,907

Modeled survival of escaped cultured fish to enter the population varied between 37% for the smallest sized fish, 42% for the mid-sized fish, and 47% for the largest sized fish (Table 3.6). Modeled survival of escaped cultured fish to survive to spawn with wild Almaco Jack varied between 5% for the smallest sized fish, 8% for the mid-sized fish, and 13% for the largest sized fish. The smallest sized escaped Almaco contributed to spawning after 6.5 years in nature, the mid-sized fish after 5.5 years, and the largest sized fish after 4.5 years in nature. This timing is based on the maturity schedule and length-weight parameters for wild Almaco Jack where 100% of fish are sexually mature by age 8 at approximately 95 cm (12.9 kg) Sagarese et al. (2016).

Table 3.7 presents cumulative numbers of escaped fish from leakage and episodic losses across various model scenarios at Years 5, 10, and 25. The data include the median, 5th percentile, and 95th percentile values from 1,000 simulations for each time point. Results indicate an increase in the cumulative number of escaped fish in the wild population across all scenarios, with median numbers rising by approximately 30% to 40% over time.

The median number of cultured Almaco Jack predicted to be in the wild population across all production scenarios and time steps ranged from 22,461 to 77,272 fish (Table 3.7). Relative to an estimated wild population size of approximately 355,000 to 786,000 age 1 and older Almaco Jack (using the model framework from Waples et al. 2011, Table 3.5), it was predicted that escaped Almaco Jack could represent approximately 3% to 12% of the total combined population of wild and escaped fish by Year 25.

In Year 5, under the 3-Farm simulations, the predicted median cumulative number of escaped fish in the wild population between 22,461 (assuming a 6% episodic likelihood) and 33,352 fish (with a 15% episodic likelihood) (Table 3.7). Simulations with the highest escape levels (95th percentile) suggested a maximum range of escaped fish from 66,198 (at the 6% likelihood) to 95,271 fish (at the 15% likelihood). The data distribution was skewed, as most simulations resulted in cumulative escape numbers well below these 95th percentile values.

In Year 25, under the 3-Farm simulations, the predicted median cumulative number of escaped fish in the wild population ranged from 28,004 fish (assuming a 6% episodic likelihood) to 39,650 fish (with a 15% episodic likelihood) (Table 3.7). For simulations reaching the highest escape outcomes (95th percentile), the maximum cumulative escape numbers ranged from 74,420 (at the 6% likelihood) to 95,332 fish (at the 15% likelihood). The results were moderately skewed, with median values closer to the lower end of the 5th and 95th percentile range.

In Year 5, the 5-Farm simulations predicted a median cumulative number of escaped fish in the wild population ranging from 37,709 fish (with a 10% episodic likelihood) to 63,904 fish (with a 25% episodic likelihood) (Table 3.7). The 95th percentile outcomes indicated maximum escape accumulations ranging from 95,651 (at the 10% likelihood) to 122,805 fish (at the 25% likelihood). Unlike the 3-Farm scenarios with lower episodic likelihoods, the 5-Farm simulations were moderately skewed for the 10% likelihood scenarios, while results for the 25% likelihood scenario were not skewed.

In Year 25, under the 5-Farm simulations, the predicted median cumulative number of escaped fish in the wild population ranged from 49,725 fish (at a 10% episodic likelihood) to 77,272 fish (at a 25% episodic likelihood) (Table 3.7). For scenarios with the highest escape outcomes (95th percentile), the simulations indicated a maximum accumulation between 103,471 fish (at the 10% likelihood) and 138,588 fish (at the 25% likelihood). The results for the 5-Farm scenarios with a 10% likelihood were moderately skewed, while the results with a 25% likelihood showed no skew.

Table 3.7. The cumulative number of cultured Almaco Jack in the wild population resulting from leakage and episodic losses under the 3-Farm and 5-Farm case study scenarios.

Case Study Scenario:	Cumulative number escaped cultured fish in population		
3-Farm, 10,500 mt	**Median**	**5th**	**95th**
Number of Cultured Fish in Year 5			
Leakage + Episodic (15% annual likelihood)	33,352	21,125	95,271
Leakage + Episodic (6% annual likelihood)	22,461	20,950	66,198
Number of Cultured Fish in Year 10			
Leakage + Episodic (15% annual likelihood)	38,979	24,629	96,394
Leakage + Episodic (6% annual likelihood)	26,710	23,966	78,380
Number of Cultured Fish in Year 25			
Leakage + Episodic (15% annual likelihood)	39,650	25,416	95,332
Leakage + Episodic (6% annual likelihood)	28,004	24,560	74,420
5-Farm, 17,500 mt			
Number of Cultured Fish in Year 5			
Leakage + Episodic (25% annual likelihood)	63,904	35,575	122,805
Leakage + Episodic (10% annual likelihood)	37,709	34,734	95,651
Number of Cultured Fish in Year 10			
Leakage + Episodic (25% annual likelihood)	73,278	42,897	135,851
Leakage + Episodic (10% annual likelihood)	47,381	40,136	101,211
Number of Cultured Fish in Year 25			
Leakage + Episodic (25% annual likelihood)	77,272	44,810	138,588
Leakage + Episodic (10% annual likelihood)	49,725	41,488	103,471

Figure 3.6 graphically illustrates the simulation outcomes, showing the cumulative number of cultured fish in the wild population (top figures), the number of cultured fish surviving to spawn (middle figures), and the percentage of escaped fish as a proportion of the total spawning abundance (bottom figures). The high episodic likelihood scenarios (15% and 25%) are presented in Figure 3.6A (left) and the low episodic likelihoods (6% and 10%) in Figure 3.6B (right). Each figure organizes results by time steps—Year 5, Year 10, and Year 25—and by low and high production scenarios. The lower and upper whiskers represent the 5th and 95th percentiles from all 1,000 simulations, while the horizontal bars denote the median values.

In Year 25, under the 3-Farm simulations with a high 15% episodic likelihood, the predicted median cumulative number of escaped fish surviving to spawn was approximately 9,500 fish, with the cumulative 95th percentile reaching approximately 20,000 fish (Figure 3.6A, middle).

For the 5-Farm simulations under a 25% episodic likelihood, the predicted median cumulative number of surviving escaped fish was approximately 17,000, while the 95th percentile was approximately 29,000 fish.

In Year 25, under the 3-Farm simulations with a low 6% episodic likelihood, the predicted median cumulative number of escaped fish surviving to spawn was approximately 6,500 fish, with the cumulative 95th percentile reaching approximately 15,000 fish (Figure 3.6B, middle). For the 5-Farm simulations under a 10% episodic likelihood, the predicted median cumulative number of surviving escaped fish was approximately 11,500, while the 95th percentile was approximately 20,500 fish.

The bottom figures in Figure 3.6 display the number of escaped fish as a proportion of the combined spawning abundance of wild and escaped fish. The 5th and 95th percentiles in these figures account for both the range of escaped fish surviving to spawn (as previously described) and the range of female spawning biomass used in the simulations (ranging from 338 mt to 750 mt). Thus, these figures reflect the simulated stochastic variability associated with the episodic escape events and the uncertainty in the population abundance of Almaco Jack. Incorporating both sources of variation expands the range of the predicted proportion of escaped Almaco Jack in spawning populations, thereby capturing the full spectrum of potential modeled outcomes.

The median proportion of cultured fish in the wild population's spawning abundance, under the low and high production scenarios and with the assumed high episodic likelihoods, varied between approximately 0.02 and approximately 0.18 over the time period and across production scenarios (Figure 3.6A, bottom). In Year 25, under the 3-Farm simulations with the high 15% episodic likelihood assumption, the predicted proportion of cultured fish in the wild ranged from approximately 0.07 (5th percentile) to approximately 0.22 (95th percentile) with a median of approximately 0.12. In Year 25, under the 5-Farm simulations with the 25% episodic likelihood assumption, the predicted proportion of cultured fish in the wild ranged from approximately 0.12 (5th percentile) to approximately 0.29 (95th percentile) with a median of approximately 0.18.

In Year 25, under the 3-Farm simulations with the low 6% episodic likelihood assumption, the proportion of cultured fish ranged from approximately 0.06 (5th percentile) to approximately 0.17 (95th percentile) with a median of approximately 0.08 (Figure 3.6B, bottom). In Year 25, under the 5-Farm simulations with the low 10% episodic likelihood assumption, the proportion of cultured fish ranged from approximately 0.095 (5th percentile) to approximately 0.225 (95th percentile) with a median of approximately 0.135.

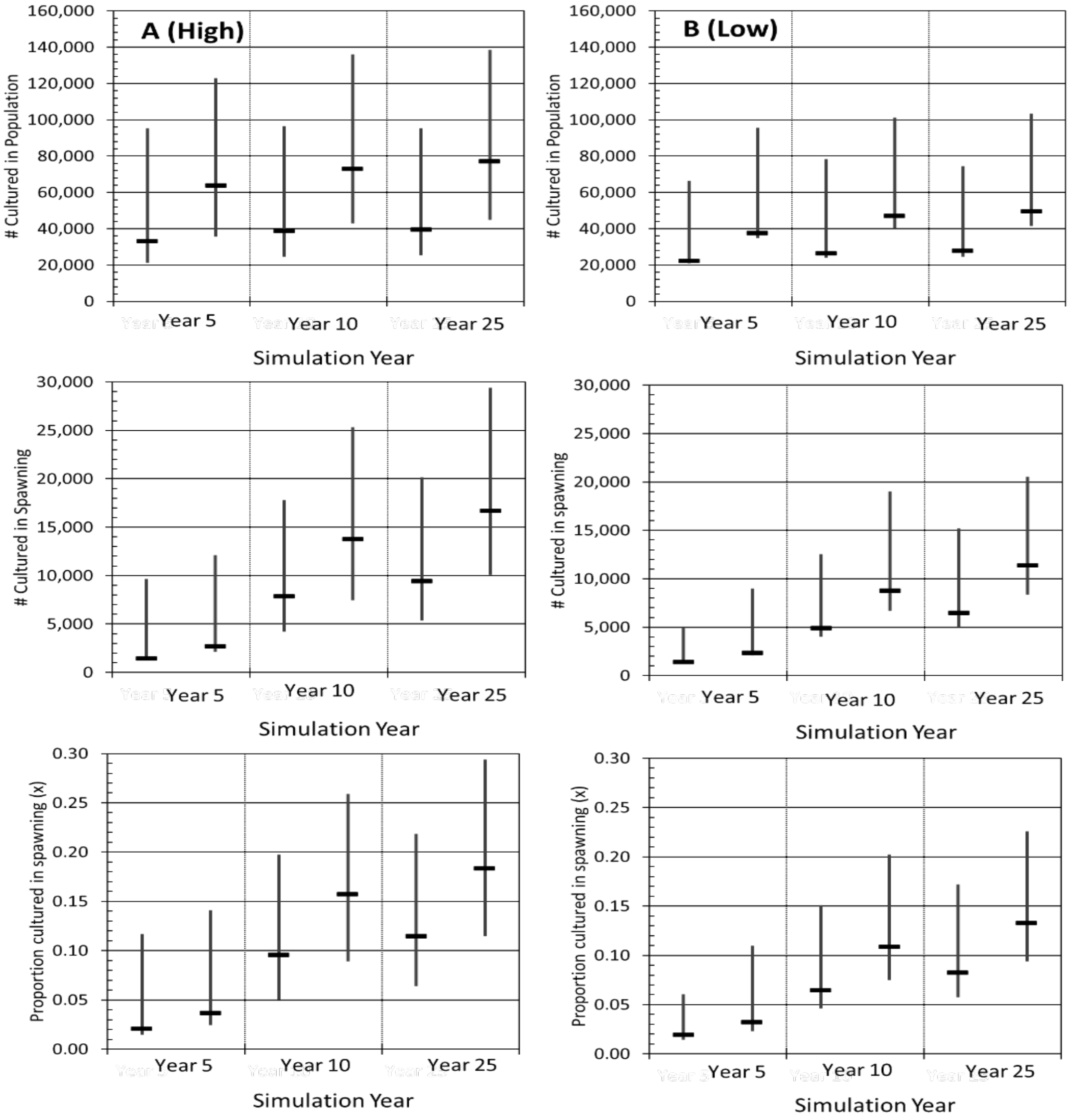

Figure 3.6. The number of cultured Almaco Jack under low (10,500 mt) and high (17,500 mt) production scenarios in the population (top), population spawning abundance (middle), and the percentage of cultured fish in spawning (bottom). A) Model results with high episodic cage failure assumptions. B) Model results with low episodic cage failure assumptions. In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year.

The median number of cultured fish in the wild population, under the low and high production scenarios with modified escape assumptions reflecting a lower potential for Almaco Jack escape and low survival of escapees, was approximately one-third of the values predicted under the high escape scenarios (Table 3.8). Again, these modified scenarios assumed: 1) low likelihood of episodic escapes (3% for the low production scenario and 5% for the high production scenario), 2) recovery of escaped fish ranging from half to three-quarters of those that escaped, 3) reduced survival (by half) of escaped fish entering the population and surviving to spawn.

The median number of cultured fish in the wild population, under the modified assumptions, varied between 11,150 and 22,091 fish across all time steps and production scenarios. When considering the estimated total number of age 1 and older Almaco Jack, as calculated using the model framework in Waples et al. (2011), which ranged from approximately 355,000 to 786,000 fish (Table 3.5), the predicted abundance of escaped Almaco Jack in the wild population would constitute only 1% to 6% of the combined population of both cultured and wild Almaco Jack.

The escape scenarios with modified assumptions, reflecting a lower potential for Almaco Jack escape and low survival of escapees, are shown graphically in Figure 3.7. In Year 25, under the 3-Farm simulations with the 3% episodic likelihood assumption, the predicted median cumulative number of escaped fish surviving to spawn was approximately 3,000 fish (Figure 3.7, middle). In Year 25, under the 5-Farm simulations with the 5% episodic likelihood assumption, the predicted median cumulative number of escaped fish surviving to spawn was approximately 5,000 fish. The proportion of escaped fish in the combined wild and escaped fish spawning abundance is displayed in the bottom figure of Figure 3.7. The median proportions of cultured fish in the wild population spawning abundance under the low and high production scenarios were 0.04 and 0.06, respectively.

Table 3.8. The cumulative number of cultured Almaco Jack in the wild population resulting from leakage and episodic losses under the 3-Farm and 5-Farm case study scenarios with low escape assumptions and low survival of escaped fish.

Case Study Scenario:	Cumulative number escaped cultured fish in population		
3-Farm, 10,500 mt	**Median**	**5th**	**95th**
Number of Cultured Fish in Year 5			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	11,150	10,395	20,064
Number of Cultured Fish in Year 10			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	12,945	11,887	21,139
Number of Cultured Fish in Year 25			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	13,223	12,184	21,090
5-Farm, 17,500 mt			
Number of Cultured Fish in Year 5			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	18,561	17,300	28,744
Number of Cultured Fish in Year 10			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	21,393	19,561	31,011
Number of Cultured Fish in Year 25			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	22,091	20,124	31,882

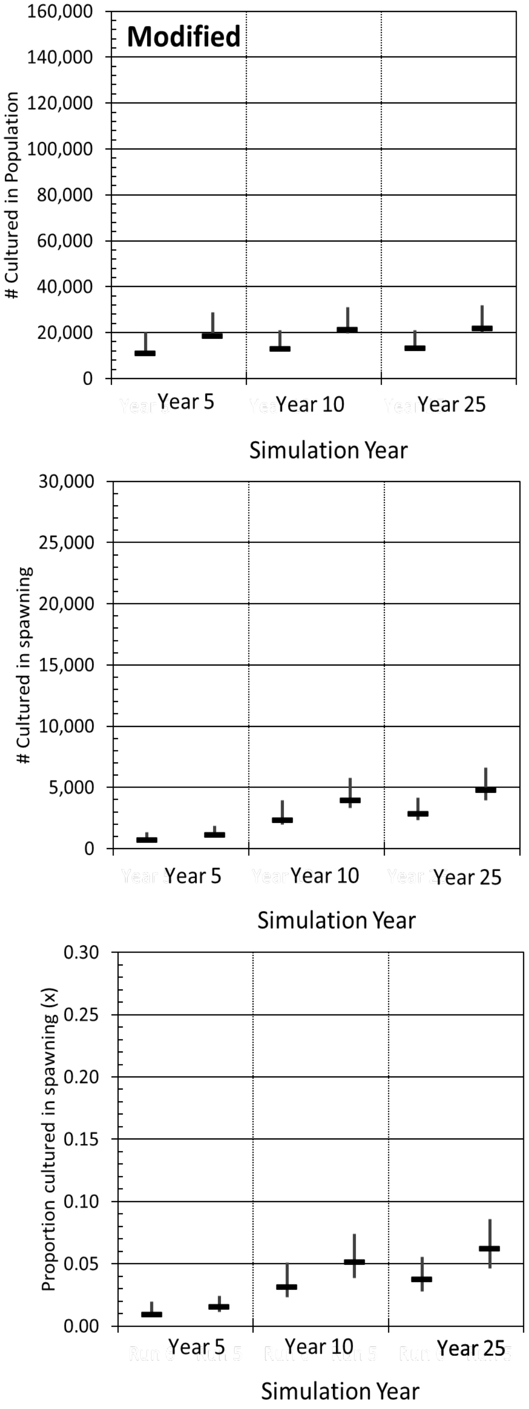

Figure 3.7. The number of cultured Almaco Jack under low (10,500 mt) and high (17,500 mt) production scenarios in the population (top), population spawning abundance (middle), and the percentage of cultured fish in spawning (bottom) with modified assumptions: low escape likelihood, recovery of escaped fish, and low survival of escaped fish. In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year.

Model simulations predicted a small loss in relative fitness from escaped Almaco Jack (Figure 3.8). The maximum relative fitness loss was 0.015, in the mixed population in Year 25 under the high production scenario and high episodic escape likelihood assumption (Figure 3.8, top, right). Under the high production scenario and low episodic escape likelihood assumption, the maximum relative fitness loss was even smaller, approximately 0.009 (Figure 3.8, top, left).

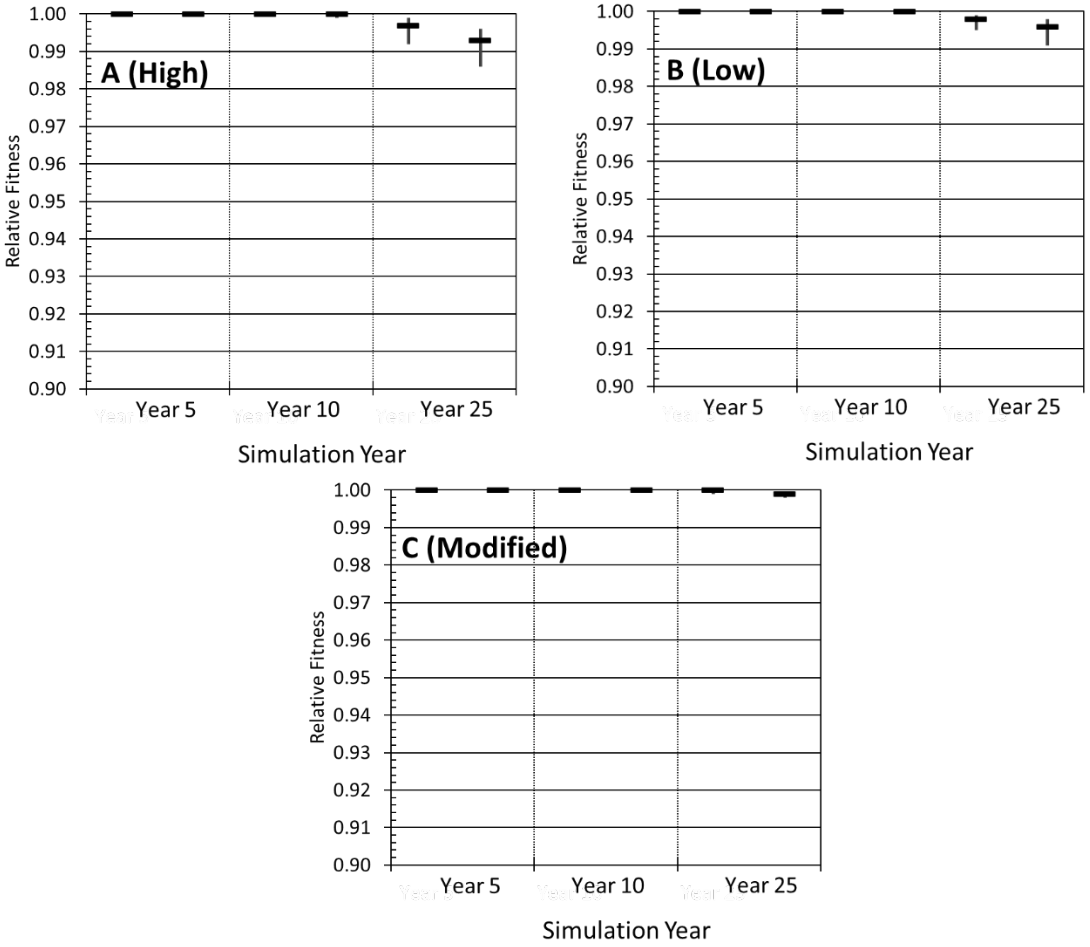

Figure 3.8. Short-term relative fitness effects for Almaco Jack under low production (10,500 mt) and high production (17,500 mt) scenarios grouped by simulation year. High, low, and modified scenarios are the same as described in previous figures.

The effects of escaped fish on fitness represent a long-term consequence for a relatively long-lived species like Almaco Jack. Model simulation results were also generated for a 90-year period (Years 10–100). Median values were calculated for each simulation iteration to capture the midpoint outcome over this extended period. The reported median value, along with the 5th and 95th percentile values, represents the median of the 1,000 iteration medians and the range of median values across all model iterations. In summary, the relative fitness results presented in Figure 3.9 are not the most extreme fitness loss predicted by the model simulations; instead, they are intended to approximate potential long-term outcomes of escapes on population fitness.

Based on the model simulations over the 90-year period, the predicted maximum median loss of fitness showed a potential for a moderate reduction from the optimum value of 1.0. Across over 1,000 simulations, the maximum predicted relative fitness loss was approximately 0.065 (95th percentile of the simulation medians) in the mixed population (Figure 3.9, high production and high episodic likelihood assumption). The median loss of fitness across all 1,000 iterations was 0.032. Fitness loss was lower under the modified scenario, with an estimation of 0.01 at the 95th percentile. The slightly greater loss of relative fitness observed in the 90-year results compared to the short-term results reflects the cumulative effect of multiple generations of escaped fish, compounded by a slight shift in the mean trait value of fish from the wild population used for broodstock.

Loss in fitness can be reduced by using wild-caught broodstock but cannot be completely avoided. Early in the simulations, escaped fish would not substantially differ from wild fish, as the traits affecting fitness in the wild population would largely remain unaffected by the escaped individuals. The greater loss of relative fitness observed in the long-term results, compared to the short-term results, reflects the cumulative effect of multiple generations of escaped fish and the shift in the mean trait value of wild fish used for broodstock. Model simulations incorporate feedback over multiple generations, with repeated escapes and spawning of escaped fish leading to a shift in the mean trait value of the combined admixed wild population of Almaco Jack. Unintended domestication selection in the culture environment would gradually cause the admixed population to shift toward the hatchery-optimal trait value. The long-term effects of escaped fish on the fitness of the wild population could be substantial, particularly at the lower end of the population abundance range, potentially impacting survival and abundance of the wild population. Thus, while the reduction in relative fitness may appear small, the proportion of cultured fish in spawning approaches 0.30 (Figure 3.6), and such a high percentage poses a risk to the wild population, which was not predicted for the two other Gulf case study species.

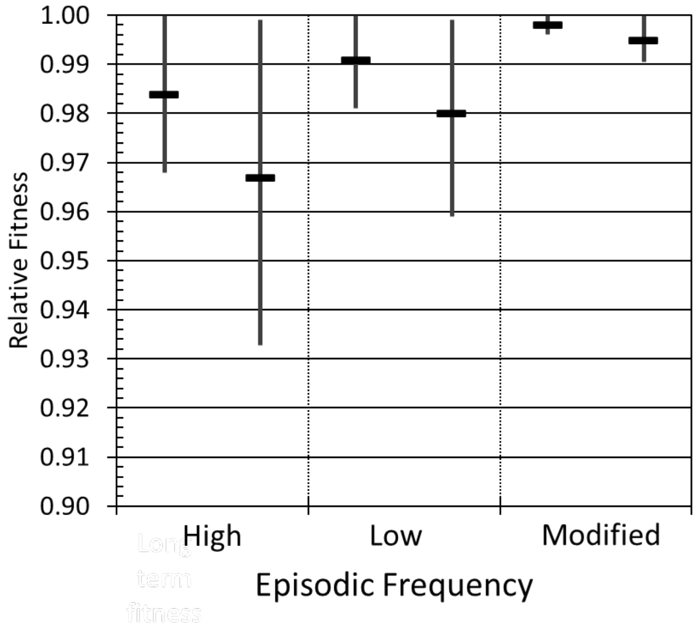

Figure 3.9. Relative fitness effects in years 10 to 100 under the low production (10,500 mt) and high production (17,500 mt) scenarios for Almaco Jack under previously described model assumptions for high, low, and modified escape assumptions. The box-whisker plots show the range of median predicted loss in fitness (5th and 95th percentiles) across the 1,000 model iterations over a 90-year period. The median predicted loss in fitness is the median of the 1,000 model iterations.

The potential for reduction in N_e is presented in Figure 3.10 with the high and low cage failure likelihoods. The potential for reduction in N_e with modified escape assumptions is presented in Figure 3.11 for the low and high production scenarios.

The results in Figure 3.10 (middle) in Year 25 under the high production scenario suggest a potential large reduction in genetic diversity when comparing N_{eT} relative to the general rule-of-thumb that N_e greater than 5,000 fish is sufficient to avoid loss of genetic diversity. It is important to note that across all cage failure frequencies, the cultured fish spawning with wild Almaco Jack in Year 25 were from multiple years of cultured fish escaping and thus the calculated N_{eT} may be a low estimate, as parents of these fish would include wild broodstock collected over multiple years (i.e., have a higher N_{eC} than calculated in the modified Ryman-Laikre model). However, the low estimated values of N_{eT} suggest higher values of N_{eC} would not change the results enough to suggest a low risk to genetic diversity. Waples et al. (2012) also recommended that a reduction in N_{eW} (i.e., ratio N_{eT}/N_{eW}) be considered in large marine populations and values less than 0.1 may result in Ryman-Laikre effects. The median reduction in N_{eW} with the highest likelihood of cage failure and under the high production scenario was just above the 0.1 rule-of-thumb and the low end of the simulation range was well below the 0.1 threshold suggesting a potential for Ryman-Laikre effects (Figure 3.10, bottom).

The modified scenario results in Figure 3.11 (middle) with low likelihood of escapes, recovery of escaped fish, and low survival of escaped fish are more favorable and do not suggest a loss of genetic diversity when comparing N_{eT} against the general rule-of-thumb that N_e greater than 5,000 fish is sufficient to avoid deleterious effects of small N_e. Additionally, the predicted reduction in N_{eW} (i.e., ratio N_{eT}/N_{eW}) (Figure 3.11 bottom) was well above the 0.1 threshold suggested by Waples et al. (2012).

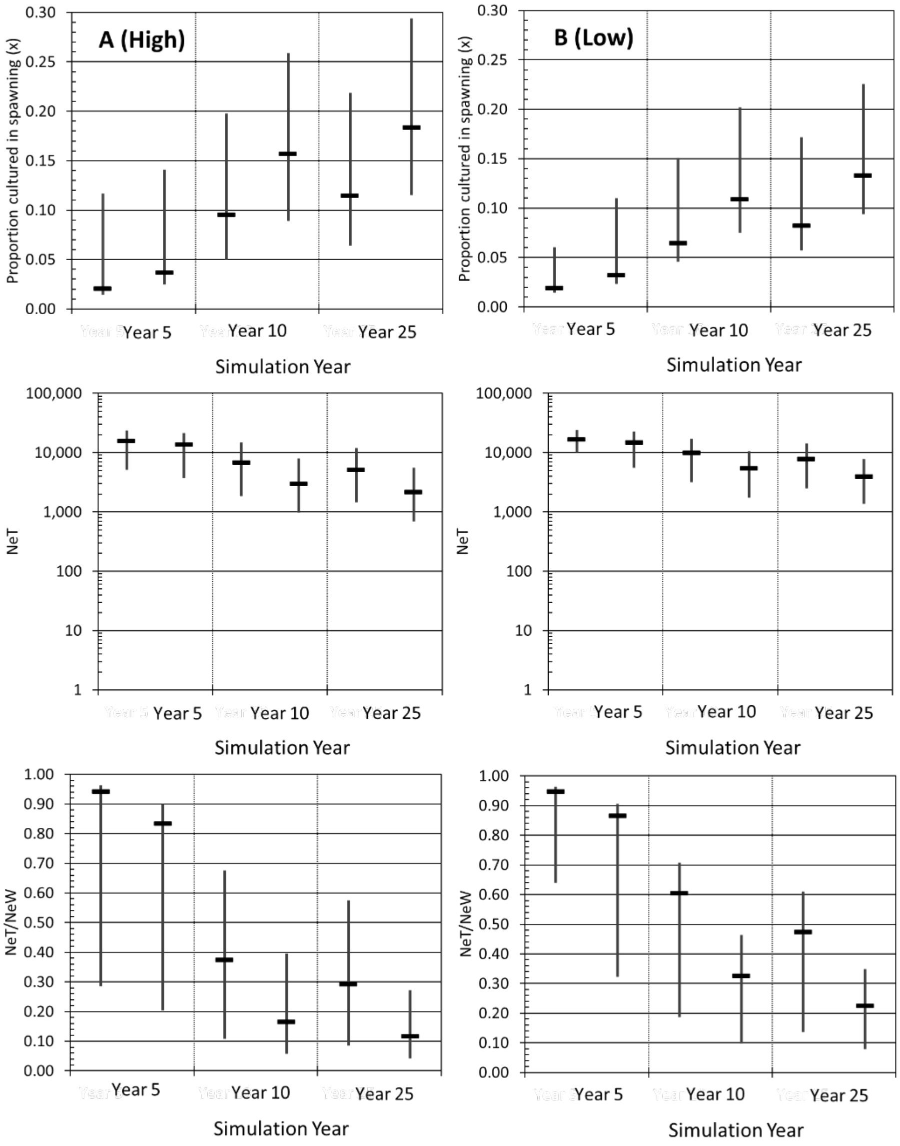

Figure 3.10. Predicted potential reduction in effective population size (N_{eT}) of Almaco Jack with high cage failure frequency (A) and low cage failure frequency (B). In each figure the 10,500 and 17,500 mt production scenarios are shown by simulation year.

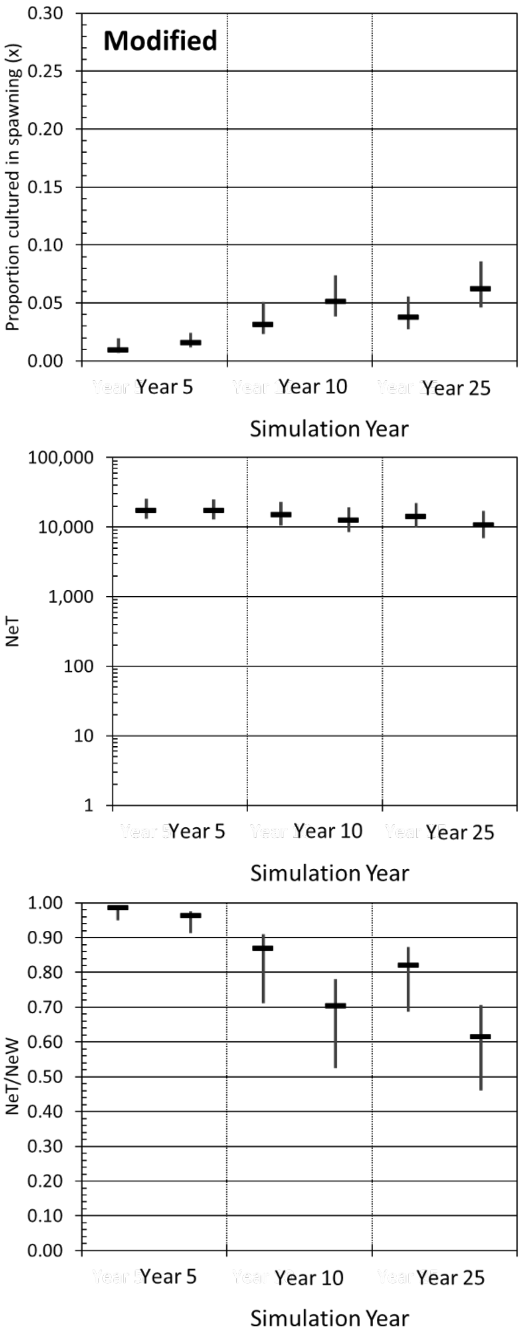

Figure 3.11. Predicted potential reduction in effective population size (N_{eT}) of Almaco Jack with low cage failure frequency, recovery of escaped fish, and low survival of escaped fish. In each figure the 10,500 and 17,500 mt production scenarios are shown by simulation year

3.3.3 Case Study: Cobia

Cobia are a highly migratory marine finfish found in tropical and sub-tropical waters, with a nearly worldwide distribution (Shaffer and Nakamura 1989).

The Cobia case study assessment was completed for the Gulf stock, which includes the Eastern Atlantic Florida coast south of the state border between Florida and Georgia (SEDAR 28 2020). Cobia are managed as a federal species in the Gulf under the Gulf and South Atlantic Fishery Management Councils in the Coastal Migratory Pelagic (CMP) Fishery Management Plan, which includes King Mackerel, Spanish Mackerel, as well as Cobia (GSMFC 2019). As such Cobia have a well-developed stock assessment model (SEDAR 28 2020) that was used to parameterize OMEGA.

The spawning stock biomass estimate of the Gulf Cobia from 2000 to 2018 varied between approximately 3,200 mt and 4,900 mt with an average of 4,020 mt (SEDAR 28 2020). Total catch (landed plus discards) in the Gulf has varied between approximately 1,700 mt to over 3,000 mt from 2000 to 2018.

Cobia are fast-growing fish that can grow to over 2 kg in their first year of life. Cobia are found in offshore and nearshore locations, and are known to be attracted to buoys, piers, and artificial structures (GSMFC 2019). The modeled Cobia maturity schedule used ages reported in SEDAR 28 (2020) with 50% of the fish mature at age 2 and 100% mature at age 3 (>700 mm fork length).

Of the three Gulf case study species, Cobia have the shortest maximum age and generation length. The maximum age is 11 years (SEDAR 28 2020) and estimated generation length was 4.0 years using the AgeNe program (Waples et al. 2011; Table 3.9). Estimates of N_e and the ratio of N_e/N_T and N_e/N_A were made assuming over-dispersed variation in reproductive success at age (i.e., a Poisson scaling factor of 3) using the AgeNe program (Waples et al. 2011). The ratio of N_e to total N was estimated to be 0.19. The ratio of N_e to adult N (N_A) was estimated to be 0.46. The number of breeders in a year (N_b) was estimated to be 402,144 adults. The total number of fish age 1 and older using the AgeNe model was estimated to be 2,493,546 fish. The estimated number of adults was estimated to be 1,026,754 fish. Note these estimates of abundance are based on the life table model framework of Waples et al. (2011) and results differ slightly from total abundance estimates in OMEGA using a life cycle simulation model framework with varying survival and fishery exploitation rates.

Table 3.9. Cobia calculated values of effective population size (N_e) with over-dispersed variation in reproductive success (Poisson factor = 3.0) using equations in Waples et al. 2011 and AgeNe program.

Scenario	Max Age	Generation Length	N_T	N_A	N_b	N_e	N_e / N_T	N_e / N_A
Over dispersed (Poisson factor = 3)	11 yrs	4.0 yrs	2,493,546	1,026,754	402,144	474,698	0.19	0.46

Notes:
N_T = Total number of individuals age 1 and older
N_A = Total number of adults
N_b = Effective number of breeders
N_e = Effective population size

This species is very fast growing in culture, reaching a harvest size of up to 6 kg in 51 weeks (Benetti et al. 2012). However, growth rate in culture varies widely by individual location. Growth is faster at lower stocking densities and higher temperatures.

Model simulations in OMEGA for the low (3-Farm, 10,500 mt annual production) and high production (5-Farm, 17,500 mt annual production) scenarios are presented in Table 3.10. Fish size is weight in kilograms at the end of each phase of grow-out in cages. Fish size at harvest is the lower end of the market weight range (4.0 to 8.0 kg) in Benetti et al. (2021). The number of fish transferred to cages was calculated based on the midpoint market weight and a harvest goal of 10,500 mt and 17,500 mt. The number of cages assumed 100,000 fish per cage at market size. Modeled size of fish when transferred to offshore cages was 10 grams (0.01 kg) and time from transfer to harvest was assumed to be approximately 52 weeks. The total number of fish escaping under the low and high production scenarios were 7,123 fish and 11,871 fish, respectively.

As described in Section 1.3.1.1, *Use of Case Studies*, leakage assumed a loss of 0.3% of fish in a cage over the entire period the fish are in cages with 65% of the total leakage occurring in the smallest bin, 10% in the mid-sized bin, and 25% in the largest bin. The estimated total number of fish escaping due to leakage under the low and high production scenarios were 7,123 fish and 11,871 fish, respectively (Table 3.10).

As described in Section 1.3.1.1, *Use of Case Studies*, episodic escapes are defined as cage failures, where escape losses ranged from half to all of the fish within a given cage. Two rates of episodic escape frequencies were modeled for the high production scenario: 1) one event every 10 years (10% annual likelihood of an episodic escape event), and 2) 2.5 events every 10 years (25% annual likelihood of an episodic escape event). In the low production scenario, the modeled episodic escape likelihoods were adjusted downward using the same ratio as the high production assumptions to account for the reduced number of cages with fish and, consequently, the lower likelihood of episodic escapes. Thus, the episodic escape frequencies for the low production scenario were: 1) 0.6 events every 10 years (6% annual likelihood of an episodic escape event), and 2) 1.5 events every 10 years (15% annual likelihood of an episodic escape event). In the “modified” escape scenarios, the low escape likelihoods were halved to 3% and 5% annual likelihood under the low and high production scenarios, respectively. The number of

fish escaping was reduced to between a quarter and half of the fish in a cage to account for partial fish escape recovery.

Table 3.10. Cobia production scenarios modeled for the case study.

Scenario	***Fish Size at Harvest (kg)***	***# Fish***	***# Cages***	***Annual # Escaping via Leakage***			**-**
				0.45 kg	***4.0 kg***	***5.0 kg***	***Total***
3-Farm, 10,500 mt	5	2,100,000	21	4,878	670	1,575	7,123
5-Farm, 17,500 mt	5	3,500,000	35	8,130	1,116	2,625	11,871

Modeled survival of escaped cultured fish to enter the population varied between approximately 16% for the smallest and mid-sized fish, and 23% for the largest-sized fish in Table 3.10. Modeled survival of escaped cultured fish to survive to spawn with wild Cobia varied between 6% for the smallest and mid-sized fish, and 19% for the largest sized fish.

The smallest and mid-sized escaped Cobia were contributing to spawning after 2.5 years in nature and the largest sized fish were contributing to spawning after 1.5 years in nature. The size of the largest escaped Cobia was approximately half the weight of age 3 sexually mature wild Cobia (5.0 kg versus approximately 10 kg, respectively. These estimates were based on wild Cobia that are 100% sexually mature at age 3 at approximately 100 cm in the Gulf (SEDAR 28 2020).

The various model scenarios predicted the cumulative number of fish from leakage and episodic losses at the three time points of the simulations (Table 3.11). The results presented are the median, 5th percentile, and 95th percentile values across the 1,000 simulations at Year 5, Year 10, and Year 25.

The median number of cultured Cobia in the wild population under the low and high production scenarios ranged from 6,856 to 17,673 fish across all time steps and production scenarios, excluding the modified scenario (Table 3.11). When placed in the context of the estimated total number of age 1 and older Cobia, approximately 2.5 million fish (using the model framework from Waples et al., 2011; Table 3.9), the results predicted that the abundance of escaped Cobia in the wild would constitute approximately 0.4% to 0.7% of the combined population of cultured and wild Cobia in Year 25 under the low and high production scenarios, respectively.

In Year 5, under the 3-Farm simulations, the predicted median cumulative number of escaped fish in the population ranged between 5,350 (with the 6% likelihood) and 6,856 fish (with the 15% likelihood) (Table 3.11). Simulations with the highest escape outcomes (95th percentile) indicated that a maximum between 30,831 (with the 6% likelihood) and 47,863 (with the 15% likelihood) escaped fish may accumulate in the wild population. The results were highly skewed with median values close to the low end of the 5th and 95th percentile range.

In Year 25, under the 3-Farm simulations, the predicted median cumulative number of escaped fish in the population ranged between 5,542 (with the 6% likelihood) and 7,249 fish (with the 15% likelihood) (Table 3.11). Simulations with the highest escape outcomes (95th percentile) indicated that a maximum between 36,135 (with the 6% likelihood) and 49,925 (with the 15% likelihood) escaped fish may accumulate in the wild population. The results were also highly skewed with median values closer towards the low end of the 5th and 95th percentile range.

In Year 5, under the 5-Farm simulations the predicted median cumulative number of escaped fish in the population ranged between 9,050 (with the 10% likelihood) and 17,186 fish (with the 25% likelihood) (Table 3.11). Simulations with the highest escape outcomes (95th percentile) indicated that a maximum between 46,175 (with the 10% likelihood) and 58,555 (with the 25% likelihood) escaped fish may accumulate in the wild population. In contrast to the highly skewed results for the 3-Farm scenarios under both episodic escape likelihoods, median values for the 5-Farm scenarios were only skewed with the low episodic escape likelihood.

In Year 25, under the 5-Farm simulations, the predicted median cumulative number of escaped fish in the population ranged between 9,471 (with the 10% likelihood) and 17,055 fish (with the 25% likelihood) (Table 3.11). Simulations with the highest escape outcomes (95th percentile) indicated that a maximum between 47,180 (with the 10% likelihood) and 58,924 (with the 25% likelihood) escaped fish may accumulate in the wild population. Like the Year 5 results, median values under the 5-Farm scenarios in Year 25 were highly skewed towards the low end of the range with the low episodic escape likelihood.

There was essentially no increase in the number of cultured Cobia in the population over time in both the 3-Farm and 5-Farm scenarios. This was because of the short generation length (4 years) of Cobia; escaped fish entering the population died out after only a few years in the population. The age structure of Cobia did not allow a cumulative increase in escaped fish in the wild population as was predicted for Red Drum, for example (see Table 3.3). The results tended to be more skewed compared to other species because of the age structure. The higher predicted escape results (95th percentile results) were simulation iterations that included a cage failure occurrence just prior to the reported Year 5, Year 10, and Year 25 results.

Table 3.11. The cumulative number of cultured Cobia in the wild population resulting from leakage and episodic losses from current year escapes and surviving fish from previous years under the 3-Farm and 5-Farm case study scenarios simulation results.

Case Study Scenario:	Cumulative number escaped cultured fish in population		
3-Farm, 10,500 mt	**Median**	**5th**	**95th**
Number of Cultured Fish in Year 5			
Leakage + Episodic (15% annual likelihood)	6,856	5,165	47,863
Leakage + Episodic (6% annual likelihood)	5,350	5,117	30,831
Number of Cultured Fish in Year 10			
Leakage + Episodic (15% annual likelihood)	7,442	5,320	48,663
Leakage + Episodic (6% annual likelihood)	5,546	5,250	31,187
Number of Cultured Fish in Year 25			
Leakage + Episodic (15% annual likelihood)	7,249	5,310	49,925
Leakage + Episodic (6% annual likelihood)	5,542	5,252	36,135
5-Farm, 17,500 mt			
Number of Cultured Fish in Year 5			
Leakage + Episodic (25% annual likelihood)	17,186	8,704	58,555
Leakage + Episodic (10% annual likelihood)	9,050	8,577	46,175
Number of Cultured Fish in Year 10			
Leakage + Episodic (25% annual likelihood)	17,673	9,039	60,321
Leakage + Episodic (10% annual likelihood)	9,423	8,788	44,440
Number of Cultured Fish in Year 25			
Leakage + Episodic (25% annual likelihood)	17,055	9,125	58,924
Leakage + Episodic (10% annual likelihood)	9,471	8,787	47,180

The simulation results are presented graphically in Figure 3.12. The top figures show the number of cultured fish in the wild population, while the middle figures display the number of cultured fish surviving to spawn. The bottom figures illustrate the percentage of escaped fish as a proportion of the population spawning abundance. The high episodic likelihood results are shown in Figure 3.12A (left), with episodic likelihoods of 15% and 25%, and the low episodic likelihoods are shown in Figure 3.12B (right), with episodic likelihoods of 6% and 10%. Both the low and high production scenarios are grouped within the Year 5, Year 10, and Year 25 time steps in the figures. The lower and upper whiskers in the figures represent the 5th and 95th percentiles predicted across all 1,000 simulations, while the horizontal bars indicate the median values.

In Year 25, under the 3-Farm simulations with the high 15% episodic likelihood assumption, the predicted median cumulative number of escaped fish surviving to spawn was approximately 3,000 fish (Figure 3.12A, middle). The predicted cumulative 95th percentile number of cultured fish surviving to spawn was approximately 13,000 fish. In Year 25, under the 5-Farm simulations with the 25% episodic likelihood assumption the predicted median cumulative number of escaped fish surviving to spawn was approximately 6,000 fish. The predicted cumulative 95th percentile number of cultured fish surviving to spawn was approximately 17,500 fish.

The number of escaped fish as a proportion of the combined wild and escaped fish spawning abundance is shown in the bottom figures in Figure 3.12. Note the 5th and 95th percentiles in these figures include the previously described range of escaped fish surviving to spawn. Model simulations include stochastic variation in population abundance, but do not include a range of possible population abundance assumptions. Thus, the range of values is mostly due to the variation in the number of escaped fish.

The median proportion cultured fish in the wild population spawning abundance under the low and high production scenarios and assumed high episodic likelihoods varied between approximately 0.003 and 0.012 across all time steps and production scenarios (Figure 3.12, bottom). In Year 25, under the 3-Farm simulations with the high 15% episodic likelihood assumption, the predicted proportion of cultured fish ranged from approximately 0.004 (5th percentile) to 0.025 (95th percentile) with a median of approximately 0.006 (Figure 3.12A, bottom). In Year 25, under the 5-Farm simulations with the 25% episodic likelihood assumption, the predicted proportion of cultured fish ranged from approximately 0.005 (5th percentile) to 0.0325 (95th percentile) with a median of approximately 0.012 (Figure 3.12A, bottom).

In Year 25, under the 3-Farm simulations with the low 6% episodic likelihood assumption the proportion of cultured fish ranged from approximately 0.002 (5th percentile) to 0.014 (95th percentile) with a median of approximately 0.003 (Figure 3.12B, bottom). In Year 25, under the 5-Farm simulations with the low 10% episodic likelihood assumption, the proportion of cultured fish ranged from approximately 0.006 (5th percentile) to 0.024 (95th percentile) with a median of approximately 0.006 (Figure 3.12b, bottom).

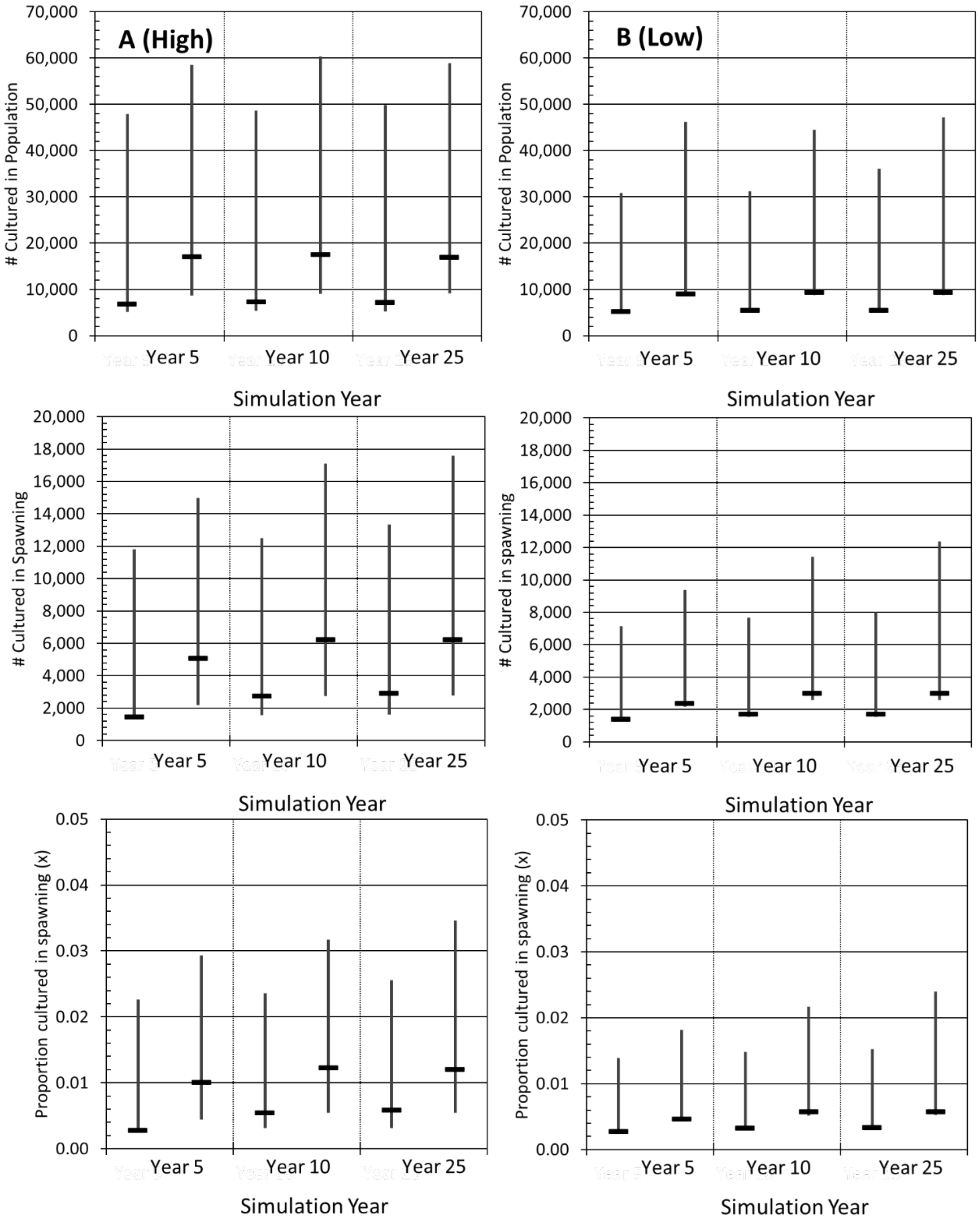

Figure 3.12. The number of cultured Cobia under low (10,500 mt) and high (17,500 mt) production scenarios in the population (top), population spawning abundance (middle), and the proportion cultured fish in spawning (bottom). A) Model results with high episodic cage failure assumptions. B) Model results with low episodic cage failure assumptions. In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year.

The median number of cultured fish in the wild population under the low and high production scenarios, with modified model assumptions reflecting a lower potential for Cobia escape and low survival of escapees, was approximately one-quarter to one-half of the numbers predicted under high escape scenarios (Table 3.12). These modified scenarios assumed: 1) low likelihood of episodic escapes (3% and 5% for low and high production scenarios, respectively); 2) recovery of escaped fish (half to three-quarters of the fish recaptured following an episodic escape); and 3) reduced survival (by half) of escaped fish to enter the population and survive to spawn.

The median number of cultured fish in the wild population under modified assumptions varied between 2,659 and 4,591 fish across all time steps and production scenarios. In the context of the estimated total number of age 1 and older Cobia, based on the model framework in Waples et al. (2011), which estimates 2.5 million fish (Table 3.9), the abundance of escaped Cobia in the wild Gulf population would be approximately 0.2% of the combined population of cultured and wild Cobia in Year 25.

Table 3.12. The cumulative number of cultured Cobia in the wild population resulting from leakage and episodic losses under the 3-Farm and 5-Farm case study scenarios with modified assumptions: low escape likelihood, recovery of escaped fish, and low survival of escaped fish.

Case Study Scenario:	Cumulative number escaped cultured fish in population		
3-Farm, 10,500 mt	**Median**	**5th**	**95th**
Number of Cultured Fish in Year 5			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	2,659	2,560	5,879
Number of Cultured Fish in Year 10			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	2,735	2,617	6,790
Number of Cultured Fish in Year 25			
Leakage + Episodic (3% annual likelihood) + Low Escapee Survival	2,732	2,614	5,771
5-Farm, 17,500 mt			
Number of Cultured Fish in Year 5			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	4,470	4,275	11,143
Number of Cultured Fish in Year 10			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	4,576	4,386	10,301
Number of Cultured Fish in Year 25			
Leakage + Episodic (5% annual likelihood) + Low Escapee Survival	4,591	4,371	11,536

The escape scenarios reflecting a lower potential for Cobia escape and low survival of escapees are displayed graphically in Figure 3.13. In Year 25, under the 3-Farm simulations with the 3% episodic likelihood assumption, the predicted median cumulative number of escaped fish surviving to spawn was approximately 1,000 fish (Figure 3.13, middle). In Year 25, under the 5-Farm simulations with the 5% episodic likelihood assumption, the predicted median cumulative number of escaped fish surviving to spawn was fewer than 2,000 fish. The proportion of escaped fish in the combined wild and escaped fish spawning abundance is shown in the bottom figure of Figure 3.13. In Year 25, the median proportion of cultured fish in the wild population spawning abundance under the low production scenario was 0.002, and under the high production scenario, it was approximately 0.003.

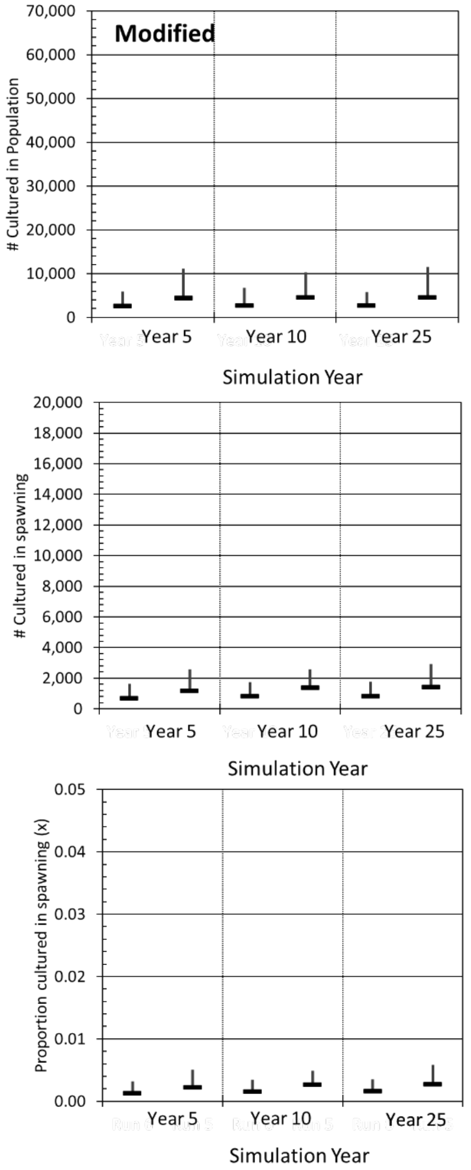

Figure 3.13. The number of cultured Cobia under low (10,500 mt) and high (17,500 mt) production scenarios in the population (top), population spawning abundance (middle), and the proportion cultured fish in spawning (bottom) with modified assumptions: low escape likelihood, recovery of escaped fish, and low survival of escaped fish. In each figure the 10,500 and 17,500 mt production scenarios are shown grouped by simulation year.

Results suggest no effect on population fitness even at the 95th percentile under the high production scenario and high episodic escape assumption; the proportion of cultured fish was predicted to be just over 0.035 of the mixed population (Figure 3.12). Simulation results with leakage, low likelihood of cage failures, recovery of a portion of escaped fish, and low survival of escaped Cobia (i.e., modified scenario) indicated a maximum proportion cultured in fish in the mixed population of less than 0.01 (Figure 3.13).

The potential for reduction in N_e is presented in Figure 3.14 with the high and low cage failure likelihoods. The potential for reduction in N_e with modified escape assumptions is presented in Figure 3.15 for the low and high production scenarios.

The results in Figure 3.14 (middle) do not indicate a potential loss of genetic diversity when comparing N_{eT} against the general rule-of-thumb that N_e greater than 5,000 fish is sufficient to avoid deleterious effects of small N_e. It is important to note that across all cage failure frequencies, the cultured fish spawning with wild Cobia in Year 25 were from multiple years of cultured fish escaping and thus the calculated N_{eT} may be a low estimate, as parents of these fish would include wild broodstock collected over multiple years (i.e., have a higher N_{eC} than calculated in the modified Ryman-Laikre model). Waples et al. (2012) also recommended that a reduction in N_{eW} (i.e., ratio N_{eT}/N_{eW}) be considered in large marine populations and values less than 0.1 may indicate a potential for populations to experience Ryman-Laikre effects. The median and 95th percentile reduction in N_{eW}, at the highest likelihood of cage failure in Year 25, were well above the 0.10 threshold, suggesting no potential Ryman-Laikre effect (Figure 3.14A, bottom).

The results in Figure 3.15 (middle) with low likelihood of escapes, recovery of escaped fish, and low survival of escaped fish (i.e., “modified” scenario) do not suggest a loss of genetic diversity when comparing N_{eT} against the general rule-of-thumb that N_e greater than 5,000 fish is sufficient. In addition, the predicted reduction in N_{eW} (i.e., ratio N_{eT}/N_{eW}) (Figure 3.15 bottom) were well above the 0.1 threshold suggested by Waples et al. (2012).

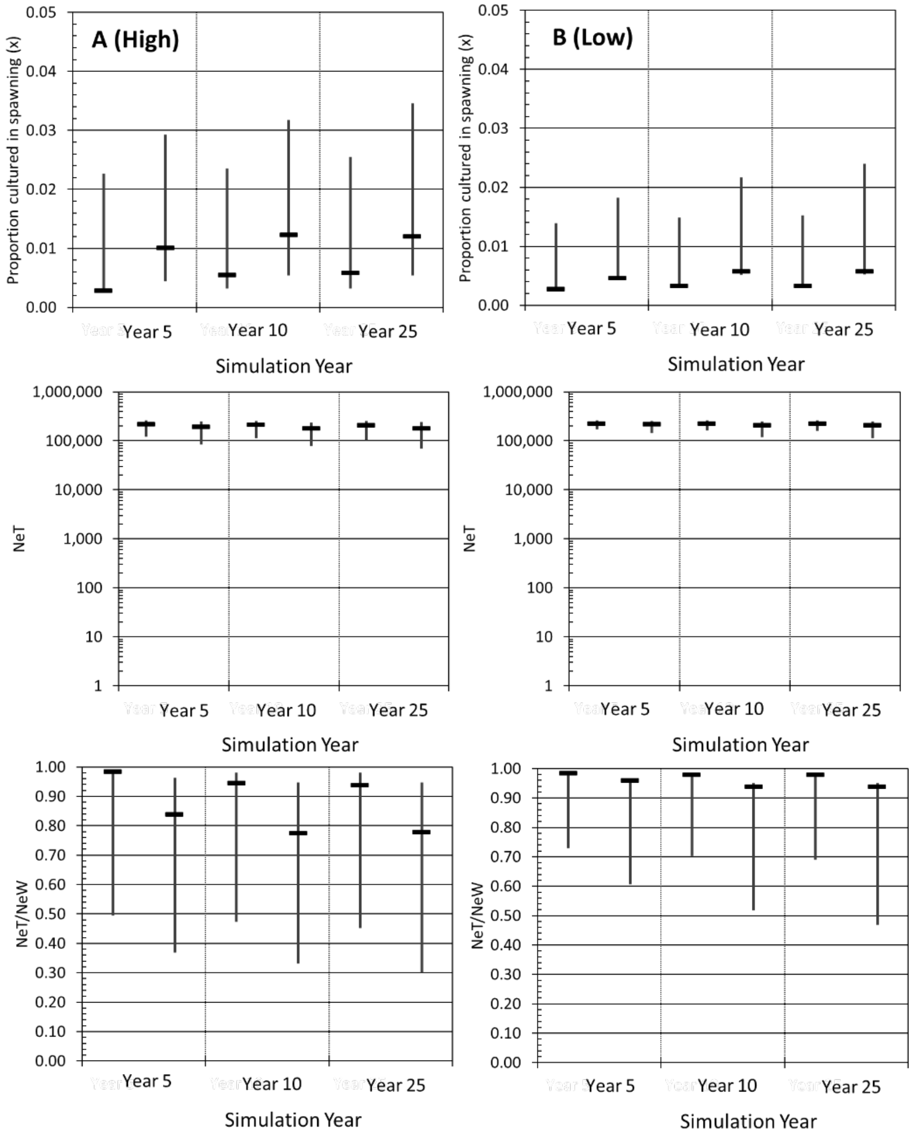

Figure 3.14. Predicted potential reduction in effective population size (N_{eT}) of Cobia with high cage failure likelihood (A) and low cage failure likelihood (B). In each figure the 10,500 and 17,500 mt production scenarios are shown by simulation year.

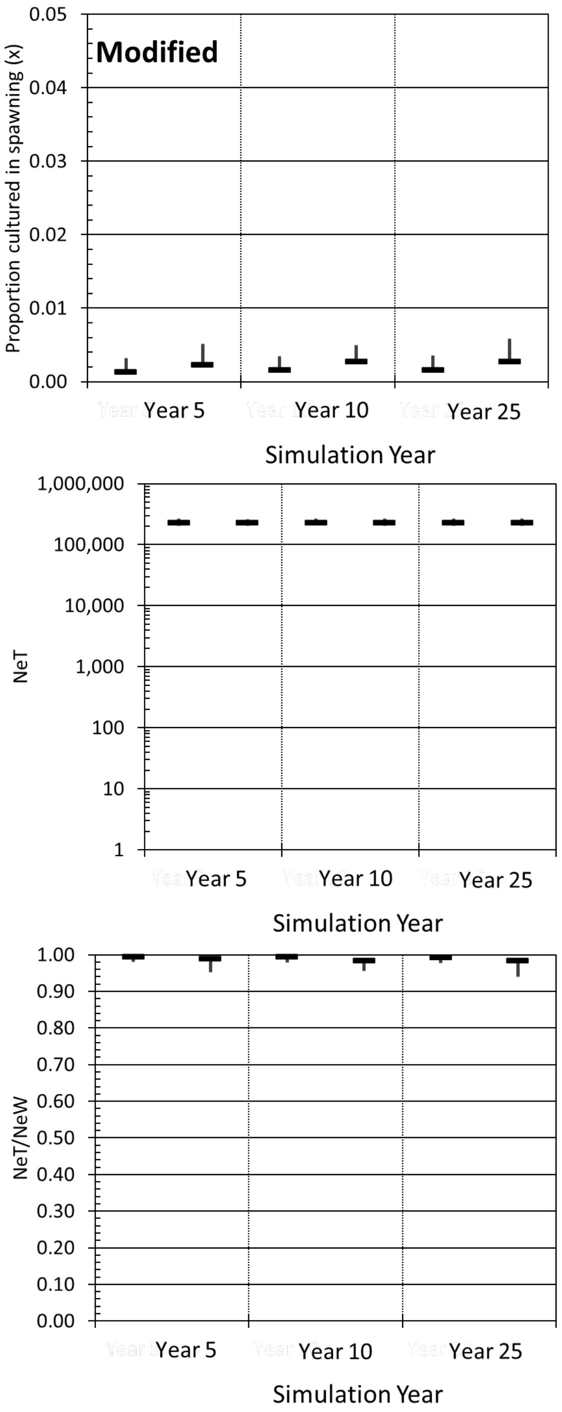

Figure 3.15. Predicted potential reduction in effective population size (N_{eT}) of Cobia with low cage failure likelihood, recovery of escaped fish, and low survival of escaped fish. In each figure the 10,500 and 17,500 mt production scenarios are shown by simulation year.

3.3.4 Gulf of America Case Study Conclusions

The OMEGA model was used to evaluate potential genetic impacts from escaped Red Drum, Almaco Jack, and Cobia on wild conspecifics in the Gulf.

The potential impacts of cultured fish escaping into nature include genetic effects from introgression of cultured fish with the wild populations leading to a loss of fitness from the unintended selection of traits during captive rearing that are maladapted in the wild population, and the reduction in the effective population size and subsequent loss of genetic diversity within the wild population. Ecological effects from escaped fish were not analyzed but could occur and may include predation, competition, or disease transfer to the wild population of conspecifics or to other species within the marine ecosystem. The focus of these case studies for the Gulf species was to evaluate the potential genetic impacts from escaped fish. The case study analyses reported the number of fish escaping from leakage and cage failure which could be used to further evaluate potential ecological effects from escaped fish.

3.3.4.1 Red Drum Conclusions

For Red Drum, simulation results under the high production scenario with the high escape likelihood suggested negligible effects on population fitness. Important factors that greatly minimize the potential for loss of fitness in the wild population include: the use of local wild-origin fish in the captive breeding program, the absence of intentional selection for specific traits in breeding program, and a large NW Florida population that appears abundant relative to the case study production scenarios. Although Red Drum are considered a data-limited species (SEDAR 49 2023), the Red Drum assessment was greatly improved by using model parameters from the stock assessment completed by Addis (2020) and the case study assessment was supported by other studies of Red Drum on the west coast of Florida (e.g., Tringali1 and Lowerre-Barbieri 2023).

Based on simulations with leakage, low likelihood of cage failures, recovery of a portion of escaped fish, and low survival of escaped Red Drum (i.e., “modified” scenario), the potential for loss of fitness was undetectable in the model simulations.

Based on simulations from leakage and episodic cage failures under the high production scenario with high episodic cage failure likelihood, the effective size of the mixed population (N_{eT}) was sufficiently large (i.e., above 5,000 fish) to avoid deleterious effects of small N_e. At the highest frequency of cage failures, the values for the higher escape outcomes in the simulations (95th percentiles) began to approach a level where the wild population could experience Ryman-Laikre effects.

Based on simulations with leakage, low likelihood of cage failures, recovery of a portion of escaped fish, and low survival of escaped Red Drum (i.e., “modified” scenario), the potential for deleterious effects of small N_e were predicted to be of minor consequence.

The case study results should only be applied to the eastern half of the Gulf after first considering the population structure and population abundances of Red Drum in this portion of the Gulf. In addition, Texas has a large annual release of 10 to 20 million hatchery Red Drum fry for stock enhancement, which may have its own effects on fitness and genetic diversity which would confound any predictions from OMEGA. The assessment did not evaluate how escaped cultured Red Drum may affect fitness and genetic diversity of subpopulations along the Texas coast that are the focus of the Texas stock enhancement program.

Additionally, the potential loss of genetic diversity among population subgroups was not evaluated. Studies have shown that Red Drum exhibit a high degree of spawning site fidelity (Tringali and Lowerre-Barbieri 2023), with fish spawning in estuaries along Florida's west coast likely not interbreeding with those spawning in Texas estuaries. This site fidelity indicates localized spawning populations that may be adapted to specific regional conditions. If escaped Red Drum move beyond the area where broodstock were originally collected and spawn with other subgroups, these localized adaptations could be disrupted, potentially impacting genetic diversity and fitness across subpopulations.

3.3.4.2 Almaco Jack Conclusions

The predicted proportion of cultured fish spawning with wild fish of the other case study species in the Gulf (Red Drum and Cobia) were low under even the high production scenario and high assumed episodic likelihoods, and the predicted loss of fitness was negligible for these two species. However, there is a potential loss of fitness in Almaco Jack.

Almaco Jack are classified a data limited species in the Gulf (SEDAR 49 2016) and, although the SEDAR 49 Gulf Data-limited Species Data Workshop urged caution when using Greater Amberjack parameter values when assessing other jack species, the group also noted that little is known about Almaco Jack and itself proceeded to use Greater Amberjack as a proxy for Almaco Jack in SEDAR 49 (Sagarese et al. 2016). Thus, updated model parameters for Greater Amberjack in SEDAR 70 (2020) were the primary guide to modeling Almaco Jack in OMEGA in the Gulf. However, abundance of Almaco Jack in the Gulf is unknown. Abundance of this species in the Gulf was inferred from catch data relative to Greater Amberjack which has a stock assessment for the Gulf (SEDAR 70 2020). Catch of Almaco Jack has averaged around 10% of the combined Almaco Jack and Greater Amberjack catch, suggesting Almaco Jack abundance is about a tenth of the Greater Amberjack abundance. However, there has been a trend in recent years of a slightly higher proportion Almaco Jack, this may possibly suggest a more abundant population or better monitoring of Almaco Jack catch. Like California Yellowtail and White Seabass, model simulations for Almaco Jack used a range of abundance assumptions to address uncertainty in population abundance. Model simulations varied female spawning biomass between 338 mt and 750 mt.

As with all case study species, low (3-Farm, 10,500 mt) and high (5-Farm, 17,500 mt) production scenarios were developed for Almaco Jack. Model simulations of Almaco Jack escape scenarios detected a loss in fitness by Year 25 and a potentially more deleterious loss of fitness over the long-term (years 1- 100) timeframe. By Year 25, under the 5-Farm production scenario with the high episodic cage failure assumption, the median proportion of cultured fish in the mixed cultured and wild population was approximately 0.20 (or 20% of that mixed population). The 95th percentile result, representing the lower end of the population range, was approximately 0.30 (or 30% of the mixed population). By Year 25 under 3-Farm production scenario, and high episodic cage failure assumptions, the median proportion of cultured fish in the mixed population was approximately 0.10 and the 95th percentile result, representing the lower end of the population range, exceeded 0.20. The predicted median loss in fitness under the 5-Farm scenario in Year 25, with the high episodic cage failure assumption, was 0.008. The median long-term loss of fitness was approximately 0.032 and the 95th percentile long-term fitness loss was 0.067. Thus, although the reduction in relative fitness was relatively small to moderate for this species, the estimated proportion of cultured fish in the spawning population nearing 0.20 poses a significant risk to the wild population. This level of introgression differs from the outcomes predicted for the other two Gulf case study species, indicating a potentially greater genetic risk for this particular species.

A more considerable impact is the potentially high reduction in the effective size of the mixed population (N_{eT}) and a loss of genetic diversity in the population. Based on simulations from leakage and episodic cage failures under the high production scenario with high episodic cage failure likelihood, the effective size of the mixed population (N_{eT}) was well below the 5,000 fish rule-of-thumb and the 0.10 ratio threshold (N_{eT}/N_{eW}). At the highest frequency of cage failures, simulation outcomes under scenarios with higher escape levels and lower population abundance indicated a ratio that suggested greater potential for Ryman-Laikre effects on the wild population.

Based on simulations with leakage, low likelihood of cage failures, recovery of a portion of escaped fish, and low survival of escaped Almaco Jack (i.e., the "modified" scenario) the potential for deleterious effects of small N_e were predicted to be of minor consequence.

3.3.4.3 Cobia Conclusions

For Cobia, simulation results under the high production scenario with the high escape likelihood suggested negligible effects on population fitness. Important factors that greatly minimize the potential for loss of fitness in the wild population include: the use of local wild-origin fish in the captive breeding program, the absence of intentional selection for specific traits in breeding program, and a relatively large Cobia population in the Gulf that appears abundant relative to the case study production scenarios. The Cobia case study was greatly improved by using model parameters developed for a recent stock assessment (SEDAR 28 2020).

Based on simulations with leakage, low likelihood of cage failures, recovery of a portion of escaped fish, and low survival of escaped Cobia (i.e., "modified" scenarios), the potential for loss of fitness was undetectable in the model simulations.

Based on simulations from leakage and episodic cage failures under the high production scenario with the high episodic cage failure likelihood, the effective size of the mixed population (N_{eT})

was sufficiently large (i.e., above 5,000 fish) to avoid deleterious effects of small N_e. At the highest frequency of cage failures, the values for the higher escape outcomes in the simulations (95th percentiles) were above a level where the wild population would experience Ryman-Laikre effects.

Based on simulations with leakage, low likelihood of cage failures, recovery of a portion of escaped fish, and low survival of escaped Cobia (i.e., “modified” scenario) the potential for deleterious effects of small N_e were predicted to be of no consequence.

There was essentially no increase in the number of cultured Cobia in the population over time in both the 3-Farm and 5-Farm scenarios. Cobia have the shortest generation length of the three Gulf case study species (e.g., Cobia – 4 years, Red Drum – 11.4 years, and Almaco Jack – 8.9 years). This life history meant that escaped fish entering the population died out after only a few years in the population. The age structure of Cobia did not allow a cumulative increase in escaped fish in the wild population as predicted for Red Drum and Almaco Jack. Also, Cobia results were more skewed with median values close to the 5th percentile range compared to other species because of this age structure. The higher predicted escape results (95th percentile results) were simulation iterations that included a cage failure occurrence just prior to the reported Year 5, Year 10, and Year 25 results. Median results were influenced largely by annual leakage from cages.

3.3.4.4 Additional Conclusions Specific to Effective Population Size (N_e) Predictions in the Gulf of America Case Study Species

Model simulations predicted a reduction in effective population size and potential loss of genetic diversity in Almaco Jack and a moderate reduction in effective population size and potential loss of genetic diversity in Red Drum loss using the modified Ryman-Laikre effect model framework in Waples et al. (2016). The potential for loss in genetic diversity was not predicted for Cobia.

See Section 2.3.4.4, *Additional Conclusions Specific to Effective Population Size (N_e) Predictions in Southern California Case Study Species* for a more in-depth discussion of the effect of a reduced effective population size (N_e) in a mixed population. Briefly, with some low level of escapement on a regular basis, or possibly infrequent larger incursions of escaped fish into the wild population from episodic cage failures, the mixed population of Almaco Jack and Red Drum may be resilient to some reduction in N_e, especially for a species with a generation length of approximately 11 years for Red Drum and an assumed high lifetime variance in reproductive success. The shorter generation length of 4 years for Almaco Jack may result in a higher potential for reduction in effective population size (N_{eT}) from escaped fish.

The impact of effective population size (N_e) on genetic diversity within Almaco Jack and Red Drum populations, along with the implications of genetic diversity for adaptive potential, is an area of great interest but also substantial uncertainty. The relatively recent realization that the N_e-to total population size (N) ratio may be orders of magnitude higher than previously estimated for many marine fish species with high fecundity and high early mortality rates (Waples et al.

2018; Jones et al. 2019; Tringali and Lowerre-Barbieri 2023) is prompting a re-evaluation of the characterization of early-life stages in fish (Tringali and Lowerre-Barbieri 2023) and driving a shift in recruitment dynamics paradigms for these species (Lowerre-Barbieri et al. 2017; Árnason et al. 2023).

Information is not available to characterize the ratio of N_e to total population size (N) for Almaco Jack. In contrast, Tringali and Lowerre-Barbieri (2023) provided empirical estimates of the ratio of Red Drum N_e to adult abundance (N_a) of between $0.09 - 0.50$ and a most likely ratio of approximately 0.21.

Quantifying or balancing the outcomes of these opposing impacts remains unfeasible given current state of knowledge. However, avoiding reductions in N_e and loss of genetic diversity may be supported by several strategies: 1) minimizing the number of escaped fish through operational designs aimed at preventing escapes; 2) using broodstock that represent a broad genetic background from the region of operation to capture local genetic diversity, with sufficient brood size and breeding protocols to maximize the N_e in cultured fish; and 3) producing fish that either cannot survive or cannot reproduce in the wild environment (e.g., through sterilization). Additional risk reduction can be achieved by increasing the number of broodstock adults, employing parentage analysis of captive breeders to monitor and optimize the effective breeder (N_b) to census size (N) ratio. One possible approach would be to develop broodstock to supply multiple farms and distributing fry/fingerlings to the farms that include offspring from the entire pool of broodstock. That would increase genetic diversity of fish in a cage as a hedge if the fish were to escape.

4.0 Genetic Risk Factors and Management Measures

Culture candidate species for Southern California and Gulf discussed in Chapters 2 and 3 are summarized in the below tables, with an emphasis on risk factors that could potentially contribute to genetic effects to wild populations. Risk factors are specifically related to reproduction and the potential for culture-wild interactions, and subsequent reduced population fitness and decline in genetic diversity.

The assessment of genetic risk levels considers specific species and population dynamics that may influence genetic impacts on wild populations due to aquaculture activities. These risk levels are determined by evaluating key factors related to species and population characteristics that could affect genetic interactions with wild counterparts. The risk factors are: potential for maturity in culture (e.g., harvest after maturity age would present greater genetic risk), size of the wild population abundance (e.g., low abundance of the local population would mean greater demographic contribution for each escaped fish, with potential for greater genetic risk), biological/life history characteristics (cultured fish more likely to migrate away from cages would present greater genetic risk, longer-lived fish may promote a cumulative effect of culture trait persisting through multiple generations), and regional population genetic structure (escaped fish may alter or homogenize signals of genetic structure and/or eliminate local adaptation among populations).

The evaluation of uncertainty in the risk level is based on available data to support findings on wild population status and genetic diversity. The Low/Moderate/High assessment for the genetic risk level and uncertainty presented in the tables is based on a broad review of the available research and scientific literature regarding wild population dynamics and characteristics for each species. The risk levels do not account for culture production levels, escape rates or other operational factors. As such the genetic risk levels in the table can be considered for factors that influence risk but should not be construed as a full assessment of genetic risk from aquaculture.

4.1 Southern California Aquaculture Candidate Species – Summary of Genetic Risk Factors

Table 4.1. Finfish Genetic Risk Factors – Southern California

Part A: Population Dynamics and Reproduction, Southern California Candidate Species

Species Name	Common Name	Native to Region	Population Status	Habitat	Spawning Type	Spawning Season
Seriola dorsalis	California Yellowtail	Yes	Annual landings vary according to ocean temperature; the stock is assumed to be healthy, but there is no stock assessment	Coastal pelagic	Broadcast batch spawning through late adulthood	Summer to early fall, temperature dependent
Atractoscion nobilis	White Seabass	Yes	Subject to overfishing, rebuilding stock through replenishment programs	Demersal as juveniles, Pelagic as adults	Pelagic batch spawning	March to September
Morone saxatilis	Striped Bass	No, introduced in 19th century and naturalized	Declined due to overfishing, rebuilding through fishery regulation	Euryhaline coastal areas	Iteroparous anadromous spawners	Late spring to early summer
Anoplopoma fimbria	Sablefish	Yes	Healthy, not overfished nor subject to overfishing	Demersal	Batch spawners	January to March
Paralichthys californicus	California Halibut	Yes	Resilient population, but there is uncertainty about the relative contributions of environmental factors and fishing pressure relative to abundance	Benthic	Pelagic batch spawning	Year round, peaking in early spring
Paralichthys olivaceus	Olive Flounder	No	Nonexistent in the U.S.	Benthic	Pelagic batch spawning	January to August

Part B: Aquaculture Information, Southern California Candidate Species

Species Name	Common Name	Maturity Size/Length	Maturity Age	Market Size	Age at attainment of Market Size	Current Aquaculture Status
Seriola dorsalis	California Yellowtail	50 to 64 cm TL	2 to 3 years	4.0 kg	24 months	Commercial program in development in California; onshore in the Netherlands, offshore in Australia and New Zealand
Atractoscion nobilis	White Seabass	60 to 80 cm TL	3 to 4 years	1 to 2 kg	18 months	Stock enhancement for the last 40 years in Southern California
Morone saxatilis	Striped Bass	25 to 46 cm FL	4 to 6 years	2 kg	24 months	Extensive onshore culture, offshore in Baja California
Anoplopoma fimbria	Sablefish	56 cm TL	5 to 9 years	2.5 kg	24 months	Offshore in Canada; experimental in U.S.
Paralichthys californicus	California Halibut	20 to 42 cm SL	2 to 5 years	1 kg	36 months	Japan, experimental in the U.S.
Paralichthys olivaceus	Olive Flounder	43 cm TL	2 to 3 years	0.8 to 1.2 kg	12 to 18 months	Extensive onshore culture in Korea and Japan

Part C: Assessment of Risk and Uncertainty, Southern California Candidate Species

Species Name	Common Name	Potential for Gamete Release in Culture	Priorities for Research	Influence of Species and Population Dynamics on Genetic Risk Level	Uncertainty in Risk Level	Management Priorities to Minimize Genetic Effects
Seriola dorsalis	California Yellowtail	Low: can be harvested before maturity	Stock assessment, genetic diversity	Low to Moderate: can be harvested before maturity; status of wild population is unknown but presumed to be healthy; also see OMEGA case study results in Part D of this table	Moderate: stock is presumed to be healthy based on limited data	Broodstock genetic management plan
Atractoscion nobilis	White Seabass	Low: harvest size occurs 1-2 years before maturity	Fine-scale stock structure and migratory behavior for the range of Southern California to South Baja California, effective population size and reproductive success of the wild mixed population	High: harvest size occurs before maturity; replenishment is contributing to stability of population, but more data are needed on abundance and genetics of the admixed population; also see OMEGA case study results in Part D of this table	High: stock is rebuilding through enhancement efforts, but effect on genetic diversity needs to be better understood. Stock assessments are needed to estimate biomass and identify the geographical extent of the Southern California population	Broodstock genetic management plan, genetic diversity monitoring
Morone saxatilis	Striped Bass	Low: harvest size occurs 1-2 years before maturity in females, however male harvest size may coincide with maturity	Culture management of sexual dimorphism, genetic diversity, population abundance	Low to Moderate: unlikely to mature in culture, replenishment is contributing to stability of population abundance, but more data are needed	Moderate: stock is rebuilding but there is limited data on stock status; as a non-native species, culture may pose risks (not evaluated here) to other species and ecosystems.	Broodstock genetic management plan, genetic diversity monitoring
Anoplopoma fimbria	Sablefish	Very Low: harvest size occurs 2-3 years before maturity	Culture management of sexual dimorphism, genetic diversity	Low to Moderate: harvest size occurs before maturity, status of wild population is healthy, however potential for encounter is high	Low: genetic research and stock assessments have been done recently	Broodstock genetic management plan, genetic diversity monitoring

Species Name	Common Name	Potential for Gamete Release in Culture	Priorities for Research	Influence of Species and Population Dynamics on Genetic Risk Level	Uncertainty in Risk Level	Management Priorities to Minimize Genetic Effects
Paralichthys californicus	California Halibut	High: Maturity occurs 1-2 years before reaching harvest size	Culture management of sexual dimorphism, genetic diversity	High: harvest size occurs before maturity; population status is uncertain	Moderate: Updated stock assessment is needed	Management of sexual dimorphism, management of gamete releases in culture, broodstock genetic management plan, genetic diversity monitoring
Paralichthys olivaceus	Olive Flounder	Low: harvest size occurs before maturity	Culture management of sexual dimorphism, genetic diversity	Low: nonexistent wild population in the U.S.	Low	Not applicable; nonexistent wild population in the U.S., however this species presents potential ecological risks

Part D: OMEGA Case Studies to Evaluate Genetic Risk of Farm Scenarios for Three Candidate Species in Southern California

Common Name of Candidate Species	Production Level, metric tons	Proportion of cultured fish in spawning population [1]			Relative Long-term Fitness [1]			Admixed Population Effective Size as a fraction of Wild Population Effective Size (N_{eT}/N_{eW}) [1, 2]		
		High	**Low**	**Modified**	**High**	**Low**	**Modified**	**High**	**Low**	**Modified**
California Yellowtail	10,500	0.007	0.004	0.002	>0.999	>0.999	>0.999	0.53	0.80	0.96
	17,500	0.013	0.007	0.003	>0.999	>0.999	>0.999	0.26	0.55	0.88
White Seabass [3]	10,500	0.225	0.190	0.105	0.946	0.958	0.988	0.03	0.05	0.17
	17,500	0.330	0.290	0.160	0.902	0.920	0.971	0.01	0.01	0.07
Striped Bass	10,500	No results available – see Section 2.3.3 for discussion [4]								
	17,500	No results available – see Section 2.3.3 for discussion								

[1] Median values of 1,000 simulations. See Section 2.3, *OMEGA Genetic Risk Modeling Case Studies for Finfish in Southern California* for details on results and model scenarios. The High, Low and Modified columns refer to likelihood of episodic events. “High” is the most conservative assumption, with an episodic event likelihood of 15% in any given year for the 10,500 mt scenario and 25% in any given year for the 17,500 mt scenario. “Low” assumes a 6% likelihood in any given year for the 10,500 mt scenario and 10% in any given year for the 17,500 mt scenario. “Modified” assumes a 3% likelihood in any given year for the 10,500 mt scenario and 5% in any given year for the 17,500 mt scenario, as well as reduced escape survival compared to the “High” and “Low” conditions. In general, “High” and “Low” are considered to be conservative in regard to escape levels that would occur during operation, while “Modified” represents an anticipated level of escape assuming best management practices are followed.

[2] The ratio of admixed population size to the wild effective population size is a key indicator of genetic diversity. A value of 1.0 is a baseline level of diversity in the wild population. A value of less than 0.1 indicates high likelihood of deleterious Ryman-Laikre effects in the wild population. See Section 1.3.1, *OMEGA Model for Assessment of Finfish Escapes* for discussion.

[3] Results in this table assume a range of White Seabass population within Southern California. Modeling was also done with a population extending into the Baja California, Mexico portion of the species range. See Section 2.3.2, *Case Study: White Seabass* for further information on modeling scenarios for this species.

[4] Striped Bass are a naturalized species and there is not enough information about California populations to determine potential genetic risks. See Section 2.3.3, *Case Study: Striped Bass* for further discussion.

4.2 Gulf of America Aquaculture Candidate Species – Summary of Genetic Risk Factors

Table 4.2. Finfish Genetic Risk Factors – Gulf of America

Part A: Population Dynamics and Reproduction, Gulf of America Candidate Species

Species Name	Common Name	Native to Region	Population Status	Habitat	Spawning Type	Spawning Season
Sciaenops ocellatus	Red Drum	Yes	Rebuilding through enhancement programs, unknown status in the Gulf EEZ	Euryhaline, adults migrate to the Gulf and return to bays in the fall	Broadcast batch spawning through late adulthood	Late summer/early fall
Seriola rivoliana	Almaco Jack	Yes	Overfishing likely occurring, overfished status unknown	Pelagic	Pelagic	April to November
Rachycentron canadum	Cobia	Yes	Stable; not overfished, but potentially undergoing overfishing based on projections	Pelagic	Broadcast batch spawning	May to September in the Gulf
Seriola dumerili	Greater Amberjack	Yes	Rebuilding through fishery regulation, overfished and subject to overfishing	Pelagic, reef-associated	Broadcast spawning	March to June
Trachinotus carolinus	Florida Pompano	Yes	Stable low abundance levels as of 2009	Pelagic	Unknown; likely multiple batch spawners	Year-round
Centropristis striata	Black Sea Bass	Yes	Declining: Overfished and undergoing overfishing (fn)	Primarily nearshore and benthic habitat	Protogynous hermaphrodite, pelagic eggs	December to April
Cynoscion nebulosus	Spotted Seatrout	Yes	Varies by state; generally abundant but prone to overfishing	Estuarine	Pelagic batch spawners	Late spring to early fall, peaking midsummer
Lobotes surinamensis	Tripletail	Yes	Unknown	Pelagic, primarily nearshore	Pelagic batch spawners	Summer months

Species Name	Common Name	Native to Region	Population Status	Habitat	Spawning Type	Spawning Season
Paralichthys lethostigma	Southern Flounder	Yes	Varies by state; in general, declining due to fishing pressure, Rebuilding	Estuarine, euryhaline	Hermaphroditic, broadcast spawning	November to January

Part B: Aquaculture Information, Gulf of America Candidate Species

Species Name	Common Name	Maturity Size/Length	Maturity Age	Market Size	Age at attainment of Market Size	Current Aquaculture Status
Sciaenops ocellatus	Red Drum	66 to 69 cm TL	4-6 years	1.2 to 1.6 kg	16 to 24 months	Stock enhancement in the Gulf
Seriola rivoliana	Almaco Jack	Insufficient data on life history	Insufficient data on life history	1.8 to 3.0 kg	8 to 18 months	Commercial in Hawaii and Japan
Rachycentron canadum	Cobia	100 cm TL (at 100% maturity)	2 to 3 years	3.5 to 6.0 kg	9 to 12 months	Japan and Mediterranean, experimental in the U.S. (HI, FL, MD)
Seriola dumerili	Greater Amberjack	90 cm FL	2 to 3 years	6.0 kg	30 to 36 months	Commercial in Mexico, Belize, Panama, Bahamas
Trachinotus carolinus	Florida Pompano	28 to 33 cm FL	1 to 3 years	0.7 kg	9 months	Commercial in Panama, Experimental in Gulf States
Centropristis striata	Black Sea Bass	12 to 21 cm TL	1 to 3 years	0.6 to 1.1 kg	20 months	Primarily experimental onshore culture
Cynoscion nebulosus	Spotted Seatrout	26 to 30 cm TL	1 to 3 years	450 g	10 months	Onshore growout; supplementation programs in the Gulf
Lobotes surinamensis	Tripletail	38 to 49 cm TL	About 1 year	1 kg	6 to 7 months	Experimental in MS and FL
Paralichthys lethostigma	Southern Flounder	20 to 37 cm TL	1 to 2 years	0.7 kg	14 months	Experimental in MS and FL

Part C: Assessment of Risk and Uncertainty, Gulf of America Candidate Species

Species Name	Common Name	Potential for Gamete Release in Culture	Priorities for Research	Influence of Species and Population Dynamics on Genetic Risk Level	Uncertainty in Risk Level	Management Priorities to Minimize Genetic Effects
Sciaenops ocellatus	Red Drum	Low: harvest size occurs before maturity	Adult abundance and population structure, Reproductive resilience to selective forces	Low: escapement rates indicate recovery, harvest size occurs before maturity, there is evidence that the wild population is resilient to selection pressures; also see OMEGA case study results in Part D of this table	Moderate: Stock assessments are needed to characterize the stock status for the Gulf at large	Broodstock genetic management plan
Seriola rivoliana	Almaco Jack	Unknown: more data needed on life history	Life history, growth parameters, abundance, genetic diversity	High: harvest size occurs before maturity, catch data suggests a low level of wild abundance; also see OMEGA case study results in Part D of this table	High: Stock assessment is needed for nearshore and offshore populations	Broodstock genetic management plan, genetic diversity monitoring
Rachycentron canadum	Cobia	Low: harvest size occurs before maturity	Sexual dimorphism, fine-scale genetic diversity, reproductive resilience to selective forces	Low: harvest size occurs before maturity; stock is not considered to be overfished; also see OMEGA case study results in Part D of this table	Low: Stock assessment update conducted in the last 5 years	Broodstock genetic management plan, siting, genetic diversity monitoring
Seriola dumerili	Greater Amberjack	Moderate: harvest size is coincident with maturity age	Migration of Gulf stock, reproduction, population structure, genetic diversity	High: status of wild population is unknown, but is overfished and considered to have low abundance	High: Updated stock assessment and more information about stock genetics are needed	Broodstock genetic management plan, siting, genetic diversity monitoring
Trachinotus carolinus	Florida Pompano	Low: harvest size occurs before maturity	Adult abundance and population structure, genetic diversity monitoring	Moderate: harvest size occurs before maturity, but status of wild population is unknown	High: Updated stock assessment is needed	Broodstock genetic management plan, delayed maturation, genetic diversity monitoring

Species Name	Common Name	Potential for Gamete Release in Culture	Priorities for Research	Influence of Species and Population Dynamics on Genetic Risk Level	Uncertainty in Risk Level	Management Priorities to Minimize Genetic Effects
Centropristis striata	Black Sea Bass	Moderate: harvest size is coincident with maturity age	Genetic diversity monitoring, reproductive behaviors, siting, population structure	High: harvest size is coincident with maturity age; stock is overfished	High: more information is needed about life history, biology, stock status, and population structure in the Gulf	Management of hermaphroditism in cultured stock, broodstock genetic management plan, siting, genetic diversity monitoring
Cynoscion nebulosus	Spotted Seatrout	Not determined -- possibly low if harvested before maturity but depends on desired harvest size for offshore culture	Spawning potential, effective population size	Low: supplementation programs stabilize wild abundance; however, population abundance is more vulnerable to degradation of habitat	Moderate: ecology of estuaries may influence abundance of species over time; genetic diversity at a subregion level is unknown	Management of cannibalism, broodstock genetic management plan, siting
Lobotes surinamensis	Tripletail	Moderate: harvest size may be coincident with maturity age	Wild stock structure, reproduction, migration, genetic structure	Moderate: harvest size may be coincident with maturity age, but abundance of wild population is unknown	High: research is needed on many aspects of life history, behavior, and population connectivity in the Gulf population	Fertilization in culture, broodstock genetic management plan, siting
Paralichthys lethostigma	Southern Flounder	Moderate: harvest size is coincident with maturity age	Adult abundance and fine-scale population structure, genetic diversity monitoring	Moderate: harvest size is coincident with maturity age, and abundance is vulnerable to degradation of habitat, but studies support a genetically diverse population	Moderate: more fine-scale speciated research is needed on life history and stock structure	Management of sexual dimorphism and hermaphroditism, broodstock genetic management plan, siting, genetic diversity monitoring

Part D: OMEGA Case Studies to Evaluate Genetic Risk of Farm Scenarios for Three Candidate Species in the Gulf of America

Common Name of Candidate Species	Production Level, metric tons	Proportion of cultured fish in spawning population [1]			Relative Long-term Fitness [1]			Admixed Population Effective Size as a fraction of Wild Population Effective Size (N_{eT}/N_{eW}) [1, 2]		
		High	Low	Modified	High	Low	Modified	High	Low	Modified
Red Drum	10,500	0.016	0.012	0.006	>0.999	>0.999	>0.999	0.13	0.20	0.55
	17,500	0.027	0.021	0.010	>0.999	>0.999	>0.999	0.05	0.08	0.30
Almaco Jack	10,500	0.120	0.080	0.040	0.984	0.991	0.997	0.29	0.48	0.82
	17,500	0.180	0.135	0.060	0.967	0.980	0.995	0.11	0.22	0.61
Cobia	10,500	0.006	0.003	0.002	>0.999	>0.999	>0.999	0.94	0.98	0.99
	17,500	0.011	0.006	0.003	>0.999	>0.999	>0.999	0.78	0.94	0.98

[1] Median values of 1,000 simulations. See Section 3.3, *OMEGA Genetic Risk Modeling Case Studies for Finfish in the Gulf* for details on results and model scenarios. The High, Low and Modified columns refer to likelihood of episodic events. “High” is the most conservative assumption, with an episodic event likelihood of 15% in any given year for the 10,500 mt scenario and 25% in any given year for the 17,500 mt scenario. “Low” assumes a 6% likelihood in any given year for the 10,500 mt scenario and 10% in any given year for the 17,500 mt scenario. “Modified” assumes a 3% likelihood in any given year for the 10,500 mt scenario and 5% in any given year for the 17,500 mt scenario, as well as reduced escape survival compared to the “High” and “Low” conditions. In general, “High” and “Low” are considered to be conservative in regard to escape levels that would occur during operation, while “Modified” represents an anticipated level of escape assuming best management practices are followed.

[2] The ratio of admixed population size to the wild effective population size is a key indicator of genetic diversity. A value of 1.0 is a baseline level of diversity in the wild population. A value of less than 0.1 indicates high likelihood of deleterious Ryman-Laikre effects in the wild population. See Section 1.3.1, *OMEGA Model for Assessment of Finfish Escapes* for discussion.

4.3 Escape Prevention Measures and Best Management Practices

Operational Procedures to Minimize Escape Risk and Action measures are procedures taken to minimize or avoid escapes leading to potential culture-wild genetic interactions from program gene flow into wild populations. While the implementation of one or a combination of these measures would not provide an absolute guarantee against unintended gene flow from the aquaculture program, these measures are designed to effectively minimize the risk of this kind of escape.

Following Operational Procedures, Action-level measures are listed for situations where a reactive response to a medium-level or large-scale escape event is required.

4.3.1 Operational Procedures to Minimize Escape Risk

Operational procedures to minimize escape risk and action measures are procedures taken to minimize or avoid escapes leading to potential cultured-wild genetic interactions from program gene flow into wild populations. While the implementation of one or a combination of these measures would not provide an absolute guarantee against unintended gene flow from an aquaculture program, these measures are designed to effectively minimize the risk of this kind of escape.

The following operational procedures, and action-level measures are listed for situations where a reactive response to a medium-level or large-scale escape event is required.

Measure Fish-1 Onshore Nursery Procedures

Use wild-caught broodstock from local sources

Broodstock used for reproduction in the hatchery should be harvested from the local population, which can be defined as the region surrounding the site that contains locally-adapted wild stock. If the aquaculture operation were to employ domestication or strain selection, additional steps would be needed to understand the risk that implementation of intentional selection would have on natural populations, and further steps may be needed to minimize the risk of maladapted traits passing from cultured lines to wild fish populations. However, mitigation steps may include developing selected strains with reduced or delayed reproductive maturity, and/or developing sterile lines.

Maximize the size of the brood program and design selection of broodstock to maximize effective population of cultured fish

Greater genetic diversity in wild populations enhances adaptive potential and strengthens the effectiveness of natural selection. However, aquaculture programs face operational constraints that limit the number of broodstock maintained in nursery settings. Despite this limitation, optimized conditions for egg, larval, and juvenile survival allow many offspring to be produced from a small number of parents. To mitigate potential genetic risks, husbandry practices should be designed to maximize the number of breeders contributing to each generation. This approach would help maintain genetic diversity within the breeding program, reduce the risk of inbreeding depression, and minimize the genetic impact of escaped fish interbreeding with wild populations.

Sterilization (if applicable)

The development and implementation of sterilization techniques in aquaculture species is an important area of ongoing research and is considered a high priority to mitigate genetic consequences from escaped cultured organisms. Approaches such as induced triploidy have been previously used in several salmonid species and shellfish species to varying degrees of success and with varying trade-offs for these species. Other approaches may be explored, such as gene editing broodstock lines to create sterile offspring with a higher success rate, if sterility is the primary goal. On a species basis, the tradeoffs for sterilization and optimization of sterilization techniques should be tested and evaluated.

If successfully implemented, sterilization techniques could virtually eliminate risks associated with culture-wild interbreeding.

Sterilization for applicable species may also be considered as an Action-level measure, as described below.

Measure Fish-2 Offshore Program siting

Locate program to minimize loading from wave action, wind and marine currents

Offshore cages should be sited in such a way that forces from wave action, wind and marine currents can be minimized, to the extent feasible. The engineering constraints of program mooring, anchor points, cages and ancillary facilities will be factored into site selection. Siting should take advantage of land features to reduce marine forces acting on the cage system where possible.

In locations where severe storms are common, such as in the Gulf, cages may be submersed to an adequate depth to reduce storm and wave impacts. However, the feasibility of this approach will depend on costs, permitting restrictions, and user conflicts.

Site program to minimize potential for culture-wild interactions

Another siting consideration is to place cage systems at a sufficient distance from areas where conspecifics have been observed, if possible. For species that aggregate near cages this could reduce the likelihood of culture-wild interactions.

Measure Fish-3 Offshore Cage System Design

Engineer cages to minimize risk of failure

Cages should be constructed of materials and designed to resist documented causes of failure in an offshore environment. Materials and engineering of cages should conform to ISO standards. The cage program should be designed by a licensed engineer and should be approved by the RAC as a component of the permit to operate.

Causes of potential failure include:

- Biofouling – utilize materials that resist biofouling over a several year time scale (e.g., copper alloy mesh is a material with high strength and rigidity that is resistant to common causes of escape leakage, biofouling and other types of net damage);
- Net biting by cultured fish or predators;
- Damage by large predators;
- Operational errors – this can occur due to a variety of factors (for examples see Yang et al. 2022).

Surround cages with predator nets

- Nets should be designed to be large enough to exclude predators and marine mammals and have a mesh size to contain fish that escape due to leakage or cage failure.
- Nets should be set back a safe distance from cages to allow for an appropriate amount of space for escape containment and for predators to be shut off from the cage system.
- Nets should be securely placed and moored.
- Nets should be designed within a reasonable factor of safety for wave, wind and current loading (e.g., built to withstand worst-case conditions over a specified time horizon, e.g., withstand a once in 50 year/100 year/etc. storm.).

Measure Fish-4 Offshore Grow-out Management

Episodic escape events occur most frequently during vulnerable operations maneuvers (Yang et. Al. 2022including, but not limited to: inventorying and handling of fish, nursery net replacement, detaching and towing harvest pens, initial seeding of pens, size-grading of fish using crowders, well-boat operations, net cleaning and repair, use of equipment to remove dead fish from pens, vessel mooring, bottom weight handling, and float line handling (Jensen et al. 2010, Atalah and Sanchez-Jerez 2020, Føre and Thorvaldsen 2021, Holmen et al. 2021). As such best practices for management during all phases of grow-out would substantially reduce risks associated with medium- to large-scale escape releases.

Continuous Surveillance of Cage System Condition

The culture site should be staffed and monitored continuously to ensure security of the program. Training of staff could be implemented to respond to various threats that may result in escape events, including:

- Rogue waves;
- Wave overtopping;
- Severe weather events;
- Cage failure;
- Mooring failure;
- Presence of predators.

Use nursery nets during grow-out transfers

Nursery nets have small mesh and are used to contain juveniles in the process of transferring to grow-out cages. These could be utilized in a way that handling occurs within the nets until fish grow to an appropriate size for the assigned cohort.

Implement periodic facility inspections and evaluation of equipment condition

Materials should be inspected and tested to determine remaining life of system components, including a replacement schedule of all systems components, including nets, fasteners, anchors, ropes, chains, and any other support systems. The replacement schedule should be evaluated for the planned facility operating period.

Best practices for inventorying

- Maintain detailed inventory operation, including mortality losses in culture to accurately account for fish that escape
- Inventory at a sufficiently high frequency and accuracy to manage any factors that may influence escape
- Use containment methods for sorting fish to prevent escape during grading procedures
- Provide a continuous record of escape through the applicable fisheries management agency.

Best practices for size-grading

- Use nursery nets
- If applicable, manage cannibalistic behavior by grading and sizing frequently and segregating as needed. This condition would require further netting procedures and other specific management measures to manage this behavior.

Best practices for cage and net maintenance

Cage and net condition should be surveyed at regular intervals and cages and nets should be maintained, repaired or replaced as required. As needed cages and nets should be rotated or relocated within the culture system. A maintenance log should contain a record of inspections and actions taken.

Prevent spawning in cages

- Minimize the potential for gamete release by harvesting fish before they reach maturity, or utilize sterilization.

Implement measures to minimize disease in cultured fish

- Disease transmission to wild fish may also influence genetic consequences, this is due to disease-based selection processes acting on wild populations or influencing wild mortality in disease transmission from culture-origin individuals. because of a selection process of wild mortality due to disease transmission from culture-origin individuals.

Measure Fish-5 Implement offshore large-scale event prevention measures

Limit access surrounding the facility using buoys, lights or other methods

The boundary of the aquaculture system should be clearly marked with signage identifying restrictions, purpose of the site and lease information. Markers should be designed to be clearly visible to vessel operators. Lighting may be incorporated into site marking where appropriate and where lighting would not cause a visual disturbance. Potential detriment to other species from such measures, including to endangered species, would need to be evaluated before implementing these approaches.

Use warning measures to restrict vessels from the area

Reactive measures such as audible sources and lights could be installed to warn vessels operating near the aquaculture boundary. However, potential detriment to other species from such measures, including to endangered species, would need to be evaluated before implementing these approaches.

Use deterrent measures to keep predators from entering the cage areas

Reactive measures such as audible sources and lights may be used to repel or deter predators from damaging seed lines or opportunistically feeding at the aquaculture site. Air bubble generators or exclusion nets can also be effective predator deterrents, if feasible. However, potential detriment to other species from such measures, including to endangered species, would need to be evaluated before implementing these approaches. *Implement submersible systems for severe weather events*

For offshore installations, aquaculture systems could implement submersible designs so they can be lowered below sea level in the event of severe weather. These systems should be designed to be raised and lowered as necessary to suspend maintenance during submerged periods and resume normal operation during moderate conditions. However, cost, permitting, and user conflicts may limit the use of this approach.

Plan for removal of ancillary equipment during severe weather events

A rapid response plan should be implemented to allow for removal or protection of surface level infrastructure to minimize potential for container system damage and loss of maintenance capabilities.

Implement alarm systems including auto-dialing to ensure rapid response to large-scale events

A recovery plan should be developed to respond to damage and equipment losses within the aquaculture system. Possible components of the plan include an alarm system, staffing and required equipment for gear recovery, repair and reinstallation methods and restoration of inventory losses.

Measure Fish-6 Offshore Harvest and Transfer procedures

Minimize opportunities for escape during transfer from nursery to well-boat or other containers

Implement reporting requirements when fingerlings or juveniles are transported to an aquaculture facility; to include the estimated number of fish transported, average size and coefficient of variation in size.

Minimize opportunities for escape during transfer from well-boat or other containers to cage system

The method of transfer of juvenile stock from holding containers to grow-out containers should eliminate potential opportunities for escape.

- An enclosed transfer system such as one that uses a vacuum method would minimize opportunities for juveniles to jump into unenclosed water during the transfer process.
- A containment net around the transfer area would create a backup enclosure for juveniles that escape during transfer.

Minimize opportunities for escape during transfer from nets to well-boat or other containers

- Maximize the volume of fish taken from cages for each harvest event to reduce the number of harvest events and potential for cage issues or failure with boat movement along the cage system.
- Use a containment net around harvest area of a sufficient size to capture any fish that may escape during crowding toward container vessel.

Minimize opportunities for escape from well-boat or other container during transport

Harvested fish could be kept in enclosed containers to prevent escape during transport from the grow-out system to shore.

Minimize opportunities for escape during transfer from well-boat to processor

Safe handling methods should be used when transferring market size fish from the harvest vessel to minimize any potential for losses.

Measure Fish-7 Advance Science of Aquaculture Genetic and Ecological Interactions

Ongoing monitoring and research of wild populations and the environment could inform sustainable carrying capacities of aquaculture in a given region, as well as risk thresholds for additional action. Much research has been done on salmonids and some of these methods are likely transferable to marine species.

Tagging culture fish

Implement a fish tagging program for fish in culture programs. Such a program can use DNA or trace-element methods to trace escapes to the farms of origin. Farm-of-origin tracing is conducted by many countries that culture fish in a natural environment.

Address data gaps of wild populations

Areas of further research for individual species are described in Chapter 3 and Chapter 4. Some items for research include genetic structure, life history, migratory behavior, reproductive behavior, population demographics, spawning abundance, and effective population size.

Environmental monitoring

Monitor the genetic status of wild populations through genetic sampling of individuals from surrounding wild populations. Genetic markers should be utilized to identify trait values that can be traced to aquaculture origin.

4.3.2 Action Level Measures

. Action level mitigation measures are implemented in the event of an escape event deemed to pose a significant genetic or ecological risk.

Action Fish-1 Recapture of escapes

This measure is applicable to any leakage, episodic or large-scale escape events that occur in the cage system. This would involve deployment of one or more vessels to identify and recapture fish of any size or age that escape from the cage system. Predator nets, described above under Measure Fish-3 would minimize the chance that a fish would escape from the facility entirely. Reporting of escape events in terms of number and size of fish would provide information in the numbers needed to be recaptured, and tagging and trace-element methods described under Measure Fish-7 would aid in the process of identifying and locating escapes in the wild.

Action Fish-2 Agency Inspection

This measure is applicable to situations where there are more than two minor escape events occurring within a 30-day period, or in the event of a cage failure or other episodic event. The aquaculture company should work with a responsible agency to identify operational deficiencies and actions to improve operations. The company should have some period of days (e.g., up to 90 days) to take corrective action. A follow up inspection should be required to approve implementation of new measures.

Action Fish-3 Expansion of fish tagging program

This measure is applicable to medium- and large-scale events. For an existing tagging program, the proportion of culture fish tagged should be increased to further assist recapture efforts in the event of a future escape event. If a tagging program is not yet implemented, then a program should be implemented.

Action Fish-4 Sterilization of fish stock

Resources should be put toward sterilization research, and if applicable, the facility could work in collaboration with the responsible agencies to develop or enhance management methods for sterilization of juveniles.

Action Fish-5 Reduction in program inventory

Program inventory reductions may be appropriate in situations where a) measures as those described need improvement, or b) declines in wild population abundance or diversity necessitate remedial action. The aquaculture company should work with a responsible agency to reduce program harvest goals to a sustainable level. Inventory reductions may be done on a temporary basis to correct identified deficiencies in standard measures described above. Documented improvement in operations, management measures, and wild population status as determined by the responsible agency could conditionally allow the program to scale back to full harvest levels.

Action Fish-6 Temporary or permanent cessation of operations

This measure would be appropriate in the event of a large-scale escape or significant change in genetic status of the wild population. Other action-level mitigation items would be implemented to correct any operational deficiencies. Documented improvement in operations, management measures, and wild population status, as determined by the responsible agency, could conditionally allow the program to recommence operations at a full or reduced level.

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Appendix A - Case Study Analyses of Genetic Effects of Escaped Marine Finfish Aquaculture in Southern California and the Gulf of America

November 2024

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1.0 Overview

This appendix presents an overview of the Offshore Mariculture Escapes Genetics Assessment (OMEGA) model structure and parameterization of the model for the six case study species.

The ways fish escape and escape levels (frequency and magnitude) are discuss in detail in Section 2.1, *Escape Background and Categories* in the body of this report and are briefly presented here to provide some context. Figure A-1 shows the five categories of ways fish escape from cages as conceptualized in the OMEGA model. Type 1 and 2 represent leakage and the escape of 10s to 100s of fish at a time. Type 3 represents episodic escapes resulting in intermediate escape numbers of 1,000s to 10,000s, Type 4 represents the rare complete failure of multiple cages or a catastrophic equipment failure and loss of 100,000s to millions of fish and Type 5 is the release of eggs/sperm or larvae from fish spawning in cages. Case study analyses evaluated escapes from Types 1 through 3, although that does not suggest large scale escapes or release of eggs/sperm and larvae would not be possible for case study species.

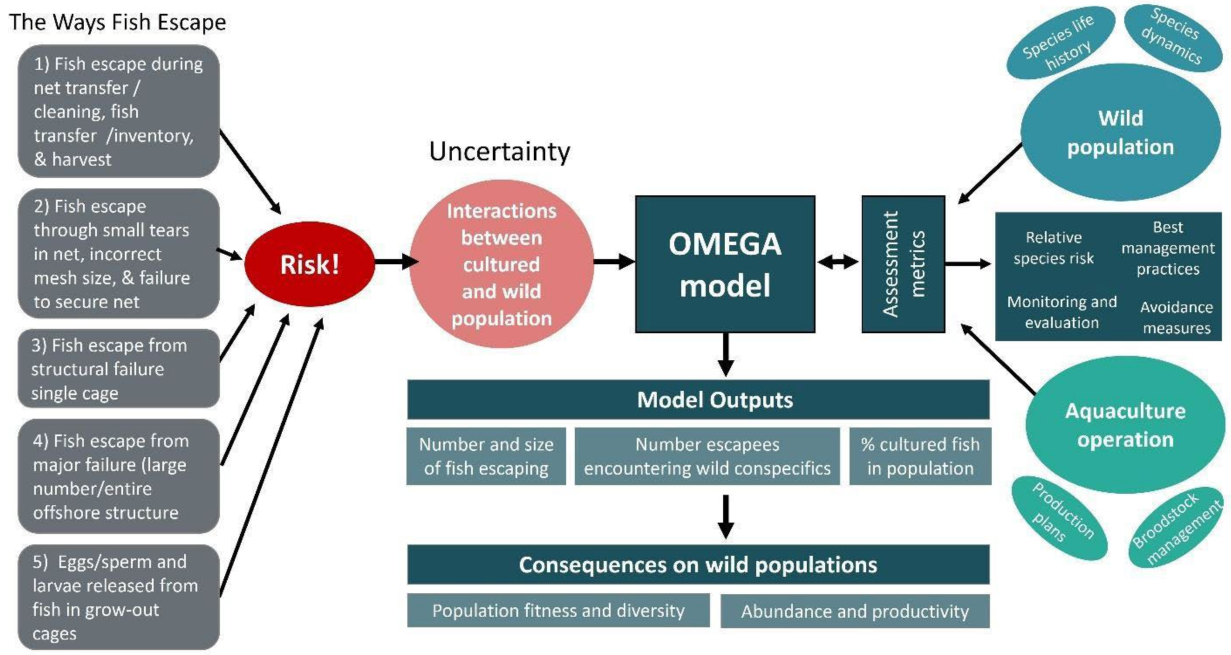


Figure A-1. The ways fish escape, and OMEGA model conceptual design.

2.0 Offshore Mariculture Escapes Genetics Assessment (OMEGA) Model

The NOAA National Marine Fisheries Service (NMFS) aided in the development of a scientific decision-support tool called the Offshore Mariculture Escapes Genetics Assessment (OMEGA) model to assess the potential risks of farmed escapees to their wild counterparts and to aid in the design of management strategies to address the potential risks of escapees to marine resources. OMEGA is intended to: 1) provide insights about factors affecting risks associated with escapes from aquaculture operations, 2) simulate the scale, frequency, and dispersal of escapes into the wild population and potential impacts to wild population fitness, genetic diversity, and long-term viability of the wild population, and 3) aid in the assessment of proposed aquaculture projects and the development of management strategies to address potential escape risk, including evaluating the effects of regulatory and technical advances on fish containment. Finally, models like OMEGA are useful to understand and predict the consequences of different management alternatives and are an important tool to support environmental regulatory decisions (National Research Council 2007).

2.1 OMEGA Model Background

The concepts used in OMEGA are an extension from the All-H-Analyzer (AHA) tool, which was used successfully in the U.S. Pacific Northwest to evaluate genetic and ecological interactions between hatchery and wild salmon and steelhead trout (Paquet et al. 2011).

A user guide for OMEGA containing model background and user instructions was produced the same year. Version 2.0 developed in 2019 used for this assessment includes a Monte Carlo simulation frontend for conducting multiple iterations of a randomized simulation, varying one or more parameters based on user-specified distributions. This feature is an add-on to OMEGA and requires @Risk for Excel, available from Palisade Software. @RISK operates by replacing one or more model input parameter values in OMEGA with a new value. The user also selects output model response variables to evaluate from the simulation. Model inputs and results are recorded for each iteration.

The OMEGA model is organized around three components (Figure A-2):

1) The biology of the cultured population and details of the aquaculture operation, including the frequency and magnitude of fish escaping from the pens.

2) Factors affecting the potential for interaction between escapees and the wild population, including survival of escapees, location of the aquaculture operation relative to the wild population, and reproductive success of escapees in the wild.

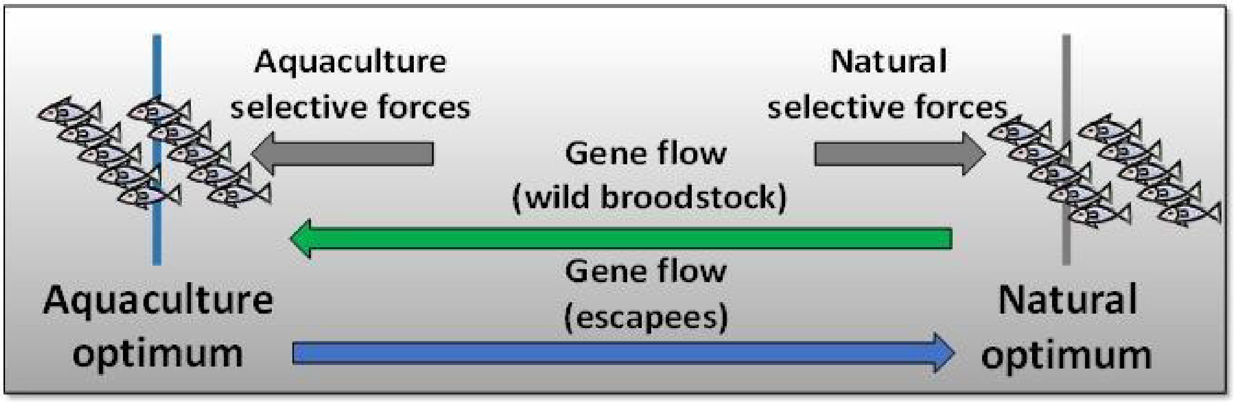
3) The biology and population dynamics of the wild population, including abundance, distribution, survival, age and size at maturity, spawning characteristics, and age-specific harvest rates.

Figure A-2. The three components of the OMEGA model.

OMEGA model input parameters describe size and growth characteristics of cultured fish, frequency and magnitude of escape events, mechanism of escape, survival of escapees in the wild, probability of escapees encountering a conspecific natural population and interbreeding, and population dynamics of the natural population. Model results describe the influence of aquaculture escapes on spawning biomass, juvenile production, and fitness of the composite population. Effects of interactions on fitness and abundance are based on the frequency and relative abundance of cultured fish that escape and survive to encounter a natural population, the difference in survival characteristics between the artificial and the natural environments, and the genetic legacy of the cultured and natural populations. More recent model developments now also evaluate potential impacts on effective population size and consequences for genetic diversity in the mixed population from escaped cultured fish.

OMEGA scenarios are modeled to assume a rate of survival of escapees based on size at escape relative to wild conspecifics. The survival rate may be adjusted to model a lower rate relative to wild conspecifics using a shaping function that is based on assumptions of predator avoidance and foraging behavior after escape, and time from escape. OMEGA also includes a parameter to describe the probability of escapees encountering the wild population. The probability of encounter is based on an understanding of distribution of wild juveniles and spawners and distance from a farm location. A third parameter is reproductive competency of escaped fish. At one extreme, cultured fish may be sterilized prior to stocking in cages and would have zero reproductive potential. At the other extreme, cultured fish from wild sourced broodstock may be as competent as spawners as wild conspecifics.

For fitness predictions and effects on wild population viability and abundance, OMEGA includes a model of stabilizing selection for a hypothetical trait, which describes the survivorship of offspring of naturally spawning wild and culture origin as described in Ford (2002). Effects on survivorship of the wild population are modeled using a relative fitness factor of the admixed wild population of conspecifics based on the modified trait value of the mixed population (Figure A-3). Over successive generations of escapees interbreeding the mixed wild population moves away from the natural optimum and relative fitness is less than 1.0 based on assumed selection in nature for the trait.



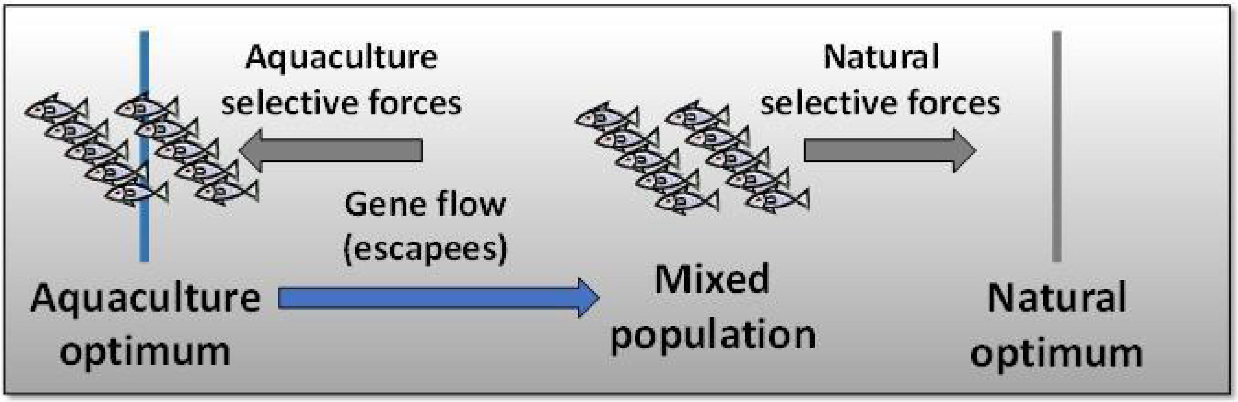


Figure A-3. Schematic of Single Trait Fitness Model (top) and Gene flow to Wild Population with Mean Trait Value Change (bottom). Conceptual fitness model based on Ford 2002.

The potential for the wild population to experience Ryman-Laikre effects because of escapees is evaluated in terms of impacts on the effective population size (N_e) and related loss of genetic diversity. Waples et al. (2016) published a model to calculate the total effective population size (N_{eT}) in an admixed cultured–wild population and the change in effective population size. The model includes parameters on the number of effective broodstock fish used to produce cultured fish in a breeding program, the demographics of the wild population, and the predicted contribution of cultured fish to natural spawning. The OMEGA model includes the AgeNe model described in Waples et al (2011) to calculate generation length and effective population size absent escapees.

Generation length and effective population size absent escapees provide context when evaluating impact of escaped fish on a wild population. Escapees persistent and accumulate in the population for species with a long generation length. The estimate of effective population size and the estimate of the ratio of N_e/N is a measure of effective population size to census population size and potential effects of escapees in a population with a potentially low genetic diversity (tiny ratio of N_e/N). The total effective population size (N_{eT}) and reduction in effective population size (N_{eT}/N_{eW}) from breeding escapees is estimated in OMEGA using Equation 8 in Waples et al (2016).

Waples et al. (2012) summarized a general rule of thumb proposed in the scientific literature for minimum effective population size to avoid genetic diversity effects of 50/500/5,000. They suggested marine large marine populations may be more susceptible to loss of genetic diversity than other species and the higher minimum effective population size may be more appropriate. OMEGA results were evaluated for potential Ryman-Laikre effect using the 5,000 minimum population size.

Waples et al. (2012) also recommended that a reduction in N_{eW} (i.e., ratio N_{eT}/N_{eW}) be considered in large marine populations and values less than 0.1 may have Ryman-Laikre effects. Both metrics were calculated in OMEGA to consider potential Ryman-Laikre effects.

2.2 Use of Case Studies

The OMEGA model was used to evaluate species-specific case studies for a subset of Southern California and the Gulf species. The case studies are intended to provide insights into how different species life histories, abundance, and population structure can affect estimates of introgression of cultured finfish in wild populations and the genetic impacts of escapees in terms of relative fitness and effective population size. Farm production scenarios developed for the case studies are hypothetical and are not intended to represent a specific farm proposal, serve as an implicit or explicit endorsement by NOAA of any species or cultivation practice, nor are they meant to serve as a policy recommendation or be prescriptive of any potential future farm proposal.

3.0 OMEGA Model Components

The following sections describe OMEGA computation steps used to assess the impacts of escaped case study species. Described are how OMEGA computes population abundance, and effects of escaped fish on fitness and an assessment of effects of escaped fish on within population genetic diversity based on potential change in effective population size of the wild population.

3.1 Population Simulations

The wild population simulation in OMEGA is an age-structured single population model with age-specific assumptions for survival, harvest, and maturity (ICF 2014). The life cycle process is separated into four phases: 1) spawning biomass, 2) egg production, 3) juvenile recruitment, and 4) subadult/adult survival. Harvest is included during the subadult and adult phase and is shaped by an age-specific double logistic function. The population model in OMEGA was developed based on many of the concepts and the life stage structure of the Stock Synthesis population assessment model for marine fish management (Methot 2000). OMEGA is a much simpler construct of the population model in Stock Synthesis and does not include the analytical components in Stock Synthesis to estimate population parameters.

The number of spawners for wild and cultured are calculated as follows:

$$N_{Wild,a,yr} = \sum_{a=1}^{A} \left(N_{Wild,a,yr} * M_a\right)$$

$$N_{Cultured,a,yr} = \sum_{a=1}^{A} \left(N_{Cultured,a,yr} * M_a\right)$$

Where $N_{a,yr}$ is the number of wild and cultured fish in the population by age a in year yr and M_a is the fraction fish mature at age a. The same maturation schedule for females and males was assumed in this model. To account for the observation that cultured fish, when they escape, would be larger than wild fish at a given age, the age of the cultured fish at the time of escape was advanced based on their size relative to size of wild fish.

Female spawning biomass (SPB) of wild fish is calculated as follows:

$$SPB_{Wild,yr} = \sum_{a=1}^{A} \left(N_{Wild,a,yr} * SexRatio_a * W_{f,a}\right)$$

and cultured fish:

$$SPB_{Cultured,yr} = \sum_{a=1}^{A} \left(N_{Cultured,a,yr} * SexRatio_a * W_{f,a} * RRS_{Cultured} * f_{Cultured}\right)$$

Where $SexRatio_a$ is ratio females to males at age a, and $W_{f,a}$ is the body weight of females at age a. For cultured fish in the population RRS is the user input relative reproductive success of escapees, and $f_{Cultured}$ is the fitness of cultured fish in nature based on calculated cultured fish trait value. Relative reproductive success and calculated fitness were included at this stage to report effective spawning biomass of cultured fish in nature versus census abundance estimated previously.

Egg production is calculated by the following for wild and cultured:

$$Eggs_{Wild} = \mathrm{SPB}_{\mathrm{Wild}} * \frac{Eggs}{Kg} * f_{Spawn}$$

$$Eggs_{Cultured} = \mathrm{SPB}_{\mathrm{Cultured}} * \frac{Eggs}{Kg}$$

Where f_{Spawn} is fitness of wild fish allocated to spawning life stage.

Egg to end of juvenile recruit period is based on the two parameter Beverton-Holt survival function (assumption of density-independent productivity and maximum number recruits or capacity). The modeled recruitment stage for the case study fish was one year. The Beverton-Holt function is as follows:

$$Recruits = (P * f_{Recruit}) * Eggs)/(1 + \frac{(P * f_{Recruit}) * Eggs}{C * f_{Recruit}})$$

where Eggs is sum of eggs following spawning from wild and cultured, *P* is the density-independent productivity, *C* is capacity and $f_{Recruit}$ is fitness of wild fish allocated to the recruit life stage.

The number of subadult and adult fish surviving to the next year is calculated by the following:

$$N_{a+1,yr+1} = N_{a,yr}e^{-Z_a}$$

where Z is age specific instantaneous mortality ($M_a + F_a$) where *M* is natural mortality and *F* fishing mortality. Natural mortality is adjusted for relative fitness allocated to subadult and adult life stage by calculating annual survival adjusted for relative fitness and then calculating fitness adjusted M_a.

To remove any initial parameter effects on results the simulation includes a 50 step/year initialization period absent stochastic variation and cultured fish escapes. This is done to eliminate any initial parameter effects prior to analysis of effects of escapees.

Model results were summarized in years 5 (Year 5), 10 (Year 10), and 25 (Year 25) of the simulations. The short-term results are presented to describe potential effects within a time frame applicable for environmental impact analyses and permitting applications.

OMEGA model simulations typically run for 300 years to include the long-term equilibrium impacts of escaped fish. Model simulations have shown that the effect of escaped, long-lived marine fish species on fitness are slow to materialize. The short-term results provide enough of a time scale to understand the population trajectory with escapes. However, in a couple of case study species that suggest a fitness impact of escaped fish we report the long-term fitness results to help better understand long-term consequences. The long-term fitness consequences were summarized as the median loss in fitness in years 10 to 100 for each iteration.

3.2 Fitness Effects (finished)

Impacts on conspecific fitness from escaped case study species were predicted using a simple phenotypic, single trait fitness model described by Ford (2002). The phenotypic fitness model is a two-population analysis of different environmental selection regimes acting on the two populations and the effect of gene flow between populations on mean trait value of the receiving populations. Assumptions of the model are as follows:

- A single trait is under selection with different optimum values for the two environments.
- The trait is normally distributed and subject to bell-shaped (Gaussian) selection.
- All mating is random; fish do not sort by origin (escapee and wild).
- Population size is large so that random drive, phenotypic plasticity, and other stochastic forces can be ignored.
- Changes in mean trait value are deterministic based on selection and gene flow.
- Selection does not reduce population size, variance or heritability of the trait over time.

Our analysis of case study species assumes 100% locally sourced wild broodstock, thus the initial condition modeled assumes the mean trait value of fish used for broodstock is equal to the wild population, representing the natural environment optimum. In our analyses, gene flow is two directions with use of 100% wild broodstock providing gene flow into the culture environment and escapees breeding with the wild population resulting in gene flow into the wild population.

The resulting condition from escapees spawning with the wild population is a change in the mean trait value of the now mixed wild population (see Figure A-3 bottom**Error! Reference source not found.**). In this case the mean trait value of the mixed wild population is intermediate between the two environmental optimums.

The deviation of the wild population from the optimum phenotypic value is $\bar{P}_{Wild} - \theta_{Nat}$.

The mean phenotypic trait values of wild and cultured progeny in year y are calculated by the following equations (Ford 2002):

$$\begin{aligned}\bar{P}_{Wild,y} = (1 - pHOS_{sp})\left[\bar{P}_{Wild,sp} + \left(\left((\bar{P}_{Wild,sp}\omega_{Nat}^2 + \theta_{Nat}\sigma^2)/(\omega_{Nat}^2 + \sigma^2)\right) - \bar{P}_{Wild,sp}\right)h^2\right] \\ + pHOS_{sp}\left[\bar{P}_{Escapee,sp}\left(\left((\bar{P}_{Escapee,sp}\omega_{Nat}^2 + \theta_{Nat}\sigma^2)/(\omega_{Nat}^2 + \sigma^2)\right)\ \bar{P}_{Escapee,sp}\right)h^2\right]\end{aligned}$$

and

$$\begin{aligned}\bar{P}_{Culture,y} = (1 - pNOB_{brood})\Big[\bar{P}_{Culture,brood}\Big(\big((\bar{P}_{Culture,brood}\omega_{Culture}^2 + \theta_{Culture}\sigma^2) \\ /(\omega_{Culture}^2 + \sigma^2)\big) - \bar{P}_{Culture,brood}\Big)h^2\Big] \\ + pNOB_{brood}\Big[\bar{P}_{Wild,brood} \\ + \left(\left((\bar{P}_{Wild,brood}\omega_{Culture}^2 + \theta_{Culture}\sigma^2)/(\omega_{Culture}^2 + \sigma^2)\right) - \bar{P}_{Wild,brood}\right)h^2\Big]\end{aligned}$$

where:

$pHOS_{sp}$ = Proportion of spawning biomass in nature that is escapees

$pNOB_{Brood}$ = Proportion of aquaculture brood stock that is wild fish

θ_{Nat}=Phenotypic optimum or expected value

(mean) of the phenotypic probability distribution for the natural environment

$\theta_{Culture}$=Phenotypic optimum or expected value

(mean) of the phenotypic probability distribution for the culture environment

σ^2=Phenotypic variance for the trait in question

h^2 = Phenotypic trait heritability

ω^2_{Nat}=Variance of the probability distribution of fitness as a

function of the phenotypic values for individuals in the natural environment

$\omega^2_{Culture}$ = Variance of the probability distribution of fitness as a function of phenotypic values for individuals in the culture environment

$\bar{P}_{Wild,sp}$ = Mean phenotypic value of the wild population spawning in year y

$\bar{P}_{Escapee,sp}$ = Mean phenotypic value of cultured adults (escapees) spawning in year y

$\bar{P}_{Wild,brood}$ = Mean phenotypic value of the wild brood stock in year y

$\bar{P}_{Culture,brood}$ = Mean phenotypic value of the cultured brood stock in year y

Because OMEGA is an annual simulation model and the trait model is a generational analysis, OMEGA includes a step that computes the average trait value for the wild population in each year that accounts for fish contributing to spawning from multiple cohorts, each with a potentially different trait value resulting from the level of escape introgression at spawning. In the above equations, $\bar{P}_{Wild,sp}$ and $\bar{P}_{Escapee,sp}$ are calculated as the mean phenotypic value of the escapee and wild adults spawning in year *y* comprised of age classes (*a*):

$$\bar{P}_{Wild,sp} = \frac{\sum_{a=i}^{A} N_{Wild,a}\bar{P}_{Wild,a}}{\sum_{a=i}^{A} N_{Wild,a}}$$

and

$$\bar{P}_{Escapee,sp} = \frac{\sum_{a=i}^{A} N_{Escapee,a}\bar{P}_{Escapee,a}}{\sum_{a=i}^{A} N_{Escapee,a}}$$

These equations assume that cohort contributions to spawning is proportional to abundance in the spawning biomass. This approach is a simplification as it overlooks the potential of unequal spawning contribution among cohorts due to differences in age specific female fecundity and, more importantly, fitness.

A similar issue arises when computing annual trait value for the cultured broodstock. In the previous equation the trait value of wild adults in the brood stock ($\bar{P}_{Wild,brood}$) is assumed to be the same as wild spawners ($\bar{P}_{Wild,sp}$).

Finally, the mean relative fitness (RF) of the wild fish cohort, offspring from spawning in year y, is calculated by the following:

$$RF_{Cohort,y} = e^{\frac{-\left(\bar{P}_{Wild,sp}-\theta_{Nat}\right)^2}{2\left(\omega_{Nat}^2+\sigma^2\right)}}$$

The effect of relative fitness on cohort survival is likely a function of the trait in question, which would possibly affect different life stages in different ways, including during spawning, subadult phase, or adult phase across multiple years up to and beyond first spawning. Allocation of fitness effect across the life cycle is included as parameter values in OMEGA.

Our use of the Ford model in OMEGA to predict fitness impacts includes several caveats:

1) The Ford model is only one of several possible ways to model domestication and although it includes several important concepts (heritability, strength of selection on trait, effects of differences in cultured and wild environments on evolutionary adaptation, and the degree of introgression during spawning) it is incomplete in its approach in that it is not modeling specific genetically controlled traits per models developed for Atlantic Salmon (see Bradbury et al. 2020),
2) We are using a single-trait model that is likely a simplification of a multi-trait phenomenon, and
3) Available data on case study species are inadequate for confident parameterization.

However, the Ford model was used because it is useful for exploring scenarios, evaluating relative impacts of escapees, and because data are incomplete on specific genotypic traits for case study species that may be subject to domestication selection.

Results from the OMEGA model are very sensitive to the input parameters in the fitness function, and as such, the model outputs of fitness effects should be considered as guidelines useful for assessment of the magnitude of potential impact of escapes, but not precise quantitative predictions. The approach used is consistent with other methods that applied phenotypic trait modeling methods (Yang et al. 2019, Baskett et al 2013, Basket and Waples 2013). For risk assessment and decision-making support, the approach used in OMEGA is scientifically sound and correctly identifies the relative consequences of cultured fish escaping and surviving to breed with a wild population.

The parameter values used in this assessment of fitness effects from escapees on wild case study species are presented in Table A- 1. To examine relative effects of escapees on fitness, the parameters were held constant in all model simulations, with one exception. With wild fish captured for broodstock, the first year of the simulations starts with the wild population trait value and then the model is configured to calculate the trait value of fish captured from the mixed wild population in subsequent years. In other words, in subsequent years the trait value of wild sourced broodstock is calculated based on selection that may occur on the F1 generation (cultured offspring of wild broodstock) and degree of introgression of escapees in the wild population.

Consistent with the intent to consider a high potential for effects approach the fitness assessment assumed strong selection. Strong selection would infer a more severe loss of fitness in the wild population as the mean trait value moves away from the wild optimum. The inverse of ω^2, i.e. $1/\omega^2$ is the intensity selection towards the phenotypic optimum. In other words, as ω^2 increases the selection intensity decreases. According to Ford (2002), $\omega^2 = 10\sigma^2$ is considered "strong selection", whereas $\omega^2 = 100\sigma^2$ would be considered "weak selection", where $\sigma^2 = 10$ in both cases. This analysis used $\omega^2 = 5\sigma^2$, a "very strong" selection assumption to evaluate a maximum potential effect on fitness for a marine fish with an unknown trait selection profile (Table A- 1). Sensitivity analyses were made to explore relative fitness effects under different selection assumptions and even under the "very strong" selection assumption effects on relative fitness were very small when assuming all wild origin broodstock in the program. Similarly, the analysis used a relatively high trait heritability assumption of 0.5. Measurements of heritability for growth rate range from 0.2 to 0.3 for Atlantic Salmon (Gjedrem 2000). Ferrari et al. (2016) reported higher heritability of behavioral traits in European Seabass (0.45 +/- 0.14). The model parameterization for case study species used a high heritability assumption to capture a potential maximum effect of escaped fish on relative fitness.

Table A- 1. OMEGA fitness model parameter values used in simulations of impacts of escapees on fitness of the case study species wild populations.

Parameter	Description	Parameter Value
Initial Trait Value	The initial phenotypic trait value for the aquaculture and wild population $\bar{P}_{Culture,Initial}$ and $\bar{P}_{Wild,Initial}$. The wild population is nearly always 100 and the aquaculture trait value something less if originating with a cultured brood stock or 100 if originating with wild fish.	100
Culture Environmental Trait Optimum:	Phenotypic optimum for the culture environment $\theta_{Culture}$. The aquaculture optimum is always something less than then natural environment optimum to represent differential selection pressure.	80
Natural Environmental Trait Optimum:	The natural optimum $\theta_{Natural}$ is always something greater than the aquaculture environment to represent differential selection pressure.	100
Trait Heritability	The analysis assumes relatively high trait heritability h^2. Trait heritability is assumed to be the same for cultured and wild fish.	0.5
Trait Variance	This is the phenotypic variance σ^2 of the trait in question. Trait variance is assumed to be the same for wild and cultured.	10
Strength of Selection	Variance of the probability distribution of fitness ω^2 as a function of phenotypic values for individuals in the population. The analysis assumed ω^2 to be the same for wild and cultured.	$\omega^2 = 5\sigma^2$

3.3 Genetic Diversity Effects

In addition to loss of fitness, a second major concern when cultured fish escape is the potential loss of genetic diversity within populations and loss of genetic diversity among populations (Waples et al. 2012). Population structure of the case study species differed. For example, California Yellowtail are a single intermixed population across their range and wild broodstock collected for the project would presumably represent the entire population; thus, loss of genetic diversity within the population is the primary concern from escapees and not loss of genetic diversity among populations. In contrast, Red Drum may have genetic differentiation across its range based on evidence of isolation by distance, where genetic differentiation increases with geographic distance and thus loss of genetic diversity among populations may be a concern. See Section 3.2.1 *Red Drum (Sciaenops ocellatus)* in the body of this report for a more detailed discussion of population structure of Red Drum.

The OMEGA model includes an assessment of effect of escaped fish on effective population size as a surrogate for effects on within population genetic diversity. As described in Section 1.2.3, *Genetic Diversity Effects* in the body of the report, conservation of genetic diversity in managed populations requires maintenance of sufficiently large (genetic) effective population sizes (N_e). Relatively few mature fish are needed to supply broodstock for a marine aquaculture project, and so offspring produced in any given cohort may be generated from only a few parents. If, or when, offspring escape and then subsequently contribute to spawning in the wild at high rates, there is potential to reduce the effective size of the mixed population due to the relatively low genetic diversity of the escaped culture fish compared to the wild population. The lower effective size may strengthen genetic drift processes acting on the population, and result in a loss of genetic diversity population-wide (Waples et al. 2012).

Waples et al. (2018) published a model to calculate the change in effective population size that includes parameters on the number of effective broodstock fish used to produce cultured fish in a breeding program, the demographics of the wild population, and the predicted contribution of cultured fish to natural spawning. Values for several of these parameters are generally unknown for the case study species but can be estimated using inputs assumed to model the species productivity and abundance in OMEGA (Section 3.1 *Population Simulations*).

Demographic estimates of effective population size across the range of abundances modeled in OMEGA for case study species were computed using the program AgeNe (Waples et al. 2011). The case study species are generally broadcast spawners, spawning in large aggregations in offshore and nearshore waters suggesting reproductive success is moderately to highly variable among individuals. Two theories propose different mechanisms dictating reproductive success among individuals. The “Sweepstakes Reproductive Success (SRS)” hypothesis (Hedgecock and Pudovkin 2011) proposes that stochastic (i.e., random) survival under variable oceanographic conditions results in the highly variable and unequal offspring distributions frequently associated with in broadcast spawning species with high fecundity and high early mortality. Alternatively, the “Recurrent Selective Sweepstakes (RSS)” hypothesis (Tringali 2023) proposes that multiple independent stages of early-life stage selection due to the variable oceanographic conditions results in the highly variable and unequal offspring distributions. Put more simply, surviving offspring (or successful breeders) either result from genetic drift or selection, respectively. For either (or both) of the dynamics impacting recruitment life stages in marine species, moderate to large variance in reproductive success may be expected. However, recent approaches to understanding population estimates that utilize very large sample sizes, revealed much higher *Ne/N* ratios in the few marine species that large scale sample studies have occurred (see Section 1.2.3.1, *Effective Population Size* in the body of this report for details).With this in mind, an intermediate assumption of variance in reproductive success was applied to all case study species.

Estimates of N_e and ratio of N_e/N were made with random reproductive success where variance in reproductive success at age x (V_x) is equal to the expected lifetime reproductive success of a group of fish that die at age x, given by $\bar{k}_x = \sum b_{i(i<x)}$, where k is the number of gametes contributed by an individual to the next generation. Also calculated were estimates of N_e and ratio of N_e/N assuming over-dispersed variation in reproductive success at age x where $V_x = 3\bar{k}_x$ (i.e., a Poisson scaling factor of 3).

Results are summarized in Table A-2 for each of the case study species excepting Striped Bass which a wild population was not modeled. Among the five species modeled the ratio of N_e to total N varied between 0.16 and 0.35. The ratio of N_e to adult N (N_A) varied between 0.25 and 0.67.

Table A-2. Case study species calculated values of effective population size (*Ne*) with over-dispersed variation in reproductive success (Poisson factor = 3.0) using equations in Waples et al. 2011 and the AgeNe program.

Scenario	Max Age	Generation Length	N_T	N_A	N_b	N_e	N_e / N_T	N_e / N_A
California Yellowtail (*Seriola dorsalis*)								
Low Population Abundance	22 yrs	7.7 yrs	5,569,338	3,753,789	1,907,650	1,710,971	0.27	0.41
High Population Abundance			11,194,899	7,552,804	3,838,284	3,442,555		
White Seabass (*Atractoscion nobilis*)								
Low Abundance	27 yrs	8.9 yrs	265,428 – 455,019	103,348 – 177,168	54,779 – 93,907	69,253 – 118,719	0.26	0.67
High Abundance			1,105,949 – 2,027,521	430,617 – 789,463	228,246 - 418,450	288,553 – 529,013		
Red Drum (*Sciaenaops ocellatus*)								
Abundance referenced to Addis (2020) NW Florida Population Unit	40 yrs	11.4 yrs	10,800,422	8,946,846	2,409,455	3,755,067	0.35	0.42
Almaco Jack *(Seriola rivoliana*)								
Low Population Abundance	22 yrs	8.9 yrs	354,666	225,650	42,014	55,323	0.16	0.25
High Population Abundance			786,166	500,183	93,131	122,632		
Cobia (*Rachycentron canadum*)								
Abundance referenced SEDAR 2020 Gulf Population	11 yrs	4.0 yrs	2,493,546	1,026,754	402,144	474,698	0.19	0.46

Notes:
NT = Total number of individuals age 1 and older
NA = Total number of adults
Nb = Effective number of breeders in a year
Ne = Effective population size

The rate of loss for genetic diversity is inversely proportional to N_e and increases rapidly as N_e declines. As discussed in Section 1.2.3, *Genetic Diversity Effects* in the body of this report, the loss of genetic diversity arising when cultured fish escape and spawn with wild conspecific fish is known as the Ryman-Laikre effect (Ryman and Laikre 1991). They showed that in assessing the effects of fish culture on genetic diversity, it is not sufficient to know only N_e in the cultured or wild population; instead, it is necessary to consider the effective size of the cultured-wild system as a whole (N_{eT}). Waples et al (2018) provided a model to calculate N_{eT} as a function of effective size of the captive (N_{eC}) broodstock and wild (N_{eW}) spawners and the proportion of cultured fish in the mixed cultured/wild spawning (x) that are offspring of the captive broodstock (i.e., escapees). The modified Ryman-Laikre model in Waples et al. was used to calculate the reduction in N_e *(i.e.,* N_{eT}*)* for the escape scenarios assessed for the POA project. Results were evaluated against a general rule-of-thumb that N_{eT} values should exceed 5,000 fish (Waples et al. 2012).

Waples et al. (2012) also recommended that an assessment of potential loss of genetic diversity consider the "proportional reduction in N_{eW}". Scenarios that satisfy the criterion that N_{eT} exceed 5,000 could mean a reduction of several orders of magnitude in N_e thus based on Waples et al. the analyses also considers the proportional reductions in N_{eW}. Waples et al. 2012 recommend this "should be considered, along with the absolute levels of N_{eT}, in evaluating risks to within-population diversity".

Results of model scenarios from OMEGA considered both criteria when evaluating potential loss of within population diversity. However, as discussed in in Section 1.2.3, *Genetic Diversity Effects,* while the concept of the Ryman-Laikre effect is undisputed, the consequences of a reduced N_{eT} in the population on long-term viability of the population is largely theoretical.

Calculated effects on N_e were explored for a range of N_e/N values for California Yellowtail (varying Poisson factor between 1 and 25) and found to have a minor effect on results, thus all calculations used the mid-range ratio (Poisson factor = 3). Tiny ratios of N_e/N (<0.001) were not considered in this sensitivity analysis as the extreme conditions to produce tiny ratios did not seem possible with the case study species (see Waples 2016). Also explored was the effect of the number of broodstock used in the program. It was found that results were insensitive to a range of reasonable broodstock abundance (100 to 500 adults) and effective broodstock spawners. All simulations used an abundance of 200 broodstock adults and the ratio of effective spawners (N_{eC} /N_c) of 0.125.

3.4 Escape and Interactions Assumptions

Leakage rates across the production cycle were based on an assumed 0.3% escape rate across all size categories. The leakage escape rate was apportioned by size category as described in Section 1.3, *Assessing Risks of Escape using Modeling Methods* in the body of this report.

In modeling episodic escape events, parameters for both the likelihood[3] of a cage failure and the magnitude loss of fish from an episodic escape event were approximated. The highly variable pattern of escape numbers by year reported in Skilbrei et al. (2015) suggest medium to large episodic escape events occur in combination with the previously discussed leakage type escape. Norwegian studies of Atlantic Salmon suggest unreported episodic escape events occur on a regular basis (Glover et al. 2008, Glover 2010). Thus, it seems reasonable to assess episodic escapes in combination with leakage escapes to anticipate a pattern of low-level escapes (leakage) interacting with the wild population with an occasional larger influx of escapees (episodic cage failures). Episodic escape assumptions are described in detail in Section 1.3, *Assessing Risks of Escape using Modeling Methods* in the body of the report.

To simulate episodic escapes more realistically, the OMEGA model was set to randomize the number of fish lost in an event between a half and a full cage of fish. The model also randomly assigned the cage loss to one of the three size bins of fish for the species.

Escaped cultured fish may survive at lower rates compared to similarly sized wild conspecifics (e.g., escaped Yellowtail Kingfish (*S. lalandi*) observed with empty stomachs or stomachs containing atypical non-food contents; see Fowler et al. 2003). However, empirical estimates of relative survival of marine fish escapees are rare. Observations of suggested lower survival, such as Fowler et al. (2003), are from fish selected for culture traits and may not reflect survival of escaped fish from wild caught broodstock. Hervas et al. (2010) found both short-term and long-term size-dependent mortality of hatchery White Seabass released for stock enhancement. In that case the time of year when released influenced post-release mortality, with highest mortality for fish released in the winter and lowest mortality for fish released in the spring. More importantly, overall hatchery-reared White Seabass had a higher mortality in the wild compared to estimates of wild fish. However, even though the limited evidence suggests survival may be lower for escaped cultured fish, the case study analyses assumed survival would be the same as the wild population size-based survival assumed in the OMEGA.

Finally, an additional scenario was modeled for each case study species to reflect a scenario that included low potential for escape of cultured fish and low survival of escapees (referred to as

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[3] Episodic events are described as the likelihood of a cage failure occurring in a year. Likelihood is synonymous with probability in this analysis. The analysis does not evaluate the likelihood that a single cage may fail in a year. If that were the case the number of cage failures in a year would depend on the likelihood of failure and the number of cages with fish. Information used to develop likelihoods were based on the reported number of cage failures over a period of time, in other words the observed frequency of an event. Information on the number of cages with fish over the period of reported cage failures was not available to calculate likelihood of any one cage failing. This lack of information to better model the likelihood of episodic escape events is an impediment to better understanding offshore genetic risks from cage failures leading to fish escaping.

“Modified” scenarios in the result figures and discussion in the body of this report). The modified scenarios were modeled to recognize that the previously described assumptions may not reflect four factors affecting the number of fish escaping and their survival in the wild. They are: 1) strong measures to minimize the likelihood of episodic escapes, 2) operation plans to recapture escaped fish, 3) the placement of offshore farms that may adversely affect the survival of escapees, and 4) the effects of the culture environment (developmental effects) adversely affecting survival of escapees. The low and high production scenarios were modeled with the modified assumptions. Specifically, cage failure likelihoods were modeled at 3% and 5% for low and high production scenarios, respectively, and half to three-quarters of the fish in a cage failure would be recovered (25% to 50% of the fish in a cage escape). Additionally, the modified scenarios assumed escaped fish would survive at half the rate of the wild population size-based survival.

4.0 Species Parameterization

The following sections describe parameter values used for each of the three components of OMEGA: 1) the cultured population and aquaculture operations, 2) the wild population biology and demographics, and 3) the interactions between wild and escaped cultured fish. Parameter values were based on information gleaned from assessment reports and values gleaned from a combination of lessons learned from use of cultured marine fish for stock enhancement, the wealth of information studying the consequences of Atlantic Salmon escapes from Norway, and the use of theoretical concepts to evaluate potential consequences of escapes.

Aquaculture parameters used in the case studies (size of fish transferred to offshore pens, time in pens and size of fish at harvest) were developed from species reviews in Richie (2021) and other sources. Case studies modeled a 3-Farm, 10,500 mt annual production scenario to represent 3 farms each producing 3,500 mt annually and a 5-Farm, 17,500 mt annual production scenario to represent 5 farms each producing 3,500 mt annually. All case study scenarios assumed 100% wild caught broodstock.

The number of fish in a cage was assumed to be 100,000 at harvest in all cases. Fish in cages were binned into three size categories (bins) in OMEGA to match a growth curve while fish were in cages (transfer to cages, intermediate growout, and size of fish at harvest). These three size categories were included in the model to evaluate escapes of different fish sizes.

4.1 California Yellowtail

The complete list of natural population parameters for California Yellowtail are summarized in Table A-3.

Natural mortality rate of adults was based on Ben-Aderet et al. (2020) and age-specific rates calculated using a logistic function approximated from a review of Greater Amberjack modeling in the Gulf (SEDAR 70 2020) (Table A-3). Fishing mortality was assumed based on a comparison of model predicted annual catch with a total population of 25,000 mt and annual combined U.S. and Mexico catch. Fecundity was from Baxter (1960). The von Bertalanffy Growth model parameters are from Ben-Aderet et al. (2020).

Table A-3. California Yellowtail OMEGA model parameter values.

Component	Parameter	Value	Range	Units	Source
von Bertalanffy Growth Model (both sexes)	VBGF L_{Max}	117.96	--	cm	Ben-Aderet et al. 2020
	VBGF $L_{Initial}$	0	--	cm	
	k	0.196	--	year	
	Max age	22	--	years	
Length (cm) to Weight (kg) (both sexes)	Ln(a)	-10.64163	--	--	Baxter 1960
	b	2.85	--	--	
Maturity schedule	~50% Mature	Age 2(50 cm; 1.7 kg)	--	Years, (cm; kg)	Ben-Aderet et al. 2020 (size at age); Baxter 1960 (maturity schedule)
	100% Mature	Age 3-4 (63 cm; 3.2 kg)	--		
Recruitment	Fecundity	2000000	--	# eggs per kg	Baxter 1960
	Recruitment DI survival	0.0000125	--	--	Assumed
	BH Capacity	--	2000 to 4000	x1,000	Assumed range
	Steepness (h)	--	0.75 to 0.90	--	Calculated range
Natural Mortality	M	0.60 – 0.26	--	Yearly instantaneous	Assumed based on size of fish and rapid growth during YOY recruitment phase, Ben-Aderet et al. 2020
Fishing Mortality	F	0.05	--	Yearly instantaneous	Assumed based on area and remote portions of range of population
Population size	Female spawning biomass	8000 to 18000		mt	Modeled range

California Yellowtail life table (Table A-4) was developed based on population demographic data from Baxter (1960) and Ben-Aderet et al. (2020). Birthrate (b_x) is assumed to be proportional to mean weight at age (Baxter 1960) and the same for males and females. Generation length varied slightly with stochastic variation in survival values used in OMEGA. The median calculated generation length was 7.7 years. S_x includes natural mortality and fishing mortality.

Table A-4. Life table for female California Yellowtail with approximately 100% of fish mature at 3-4 years and maximum age of 22 years. Notation is from Waples et al. (2011).

Age (x)	s_x	m_x	b_x	l_x	b_xl_x	b'_x	b'_xl_x	N_x	B_x	$xB_x/N1$
Females										
1	0.55	0.0	0.00	1.00	0.00	0.00	0.00	1623537	0	0.000
2	0.73	0.4	0.10	0.55	0.03	0.07	0.04	891322	64248	0.040
3	0.75	0.9	0.30	0.40	0.13	0.38	0.15	650665	247162	0.228
4	0.73	1.0	0.60	0.30	0.19	0.74	0.22	485396	357102	0.440
5	0.73	1.0	1.00	0.22	0.21	1.11	0.24	356281	394189	0.607
6	0.73	1.0	1.30	0.16	0.21	1.48	0.24	261154	386350	0.714
7	0.73	1.0	1.60	0.12	0.19	1.84	0.22	191426	352405	0.760
8	0.73	1.0	1.90	0.09	0.16	2.18	0.19	140315	305352	0.752
9	0.73	1.0	2.20	0.06	0.14	2.48	0.16	102851	255125	0.707
10	0.73	1.0	2.40	0.05	0.11	2.75	0.13	75390	207277	0.638
11	0.73	1.0	2.60	0.03	0.09	2.98	0.10	55261	164896	0.559
12	0.73	1.0	2.80	0.03	0.07	3.19	0.08	40506	129072	0.477
13	0.73	1.0	2.90	0.02	0.05	3.36	0.06	29691	99739	0.399
14	0.73	1.0	3.10	0.01	0.04	3.51	0.05	21763	76296	0.329
15	0.73	1.0	3.20	0.01	0.03	3.63	0.04	15953	57896	0.267
16	0.73	1.0	3.30	0.01	0.02	3.73	0.03	11693	43656	0.215
17	0.73	1.0	3.30	0.01	0.02	3.82	0.02	8571	32745	0.171
18	0.73	1.0	3.40	0.00	0.01	3.89	0.02	6283	24455	0.136
19	0.73	1.0	3.50	0.00	0.01	3.95	0.01	4605	18199	0.106
20	0.73	1.0	3.50	0.00	0.01	4.00	0.01	3376	13510	0.083
21	0.73	1.0	3.50	0.00	0.01	4.04	0.01	2474	10005	0.065
22	0.00	1.0	3.60	0.00	0.00	4.08	0.01	1814	7396	0.050
									Generation Length (years)	7.7

4.2 White Seabass

The case study analysis of White Seabass was completed for two scenarios, a U.S. population simulation (low abundance simulation) consistent with the assessment by Valero and Waterhouse (2016) and an extended population (high abundance simulation) that includes the Baja California portion of the species range. The high abundance scenario was modeled to consider the possible distribution of escaped White Seabass south into Baja California, Mexico to spawn, thus diluting the contribution of escaped fish to spawning aggregations in California.

The low abundance case study simulation modeled a spawning biomass of 400 mt to 1,200 mt and the high abundance case study simulation modeled a spawning biomass of 1,600 mt to 5,100 mt. The high abundance model was approximated based on catch data from California and Baja California, Mexico. Total catch ranged from 743 to 1,249 mt from 2005 to 2019, with an average of 80% of the catch from Baja California.

The complete list of natural population parameters for White Seabass are summarized in Table A-5Table A-5Table A-3.

Table A-5. White Seabass OMEGA model parameter values.

Component	Parameter	Value	Range	Units	Source
von Bertalanffy Growth Model (both sexes)	VBGF L_{Max}	141.8	--	cm	Romo-Curiel et al. 2015
	VBGF $L_{Initial}$	0	--	cm	
	k	0.17	--	year	
	Max age	27	--	years	
Length (cm) to Weight (kg) (both sexes)	Ln(a)	-11.81	--	--	Velero and Waterhouse 2016
	b	3.0335	--	--	
Maturity schedule	~50% Mature	Age 4(87 cm; 5.7 kg)	--	Years, (cm; kg)	Velero and Waterhouse 2016
	100% Mature	Age 6 (100 cm; 9.4 kg)	--		
Recruitment	Fecundity	80,000	--	# eggs per kg	Based on 0.76 to 1.5 million eggs per female, CDFG 1994
	Recruitment DI survival	0.000015	--	--	Assumed
	BH Capacity	--	100 to 144 (US) 420 to 770 (US/Mexico)	x1,000	U.S. Velero and Waterhouse 2016 and US/Mexico Assumed range
	Steepness (h)	--	0.70 to 0.80	--	Calculated range
Natural Mortality	M	0.225	--	Yearly instantaneous	Velero and Waterhouse 2016
Fishing Mortality	F	0.2	--	Yearly instantaneous	Assumed based on reported commercial catch in Farado-Yamamoto et al. 2022 and recreational catch in Velero and Waterhouse 2016
Population Size	Female spawning biomass	400 to 1,200 Low 1,600 to 5,100 High		mt	Modeled range Low US and High US/Mexico

White Seabass life table (Table A-6) was developed based on population demographic data from Valero and Waterhouse (2016). Birthrate (b_x) is assumed to be proportional to mean weight at age and the same for males and females. The median calculated generation length was 8.9 years. Abundance (N_x) is the high end of the U.S. population simulation in Valero and Waterhouse (2016). S_x includes natural mortality and fishing mortality.

Table A-6. Life table for female White Seabass with 100% of fish mature at 5 years and maximum age of 27 years. Notation is from Waples et al. (2011).

Age (x)	s_x	m_x	b_x	l_x	b_xl_x	b'_x	b'_xl_x	N_x	B_x	$xB_x/N1$
Females										
1	0.50	0.00	0.00	1.00	0.00	0.00	0.00	74440	0	0.000
2	0.75	0.00	0.00	0.50	0.00	0.00	0.00	36996	0	0.000
3	0.77	0.00	0.00	0.37	0.00	0.00	0.00	27562	0	0.000
4	0.76	0.56	0.50	0.29	0.15	0.53	0.15	21306	11179	0.300
5	0.76	1.00	1.30	0.22	0.27	1.26	0.27	16192	20314	0.682
6	0.76	1.00	1.60	0.17	0.26	1.57	0.26	12290	19236	0.775
7	0.76	1.00	1.90	0.13	0.24	1.87	0.23	9340	17419	0.819
8	0.76	1.00	2.20	0.10	0.21	2.15	0.21	7099	15224	0.818
9	0.76	1.00	2.40	0.07	0.17	2.40	0.17	5395	12962	0.784
10	0.76	1.00	2.60	0.06	0.15	2.64	0.15	4100	10806	0.726
11	0.76	1.00	2.90	0.04	0.12	2.84	0.12	3116	8858	0.654
12	0.76	1.00	3.00	0.03	0.10	3.03	0.10	2368	7168	0.578
13	0.76	1.00	3.20	0.02	0.08	3.19	0.08	1800	5737	0.501
14	0.76	1.00	3.30	0.02	0.06	3.33	0.06	1368	4552	0.428
15	0.76	1.00	3.50	0.01	0.05	3.45	0.05	1040	3586	0.361
16	0.76	1.00	3.60	0.01	0.04	3.55	0.04	790	2808	0.302
17	0.76	1.00	3.70	0.01	0.03	3.64	0.03	600	2188	0.250
18	0.76	1.00	3.70	0.01	0.02	3.72	0.02	456	1698	0.205
19	0.76	1.00	3.80	0.01	0.02	3.79	0.02	347	1313	0.168
20	0.76	1.00	3.90	0.00	0.01	3.84	0.01	264	1013	0.136
21	0.76	1.00	3.90	0.00	0.01	3.89	0.01	200	780	0.110
22	0.76	1.00	3.90	0.00	0.01	3.93	0.01	152	599	0.088
23	0.76	1.00	4.00	0.00	0.01	3.97	0.01	116	459	0.071
24	0.76	1.00	4.00	0.00	0.00	4.00	0.01	88	351	0.057
25	0.76	1.00	4.00	0.00	0.00	4.02	0.00	67	269	0.045
26	0.76	1.00	4.10	0.00	0.00	4.04	0.00	51	205	0.036
27	0.00	1.00	4.10	0.00	0.00	4.06	0.00	39	157	0.028
									Generation Length (years)	8.9

4.3 Striped Bass

The complete list of natural population parameters for Striped Bass are summarized in Table A-7Table A-5Table A-3. Growth, maturity and survival were modeled based on Northeast Atlantic Striped Bass (NEFSC 2019) to evaluate escape scenarios of Striped Bass in California waters. A natural population was not modeled for Striped Bass.

Table A-7. Striped Bass OMEGA Model Parameter Values

Component	Parameter	Value	Range	Units	Source
von Bertalanffy Growth Model (both sexes)	VBGF L_{Max}	162.0	--	cm	NEFSC 2019
	VBGF $L_{Initial}$	-0.71	--	cm	
	k	0.069	--	year	
	Max age	31	--	years	
Length (cm) to Weight (kg) (both sexes)	Ln(a)	-11.322	--	--	NEFSC 2019
	b	3.007	--	--	
Maturity schedule	~50% Mature	Age 6 (60 cm; 2.7 kg)	--	Years, (cm; kg)	NEFSC 2019; used to estimate maturity of escaped Striped Bass
	100% Mature	Age 8 (73 cm; 4.9 kg)	--		
Recruitment	Fecundity	Not Modeled		# eggs per kg	
	Recruitment DI survival			--	
	BH Capacity			x1,000	
	Steepness (h)			--	
Natural Mortality	M	0.70 – 0.23	--	Yearly instantaneous	NEFSC 2019; Used to estimate survival of escaped Striped Bass
Fishing Mortality	F	Not modeled	--	Yearly instantaneous	
Population size	Female spawning biomass	Not modeled		mt	

4.4 Red Drum

The complete list of natural population parameters for Red Drum are summarized in Table A-7Table A-5Table A-3. Model parameters were taken from Addis (2020) for the NW Florida population of Red Drum. See Section 3.3.1, *Case Study: Red Drum* in the body of this report for more details.

Table A-8. Red Drum OMEGA Model Parameter Values

Component	Parameter	Value	Range	Units	Source
von Bertalanffy Growth Model (both sexes)	VBGF L_{Max}	73.76	--	cm	Addis 2020
	VBGF $L_{Initial}$	0	--	cm	
	k	-0.17	--	year	
	Max age	40	--	years	
Length (cm) to Weight (kg) (both sexes)	Ln(a)	-11.15	--	--	Addis 2020
	b	2.94	--	--	
Maturity schedule	~50% Mature	Age 3(60 cm; 2.4 kg)	--	Years, (cm; kg)	Addis 2020
	100% Mature	Age 4 (65 cm; 3.1 kg)	--		
Recruitment	Fecundity	7,500,000	--	# eggs per kg	Wilson and Nieland 1994
	Recruitment DI survival	0.00000032	--	--	Assumed
	BH Capacity	1,965	--	x1,000	Addis 2020 for NW Florida Population Unit
	Steepness (h)	--	~0.90	--	Calculated mid-pointe
Natural Mortality	M	0.40 – 0.11	--	Yearly instantaneous	Addis 2020
Fishing Mortality	F	0.16	--	Yearly instantaneous	Addis 2020
Population size	Female spawning biomass	10,200 to 13,700		mt	Modeled range

Red Drum life table (Table A-9) was developed based on population demographic data from Addis (2020) for the NW Florida population unit. Birthrate (b_x) is assumed to be proportional to mean weight at age and the same for males and females. The median calculated generation length was 11.4 years. S_x includes natural mortality and fishing mortality.

Table A-9. Life table for female Red Drum with 100% of fish mature at 4 years and maximum age of 40 years. Notation is from Waples et al. (2011).

Age (x)	s_x	m_x	b_x	l_x	b_xl_x	b'_x	b'_xl_x	N_x	B_x	$xB_x/N1$
Females										
1	0.80	0.00	0.00	1.00	0.00	0.00	0.00	926787	0	0.000
2	0.80	0.00	0.00	0.80	0.00	0.00	0.00	737722	435	0.000
3	0.78	0.59	0.60	0.64	0.41	0.19	0.12	588703	112487	0.182
4	0.76	0.98	1.40	0.49	0.70	0.42	0.21	456833	190476	0.411
5	0.78	1.00	1.70	0.38	0.62	0.49	0.18	347650	170785	0.461
6	0.83	1.00	1.80	0.29	0.53	0.54	0.16	270124	144807	0.469
7	0.88	1.00	1.90	0.24	0.46	0.56	0.14	223933	126186	0.477
8	0.90	1.00	2.00	0.21	0.42	0.58	0.12	197509	114616	0.495
9	0.90	1.00	2.00	0.19	0.38	0.59	0.11	176968	104470	0.507
10	0.90	1.00	2.00	0.17	0.35	0.60	0.10	158563	94587	0.510
11	0.90	1.00	2.00	0.15	0.31	0.60	0.09	142073	85253	0.506
12	0.90	1.00	2.00	0.14	0.28	0.60	0.08	127297	76649	0.496
13	0.90	1.00	2.00	0.12	0.25	0.60	0.07	114058	68846	0.483
14	0.90	1.00	2.00	0.11	0.23	0.60	0.07	102196	61746	0.466
15	0.90	1.00	2.10	0.10	0.20	0.61	0.06	91568	55378	0.448
16	0.90	1.00	2.10	0.09	0.18	0.61	0.05	82045	49643	0.429
17	0.90	1.00	2.10	0.08	0.16	0.61	0.05	73512	44480	0.408
18	0.90	1.00	2.10	0.07	0.15	0.61	0.04	65867	39874	0.387
19	0.90	1.00	2.10	0.06	0.13	0.61	0.04	59017	35727	0.366
20	0.90	1.00	2.10	0.06	0.12	0.61	0.04	52879	32011	0.345
21	0.90	1.00	2.10	0.05	0.10	0.61	0.03	47380	28682	0.325
22	0.90	1.00	2.10	0.05	0.09	0.61	0.03	42452	25699	0.305
23	0.90	1.00	2.10	0.04	0.08	0.61	0.03	38037	23027	0.286
24	0.90	1.00	2.10	0.04	0.08	0.61	0.02	34081	20632	0.267
25	0.90	1.00	2.10	0.03	0.07	0.61	0.02	30537	18486	0.249
26	0.90	1.00	2.10	0.03	0.06	0.61	0.02	27361	16564	0.232
27	0.90	1.00	2.10	0.03	0.05	0.61	0.02	24515	14841	0.216
28	0.90	1.00	2.10	0.02	0.05	0.61	0.01	21966	13297	0.201
29	0.90	1.00	2.10	0.02	0.04	0.61	0.01	19681	11915	0.186
30	0.90	1.00	2.10	0.02	0.04	0.61	0.01	17634	10675	0.173
31	0.90	1.00	2.10	0.02	0.04	0.61	0.01	15801	9565	0.160
32	0.90	1.00	2.10	0.02	0.03	0.61	0.01	14157	8570	0.148
33	0.90	1.00	2.10	0.01	0.03	0.61	0.01	12685	7679	0.137
34	0.90	1.00	2.10	0.01	0.03	0.61	0.01	11366	6880	0.126
35	0.90	1.00	2.10	0.01	0.02	0.61	0.01	10184	6165	0.116
36	0.90	1.00	2.10	0.01	0.02	0.61	0.01	9125	5524	0.107
37	0.90	1.00	2.10	0.01	0.02	0.61	0.01	8176	4949	0.099
38	0.90	1.00	2.10	0.01	0.02	0.61	0.01	7325	4435	0.091
39	0.90	1.00	2.10	0.01	0.01	0.61	0.00	6563	3973	0.084
40	0.00	1.00	2.10	0.01	0.01	0.61	0.00	5881	3560	0.077
									Generation Length (years)	11.4

4.5 Almaco Jack

The complete list of natural population parameters for Almaco Jack are summarized in Table A-10Table A-7Table A-5Table A-3. Sagarese et al. 2016 and updated model parameters from SEDAR 70 (2020) for Greater Amberjack were the primary guide to modeling Almaco Jack in the Gulf. A definitive estimate of population abundance of Almaco Jack was not available so a range of abundances were modeled based on catch data of Almaco Jack relative to Greater Amberjack. See Section 3.3.2, *Case Study: Almaco Jack* in the body of this report for more details.

Table A-10. Almaco Jack OMEGA Model Parameter Values

Component	Parameter	Value	Range	Units	Source
von Bertalanffy Growth Model (both sexes)	VBGF L_{Max}	143.6	--	cm	Murie and Parkyn 2008
	VBGF $L_{Initial}$	0	--	cm	
	k	0.130	--	--	Farmer et al. 2016; Sagarese et al. 2016
	Max age	22	--	years	
Length (cm) to Weight (kg) (both sexes)	Ln(a)	-10.096	--	--	Sagarese et al. 2016
	b	2.76	--	--	
Maturity schedule	~50% Mature	Age 5(76 cm; 4.5 kg)	--	Years, (cm; kg)	Sagarese et al. 2016
	100% Mature	Age 7 (92 cm; 10.8 kg)	--		
Recruitment	Fecundity	4020572	--	# eggs per kg	Harris et al. 2007; SEDAR 33 2014 Greater Amberjack
	Recruitment DI survival	0.0000002	--	--	Assumed
	BH Capacity		246 to 546	x1,000	Assumed range because of uncertainty population size
	Steepness (h)	--	0.75 to 0.85	--	Calculated range
Natural Mortality	M	0.52 – 0.26	--	Yearly instantaneous	SEDAR 70 2020 for Greater Amberjack
Fishing Mortality	F	0.10	--	Yearly instantaneous	Approximated based on assumed catch of Almaco Jack
Population size	Female spawning biomass		250 to 750	mt	Modeled range

Almaco Jack life table (Table A-11) was developed based on population demographic data from Sagarese et al. (2016) and Greater Amberjack described in SEDAR 70 (2020). The median calculated generation length was 8.9 years. Abundance (N_x) is the modeled low population abundance scenario. S_x includes natural mortality and fishing mortality.

Table A-11. Life table for female Almaco Jack with 100% of fish mature at approximately 7 to 8 years and maximum age of 22 years. Notation is from Waples et al. (2011).

Age (x)	s_x	m_x	b_x	l_x	b_xl_x	b'_x	b'_xl_x	N_x	B_x	$xB_x/N1$
Females										
1	0.60	0.00	0.00	1.00	0.00	0.00	0.00	64508	0	0.000
2	0.63	0.00	0.00	0.60	0.00	0.00	0.00	38511	76	0.001
3	0.65	0.02	0.00	0.38	0.00	0.03	0.01	24416	623	0.014
4	0.66	0.14	0.10	0.25	0.03	0.24	0.06	15993	3893	0.121
5	0.68	0.47	0.60	0.16	0.10	1.16	0.19	10523	12229	0.474
6	0.69	0.79	1.30	0.11	0.15	2.61	0.29	7124	18601	0.865
7	0.69	0.93	2.00	0.08	0.15	3.85	0.29	4894	18832	1.022
8	0.70	0.98	2.50	0.05	0.13	4.85	0.26	3397	16456	1.020
9	0.70	0.99	2.90	0.04	0.11	5.72	0.21	2367	13543	0.945
10	0.70	1.00	3.30	0.03	0.09	6.53	0.17	1657	10814	0.838
11	0.70	1.00	3.70	0.02	0.07	7.28	0.13	1165	8476	0.723
12	0.71	1.00	4.10	0.01	0.05	7.97	0.10	821	6548	0.609
13	0.71	1.00	4.40	0.01	0.04	8.61	0.08	582	5009	0.505
14	0.71	1.00	4.70	0.01	0.03	9.20	0.06	413	3800	0.412
15	0.71	1.00	5.00	0.01	0.02	9.74	0.04	294	2864	0.333
16	0.71	1.00	5.20	0.00	0.02	10.23	0.03	210	2147	0.266
17	0.71	1.00	5.40	0.00	0.01	10.67	0.03	150	1599	0.211
18	0.71	1.00	5.60	0.00	0.01	11.07	0.02	107	1184	0.165
19	0.71	1.00	5.80	0.00	0.01	11.42	0.01	76	873	0.129
20	0.71	1.00	6.00	0.00	0.01	11.74	0.01	55	641	0.099
21	0.71	1.00	6.10	0.00	0.00	12.03	0.01	39	469	0.076
22	0.00	1.00	6.30	0.00	0.00	12.28	0.01	28	342	0.058
									Generation Length (years)	8.9

4.6 Cobia

The complete list of natural population parameters for Cobia are summarized in Table A-10Table A-7Table A-5Table A-3Table A-12. Model parameters are based on SEDAR 28 (2020). The modeled Gulf stock includes the Eastern Atlantic Florida coast south of the state border between Florida and Geogia. See Section 3.3.3, *Case Study: Cobia* in the body of this report for more details.

Table A-12. Cobia OMEGA Model Parameter Values

Component	Parameter	Value	Range	Units	Source
von Bertalanffy Growth Model (both sexes)	VBGF L_{Max}	136.26 (F); 122.17 (M)	--	cm	SEDAR 28 2020
	VBGF $L_{Initial}$	0	--	cm	
	k	0.410 (F); 0.360 (M)	--	year	
	Max age	11	--	years	
Length (cm) to Weight (kg) (both sexes)	Ln(a)	-12.684 (F); 13.233 (M)	--	--	SEDAR 28 2020
	b	3.278 (F) 3.392 (M)	--	--	
Maturity schedule	~50% Mature	Age 2(100 cm; 12.6 kg)	--	Years, (cm; kg)	SEDAR 28 2020
	100% Mature	Age 3 (115 cm; 17.5 kg)	--		
Recruitment	Fecundity	607489	--	# eggs per kg	Brown-Peterson et al. 2001
	Recruitment DI survival	0.0000024	--	--	Assumed
	BH Capacity	1,906	--	x1,000	SEDAR 28 2020
	Steepness (h)	--	0.75 to 0.90	--	Calculated range
Natural Mortality	M	0.546 – 0.360	--	Yearly instantaneous	SEDAR 28 2020
Fishing Mortality	F	0.330	--	Yearly instantaneous	SEDAR 28 2020
Population size	Female spawning biomass	3,500 to 5,500		mt	Modeled range

Cobia life table (Table A-13) was developed based on population demographic data from SEDAR 28 (2020) for the Gulf. The median calculated generation length was 4.0 years. S_x includes natural mortality and fishing mortality.

Table A-13. Life table for female Cobia with 100% of fish mature at approximately 3 to 4years and maximum age of 11 years. Notation is from Waples et al. (2011).

Age (x)	s_x	m_x	b_x	l_x	b_xl_x	b'_x	b'_xl_x	N_x	B_x	$xB_x/N1$
Females										
1	0.41	0.00	0.00	1.00	0.00	0.00	0.00	880075	0	0.000
2	0.39	0.20	0.50	0.41	0.20	0.49	0.20	357311	173929	0.237
3	0.44	0.83	3.60	0.16	0.58	3.52	0.56	140780	495395	1.013
4	0.47	0.97	5.90	0.07	0.41	5.72	0.40	61662	352650	0.962
5	0.49	0.99	7.40	0.03	0.24	7.14	0.24	28981	206774	0.705
6	0.49	1.00	8.40	0.02	0.13	8.14	0.13	14085	114573	0.469
7	0.50	1.00	9.10	0.01	0.07	8.84	0.07	6958	61497	0.293
8	0.50	1.00	9.60	0.00	0.04	9.32	0.04	3465	32306	0.176
9	0.50	1.00	10.00	0.00	0.02	9.66	0.02	1733	16729	0.103
10	0.50	1.00	10.20	0.00	0.01	9.88	0.01	868	8577	0.058
11	0.00	1.00	10.30	0.00	0.01	10.03	0.01	435	4362	0.033
									Generation Length (years)	4.0

5.0 References

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