occurrence of a positive sea surface temperature anomaly registered in the area. During the strandings events high positive anomalies (0.5 - 1.5) were observed along the Uruguayan and southern Brazil continental shelf and oceanic region. This sustained temperature anomaly is associated with a strong influence of Tropical and Subtropical waters, advected southward by the Brazil Current. Probably these turtles reached the Uruguayan coast owing the favorable thermal conditions during the austral summer where an intrusion of warm oceanic waters is expected. The strandings reported above are of specially interest, since the hawksbill turtle is not frequently reported for temperate waters. Our records extend the geographic range of this species almost 250 km southward. The sporadic occurrence of this critically endangered species in Uruguayan waters implies a fifth species of marine turtle for this zone and reinforces the importance of continue monitoring the Uruguayan coast. This evidence altogether affords a new evaluation of the distribution of this species in the South Western Atlantic ocean.

USING CUSTOM-DESIGNED CAPTURE ARRAYS AND NEXT-GENERATION SEQUENCING FOR SNP DISCOVERY IN LEATHERBACKS (*DERMOCHELYS CORIACEA*)

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We describe an approach that combines custom micro-array capture technology and next-generation sequencing to discover SNPs for use in population structure analyses. The samples were chosen primarily as part of an ongoing study of fine scale population structure of leatherbacks nesting in the western Pacific, with a few additional samples representing the global distribution of the species. Nuclear loci sequences were compiled from a variety of sources, including Genbank, as well as flanking regions from microsatellites developed for either loggerheads or green turtles. Additionally some fragments were characterized during SNP discovery for green turtles using AFLP fragments. Genomic library enrichment was completed using tiled complimentary sequence probes designed specifically for the Agilent custom micro-array. Probes were designed to cover the entire mitochondrial genome as well as eighty nuclear loci. In order to multiplex 100 turtles in the array, the individual turtle genomes were fragmented and labeled with short a unique sequence or index tag. The indexed libraries were then pooled in equal concentrations. The pooled library was then hybridized to the capture array and subsequently eluted and amplified for sequencing on an Illumina genome analyzer. This is a streamlined method for collecting large amounts of nuclear and mitochondrial sequence data for SNP discovery as well as population genetic studies of wild populations.

CONSERVATION OF SANDY BEACHES: HOW ANTHROPOGENIC AND NATURAL FACTORS IMPACT SEA TURTLE NESTING ON A REGIONAL SCALE

Ikuko Fujisaki[1] and Margaret Lamont[2]

[1] University of Florida, Department of Wildlife Ecology and Conservation/Ft. Lauderdale Research and Education Center
[2] University of Florida, Florida Cooperative Fish and Wildlife Research Unit

Coastal areas provide critical habitats for a variety of wildlife species which helps maintain high biodiversity in this scarce habitat. Although conservation of this habitat is a priority, it is challenging due to

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U.S. DEPARTMENT OF COMMERCE
Dr. Rebecca Blank, Acting Secretary

NATIONAL OCEANIC AND ATMOSPHERIC ADMINISTRATION
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