NOAA Technical Memorandum NMFS

January 1981

An Annotated Computerized Bibliography of the Use of Karyotypic Analysis in the Subspecific Taxonomy of Mammals

Gary L. Worthen

NOAA-TM-NMFS-SWFC-9

U.S. DEPARTMENT OF COMMERCE
National Oceanic and Atmospheric Administration
National Marine Fisheries Service
Southwest Fisheries Center

NOAA Technical Memorandum NMFS

This TM series is used for documentation and timely communication of preliminary results, interim reports, or special purpose information; and have not received complete formal review, editorial control, or detailed editing.

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Research Associate
Biomedical Laboratory
Exceptional Child Center
Utah State University
Logan, Utah 94322

This report was prepared by Gary L. Worthen, Utah State University, under contract No. NOAA/79-ABC-00205 for the National Marine Fisheries Service, Southwest Fisheries Center, La Jolla, California. The statements, findings, conclusions and recommendations herein are those of the author and do not necessarily reflect the views of the National Marine Fisheries Service. Dr. William F. Perrin of the Southwest Fisheries Center served as Chief Official Technical Representative for this contract.

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Philip M. Klutznick, Secretary
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INTRODUCTION

As one of the task objectives to be completed in fulfilling our contract (#NOAA/79-ABC-00205) on the Stock Assessment of Pacific Ocean Delphinids by G and C Chromosome Banding, we agreed to compile an annotated computerized bibliography on the use of karyotypic analysis in the subspecific taxonomy of mammals.

We stated under "Research Design" on page 7 of our original grant proposal, that:

> . . .an annotated bibliography of articles will be constructed discussing the use of karyotypic analyses in subspecific taxonomy of mammals. Techniques used will include a computerized bibliographic search of titles and abstracts, references found in citation in known relevant articles, and manual searches. Any available article found in such a reference will be obtained and a brief abstract written for use as an annotation. All bibliographic entries will be. . .keypunched, verified, and run through a computer program which will be developed by our staff for a B6700 computer to display the entries. The end product of this process will be a listing of each key word in the title of the article (or other key words we may select) in alphabetical order in the context of the remainder of the title. This format is similar to what is found in Biological Abstracts and should be very useful to both our research staff and to NMFS personnel. In addition, a list of authors (including junior authors) of articles will appear in alphabetical order. A third section (which, to save expense, may be typed rather than listed on the computer) will appear with a full citation of each article followed by a brief annotation."

This document, then, is a summary of the most pertinent and most recent literature related to that subject. It should be noted, however, that a document such as this one is a dynamic entity, and will be, by its very nature, in a continual state of flux. Continual additions will be made as new literature is published, or as other articles in the existing literature come to light. Articles will also

be removed from the bibliography, as they become outdated and no longer substantially contribute to the scientific advancement of the field. This document, then, is an attempt to capture at this moment in time the most relevant literature related to the use of karyotypic analysis in the subspecific taxonomy of mammals.

As a result of the dates of available listings from the search service (see the following section), this bibliography covers primarily the period from 1969 to May of 1980, which coincides nicely with the time frame of the bulk of relevant cytogenetic work in the subject area (see Discussion). However, as a result of other search techniques (described below), some articles are included as far back as 1959. Any article that was found by any of the search techniques is included in this bibliography regardless of the language in which it was written.

Literature Search and Information Retrieval Techniques

A computerized literature search was conducted in the Biosis Previews, which is a computerized literature search service that abstracts from Biological Abstracts, Biological Abstracts/RRM, and Bioresearch Index in their entirety. In actuality the Biosis Previews will list more articles on a given subject than a hand search in the above sources, as all articles or abstracts are not available in those sources, but are available to the computer service. Biosis Previews are broken down into two major sections--one running from 1969 to 1973 inclusive, and the other running from 1974 to present. In May of 1980 an update on the most recent Biosis Preview was conducted in order to assure that the most recent articles would be included in this bibliography. The most recent articles are included, because the articles are placed on the Biosis Preview computer index before they are actually printed in reference form.

Several key words were used in the search to isolate articles relevant to the subject at hand. These key words were then linked together with Boolean logic. Three major components were used in the logic system:

(1) A component referring to subspecific taxonomy and related areas. In addition to terms relating strictly to subspecific taxonomy and subspeciation, terms relating to species and speciation were also added. This addition was made because of the frequent intermixing within articles of both subspecific and specific taxonomy (without clear designation in the title which taxon was being discussed). The species component was added also for a second reason--that being a very low yield (when linked to the other components) of articles relating strictly to subspecific taxonomy.

(2) A component referring to a suite of cytogenetic terms intended to isolate all relevant articles on any form of karyotypic analysis.

(3) A component used to isolate articles referring to mammals.

In this situation, the use of a concept code was extremely useful, inasmuch as it would be impossible to list all the terms which referred to mammals in titles of articles. By using the concept code, all articles referring to mammals were In scanned. addition, the term "mammal" was also scanned.

In all three components of the logic system, whenever applicable, a code was used (in this case a question mark); such that a root word could be listed, and all words containing that word would be retrieved in the bibliographic search. For example, the word "mammal" immediately followed by a question mark (MAMMAL?) would yield all articles which contained the words "mammal," "mammals," "mammalogy," "mammalian," etc. Within each of the three logical components, each of

the words was linked together with "or" such that the presence of any one of the words in the group registered the article into that logical component. In contrast, each of the logical components was linked together with "AND" such that an article had to be registered in each of the logical components to be referenced for this bibliography. Figure 1 gives a graphic presentation of the Boolean logic used in the original computer search.

This computerized literature search formed the nucleus, and the majority, of articles which are referenced here. However, as each article was obtained, the Literature Cited section in that article was scrutinized in an attempt to find other related articles. In addition, some articles were added strictly as a result of the author's familiarity with cytogenetic literature. Through a combination of these procedures, a comprehensive list of articles relating to the use of karyotypic analysis on subspecific taxomony of mammals has been constructed.

Articles were obtained either from the Utah State University Library, the University of Utah Library, or the Interlibrary Loan facility at Utah State University. Xerox copies of each of the abstracted articles are on file in the Biomedical Laboratory of the Exceptional Child Center at Utah State University.

The great majority of articles found were in English; however, a few were in foreign languages. In most cases, an English abstract was provided, or enough of the article could be read to understand its contents. In only one instance was it necessary to have an article translated by staff external to our facility.

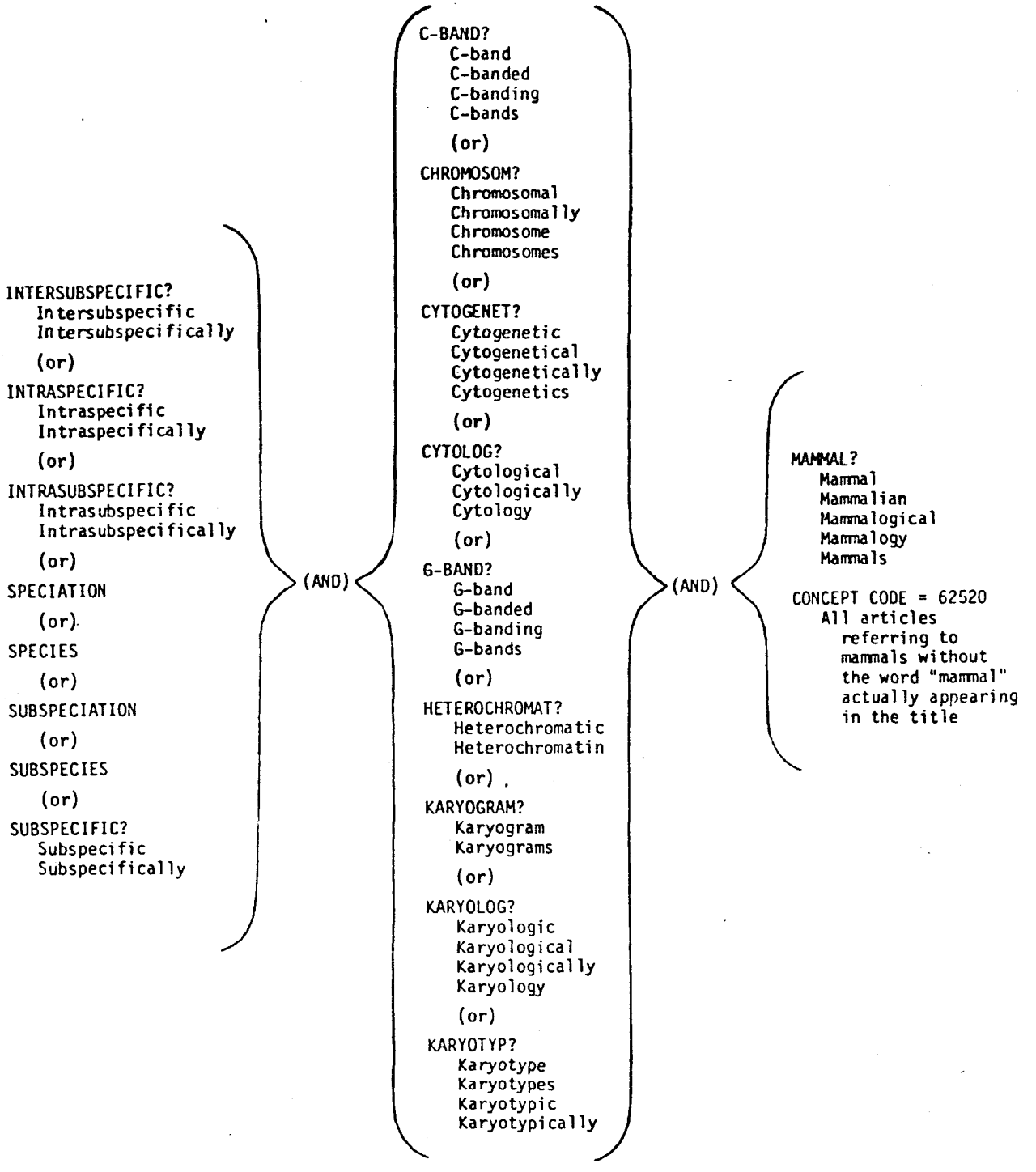

Figure 1. Boolean logic used to find articles pertinent to the use of karyotypic analysis in subspecific taxonomy of mammals, displaying the root word (or portion thereof) used in the search and some of the more common words scanned by the search program under each root word (see text for details).

DISCUSSION

The articles abstracted in this computerized bibliography cover a wide range of subject matter. Most of the articles, by virtue of the intended scope of this bibliography, center around the use of karyotypic analysis in subspecific taxonomy of mammals. Some articles, however, are only peripherally related to that subject in its narrowest interpretation. They do, however, have relevance to that subject in a broader sense.

All types of mammals for which literature could be found are covered in this bibliography, and no attempt was made to select for or against any group of mammals. Many of the mechanisms presented in this bibliography are not commonly found in cetaceans, but are common to other mammalian groups (such as rodents). The relevance (or irrelevance) of these articles to cetaceans will not be discussed here--such discussion will be saved for the final report.

Because of the time profile involved, the articles covered in this bibliography, cover a wide range of cytogenetic techniques and schools of thought. For example, during the 1960's the common method of karyotyping was by the use of gross karyotypes. Such methodology meant that only number, shape, and general configuration of the chromosome complement could be ascertained. Karyotypic work in the 70's, however, is much more refined because of a major scientific breakthrough in the early 70's which allows for the banding of chromosomes. In this manner, homologous chromosomes can be completely matched. As a result of this breakthrough, the old gross karyotypes had to be entirely re-examined in light of the new banding data. In many cases,

the old interpretations were found to be incorrect. These erroneous conclusions resulted because it was frequently impossible to tell from the gross karyotype, which chromosomes had undergone centric fusion (a process by which two chromosomes are united to form one larger chromosome). As chromosome number, size, shape, and arm ratio were the only indicators of what had evolutionarily transpired, many incorrect assumptions were made. For example, if three pair of acrocentric chromosomes (A, B, and C) existed in some ancestral type, where chromosomes B and C were identical in size and shape, interpretational problems could result. If in one evolved species, chromosome A fused to B, and in another closely related species A fused to C, the resulting chromosomes would, with gross karyotyping, appear identical. If these chromosomes were the only delineator between the two species, the two species may be incorrectly synonymized as one, when in reality the two karyotypes were quite distinct. The banding protocols now used would elucidate that fact.

Although the abstracted articles comprise more or less of a continuum, I have somewhat arbitrarily categorized each article into one or more subject groupings. Each of these groupings constitutes an appendix to this report, and all articles dealing with a particular grouping can be found listed in the appropriate appendix (A through H).

The bulk of the articles covered in the bibliography, in the broad sense, refer to karyotypic or cytogenetic analysis of subspecific taxa. These papers are listed in Appendix A, and include articles on a wide range of animal groups ranging from rodents, lemurs and deer to pigs but weighted heavily with articles covering various species of rodents.

For example, a large suite of articles exists on chromosomal polymorphism of various geographic forms of the black rat (Rattus rattus).

Various approaches have been used to analyze the diverse subspecific taxa being studied. Many of the papers are on chromosome number (exemplified by the series of papers by Yosida, et al. on black rats), and many include a comment on the fundamental number of chromosome arms (for example, see Rausch and Rausch, 1972). Other articles (for example, Greenbaum, Baker and Ramsey, 1978) use a combination of G and C banding pattern analysis to elucidate chromosomal evolution; while still other papers (for example, Sharma and Garg, 1975) heavily utilize C-banding to analyze constitutive heterochromatin.

In many instances, cytogenetic analysis has been used to substantiate the existence of a full species where only a subspecies was previously thought to exist. Articles covering this subject are listed in Appendix B, as well as in appropriate positions in other appendices. In this category, studies on rodents again predominate the literature; however, articles on artiodactyls and insectivors are also found. The concept of sibling species or a super species containing many closely related forms, has also received wide recognition. These articles are listed in Appendix C.

Articles abound in the literature on karyotypes and cytogenetics of taxa at specific or higher levels. The great majority of these articles have been omitted here for reasons of brevity, space limitations, and because they are out of the scope of the present work. A few of the articles, however, have been included when they: (1) show

relevance to one of the other major categories in the bibliography, (2) when they show a parallel in technique or interpretation to subspecific taxonomy, (3) when they show clear-cut relevance to one or more of the other articles contained in the bibliography, (4) when they show particular interest to the cytogenetics of cetaceans, or (5) when they serve as an example of a particular type of paper which is being discussed. Many articles (such as Arnason 1970) simply present a karyotype for a particular species of mammal. Other articles (for example, Haiduk, Bickham, and Schmidley 1979) describe karyotypes for several species within a particular genus. Other articles (such as Schroder and Van Der Loo 1979) compare the karyotypes of several genera within the same family. A synopsis of the few abstracted articles relating to the cytogenetics of taxa at specific or higher levels can be found in Appendix D.

A section (Appendix E) has been included on the cytogenetics of domestic mammals because of certain parallels between selected breeding in domestic animals and evolution of subspecies per se. Another section (Appendix F) has been included on individual variation, inter-populational variabiity, and sibling diversity. These articles cover a wide range of taxa including rodents, lagomorphs, pigs, chiropterans, and primates (including man). Articles included in this group show the potential scope of variability within some animal groups below the subspecies level (in some cases within a single individual).

Because of its relevance to cytogenetic interpretations of mammalian taxonomy, a separate section has been included on constitutive heterochromatin (C-band) variability in mammals (Appendix G). This section perhaps has the greatest relevance to cetacean chromosomal classification inasmuch as most of the variation found

within cetacean chromosomes are found in variation in regions of constitutive heterochromatin. This phenomenon will be discussed in greater detail in the final report. A general pattern is frequently apparent within mammalian groups for C-banding to show more variability between populations than corresponding G-banding.

The articles in the remaining category (listed in Appendix H) cover cytological aspects of speciation and chromosomal evolution. Bush, Case, Wilson and Patton (1977) state that speciation rate is strongly correlated with the rate of chromosomal evolution. Bush (1975) states that the highest rates of chromosomal evolution occur in parapatric situations and that the lowest chromosome evolution rate occurs in allopatric siutations where speciation occurs by subdivision. In the latter case there is little or no directed chromosomal evolution. In allopatric situations where the founder effect is the rule, and also in sympatric situations, the rate of chromosomal evolution is intermediate. Schroeder, Antoni, and Vanderloo (1978) also indicate that speciation is encouraged by geographic proximity and that geographically isolated species and subspecies have no need to develop divergent karyotypes. Nevo and Cleve (1978) also indicate that as a general rule, habitat specialists display significantly lower genetic variability than do habitat generalists. Arnason (1972 and 1974) indicates that cetaceans are characterized by a remarkable stability of their karyotypic patterns. Most of the existing variability is found within the C-band areas of constitutive heterochromotin. Arnason (1972) further points out that the orders Insectivora and Rodentia conversely, both display great karyotypic variability and would thus represent a different mode of speciation than that found in cetaceans.

Chromosomal evolution historically has been considered a unidirectional evolutionary process in the direction of centric fussion of small acrocentric chromosomes to form large metacentric chromosomes. Lawlor (1974) suggests that cytological evidence provided by studies of mammalian chromosomes suggests that "fission" - a process by which biarmed chromosomes divide to create small acrocentric chromosomes (and thus create a higher diploid number) - has also played an important role in chromosomal evolution. Evidence suggests no obvious trend of evolutionary change in the number of chromosomal arms.

Other subject categories could be split out from the articles in the bibliography. I felt, however, that those that have been covered are the most important. If information on other subtopics covered in the bibliography is desired, use of the key-word-in-context listing will help in the location of that material.

DESCRIPTION OF COMPUTERIZED LISTING

The program which generated the computerized listing for this bibliography was written in Cobol for a Burroughs 6700 computer. A slightly revised version of the program was used to make these actual runs on the Utah State University Computer Center's Burroughs 6800, now in operation.

The computerized portion of the bibliography contains four separate listings which serve to expedite the location of references according to different criteria. Included are elements in the bibliography listed according to: (1) date of publication, (2) name of author or authors (principal and junior), (3) title of articles referenced by key words, and (4) complete bibliographic citation.

Throughout each of the listings generated by the computerized bibliography program, an indexing identification code can be found to facilitate cross-referencing between the listings. This identification code consists of an author identification field and a numerical index field. The author identification field consists of an eight-column field bearing as much of the principal (or sole) author's name as space permits. If the author's last name exceeds eight characters, the first eight letters of the name will appear. In the case of shorter names, one or more initials will follow the complete last name of the author, as space permits.

Immediately following (and adjacent to) the author field is a 4-digit numerical index field. The index number corresponds to the numerical position in the full bibliography of that reference. Using the example in Figure 2, the first entry (by Craig-Holmes) will be the 24th reference to appear in the alphabetical citation list.

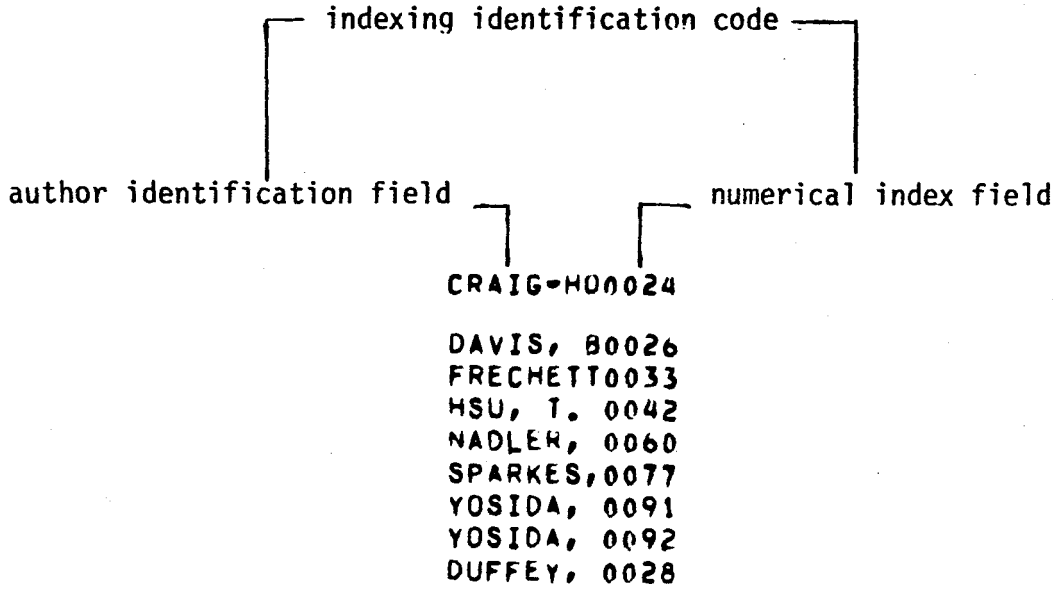

Figure 2. An example of a series of indexing identification codes, showing their two principal components (see text for details).

The first list that appears on the printout displays all references in the bibliography chronologically according to the date of publication. Within each date, the entries are listed alphabetically according to the author index field. Each date entry is followed by its complete corresponding indexing identification code (see Figure 3).

The next list which appears on the printout is an alphabetical compilation of all authors and co-authors in the left-hand 20-character field, followed by the index identification code previously mentioned. If an author listed in the first field is the sole or principal author of a reference, the name will appear in both the author and identification fields. In Figure 4 the first line, for Selander, would be an example.

This list is meant to be used primarily to locate a reference for which the principal author is not known, or if the work of a particular author is of special interest. For example, if the work of T. Sharma is being researched, one would find his name in the left column, identify him as co-author with R. Ramen, whose name appears in the author identification field, and then find the full citation by using the identification code (see line 2 in Figure 4). All authors and co-authors are listed in this manner.

In the next list, key words in the titles of articles are arranged alphabetically for easy reference to specific subject areas. All words that appear within a title, except words statistically found to be of little use in suggesting the subject matter of a title (articles, conjunctions, and such words as "several," "relative," and "typical"), are included in this list (see Table 1 for a full list of excluded

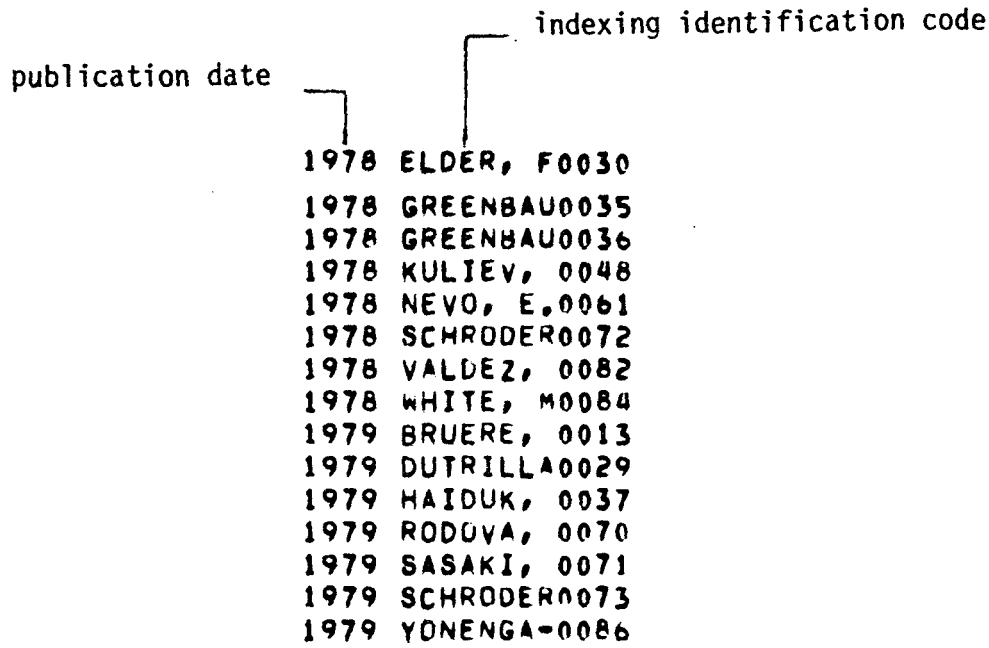

Figure 3. An example of the publication date listing, showing the arrangement of publication date and indexing identification code (see text for details).

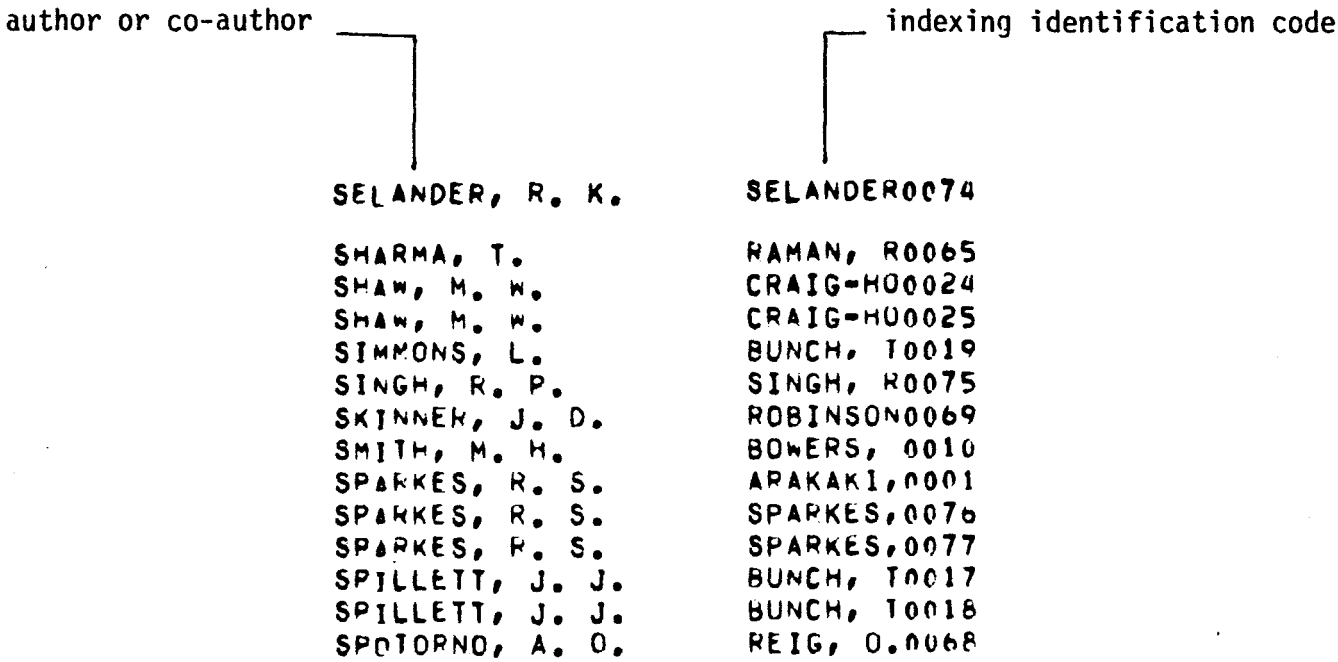

Figure 4. An example of the author listing, showing the arrangement of authors and co-authors in relationship to the indexing identification code (see text for details).

Table 1. Words excluded from the key-word-in-context listing in the annotated computerized bibliography

A
ABILITY
ACTION
ACTIVITY
ADDITIONAL
ADMINISTERED
AFFECT
AFFECTED
AFFECTING
AFTER
AGAINST
ALL
ALONG
ALTERNATING
AMONG
AN
ANALYSES
ANALYSIS
ANALYTICAL
AND
ANIMAL
ANIMALS
ANOTHER
APPARATUS
APPROPRIATE
AREA
AREAS
ARRANGEMENT
ARTIFICIAL
AS
ASPECTS
AT
ATTACHED
AVERAGE
BASED
BASIS
BEFORE
BETWEEN
BOTH
BUT
BY
CALCULATION
CAPACITY
CENT
CERTAIN
CHARACTERISTICS
CHEMICAL
CLOSED
COLLECTION
COMMENTS
COMMON
COMMUNICATION
COMPLETE
COMPUTATIONS
CONCERNING
CONDITION
CONNECTION
CONSIDERATION
CONSIDERATIONS
CONSTRUCTION
CONTAINED
CONTINENT
CONTINUOUS
DATA
DE
DEGREE
DEGREES
DEN
DER
DETERMINATION
DETERMINATIONS
DETERMINING
DIE
DIFFERENT
DO
DOES
DUE
DURING
EFFECT
EIN
ELEMENTS
EMPHASIS
EQUILIBRATION
ESTIMATION
EVALUATION
EVIDENCE
EXPERIMENTAL
EXPERIMENTS
EXTREME
EXTREMELY
FACTOR
FACTORS
FEW
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FOUND
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FUNCTION
FURTHER
GENUS
HIGH
I
II
III
IMPLICATIONS
IMPORTANCE
IN
INFLUENCE
INSTRUMENT
INSTRUMENTAL
INTERNATIONAL
INTERPRETATION
INTO
INVESTIGATION
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MEASUREMENTS
MEASURING
MECHANISM
MECHANISMS
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NORTHWESTERN
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OBSERVATIONS
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ORGANISM
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PARTS
PATTERNS
PECULIAR
PER
PERFORMANCE
PERIOD
POSSIBLE
POTENTIAL
PRELIMINARY
PRINCIPLES
PRODUCE
PRODUCTION
PROGRAM
PROPERTIES
PROPOSED
QUALITATIVE
QUANTITATIVE
RAPID
REFERENCE
REGARD
RELATION
RELATIONS
RELATIONSHIP
RELATIONSHIPS
REQUIREMENTS
RESPONSE
RESPONSES
REVEALED
ROLE
SEVERAL
SIGNIFICANCE
SIMPLE
SOME
SPECIES
STUDIED
STUDIES
STUDY
SYSTEM
TECHNIQUE
TECHNIQUES
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THEORETICAL
THEORY
THROUGH
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UNUSUAL
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WARM
WHICH
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WITHIN
WITHOUT

words). Key words within a title appear beginning in the 21st column of the printout, following a blank space in column 20. As much of the title to which the key word belongs as will fit on one line is printed. An asterisk indicates the end of an article title.

Following any asterisk is the beginning of the title which, when the title is short enough, wraps with the first 19 columns of the title. Where a title is longer than one line of printout can accommodate, a portion of the title is omitted. Enough of the title is present, however, to facilitate assessment of the importance of the article by seeing the key word in context. Following the title field is another blank space and the indexing identification code which corresponds to the reference's appearance in the full bibliography.

A title will appear within this listing as many times as the number of key words within it (which totals the number of words in the title minus the trivial words that have been excluded as indicated above). The title, "CHROMOSOME POLYMORPHISM IN INBRED SUBSPECIES OF PEROMYSCUS MANICULATUS," for instance, will appear first with "CHROMOSOME" being the isolated key word in column 21; again with "INBRED" isolated; later with "MANICULATUS" as the key word, and so on. Figure 5 illustrates the position of the elements from an excerpt of this list.

The final listing on the printout is an alphabetical (by author) bibliography of complete citations. Each citation consists of five elements, each including one or more lines. The first element is the cross-reference indexing identification code which appears in the upper right-hand corner of each citation. The identification codes correspond to those found on the preceding lists. Next, the authors

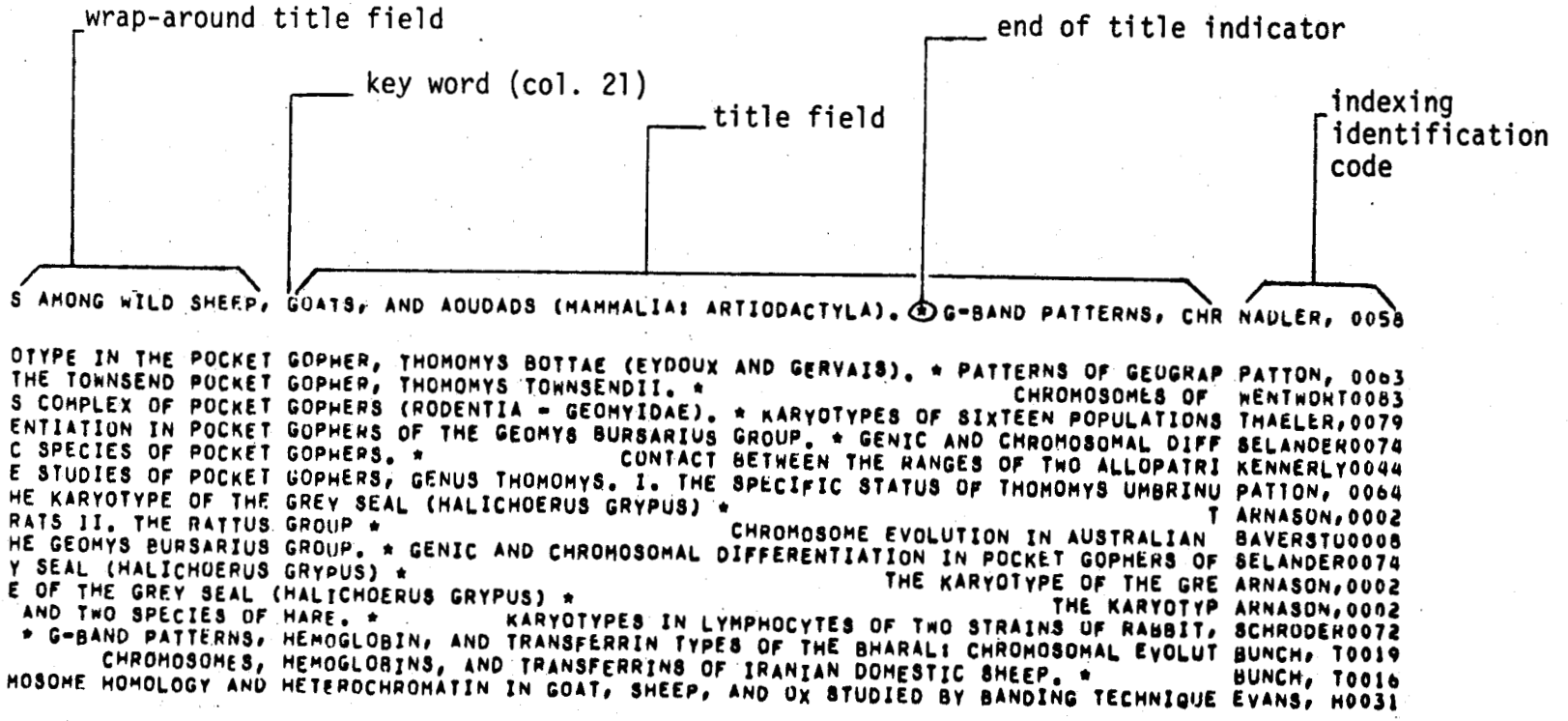

Figure 5. An example of the key word listing, showing the arrangement of the alphabetized key words, title field, wrap-around title field, end of title indicator, and indexing identification code (see text for details).

are listed. If there are more than three authors, the author list will exceed one line. The principal author, listed first, is the basis for the alphabetization of this list. The date of publication is next, located on a separate line near the right-hand side of the list.

The title of the article follows the date on the next line and appears directly below the author list. If the title exceeds 60 characters, it will appear on two or more lines. The last element of a citation in this bibliography is the source. The title of the journal from which the reference came is indented and appears directly below the title of the article. Volume, number (where applicable), and pages are found on the same line to the right of the journal name. In some instances, where a journal title is extremely long, or in the case of books, more than one line of citation may be used. See Figure 6 for an example of a few standard bibliographic entries.

CRAIG-H00025 ——— indexing identification code

CRAIG-HOLMES, A. P. SHAW, M. W. ——— author names

1971 ——— date of publication

POLYMORPHISM OF HUMAN CONSTITUTIVE HETEROCHROMATIN. ——— title of reference

SCIENCE 174 : 702- 704 ——— source

DAVIS, B0026

DAVIS, B. L. BAKER, R. J.

1971

CHROMOSOME MORPHOLOGY OF NORTH AMERICAN RATTUS RATTUS (L.) (MURIDAE).

CYTOLOGIA 36 : 417- 420

DEV, V. 0027

DEV, V. G. MILLER, D. A. TANTRAVAHI, R.
SCHRECK, R. R. RODERICK, T. H. ERLANGER, B. F.
MILLER, O. J.

1975

CHROMOSOME MARKERS IN MUS MUSCULUS: DIFFERENCES IN C-BANDING BETWEEN THE SUBSPECIES M. M. MUSCULUS AND M. M. MOLOSSINUS.

CHROMOSOMA 53 : 335- 344

DUFFEY, 0028

DUFFEY, P. A.

1972

CHROMOSOME VARIATION IN PEROMYSCUS: A NEW MECHANISM.

SCIENCE 176 :1333-1334

DUTRILLA0029

DUTRILLAUX, B. FOSSE, A. M. CHAUVIER, G.

1979

CYTOGENETIC STUDY OF SIX SPECIES OR SUBSPECIES OF MANGABEYS MONKEYS, PAPIINAE CERCOPITHECIDAE.

ANN. GENET. 22 (2): 88- 92

ARTICLE IN FRENCH WITH ENGLISH SUMMARY.

Figure 6. An example of the full bibliographic citation list, showing the four major elements of each citation and the indexing identification code (see text for details).

COMPUTERIZED LISTING OF ARTICLES:

Publication Date List

1959 KENNERLY0056
1965 YOSIDA, 0115
1965 YOSIDA, 0119
1966 HSU, T. 0051
1966 MCFEE, A0071
1966 SINGH, R0097
1966 SPARKES,0100
1967 BAKER, R0008
1967 BRUERE, 0018
1968 HSU, T. 0052
1968 MEIER, M0072
1968 NELSON-R0078
1968 PATTON, 0082
1968 THAELER,0103
1968 WROBLEWS0111
1968 WURSTER,0113
1968 ZIMMERMA0126
1968 ZIVKOVIC0127
1969 BIANCHI,0012
1969 MCFEE, A0070
1969 MEIER, M0073
1969 SOLDATOV0099
1969 WENTWURT0109
1969 YOSIDA, 0123
1970 ARAKAKI,0001
1970 ARNASON,0002
1970 BADR, F.0006
1970 CAPANNA,0028
1970 HOLDEN, 0050
1970 MALYGIN,0066
1971 CRAIG-HU0030
1971 DAVIS, B0031
1971 FRECHETT0039
1971 HSU, T. 0053
1971 KOZLOVSK0059
1971 NADLER, 0077
1971 SPARKES,0101
1971 YOSIDA, 0116
1971 YOSIDA, 0124
1972 ARNASUN,0003
1972 DUFFEY, 0033
1972 GLADKINA0042
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1978

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HEREDITAS 91 : 27- 30

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1974

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1968

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1972

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CHROMOSOMA 60 : 391- 398

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YOSIDA, T. H. AMANO, K.

1965

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CHROMOSOMA 16 : 658- 667

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MORIWAKI, K.

1971

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CHROMOSOMA 34 : 40- 50

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SAGAI, T. MORIWAKI, K.

1972

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JAP. J. GENET. 47 (6): 451- 454

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YOSIDA, T. H. KATO, H. TSUCHIYA, K.
SAGAI, T. MORIWAKI, K.

1974

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SOUTHWEST AND CENTRAL ASIA, WITH SPECIAL REGARD TO THE EVOLUTIONAL RELATIONSHIP BETWEEN THREE GEOGRAPHICAL TYPES.
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1965

CHROMOSOMAL POLYMORPHISM IN RATTUS RATTUS (L.) COLLECTED IN KUSUDOMARI AND MISIMA.
CHROMOSOMA 16 : 70- 78

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CHROMOSOMA 37 : 387- 394

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CHROMOSOMA 41 : 93- 101

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KARYOTYPIC DIFFERENCES OF BLACK RATS, RATTUS RATTUS, COLLECTED IN VARIOUS LOCALITIES OF EAST AND SOUTHEAST ASIA AND OCEANIA.
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VARIATION IN CHROMOSOMES OF THE COTTON RAT, SIGMODON HISPIDUS. 1968
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ZIVKOVIC, S. SOLDATOVIC, B. MILOSEVIC, M. SAVIC, I. ZIVKOVIC0127

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ABSTRACTS OF ARTICLES

The abstracts of the articles in this section follow standard bibliographic order, which is the same order that is followed in the Bibliographic Citation section of the computerized listing of articles. For each abstract a full bibliographic citation is given.

Wherever possible the abstracts themselves were drawn from the literature: the rationale being that an author of an article would be the best person to abstract that article because of his familiarity with subject content. Where an author's abstract was not available an author's summary was frequently used. When an abstract or a summary were not available from the author, either the abstract contained in Biological Abstracts or an abstract written by myself was used. The abstracting source (which is bracketed) immediately follows each abstract and is denoted as: "author's abstract," "author's summary," "authors' abstract," "authors' summary," "abstract from Biological Abstracts," or "abstract by GLW" (Gary L. Worthen).

In the right margin of the first line of each abstract listing is a three-digit number which has been added to facilitate cross-referencing within the text. This number corresponds to the last three digits of the indexing identification code used throughout this work.

Arakaki, D. T., I. Veomett, and R. S. Sparkes 1970. Chromosome polymorphism in deer mouse siblings (Peromyscus maniculatus). Experientia 26:425-426. 001

Sibling offspring of P. maniculatus subspecies from the same parents have been found to demonstrate chromosome polymorphism. Comparison between chromosomes of the sibling animals was made based on the numbers of large acrocentric and submetacentric chromosomes; and small, metacentric and submetacentric chromosomes (3 groups). A constant diploid number of 48 was confirmed, although the number acrocentric chromosomes varied between 12 and 16 among the animals studied. [Abstract by GLW]

Arnason, U. 1970. The karyotype of the grey seal (Halichoerus grypus). Hereditas 64:237-242. 002

The somatic chromosomes of the grey seal, Halichoerus grypus Fabr., and their autoradiographic pattern were studied in cultures of lung tissue. An idiogram was made based on measurements of 6 male and 14 female cells. The chromosome number of the grey seal is 2n=32. Some comments were made on the karyological interrelationships among the species so far studied of the family Phocidae. [Author's abstract]

Arnason, U. 1972. The role of chromosomal rearrangement in mammalian speciation with special reference to Cetacea and Pinnipedia. Hereditas 70(1):113-118. 003

The karyotypes of 17 cetaceans and 18 pinnipeds are surveyed. Within the Cetacea only two different chromosome numbers have been found, viz. 2n = 42 and 2n = 44. Within the Pinnipedia three different chromosome numbers have been described, viz. 2n = 32, 2n = 34 and 2n = 36. The material indicates that the orders Cetacea and Pinnipedia are characterized by a remarkable stability of their karyotypic patterns. Factors cooperating towards karyotypic stability may be sought in the reproductive biology of these animals - late sexual maturity and small progeny - as well as in their ecology - good mobility in an environment without distinct niches. In such animals, the main mode of speciation should be a allopatric.

The orders Insectivora and Rodentia on the other hand which both display great karyotype variability would accordingly represent a different mode of speciation. The species belonging to these orders have early sexual maturity and large progeny; their mobility is often limited and the distribution discontinuous. Consequently, in Insectivora and Rodentia stasipatric speciation should be frequent. [Authors' abstract]

Arnason, U. 1974. Comparative chromosome studies in Cetacea. Hereditas 77:1-36. 004

The karyology was studied in 9 species of cetaceans, viz. in 5 odontocetes and 4 mysticetes. Chromosome measurements and idiograms of 8 species are presented. Comparisons were made between the karyotypes of the different species on the basis of conventional staining methods as well as by autoradiography and by Q-, G-, and C-banding techniques. All cetaceans so far studied have 2n=44, except the sperm and pygmy sperm whales, which have 2n=42 and karyotypes entirely different from those of the 2n=44 species. All of the latter, except the killer whale, have closely concordant karyotypic morphology. Specific attention was payed to the C-heterochromatin, both because of its large amount and its striking pattern. The amount of C-heterochromatin varied from 10-15% of the total chromosome length in the odontocetes to 25-30% in the mysticetes. In both of them the distribution of C-heterochromatin in the karyotypes was mainly interstitial and terminal and to a lesser extent centromeric. Size heteromorphism in C-bands was frequently observed between the homologues of the same pair. The pronounced karyotypic agreement between the odontocetes and mysticetes, both in general chromosome morphology and C-band pattern, is incompatible with the theory of a diphyletic origin of the Odontoceti and Mysticeti. [Author's abstract]

Arrighi, F. E., A. D. Stock, and S. Pathak 1974. Chromosomes of Peromyscus (Rodentia, Cricetidae). V. Evidence of percentric inversions. Chromosomes Today 5:323-329 005

Cytological studies were conducted on three species of Peromyscus (deer mouse). G-banding revealed structural stability in euchromatin, whereas constitutive heterochromatin was found to be very flexible in amount and position among species and within a species. [Abstract by GLW]

Badr, F. M. and R. S. Badr 1970. The somatic chromosomes of a wild population of rats: numerical polymorphism. Chromosoma 30:465-475. 006

The karyotype and quantitative characteristics of a wild population of rats, Rattus rattus, were studied. Individuals of the population were classified into three distinct groups, each with a characteristic chromosome number of 38, 42 and ±54 respectively. The frequency distribution of the three groups of rats in the sample studied was as follow: group I with 38 chromosomes formed 14%, group II with 42 chromosomes formed 54% and group III rats have had chromosome numbers varying between 50-60 formed 32%. The rats with 38 chromosomes had two pairs of marker chromosomes (2 long metacentric pairs). Those of group III were characterised by having a marked decrease or complete absence of short metacentric chromosomes with a simultaneous increase in the frequency of short telocentric chromosomes. Group II rats had more or less the chromosomal characteristics established for laboratory rats studied by previous workers. The total chromosomal length of somatic cells in either group I and II were found to be similar. The notable chromosomal polymorphism in number was explained in terms of centromeric fusion or dissociation. [Authors' abstract]

Baker, R. J., W. J. Bleier, and W. R. Atchley 1975. A contact zone between karyotypically characterized taxa of Uroderma bilobatum (Mammalia: Chiroptera). System. Zool. 24(2):133-142 007

A total of 191 specimens of Peters' tent-making bat, Uroderma bilobatum, were collected from the zone where two chromosomal races, representing two subspecies, meet. Eighty-eight specimens had 2n=38, four had 2n=39, one had 2n=40, one had 2n=41, one had 2n=42, 14 had 2n=43, and 82 had 2n=44. This chromosomal variation is best explained as resulting from hybridization between two cytotypes with the 2n=38 and the 2n=44 being the parental (pure) types, the 2n=41 individual being of the F1 type and the 2n=43, 42, 40, and 39 individuals representing backcross or F2 products. The two parental cytotypes were not found to be sympatric at any individual collecting station. The zone of hybridization is approximately 200 kilometers long on the Pacific versant of Honduras, eastern El Salvador and northwestern Nicaragua. Some chromosomally intermediate individuals were reproductively active although the frequency of reproductive activity was not so great as in individuals with parental cytotypes. Measurements of the cranial and wing morphology of chromosomally intermediate individuals indicated that in general there was a correspondence between chromosome number and phenetic similarity to one or the other of the two parental stocks. Chromosomal and cranial and wing morphological data suggest that there is considerable gene flow between the two cytotypes and that chromosomal divergence has occurred in the absence of speciation. The magnitude of chromosomal differentiation between the two subspecies serves as a caveat to those cases where specific recognition is based on chromosomal distinctness of allopatric samples. (Karyotypes; Chiroptera; Uroderma.) [Authors' abstract]

Baker, R. J. and J. L. Patton, 1967. Karyotypes and karyotypic variation of North American vespertilioned bats. J. Mammalogy 48(2):270-286. 008

Karyotypes of 32 species of North American vespertilioned bats are described. Individual, population, subspecific, specific, and generic karyotypic variation are discussed. The use of karyotypes as taxonomic tool and phylogenetic indicator in bats is discussed. [Authors' abstract]

Baverstock, P. R., C. H. S. Watts, J. T. Hogarth, A. C. Robinson, and J. F. Robinson 1977. Chromosome evolution in Australian rodents II. The Rattus group. Chromosoma (Berl.) 61, 227-241. 009

A total of 219 wild caught specimens representing 12 of the currently recognised 13 species and subspecies of Australian Rattus have been karyotyped. No two species possessed karyotypes in common, most species and several subspecies differing markedly in chromosome number. While the diploid number varied from 2n=32 to 2n=50, the fundamental number (FN) varied only from 60 to 62, suggesting that Robertsonian rearrangements have played a major role in karyotypic evolution in the group. - Karyotypically the Australian species of Rattus fall into two groups - the R. lutreolus group and the R. sordidus group. Of the karyotypic forms encountered in the former group, that of R. lutreolus is probably most ancestral because it is identical to that of many Asian species of Rattus. Other karyotypic forms in the R. lutreolus group can be derived as follows: That of (1) R. tunneyi tunneyi and R. t. culmorum by a single fixed pericentric inversion: (2) R. fuscipes fuscipes, R. f. greyi, R. f. assimilis and R. f. coracius by two fixed fusions: (3) R. leucopus cooktownesis by three fixed fusions: and (4) R. leucopus leucopus by four fixed fusions. Of the R. sordidus groups, R. s. villosissimus may possess the most ancestral karyotype with 2n=50 (FN=60), from which R. s. colletti (2n=42; FN=60) is derived by four fusions and R. s. sordidus (2n=32; FN=60) by nine fusions, four of which appear to be homologous with those R. s. colletti. - The karyotypic data are in accord with Taylor and Horner's (1973) suggestions that (1) R. t. tunneyi and R. t. culmorum belong to one species; (2) R. lut. luteolus and R. lut. velutinus belong to one species; (3) R. leu. leucopus and R. leu. cooktownensis belong to one species and (4) R. f. fuscipes, R. f. greyi, R. f. assimilis and R. f. coracius belong to one species. However, the large karyotypic difference between R. s. sordidus and R. s. coletti and R. s. villosissimus may indicate that these groups belong to different biological species. - Supernumerary or B-chromosomes were found in R. f. assimilis and R. t. tunneyi. A single R. t. culmorum was heterozygous for a centric fusion. [Authors' abstract]

Belcheva, R. G. and D. T. Peshev 1979. Intersubspecific sex chromosome difference in Citellus citellus L. (Rodentia, Sciuridae). Experientia 35(5):595-596. 010

The autosomal karyotypes of all subspecies studied of Citellus citellus from Bulgaria do not differ. The X chromosome, by contrast, is different in 1 of the subspecies where it seems to have undergone a pericentric inversion. [Authors' abstract]

Benado, M., M. Aguilera, O. A. Reig and F. J. Ayala 1979. Biochemical genetics of chromosome forms of Venezuelan spiny rats of the Proechimys guairae and Proechimys trinitatis superspecies. Genetica 50(2):89-98. 011

Spiny rats from Venezuela show an extensive karyotypic diversification (2n = 24 to 2n = 62) and little morphological differentiation. This study reports genetic distance, heterozygosity and polymorphism based upon 22 loci in semispecies and allospecies of the Proechimys guairae superspecies from N Central Venezuela, as compared with Proechimys urichi, a member of the Proechimys trinitatis superspecies from eastern Venezuela. Four chromosome forms of the P. guairae complex are included, each characterized by karyotypes of 2n = 46 (Fundamental Number = 72), 2n = 48 (FN = 72), 2n = 50 (FN = 72), and 2n = 62 (FN = 74). Proechimys urichi has a distinctive karyotype of 2n = 62 (FN = 88). The overall mean value of Nei's genetic identity index for all pair-wise comparisons is I = 0.942 ± 0.011. Mean identity within the P. guairae complex is I = 0.969 ± 0.033. Mean identity between P. urichi and members of that complex is I = 0.889 ± 0.011. Within the P. guairae complex, increased genetic divergence is correlated with higher karyotypic divergence. Heterozygosity varies from H = 0.059 to H = 0.153, with a mean value of H = 0.088 ± 0.014. The mean percent of polymorphic loci is P = 18.2 ± 3.9 after the '0,95%' polymorphism criterion, and P = 20,5 ± 5.2 after the '0.99%' criterion. These results are compared with similar data from fossorial and non-fossorial rodents. Spiny rats are non-fossorial, forest-dwelling rodents which have undergone a speciation process with little genetic divergence and extensive chromosome rearrangements. [Authors' abstract]

Bianchi, N. O., J. Paulete-Vanrell, and L. A. De Vidal Rioja 1969. complement with 38 chromosomes in two South American populations of Rattus rattus. Experientia 25:1111-1112 012

The chromosomal complements of 16 specimens of Rattus rattus from two populations, one from Argentina and the other from Brazil, are observed to be 2n=38. The South American populations are believed to have been derived from a European ancestor having 2n=42. [Abstract by GLW]

Bosma, A. A. 1976. Chromosomal Ploymorphism and g-banding Patterns in the wild boar (Sus scrofa L.) from the Netherlands. Genetica 46:391-399. 013

Cytogenetic examination of 15 wild pigs (Sus scrofa L.) from the Netherlands has revealed intrapopulation polymorphism for the diploid chromosome number. Eleven pigs showed 2n = 36 chromosomes, three pigs showed 37 chromosomes, and one pig showed 38 chromosomes. The cause of these differences in chromosome number is discussed.

With the aid of a Giemsa banding technique it is demonstrated that the "extra" submetacentric chromosome (chromosome No. 1a) of the wild boar is homologous with chromosomes Nos. 15 and 17 of domestic pigs. [Author's abstract]

Bosma, A. A. 1978. The chromosomal g-banding pattern in the wart hog, Phacochoerus aethiopicus (Suidae, Mammalia) and its implications for the systematic position of the species. Genetica 49(1):15-19. 014

It appears from the G-banding patterns that the karyotypes of the wart hog (Phacochoerus aethiopicus), the European wild boar (Sus scrofa) and the domestic pig (Sus scrofa) are very similar, the differences in karyotype between these species consisting of Robertsonian translocations only. This close similarity in karyotype suggests a close phylogenetic relationship between the genera Phacochoerus and Sus. [Author's abstract]

Bowers, J. H., R. J. Baker, and M H. Smith 1973. Chromosomal, electrophoretic, and breeding studies of selected populations of deer mice (Peromyscus maniculatus) and black-eared mice (P. melanotis). Evolution 27(3):378-386. 015

An unusual amount of chromosomal polymorphism and geographic variation in chromosomes and electrophoretic pattern have been reported for Peromyscus maniculatus. Karyological, electrophoretic and breeding data indicate that populations of Peromyscus from the Chiricahua, Pinaleno and Santa Catalina Mountains in southern Arizona are conspecific with P. melanotis, not with P. maniculatus. These data also argue against the assumptions that monomorphism in the isolated populations arose by drift. Rather they support a model of centrifugal speciation. [Authors' summary]

Brown, R. J. 1974. A comparative study of the chromosomes of three species of shrews,, Sorex bendirii, Sorex trowbridgii, and Sorex vagrans. Wasmann J. Biol. 32(2):303-326. 016

Three subspecies of Sorex trowbridgii, (S. t. trowbridgii, S. t. humboldtensis, S. t. montereyensis), have identical karotypes (2n = 34, FN= 38). The single specimen of S. bendirii karyotyped had 2n = 54 and FN = 70. Seven subspecies of S. vagras (S. v. vagras, S. v. halicoetes, S. v. pacificus, S. v. yaquinae, S. v. permiliensis, S. v. bairdi, S. v. setosus) were karotyped and show inter- and intrapopulational variation. With the exception of 1 individual of S. v. bairdi with a diploid number of 53 (attributed to Robertsonian fusion) all subspecies have a diploid number of 54. The fundamental number varies from 58 and 59 in S. v. pacificus and S. v. yaquinae at the southern end of the range to 62 and 63 in S. v. setosus at the northern end. Graphically intermediate populations, S. v. bairdi and S. v. permilliensis have fundamental numbers varying from 58-62. The karotypic differences in the S. vagras complex are presumably due to pericentric inversions. [Abstract from Biological Abstracts]

Bruere, A. N., H. M. Chapman, P. M. Jaine, and R. M. Morris 1976. Origin and significance of centric fusions in domestic sheep. J. Heredity 67:149-154. 017

The karyotypes of 731 sheep of various breeds were studied and considered in association with previous chromosome studies of domestic sheep. A high incidence of the T_2 translocation was found in two pedigree flocks of New Zealand Romney sheep. One of these flocks was established over 100 years ago and it is suggested that this translocation originated in the Romney Marsh breed of sheep in England. A naturally occurring double translocation heterozygote $52t_1t_2$ was reported for the first time.

A further flock of sheep of the Perendale breed was found with a high incidence of dicentric chromosome fusion that was identified as the t_3 translocation. The apparently common occurrence of chromosome polymorphism, due to centric fusions, in domestic sheep is discussed in relation to karyotype evolution among both domestic and wild sheep. [Authors' summary]

Bruere, A. N. and R. D. McLaren 1967. The idiogram of the sheep with particular reference to secondary constrictions. Can. J. Genetic Cytol. 9:543:553. 018

Peripheral leucocyte cultures from 22 normal sheep aged less than two years have shown that the modal diploid chromosome number (54) was present in 87.44% of cells counted from a total of 1831. The modal number of 54 chromosomes is verified for five previously unreported breeds of sheep, including the Scottish Blackface, Grey Face, Clun Forest, Welsh Montain and Soay. Karyotype observations showed that the short arms of the X chromosome are noticeably larger than those on other members of the acrocentric group of chromosomes, and that the Y chromosome is clearly submetacentric. Secondary constrictions were seen on a number of the 333 "photographic" karyotypes prepared from the best metaphases of 3280 counted cells. The incidence of these was highest on the six large metacentric chromosomes and suggested sites of regular occurrence, which may be associated with nucleolus formation. An increase in the incidence of secondary constrictions was recorded in preparations made from cultures in which hypotonic sodium citrate was used instead of hypotonic Hanks balanced salt solution. [Authors' summary]

Bruere, A. N., D. L. Zartman, and H. M. Chapman 1974. The significance of the G-bands and C-bands of three different Robertsonian translocations of domestic sheep (Ovis aries). Cytogen. Cell Genet. 13:479-488. 019

G-banding of three different Robertsonian translocations of domestic sheep (MI, MII, and MIII) has shown that the arm components of each are nonhomologous. The C-bands of the MI and MIII translocation chromosomes showed heavy blocks of centric heterochromatin which were distributed evenly on either side of the centromeric constriction and which suggested a dicentric structure. The C-band pattern of the MII translocation was regularly exocentric, suggesting that it may be formed by reciprocal translocation. The need for caution on the use of the term "Robertsonian translocation" is discussed. The amounts of centromeric heterochromatin in each of the translocation chromosomes is apparently greater than in the regular metacentrics, which suggests that they are of a more recent origin. [Authors' abstract]

Buettner-Janusch, J. and A. E. Hamilton 1979. Chromosomes of Lemuriformes: IV. Karyotype evolution in Lemur fulvus collaris (E. Geoffroy 1812). Am. J. Phys. Anthropol. 50(3): 363-366. 020

The G[Giemsa]-banded karyotype of a feral L. fulvus collaris has a diploid number of 52; the nombre fondamental (number of chromosome arms) is 64. The karyotype consists of 6 pairs of biarmed autosomes, 19 pairs of acrocentric autosomes and acrocentric sex chromosomes. Comparisons of the 2N = 52 complement with the 2N = 50 and 2N = 51 karyotypes published by Hamilton, et al. (1977) supports the view that hybridization occurs naturally between animals with diploid numbers of 50 and 52. [Abstract from Biological Abstracts]

Bunch, T.D. 1978 Fundamental karyotype in domestic and wild species of sheep: Identity and ranking of autosomal acrocentrics involved in biarmed formations. J. Heredity 69:77-80. 021

The fundamental karyotype of Ovis is described according to G-band analysis of Ovis vignei, O. ammon, O. orientalis, O. musimon, O. dalli, O. canadensis, O. aries (to include the Massey T1, T2, and T3 translocations) and O. nivicola. The acrocentrics involved in their biarmed fusions were identified from G-banded idiograms of Capra. Acrocentrics involved in the M1, M2, M3, M4, T1, T2 and T3 centric fusions were: 1/5, 3/10, 4/9, 11/17, 8/30, 12/15, and 11/29, lower and upper arms, respectively. The significance of partial homology in the M4 and T3 biarmed chromosomes as an evolutionary occurrence leading to speciation is discussed. [Author's summary]

Bunch, T. D. and W. C. Foote 1976. Chromosomes, hemoglobins, and transferrins of Iranian domestic sheep. J. Heredity 67:167-170. 022

Twelve breeds of Iranian domestic sheep were cytogenetically analyzed. The diploid chromosome number of 2n=54 is identical to that of most breeds of domestic sheep, which is comprised of 3 pairs of metacentric and 23 pairs of acrocentric autosomes. The sex chromosomes consist of a large acrocentic X and a small bi-armed Y. Hemoglobin analysis by isoelectric focusing for these 12 breeds resulted in the identification of 2 protein fractions: Hb AB and B. The A allele was observed in 7 percent of the 506 sheep sampled, in 6 of the 12 breeds, and then only in the heterozygous form. Transferrins were analyzed by starch-gel electrophoresis and comparisons made between breeds. Nine alleles, pooled frequency of occurrence in descending order, B, C, D, A, M, E, G, P, and I were identified and resulted in 19 phenotypes. Tfs A, B, C, and D were observed in all breeds, whereas I was found in 2, G in 1, M in 8, E in 6, and P in 2. Significant differences in allelic occurrence of Tfs A, B, C, and D were observed in seven breeds. [Authors' summary]

Bunch, T. D., W. C. Foote, and J. J. Spillett 1976. Translocations of acrocentric chromosomes and their implications in the evolution of sheep (Ovis). Cytogen. Cell Genet. 17:122-136. 023

Cytogenetic evidence suggests that the caprids (sheep and goats) evolved from a common ancestor with a 2n=60 karyotype. Although goats (Capra) retained the primitive 2N=60 karyotype, sheep (Ovis) underwent a sequential reduction in the number of chromosomes by means of acrocentric translocation. The formation of the first metacentric autosome (M1) occurred in the aoudad (Ammotragus) and urial (O. vignei), resulting in a 2N=58 karyotype. The G-bands are homologous, which implies both genotypes arose from a common ancestor, possibly a rupicaprid. Based on G-bands, acrocentric chromosomes 1 and 7 of the 2n=60 karyotype formed the M1. The X chromosome, which is the second longest acrocentric in the 2n=60 karyotype, became the longest acrocentric in Ammotragus and Ovis (2n=58). The second pair of metacentrics to evolve, which is ranked in the M3 position of the 2n=54 karyotype, resulted from the translocations of acrocentric chromosomes 4 and 14 or 15 in the 2n=60 karyotype. The M2 was the third pair of metacentrics to be formed and resulted from the translocations of acrocentric chromosomes 3 and 12 or 13 in the 2n=60 karyotype. The G-bands of all 2n=54 karyotypes are homologous, which indicates origin from a common ancestor. Evidence is presented that suggests a prezygotic selection is bringing about a reduction in diploid chromosome numbers. The possible roles of fission and fusion in the karyotypic evolution of Ovis are discussed. [Authors' abstract]

Bunch, T. D., C. F. Nadler, and L. Simmons 1978. G-band patterns, hemoglobin, and tranferrin types of the bharal: Chromosomal evolutionary relationships with sheep and goats. J. Heredity 69:316-320. 024

G-band patterns of the bharal (Pseudois nayaur), 2n = 54, were compared with those of wild sheep (Ovis dalli stonei), 2n = 54, and the Persian wild goat (Capra hircus), 2n = 60. Patterns of the longer segments of the biarmed chromosomes of Pseudois were similar to those of the longer biarmed segments of Ovis, whereas the shorter segments differed. Biarmed chromosomal segments had G-band homologies with specific acrocentric autosomes of Capra and were ranked as follows in descending order of relative lengths: Pseudois 1:4/13; 2:1/27 and 3:3/29; and for Ovis 1:1/5; 2:3/10 and 3:4/9. Arm ratios and relative lengths of the biarmed chromosomes were compared. The Y chromosome of Pseudois is a small biarmed chromosome that resembles those of Capra and Ovis.

Hemoglobin B was observed in the bharal and was indistinguishable from Hb B of Ovis using starch-gel electrophoresis. The transferrin "zone pair" of Pseudois migrated more slowly in starch-gel electrophoresis than do any of the known transferrin types in sheep and goats. We refer to this transferrin as Pseudois Tf A.

Bush, G. L. 1975. Modes of animal speciation. Annual Rev. Ecol. Syst. 6:339-364. 025

The author presents an excellent treatise on speciation in animals. A portion of his discussion deals with the role of chromosomal rearrangements in speciation. Only this portion of the paper is abstracted here. In allopatric situations where speciation occurs by subdivision, there is little or no directed chromosomal evolution. Any chromosomal rearrangements that may be present are generally not associated with speciation. In allopatric situations where speciation occurs by the founder effect, and also in sympatric situations, chromosome rearrangements may or may not be associated with speciation. In parapatric situations, chromosome rearrangements are frequently associated with speciation. These broad generalities apply to the entire animal kingdom, and are not limited to any particular group (such as mammals). [Abstract by GLW]

Bush, G. L., S. M. Case, A. C. Wilson, and J. L. Patton 1977. Rapid speciation and chromosomal evolution in mammals. Proc. Natl. Adac. Sci. USA 74(9):3942-3946. 026

To test the hypothesis that population subdivision into small demes promotes both rapid speciation and evolutionary changes in gene arrangement by inbreeding and drift, we estimated rates of speciation and rates of chromosomal evolution in 225 genera of vertebrates. Rates of speciation were estimated by considering the number of living species in each genus and the fossil record of each genus as well as information about extinction rates. Speciation rate was strongly correlated with rate of chromosomal evolution and average rates of speciation in lower vertebrate genera were one-fifth those in mammalian genera. Genera with high karyotypic diversity and rapid speciation rates may generally have small effective population size (N_e), whereas large N_e values may be associated with karyotypically uniform genera and slow rates of speciation. Speciation and chromosomal evolution seem fastest in those genera with species organized into clans or harems (e.g., some primates and horses) or with limited adult vagility and juvenile dispersal, patchy distribution, and strong individual territoriality (e.g., some rodents). This is consistent with the above hypothesis regarding the evolutionary importance of demes. [Authors' abstract]

Caire, W. and E. G. Zimmerman 1973. Chromosomal and morphological variation and circular overlap in the deer mouse, Peromyscus maniculatus, in Texas and Oklahoma. Syst. Zool. 24(1):89-95. 027

Mitotic chromosomes were analyzed from 74 specimens representing three subspecies of Peromyscus maniculatus from Oklahoma and Texas. Two distinct chromosomal forms were found. One form, occurring predominantly north of the Red River in Oklahoma and representing P. m. ozarkiarum, had 11 pairs of subtelocentric, six pairs of metacentric or submetacentric and six pairs of acrocentric autosomes. A second form, occurring south of the Red River in Texas and representing P. m. pallescens, had ten pairs of subtelocentric, eight pairs of metacentric or submetacentric, and five pairs of acrocentric autosomes. Both karyological types were found in the same habitat at two localities in north-central Texas, but no chromosomal hybrids were found in this area. Meiotic analysis of hybrids from laboratory crosses between the two types indicated partial sterility. A morphological analysis revealed that gene flow is restricted in eastern Oklahoma, west-central Texas, and eastern Texas. The most plausible explanation for the observed variation is the existence of circular overlap. [Authors' abstract]

Capanna, E., M. V. Civitelli, and R. Nezer 1970. The karyotype of the black rat (Rattus rattus L.): another population with a 38-chromosome complement. Experientia 26:422-425. 028

In one Italian population of Rattus rattus, the karyotype is constantly characterized by a diploid complement of 2n=38. Differences in diploid number in populations of rats collected in other parts of the world are believed to be caused by independent centric fusions involving both Robertsonian and non-Robertsonian translocations. [Authors' abstract]

Craig-Holmes, A. P., F. B. Moore, and M. W. Shaw 1973. Polymorphism of human C-band heterochromatin. I. Frequency of variants. Amer. J. Human Genet. 25:181-192. 029

The constitutive heterochromatin of human chromosomes is subject to a high rate of variation. Among 20 unrelated individuals, 31 C-band variants were discovered. In two families, three of six variants were transmitted.

The high frequency of variants in constitutive heterochromatin is presumably due to the highly repetitious DNA present in these regions. The polymorphic spectrum of C-band heterochromatin, therefore, should be dependent on the degree of heterogeneity of the repetitious families within a region as well as the complexity of the repeated sequences. [Authors' abstract]

Craig-Holmes, A. P. and M. W. Shaw 1971. Polymorphism of human constitutive heterochromatin. Science 174(4010): 702-704. 030

Genetic polymorphism has been demonstrated in man for many characteristics including blood groups, serum proteins, tissue enzymes, and hemoglobins. A class of chromosomal polymorphism involving constitutive heterochromatin has now been found. Through the use of a special technique that permits visualization of heterochromatin, seven heterochromatin variants have been found among four individuals. These results suggest a very high frequency of variability of heterochromatin in the population. [Authors' abstract]

Davis, B. L. and R. J. Baker, 1971. Chromosome morphology of North American Rattus rattus (L.) (Muridae). Cytologia 36:417-420 031

Although the present distribution of Rattus rattus is cosmopolitan, the three subspecies reported from North America were introduced by man in recent times. Specimens for our study were collected from feral populations. Karyotypic preparations were by in vivo culture of bone marrow, sodium citrate, Carnoy's fixative, blaze dry method; stain was by Giemsa's blood stain. Specimens of the three subspecies all had the same karyotype, characterized by a diploid number of 2n=38. Subspecific assignment was made on the basis of characteristics of external morphology. [Abstract by GLW]

Dev, V. G., D. A. Miller, R. Tantravahi, R. R. Schreck, T. H. Roderick, B. F. Erlanger, and O. J. Miller 1975. Chromosome markers in Mus musculus: differences in C-banding between the subspecies M. m. musculus and M. m. molossinus. Chromosoma 53: 335-344. 032

Quinacrine (Q-band) and centromeric heterochromatin (C-band) patterns of metaphase chromosomes of two subspecies of Mus musculus were compared. M. m. musculus (the laboratory mouse) and M. m. molossinus (a subspecies from southeast Asia) had similar Q-band patterns along the length of the chromosomes, but differences were observed in the centromeric region of some chromosomes. The two subspecies had very different distributions of C-band material. Antibodies to 5-methylcytosine were bound to regions of the chromosome corresponding to the C-bands in each animal. These findings support the idea that satellite DNA, which is concentrated in the C-band region, changes more quickly than bulk DNA. The interfertility of these two subspecies permits the development of a musculus strain carrying normal marker chromosomes for genetic studies. [Authors' abstract]

Duffy, P. A. 1972. Chromosome variation in Peromyscus: A new mechanism. Science 176:1333-1334 033

Differences in total chromosome lengths between two karyotypically divergent groups of Permoyscus maniculatus are taken as evidence for an addition-deletion mechanism of chromosomal variation in the species. The differences may be due in part to variation in the amount of constitutive heterochromatin present in the two karyotypes. [Author's abstract]

Dutrillaux, B., A.M. Fossee, and G. Chauvier 1979. Cytogenetic study of six species or sub-species of Mangabeys monkeys (Papiinae cercopithecidae). Ann. Genet. 22(2):88-89 034

Chromosome banding patterns of six Mangabey species or sub-species are studied and compared. By comparison with the other Papiinae previously studied (Papio and Macaca) Lophocebus albigena and L. aterrimus possess very similar karyotypes, differing at most by a pericentric inversion of the Y chromosome. The other four, Cercocebus torquatus torquatus, C. t. fuliginosus, C. galeritus galeritus and C. g. chrysogaster differ by a complex rearrangement of chromosome N° 10 and by acquisition of heterochromatin on chromosome N° 12. No difference was detected nor [sic.] between the two Lophocebus nor between the four Cercocebus. Cytogenetic criteria are thus in agreement with the morphological, immunological and hematological data, separating the two genuses,[sic.] and placing Lophocebus closer to the Papio and Macaca than to Cercocebus. [Authors' abstract]

Dutrillaux, B. and Y. Rumpler 1977. Chromosomal evoluation in Malagasy lemurs: II. Meiosis in intra- and interspecific hybrids in the genus Lemur. Cytogenet. Cell Genet. 18(4):197-211. 035

The chromosome analysis of meiosis in 4 lemurs, L. fulvus fulvus, L. f. collaris, L. f. albocallaris and L. macaco and particular hybrid crosses is reported. In metaphase I, trivalents and chain elements were detected and identified with T-banding. The absence of chain multivalents elements in the pachytene stages of hybrid meiosis, where a chain is detected later in diakinesis, may offer evidence on the possible existence of a 2-step pairing mechanism in meiotic homolog pairing. Considerations about the role of the chromosome rearrangements in establishing a gametic barrier in speciation are developed. [Abstract from Biological Abstracts]

Elder, F. F. B. 1978. Chromosomal evolution of the cotton rats, Genus Sigmodon (Rodentia, Muridae). Diss. Abstr. 39(5):2171-B 036

The chromosomes of five species of cotton rats were analyzed using C- and G-banding techniques. The chromosomal evolution was discussed in the context of known ecological and populational parameters of the species. Limited paeontological and biochemical data suggest that chromosome evolution has proceeded rapidly, the time span from an ancestral form (Sigmodon hispidus) to the derived S. arizoniae being about 100,000 years. Chromosomal relationships were identified and biogeography and evolution of the species were discussed. A phylogeny based on the available data was proposed. [Abstract by GLW]

Evans, H.J., R. A. Buckland, and A. T. Sumner 1973. Chromosome homology and heterochromatin in goat, sheep, and ox studies by banding techniques. Chromosoma 42:383-402. 037

Peripheral blood lymphocyte metaphase chromosomes of three Bovoidean species have been studied using Quinacrine flourescence and Giemsa banding techniques to give Q-, G-, and C-banding patterns. Q- and G-banding characteristics, coupled with chromosome length, enabled all of the chromosomes in each of the chromosome complements to be clearly distinquished, although some difficulties were encountered with the very smallest chromosomes. A comparison of G-banding patterns between the species revealed a remarkable degree of homology of banding patterns. Each of the 23 differenct acrocentric autosomes of the domestic sheep (2n = 54) was represented by an identical chromosome in the goat (2n = 60) and the arms of the 3 pairs of sheep metacentric autosomes were identical matches with the remaining 6 goat acrocentrics. A similar interspecies homology was evident for all but two of the autosomes in the ox (2n = 60). This homology between sheep metacentric and goat acrocentric elements confirms a previously suggested Robertsonian variation. The close homology in G-banding patterns between these related species indicates that the banding patterns are evolutionarily conservative and may be a useful guide in assessing interspecific relationships. - The centromeric heterchromatin in the autosomes of the three species was found to show little or no Q- or G-staining, in contrast to the sex chromosomes. This lack of centromeric staining with the G-technique (ASG) contrasts markedly with results obtained with other mammalian species. However, with the C-banding technique these regions show a normal intense Giemsa stain and the C-bands in the sex chromosomes are inconspicuous. The amount of centromeric heterchromatin in the sheep metacentric chromosomes is considerable less than in the acrocentric autosomes or in a newly derived metacentric element discovered in a goat. It is suggested that the pale G-staining of the centromeric heterochromatin in these species might be related to the presence of GC-rich satellite DNA. [Authors' abstract]

Forejt, J. 1973. Centromeric heterchromatin polymorphism in the house mouse. Chromosoma 43(2):187-201. 038

Polymorphism of Giemsa-specific centromeric heterochromatin (C.H.) has been described in the laboratory and wild mice. All examined wild mice and inbred mouse strains display some chromosomes with considerably reduced or enlarged C.H. regions. The quantity of C.H. could be an inherent property of a chromosome as inferred from (a) the finding of the identical C.H. pattern within inbred strains, (b) the finding that two genetically related inbred strains, C3H and CBA, separated from each other for more than 150 generations, possess the same two chromosome pairs with tiny C.H. marker regions. These chromosomes were identified as No. 1 (l.g. XIII) and No. 14 (l.g.III) by means of T(14;15)6Ca translocation, and C- and G-band analysis. The neutrality of C.H. polymorphism in murine genome is inferred from the "heterozygosity" for the C.H. variants found in all studied wild mice. The possible relationship of C.H. polymorphism to the centromere interference phenomenon is hypothesized. [Author's abstract]

Frechette, A. G. and S. M. Jalal 1971. Karyological study of two subspecies of the red back vole. Mammalian Chromosome Newsletter 12:38-39. 039

Karyotypes of Clethrionomys gapperi gapperi Vigors and Clethrionomys gapperi loringi V. Bailey were established from specimens collected within their respective geographical ranges from south-western Ontario (Quetico Provincial Park) and northeastern North Dakota.

Chromosomal counts revealed the same modal diploid number of 56 for both subspecies. Karyotypic and idiogram analysis indicated the presence of one pair of large subtelocentrics, one pair of small metacentrics, 25 pairs of telocentrics, a telocentric X, and a subtelocentric Y. This karyotype study, at the subspecific level, differs from Mathey's (1956) who reported 56 acrocentric chromosomes. The presence of the small autosomal metacentric at the species level was confirmed. The NF ("nombre fondamentale") should thus be changed from 56 as previously recorded to 48 without consideration of the subtelocentric chromosomes. [Abstract by GLW]

Garcia, M., R. Miro, L. Freitas, and J. Egozcue 1978. Banding patterns of the chromosomes of Cebus apella: Unstable chromosomes and pericentric inversion. Folia Primatol. 29(3):196-205. 040

Quinacrine- and Giemsa-banding studies of the chromosomes of C. apella permitted the establishment of a pattern for the species and revealed an extreme chromosome unstability [sic.] in the specimens studied. The male showed a pericentric inversion in 1 of its chromosomes, while the female had 4 different cell lines, with multiple structural changes involving several pericentric inversions and 1 deletion. The existence of a marked intra- and interspecific chromosome variability is indicated. [Abstract from Biological Abstracts]

Gileva, E. A. 1973. B-chromosomes, unusual inheritance of sex chromosomes, and sex ratio in the Artic lemming (Dicrostonyx torquatus torquatus Pall. 1779). Doklady Akad. Nauk SSSR, 213(4):952-955. 041

The karyotype of the Arctic lemming is characterized by complex variability. In particular, the diploid number of chromosomes in the 68 animals examined varied from 45 to 51, primarily because of the presence of B-chromosomes.

Apparently, all male Arctic lemmings each have two true X-chromosomes. This situation differs in principle from the system of multiple X=chromosomes known in mammals up to the present, where males have only one true X-chromosome, and the second is an autosome, lacking its homolog because of its translocation into a Y-chromosome. It is known that polysomy with regard to the X-chromosome leads to sterility in male mammals. The normal fertility in male Arctic lemmings may be due either to total genetic inactivation of one of the X-chromosomes or to peculiarities in the organization of the X-chromosome.

The karyological differences between the two forms discussed (D. t. torquatus and the Nearctic forms of D. torquatus) are very large (in D. t. stevensoni 2n = 34, NF = 54), and therefore their inclusion in the same species must be regarded as doubtful. [Abstract by GLW]

Gladkina, T. S. 1972. Georgaphical variability of two subspecies of common vole (Microtus arvalis). Zool. Zh 51(2):267-279. 042

Investigations were performed during 5 generations on two common vole subspecies; M. arvalis caspicus Ogn. from the Kustanai region and M. a. duplicatus Rorig et [=and] Born with different karyotypes from the Leningrad and Kaliningrad regions respectively. The subspecies were distinguished by ecologo-physiological features of an adaptive character. However, adaptation mechanisms are different in them and are similar to those of rodent species populating the same regions. Temperature adaptations in subspecies are of a comparatively stable character. The geographical forms of M. a. duplicatus did not have any distinctions as to the characters under investigation in spite of differences in caryotypes [sic.]. On the whole, a high capability for both phenotypical and genotypical variability is characteristic of common vole which ensures its fast adaptation to the new condition of tilled lands. [Author's summary]

Greenbaum, I. F., R. J. Baker, and J. H. Bowers 1978. Chromosomal homology and divergence between sibling species of deer mice: Peromyscus maniculatus and Peromyscus melanotis (Rodentia, Cricetidae). Evolution 32(2):334-341. 043

Chromosomal homology and amount and location of heterochromatin, as revealed by G-banding and C-banding analyses, were examined for Peromyscus maniculatus bairdii and P. melanotis. These procedures enabled determination of interspecific homology of all euchromatic autosomal segments. Autosomally, the karyotypes of P. maniculatus bairdii and P. melanotis are related as follows: 12 pairs of chromosomes are unchanged, five pairs differ in the presence (in P. m. bairdii) and absence (in P. melanotis) of heterochromatic short arms, and six pairs differ by pericentric inversions. The acrocentric condition of two pairs of chromosomes found to be polymorphic in P. maniculatus is homologous to the acrocentric condition of the corresponding pairs in P. melanotis.

Intraspecific polymorphism in our sample was restricted to two pairs of autosomes in P. m. bairdii. One polymorphism involves heteromorphism for a heterochromatic short arm, whereas the other may be either the result of a pericentric inversion, translocation of a small segment, or polymorphism for undetected heterochromatin.

In P. maniculatus heterochromatin is centromeric on all chromosomes. Additionally, the short arms of five autosomal pairs are heterochromatic (one pair is reported polymorphic for the heterochromatic short arm). In both species, the short arm of the X and the Y are heterochromatic. The amount of C-band material in P. melanotis is reduced relative to that characteristic of the P. maniculatus examined. Autosomal heterochromatin in P. melanotis is confined to the centromeric regions.

Heterochromatic arms and pericentric inversions are important in the evolution of the karyotype of the genus. [Authors' summary]

Greenbaum, I. F., R. J. Baker, and P. R. Ramsey 1978. Chromosomal evolution and the mode of speciation in three species of Peromyscus. Evolution 32(3):646-654. 044

Analysis of G- and C-banding patterns of Peromyscus polionotus reveals intra-specific variation in three chromosome pairs (numbers 16, 18 and 19). All three cases involve segments of heterochromatin. Chromosomal homologies (based on G-banding patterns) between P. polionotus, P. maniculatus and P. melanotis suggest that the ancestral karyotype for the three species was composed of a large number of acrocentrics (probably near 30). The data indicate the P. maniculatus and P. polionotus have increased the number of biarmed chromosomes in their karyotypes by additions of heterochromatin and pericentric inversions. Four inversion product are unique to P. maniculatus, whereas two inversions are shared by P. maniculatus and P. polionotus. Peromyscus maniculatus and P. polionotus also share derived heterochromatic additions. These data indicate that P. maniculatus and P. polionotus had a common ancestor after P. melanotis diverged from the line. Chromosomal data for these three species are discussed in light of the centrifugal speciation model. As predicted by this model, P. maniculatus has the most derived karyotype and the most intraspecific variation. [Authors' summary]

Gropp, A. A., J. Markwong, J. Marshall, and Y. J. Kim 1972. Robertsonian chromosomal variation in the longtailed tree mouse (Vandeleuria). Z. Zool. Syst. Evolutionsforsch 10(3):210-214. 045

In Vandeleuria oleracea the sex chromosomes could not be identified. The occurrence of an autosomal polymorphism of the Robertsonian type is suggested. The presence of Robertsonian variation may be linked with the existence of different local forms or subpsecies of this widely distributed taxon. [Abstract from Biological Abstracts]

Gropp, A., J. Marshall, and A. Markwong 1973. Chromosomal findings in the spiny mice of Thailand (genus Mus) and occurrence of a complex intraspecific variation in M. shortridgei. Z. Saugetierkunde 38(3):159-168. 046

The karyotypes of M. shortridgei and M. pahari belonging to the subgenus Leggadilla and Coelomys respectively, differ radically from those of most members of the genus Mus. A complex and mixed type of intraspecific polymorphism is responsible for a numerical and structural variation of the chromosomal complement of M. shortridgei (2n = 46-49; N.F. = 48-52), but the occurrence of supernumerary autosomes seems to be the most prominent feature besides pericentric inversion. -On the contrary, M. pahari, is revealed by the study of a limited number of specimens belonging to one colony, was shown to possess a stable karyotype with 48 acrocentric chromosomes. [Authors' summary].

Hafner, D. J., J. C. Hafner, and M. S. Hafner 1979. Systematic status of kangaroo mice, genus Microdipodops: Morphometric, chromosomal, and protein analyses. J. Mammalogy 60(1):1-10. 047

The systematic status of Microdipodops megacephalus and M. pallidus is investigated at the genic, karyotypic, and morphologic levels at a purported hybrid zone. Instances of hybridization are shown to be either nonexistent or present at extremely low levels (<0.6%), and full specific status of the two taxa is affirmed. Amounts of genic variability and polymorphism are approximately equal for the species (H = 0.064) and fall well within the range observed for other vertebrate species. Estimates of the timing of the speciation event, based upon allozymic data, range from 1.2 to 6 million years before present. Possible means of ecological separation of the two sibling species in sympatry are suggested. [Authors' abstract]

Haiduk, M. W., J. W. Bickham, and D. J. Schmidley 1979. Karyotypes of six species of Oryzomys from Mexico and Central America. J. Mammalogy 60(3): 610-615. 048

The karyotypes of six species of Oryzomys from Mexico and Central America were described. Data were analyzed in light of the groupings proposed by Gardner and Patton (1976); additionally, a preliminary comparison of G- and C-banding was presented. [Abstract by GLW]

Halkka, L. and O. Halkka 1974. Karyotype Q- and G-banding in three species of the genus Sorex. Hereditas 78(2):314. 049

In Kuhmo, NE Finland, the Sorex species minutus, caecutiens and isodon, all with 2n=42, live apparently sympatrically in the forest along the river Kuusijoki. The goniomitotic metaphase chromosomes of these species were analyzed with the Q- and G-banding techniques.

The chromosome sets of caecutiens and isodon were found to be quite similar. The NFa is 60 in both species, and the large chromosomes are mostly meta- or submetacentric, the small ones mostly telo- or subtelocentric. In contrast to these two species, minutus has several telocentrics among the large chromosomes of the set, and accordingly the NFa is only 54.

A number of chromosome arms appear similar in banding patterns in all three species, but the parallelisms are much more frequent between caecutiens and isodon than between these and minutus. The divergence between the NFa 60 and NFa 54 karyotypes probably results from a number of pericentric inversions and possibly also from translocations. The direction of the change has perhaps been towards a more metacentric condition at the expense of telocentrics. If this is true, then the caecutiens and isodon sets could be divergent derivatives of a highly telocentric ancestral condition from which the minutus set deviates less than these two.

The chromosal differences are certainly sufficient to keep all three species reproductively isolated. Primarily, however, hybridization of these sympatric species appears to be prevented by psychological isolation. [Authors' abstract]

Holden, H. E. and H. S. Eabry 1970. Chromosomes of Sylvilagus floridanus and S. transitionalis. J. Mammalogy 51(1):166-168. 050

The karyotypes of four species of Sylvilagus were studied. Three species possessed a diploid chromosome number of 42; the fourth (S. transitionalis) had 2n=52. Because of the great difference in chromosome number, it is difficult to explain an evolutionary mechanism; further, the high proportion of biarmed chromosomes belongs to the species with a higher diploid number. Therefore, centric fusion theory can not explain the divergence. [Abstract by GLW]

Hsu, T. C. and F. E. Arrighi 1966. Chromosomal evolution in the genus Peromyscus (Cricetidae, Rodentia). Cytogenetics 5:355-359. 051

The diploid number of species and subspecies in genus Peromyscus is 48. The number of total chromosome arms (fundamental number), however, varies from 56 to 96. Apparently the changes were accomplished by reciprocal translocations and pericentric inversions, but not by the Robertsonian process. [Authors' abstract]

Hsu, T. C. and F. E. Arrighi 1968. Chromosomes of Peromyscus (Rodentia, Cricetidae) 1. Evolutionary trends in 20 species. Cytogenetics 7:417-446. 052

The somatic metaphase chromosome constitutions of 20 Peromyscus species (188 specimens) were described and compared. Peromyscus (Ochrotomys) nuttali, which has been considered by many mammalogists as a member of a separate genus, Ochrotomys, has a diploid number of 52. All other 19 species possess a diploid number of 48. The lowest number of total chromosome arms is 56 (P. crinitus and P. boylei) and the highest is 96 (P. eremicus and P. collatus). Since the number of centromeres remains the same, Robertsonian fusion is not found in the genus Peromyscus. The X chromosome, with one doubtful exception, is always a large, biarmed element, but the Y chromosome is extremely variable in size as well as in centromeric position. Intraspecific polymorphism is extensive in many species, and in some cases, e.g., P. truei, cytological data strongly suggest that there may be more than one species under one name. The survey indicates that it may be extremely profitable to use Peromyscus cytology to analyze species relationships, population structure, population dynamics and other evolutionary processes. Phylogenetic relationships among the species thus far analyzed are discussed. [Authors'abstract]

Hsu, T. C. and F. E. Arrighi 1971. Distribution of constitutive heterochromatin in mammalian chromosomes. Chromosoma 34:243-253. 053

Using a special staining technique, a survey of the chromosomes of many mammalian species showed that constitutive heterochromatin is present in all cases and that the heterochromatin pattern appears to be specific and consistent for each chromosome and each taxon. Usually heavy heterochromatin is found in the centromeric areas, but terminal heterochromatin is not uncommon. Occasionally interstitial heterochromatin bands occur. In some species, such as the Syrian hamster and Peromyscus, many chromosome arms are completely heterochromatic. [Authors' abstract]

Jalal, S. M., R. W. Clark, T. C. Hsu, and S. Pathak 1974. Cytological differentiation of constitutive heterochromatin. Chromosoma 48:391-403 054

The constitutive heterochromatin, as demonstrated by the C-band technique, may be subdivided into a number of categories when other characteristics are considered. The responses to flourochromes QM and 33258 Hoechst, the behavior following G band staining, the repetitive DNA content, and many other criteria are useful for the classification of heterochromatin. The heterochromatin patterns of three mammalian species are presented to demonstrate that within each karyotype there may be several different types of C bands. In general, a correlation may also be made between GC-rich satellite DNA and dull (or negative) Q flourescence, and between AT-rich satellite DNA and bright Q flourescence. [Authors' abstract]

Kato, H., K. Tsuchiya, and T. H. Yosida 1974. Constitutive heterochromatin of indian muntjac chromosomes revealed by DNase treatment and a C-banding technique. Can. J. Genet. Cytol. 16:273-280. 055

A karyotype of a female Indian muntjac, Muntiacus muntjak vaginalis, was described. The karyotype was unique in that No. 1 and No. 3 homologous pairs were hetermorphic with respect to the size of their secondary constrictions. In these pairs, one of the homologs always had a longer secondary constriction than that on the corresponding homolog. Heterochromatin in the secondary constriction region was visualized with difficulty by a C-banding technique, but was demonstrated clearly by a DNase treatment followed by Giemsa staining, which also revealed the size difference of the secondary constriction. Centromeric constitutive heterochromatin of No. 1 chromosome was also found to differ in size between the homologs. On the basis of the hetermorphic character of No 3 chromosome, or an X-autosome complex, it was possible to confirm autoradiographically that X-inactivation had occurred at random. [Authors' abstract]

Kennerly, T. E., Jr. 1959. Contact between the ranges of two allopatric species of pocket gophers. Evolution 13:247-263. 056

The biological dynamics of contact between the ranges of two allopatric species of pocket gophers, Geomys personatus and G. bursarius, in southern Texas were investigated. Ninety-one specimens of G. bursarius and 113 specimens of G. personatus were trapped. Field work proceeded irregularly between December 12, 1952 and April 6, 1955. The ranges of these two species approach one another at seven localities. At one trapping site both species were collected. No abrupt ecological changes coincide with the area of approximation between the ranges of the two species. Both species appear to have similar ecological requirements though different tolerances. Indurate soils are thought to constitute the most formidable barriers to dispersal in the area studied. Interspecific competition is thought to be largely responsible for separation of ranges. No evidence of hybridization or introgression was observed. [Author's summary]

Korobitsyna, K. V., C. F. Nadler, N. N. Vorontsov, and R. S. Hoffman 1974. Chromosomes of the Siberian snow sheep, Ovis nivicola, and implications concerning the origin of amphiberingian wild sheep (Subgenus Pachyceros). Quat. Res. 4:235-245. 057

The chromosomes of Ovis nivicola, described for the first time, exhibit 2n=52, the lowest diploid number to be reported for wild sheep and goats. The new chromosomal data, together with a review of the fossil history of the genus, lead us to conclude that the bighorned wild sheep (subgenus Pachyceros) evolved their distinctive characteristics while isolated in the ice-free Beringian refugium, and then migrated southward into western North America when the glacial barriers melted, as first suggested by Cowan (1940). [Authors' abstract]

Kozlovskii, A. I. 1974. Karylogical differentiation of North American subspecies of hoofed lemmings. Doklady Biol. Science 219:499-502. 058

The hoofed or collared lemming Dicrostonyx torquatus Pall. occupies the circumpolar area. In Eurasia, 4 subspecies are usually recognized; in North America, 12 subspecies are distinguished.

In Dicrostonyx torquatus vinogradovi a diploid set of 28 chromosomes, N.F. = 54 is found. The chromosomes represent three morphological types: meta-, submeta-, and subtelocentric. The chromosome compliments in each groups are described. The population of hoofed lemmings from the Chaunsk region proved to be polymorphous, having a diploid number from 57 to 60 chromosomes. This polymorphism is related to variability in the number of microchromosomes.

Both continental subspecies (D. t. chionopaes and D. t. torquatus) display an evident similarity of karyotypes, in which subtelo- and telocentric chromosomes of the most diverse sizes predominate, along with a few rather small metacentric chromosomes. Chromosome polymorphism is observed in populations of these sub-species. Their chromosome sets are similar, although they are by no means identical. The differences are quite essential, though not as striking as the differences among the northeastern subspecies. The differences in diploid number (45-51; 57-60) and in the form of sex chromosomes are most important and most notable in the subspecies investigated.

A comparison of the chromosome sets of hoofed lemmings from Vrangel' Island and from North America suggests their genetic affinity, since the karyotypes have the same structure and a similar N.F., despite their somewhat diverse diploid numbers.

Chromosome sets have been described for half of the 16 subspecies of Dicrostonyx torquatus from the Arctic territory. Two types of chromosome sets may be noted: the "Asiatic type" which seems older -- perhaps even the original type (at present this type is known only in the two continental sub-species - D. t. chionopaes and D. t. torquatus; and the "North American type," represented in the 5 non-arctic subspecies and in the hoofed lemming of Vrangel' Island. It should be emphasized that the chromosome sets of the northeastern subspecies of hoofed lemmings represent extreme variants of these types.

Hybridization between D. t. stevensoni and four other subspecies with the "North American type" of chromosome set (exsul, nelsoni, rubricatus, richardsoni) does not proceed beyond the first generation. This indicates the plausibility of regarding the nonarctic subspecies as a group of close, but reproductively isolated, independent species within the superspecies Dicrostonyx torquatus. [Abstract by GLW]

Kozlovskii, A. I., and V. N. Orlov 1971. Karyological evidence for species independence of Sorex isodon Turov (Soricidae, Insectivora). Zool. ZH 50(7):1056-1062 059

Karyotypes of S. isodon from the Magadan and Kemerovo Districts were studied and were identical. The chromosome set contains 40 autosomes and 1 pair of sex chromosomes, NF = 68. Among the autosomes, 9 pairs were metacentric, 5 pairs submetacentric, and 7 pairs subtelo- and telocentric. X-chromosome was telocentric and measured 5.47% of the haploid female set length. Y-chromosome was the smallest submetacentric. Quantitative characteristics of chromosomes were obtained when measuring 10 chromosome sets. Possibilities of identification of individual chromosome pairs by polykaryograms are discussed. The karyological data confirm the species status of S. isodon. Differences in chromosome sets of S. araneus and S. isodon are so sharp that it appears impossible to distinguish common features. By the karyotype structure, S. isodon is most closely related to S. caecutiens, S. unguiculatus, and S. Vir. [Abstract from Biological Abstracts]

Kral, B., E. Von Lehmann, and J. Zejda 1972. The hybrids of two subspecies of the red-backed vole (Clethrionomys glareolus Schreb). Zool. Listy 21(1):43-61. 060

The karyotype, body and skull dimensions as well as fecundity were examined in the subspecies Clethrionomys glareolus glareolus Schreber, 1780, Clethrionomys glareolus garganicus Hagen, 1958, and their crosses. C. g. garganicus differs from the nominate form by larger body and skull dimensions, among which the length of hind foot and the height of skull appear to be dominant in male line hybrids. The same holds for the inheritability of fur colour. In the karyotype of C. g. garganicus, the sex chromosome Y is distinctly acrocentric to feebly subtelocentric and is the smallest one of the set. Therein the karyotype of C. g. garagnicus differs from that of the hitherto examined central European populations of the nominate form, showing a mediocentric sex chromosome Y. Also this character of C. g. garganicus is inheritable in the male line. Both subspecies show a certain degree of sexual differentiation; that is to say, the hybrids in the female line of C. g. garganicus appear to attain sexual maturity later than those in the female line of C. g. glareolus. The crossing of individuals of the F_2 generation inter se was unsuccessful. [Authors' summary]

Kuliev, G. N., G. K. Kuliev and S. I. Radzhabli 1978. Karyotype differences between populations of the water vole Arvicola terrestris (Rodentia, Cricetidae). Zool. ZH 57(9): 1409-1411. 061

Water voles from 4 populations of the Caucasus and the Novosibirsk Distinct [sic] (USSR) were studied by means of G[Giemsa]- and C[constitutive heterochromatin]- methods of differential staining of chromosomes. In all animals studied 2n = 36. Differences were found by the values of NF (number of chromosome arms) and the size of Y-chromosome. In water voles of 3 Caucasian populations and in those from the Novosibirsk District NF = 72 and Y-chromosome is the smallest acrocentric of the set. In water voles from the Pushkinsky region of the Azerbaijan SSR NF = 66 and Y-chromosome is almost X larger. A comparative analysis of the chromosomes showed that the differences in the number of chromosome arms are due to the absence of short fully heterochromatic arms in 3 pairs of autosomes of the water voles from the Pushkinsky population. Y-chromosome of A. terrestris consists almost completely of heterochromatic material, and differences in the size of this chromosome determine the differences in the amount of heterochromatin as well. [Abstract from Biological Abstracts]

Lakhotia, S. C., S. R. V. Rao, and S. C. Jhanwar 1973. Studies on rodent chromosomes VI. Co-existence of Rattus rattus with 38 and 42 chromosomes in south western India. Cytologia 38:403-410 062

Chromosomes of two subspecies of Rattus rattus, namely, R. r. Wroughtoni and R. r. rufescens, from Sagar, Mysore State, South Western India, have been examined. R. r. wroughtoni has 42 chromosomes typical of Rattus rattus, while R. r. rufescens shows 2n = 38. The karyotype of the latter is similar to that described by other workers for Rattus rattus populations with 2n = 38 from other parts of the world. This is the first report of Rattus rattus with 38 chromosomes from India. It is proposed that the 2n = 38 karyotype is evolved from the basic Rattus rattus karyotype with 2n = 42 by centric fusion and pericentric inversions. [Authors' summary]

Lawlor, T. E. 1974. Chromosomal evolution in Peromyscus. Evolution 28(4):689-692. 063

Mechanisms for chromosome evolution were discussed in light of cytological evidence for their occurrence. Centric fusion, a process responsible for the reduction of the diploid number by creating biarmed chromosomes from the fusion of acrocentrics, has been considered a unidirectional evolutionary process. Cytological evidence provided by studies of mammalian chromosomes suggests that "fission" by which biarmed chromosomes divide to create acrocentrics (and thus create a higher diploid number), has also played an important role in chromosome evolution. Evidence suggests no obvious trend of evolutionary change in the number of chromosomal arms. [Abstract by GLW]

Lee, M. R., D. J. Schmidly, and C. C. Huheey 1972. Chromosomal variations in certain populations of Peromyscus boylii and its sytematic implications. J. Mammalogy 53(4):697-707. 064

The karyotype of Peromyscus boylii attwateri is contrasted with that of P. b. boylii, p. b. rowleyi and P. b. utahensis. The latter three taxa have identical karyotypes. Chromosomal and morphological evidence indicate that attwateri is specifically separated from the boylii-rowleyi-utahensis assemblage. Limited samples from Mexican populations of P. boylii imply that current taxonomic alignments in this species require reevaluation. The karyotype of Peromyscus difficilis comanche is described and it appears to be identical to that of Peromyscus truei truei and unlike those of northern populations of P. difficilis. [Authors' abstract]

Lyapunova, E. A. and N. N. Vorontsov 1978. Genetics of Ellobius (Rodentia): I. Karyological characteristics of 4 Ellobius species. Genetika 14(11):2012-2014. 065

Ellobius is a cytogenetically unique group of animals. A review is given on the problem of sex determination in E. lutescens (2n = 17 in both males and females) and on the chromosome divergence of the Ellobius genus. Karyotypes of 83 animals of 4 Ellobius spp. are studied. E. lutescens from 2 Armenian regions has 2n = 17 in ♂ and ♀. No translocation of a sex chromosome on an autosome was morphometrically observed. A male karyotype of E. fuscocapillus (2n = 36), the only species having heteromorphic X and Y chromosomes, is described for the 1st time. The length of the X chromosome is 5.7% and the length of the Y chromosome 1.7% of the haploid set length. The distribution of west and east karyotypes is described on the basis of the investigation of E. talpinus from 14 points. No intrapopulational chromosome polymorphism was observed in all the 14 populations. E. alaicus, a chromosomal sibling species, has 2n = 52, NF = 56. It originated from the east E. talpinus variant by means of Robertsonian fusion. E. alacius was found in the Alai valley and in the Alai mountains, E. talpinus and E. alaicus are characterized by sex chromosome isomorphism, which is unusual for other Ellobius spp. [Abstract from Biological Abstracts]

Malygin, V. M. 1970. The systematics of the subspecies of the common field mouse. Vestnik Moskovskogo Universiteta, Seriya V. Biologiya Pochvovedenie 25(5): 89-91. 066

The common field mouse Microtus arvalis Pallas is a well studied species covered in more than 500 works. The forms which have been combined under the heading "common field mouse" constitute a young group characterized by an active process of species formation. The common field mice, then, as a group, comprise a superspecies consisting of a group of closely related (sibling) species. 190 common field mice consisting of both the 46 and 54 chromosome varieties from 17 geographical locations in USSR were studied. The chromosomal makeup of the trans-Caspian field mouse was also studied. The 46 chromosome type common field mouse showed marked karyotypic differences in different portions of its geographic range. The 54 chromosome type is, again, completely different.

Among the hundreds of field mice caught in the wild, not a single sibling species hybrid was found. In order to prove the species independence of these forms individuals were hybridized to demonstrate the reproductive isolation between the sibling species. The hybrids have 50 chromosomes (23 chromosomes from 46 chromosome field mice and 27 chromosomes from 54 chromosome species) and are sterile. Chromosomal differences between these sibling species is so great that in meiosis the conjugation of homologous chromosomes is completely violated leading to total sterility in hybrids.

The diploid complement of M. transcaspicus elaeus Thom. has 54 chromosomes. In the hybrid males resulting from crossing 54 chromosomal common field mice with transcaucusus mice, spermatogenesis progresses almost to the end, but there are no mature spermatozoons and the hybrids are sterile. The results of karyotypic and hybridologic analyses attest to the species independence of the transcaucusus field mouse.

The discovery of sibling species as well as the description of several new karyotypic forms of the common field mouse totally alters the present concept of the species Microtus arvalis Pallas and its intra-species differentiation. The study reveals that because of sympatry M. a. duplicatus and M. a. transcaucasicus are without a doubt mixed subspecies and a radical systematic review of these subspecies is indicted.

It is postulated that the 54-chromosome karyotype is ancestral and that the 46-chromosome form derived by centric fusions in the large chromosomes and pericentric inversions in the small chromosomes. [Abstract by GLW]

Malygin, V. M. and V. N. Orlov 1974. Range of 4 species of voles (superspecies Microtus arvalis) by karyological data. Zool. ZH 53(4):616-622. 067

Karyotypes of over 400 voles from 8 regions were studied and a distribution map of closely related species within the range of the superspecies M. arvalis is given. M. subarvalis occurs in eastern Europe, the Urals and Armenia [USSR]. M. transcaspicus inhabits the Kopetdag Mountains and M. ilaeus is an endemic of Tien-Shan. 8 chromosome forms of M. arvalis replace one another geographically. The M. a. forma obscurus was found in Altai, South-West Siberia, Ural, Caucasus, in the basins of the Volga and Don, and the Crimea and M. a. forma arvalis in Europe. Ranges of sibling species, M. arvalis - M. subarvalis, are sympatric in the eastern Europe, the Urals, and Armenia. Contacts between the colonies of these species were found in 8 regions. [Abstract from Biological Abstracts]

Mascarello, J. T., A. D. Stock, and S. Pathak 1974. Conservatism in the arrangement of genetic material in rodents. J. Mammalogy 55(4):695-704. 068

The Giemsa banding pattern of the karyotype of Neotoma micropus is compared with the banding patterns of seven other rodent species that are progressively more distantly related to N. micropus. Results of comparisons imply that there is a tendency for arrangement of genetic material on chromosomes to be conserved. Results also lend support to systematic inferences based on characters of the glans penis and suggest that the type of approach employed here may be useful in characterizing phylogenetic relationships between genera, tribes, subfamilies, and families of rodents. [Authors' abstract]

Mascarello, J. T. and J. W. Warner 1974. Chromosome variations in the plains woodrat: A pericentric inversion involving constitutive heterochromatin. Experientia 30(1):90-91 069

The chromosomes of the plains woodrat (Neotoma micropus Baird) were studies using C- and G-banding, and compared with the chromosomes of other members of the genus Neotoma. G-bands revealed distinct homologies between the two largest autosomes in every case. The only regions not matching band-for-band were those regions having been stained positive for constitutive heterochromatin. C- and G-band patterns of the heteromorphic autosomal pair were interpreted as clear indications that the large submetacentric and large acrocentric chromosomes are homologous, except that one has sustained a pericentric inversion in the region containing constitutive heterochromatin.

Neotoma micropus and N. floridana appear to be very closely

McFee, A. F. and M. W. Banner 1969. Inheritance of chromosome number in pigs. J. Reprod. Fert. 18:9-14. 070

All possible crosses were made between European wild pigs with either 36 or 37 chromosomes and domestic swine with 38. The 36 X 36 cross produced only pigs with 36; the 36 X 37 and 37 X 38 crosses t yielded the paren numbers in about equal numbers of pigs. All pigs resulting from the 36 X 38 cross had 37, while crossing 37 X 37 gave a progeny with 36, 37 or 38 in about 1:2:1 ratio. It is surmised that the three unpaired members in the 37-chromosome animal act as a trivalent during meiosis with two telocentric chromosomes behaving as a unit. No firm evidence indicated reduced fertility in any of the animals nor were any physical changes evident which could be associated with different chromosome forms. [Authors' summary]

McFee, A. F., M. W. Banner, and J. M. Rary 1966. Variation in chromosome number among European wild pigs. Cytogenetics 5:75-81. 071

Peripheral leukocyte cultures from 36 European wild pigs have shown that 73% of the animals possessed 36 chromosomes while 27% had 37. Karyotypes of 36-chromosome individuals differed from those of domestic swine in that they possessed one pair of submetacentric chromosomes not found in domestic pigs and lacked two pairs of the domestic's telocentrics. The 37-chromosome animals had one chromosome of each of these three pairs but lacked their homologous members. Matings between animals with 36 and 38 chromosomes have produced fertile offspring with 37. A single litter from a 36 X 37 mating consisted of three pigs with 36 and three with 37 chromosomes, while one from a 37 X 37 mating contained progeny with 36, 37, or 38 chromosomes. The odd number of chromosomes in some wild pigs is postulated to have resulted from the entry of domestic breeding into the wild herd. [Authors' abstract]

Meier, M. N. 1968. Complex taxonomic analysis of the species based on the study of common voles (genus Microtus). The Zool ZH 47(6): 850-859. 072

The taxonomic status of 3 forms of common voles: Microtus fortis Buchner, M. ungurensis, Kostschenko and M. Mongolicus Radde was studied. The species independence of all the 3 forms is established after complex methods of investigation (morphological, hybridization and karyological). Stable morphological differences, as well as large differences in the number and form of chromosomes were found between M. fortis and M. ungurensis. These forms do not cross due to the above cited differences. No morphological differences are observed between M. mongolicus and M. arvalis (formerly thought to be subspecies of the same species), nevertheless both forms are strictly isolated genetically. [Abstract from Biological Abstracts]

Meier, M N., V. N. Orlov, and E. D. Skhool' 1969. Use of data on karyological, phsyiological and cytophysiological analyses for isolating a new species of rodent (Rodentia, Mammalia). Dokl Akad Nauk SSSR 188(6): 1411-1414. 073

The isolation of a new species of vole of the genus Microtus by means of karyological, physiological, and cytophysiological criteria was established. The form proposed as an independent species is Microtus arvalis Pallas. A study of the karotype of this vole showed that in the USSR there are 2 distinctly different forms, which are designated as forms A and B. A comparison of all the data obtained led to the conclusion that forms A and B of the common vole, having different karyotypes, differing in heat resistance of the cells, and reproductively isolated, can be regarded as independent species despite the absence of differences in the morphological characters studied. The name M. arvalis Pallas can be left for form A, since its original description sooner pertain to the 46-chromosome form, and the 54-chromosome form B can be given the name of some subspecies, for example Microtus arvalis Caspicus, if it turns out that this subspecies belongs wholly to form B or only B is found in the locale from where it is described. [Abstract from Biological Abstracts]

Nadler, C. F., R. S. Hoffmann, and A. Woolf 1973. G-band patterns as chromosomal markers, and the interpretation of chromosomal evolution in wild sheep (Ovis). Experientia 29:117-119. 074

Results of G-banding in wild sheep suggest the following hypotheses may apply: Chromosomal convergence among populations of European and Asiatic sheep implies that they have been derived from a common ancestor, possibly in Asia Minor or Europe, in which centric fusions have resulted in the present 2n=54 populations. Independently and earlier, another ancestral population was isolated somewhere to the east, perhaps in middle or central Asia. Centric fusion in that population resulted in sheep with a diploid number of 56, eventually giving rise to modern arkhar/argali, which in turn was the source for amphi-Beringian populations. Ancestral 2n=56 sheep migrated across the Bering land bridge in the Pliestocene and became isolated from their ancestral populations. Through additional centric fusion, they developed into modern Dall and Bighorn sheep. Fusions between specific acrocentric chromosomes is suggested as a means by which North American 2n=54 populations evolved. [Abstract by GLW]

Nadler, C. F., R. S. Hoffmann, and A. Woolf 1974. G-band patterns, chromosomal homologies, and evolutionary relationships among wild sheep, goats, and auodads (Mammalia: Artiodactyla). Experientia 30:744-746. 075

The tribe Caprini (family Bovidae) contains five genera, among which the wild sheep (Ovis) and goats (Capra) are most closely related. Chromosome analyses of three genera demonstrated a common fundamental number (NF=60). Other members of the tribe, particularly the genus Ovis, have divergent 2n numbers. Analyses suggest that the diploid number of 60 is ancestral, having evolved by Robertsonian translocation into forms with lower diploid numbers. [Abstract by GLW]

Nadler, C. F., K. V. Korobitsyna, R. S. Hoffmann, and N. N. Vorontsov 1973. Cytogenetic differentiation, geographic distribution, and domestication of palearctic sheep.(Ovis) Z. Saugetierkunde 38:109-125. 076

Old World sheep may be divided into four groups, with different diploid chromosome numbers and morphological characters. There are, from west to east, mouflon (2n=54) in the Mediterranean region and the Near East; urial (2n=58) in Middle Asia from eastern Iran to Tadzhikistan and probably West Pakistan; arkhar/argali (2n=56) in Middle and Central Asia; and snow sheep (2n=?) (subgenus Pachyceros) in eastern Siberia. The systematic status of sheep from Europe to Central Asia (subgenus Ovis) remains uncertain; in this broad area wild sheep are distributed in interconnected rings many of which have been repeatedly broken and rejoined during the Pleistocene, leading to differentiation of isolates and subsequent introgression. Domestic breeds of sheep so far studied all appear to be derived from a mouflon (2n=54) ancestor in the Near East. [Authors' summary]

Nadler, C. F., D. M. Lay, and J. D. Hassinger 1971. Cytogenetic analyses of wild sheep populations in Northern Iran. Cytogenetics 10:137-152. 077

Seven populations of wild sheep (Ovis ammon) were studied in northern Iran. Analysis of 34 individuals demonstrated that the eastern populations possess a 2n=58, including 1 pair of metacentric and 27 pairs of acrocentric autosomes. The 2n for the three western localities is 54, characterized by 3 pairs of metacentric and 23 pairs of acrocentric autosomes. In two intermediate localities animals with the following diploid numbers were collected: 2n=54, identical to western locality animals; 2n=55, containing five metacentric autosomes; 2n=56, containing four metacentric autosomes; 2n=57, with three metacentric autosomes; 2n=58, identical to the eastern two localities. The X and Y chromosomes are a large acrocentric and a small biarmed chromosome, respectively, in every specimen. The taxonomy of Iranian wild sheep and several evolutionary factors are considered in the light of these chromosomal data. The nonconformity of currently accepted theories on the

Nelson-Rees, W. A., A. J. Kniazeff, R. J. Baker, and J. L. Patton 1968. Intraspecific chromosome variation in the bat, Macrotus waterhousii Gray. J. Mammalogy 49(4):706-712. 078

The karyotypes of two subspecies of bat, Macrotus waterhousii Gray (Phyllostomatidae), have been studied and compared. Specimens of M. waterhousii mexicanus from Morelos and Guerrero, Mexico, as well as specimens in one sample of M. waterhousii californicus from Sonora, had a karyotype with a diploid number of 46 including a telocentric Y-chromosome in the male complement. Another sample of M. waterhousii californicus from Sonora, as well as samples from Arizona and California, had a diploid number of 40. Of these samples, the Arizona specimens also revealed a telocentric Y-chromosome and in addition a secondary constriction on the supposed X-chromosome, whereas the California sample was characterized by a pronounced achromatic region near the centromere on one of the large pairs of telocentric chromosomes and the existance of a meta or sub-metacentric Y-chromosome in the male. This appears to be the first major karyotypic variation of bats reported at the subspecific level. [Authors' abstract]

Nevo, E. and H. Cleve 1978. Genetic differentiation during speciation. Nature 275:125-126. 079

Karyotypes of the subterranean mammal Spalax ehrenbergi were studied in light of genetic differentiation. Results support the hypothesis that habitat specialists (such as the mole rat, S. ehrenbergi) display significantly lower genetic variation than do habitat generalists. Concerning speciation theory, the S. ehrenbergi complex represents a remarkable case of speciation with relatively few genomic changes. [Abstract by GLW]

Pathak, S., T. C. Hsu, and F. E. Arrighi 1973. Chromosomes of Peromyscus (Rodentia, Cricetidae) IV. The role of heterochromatin in karyotypic evolution. Cytogenet. Cell Genet. 12:315-326. 080

All species in the genus Peromyscus possess a diploid number of 48, but the number of total chromosome arms varies from 56 (e.g., P. crinitus) to 96 (e.g.,P. eremicus). Data are presented, using these two extreme cases, to illustrate that all short arms of biarmed chromosomes are made of constitutive heterochromatin. G-banding preparations revealed that the long arms (euchromatin) of the two species are essentially the same. Since constitutive heterochromatin contains few, if any, stuctural genes, the two species, and presumably other species as well, do not differ drastically in their information content, but differ in the amount of chromatin material, including DNA. The results indicate that in studying karyotypic evolution, C-banding and G-banding (or Q-banding) are essential tools without which erroneous conclusions may be reached. [Authors' abstract]

Patton, J. L. 1972. Patterns of geographic variation in karyotype in the pocket gopher, Thomomys bottae (Eydoux and Gervais). Evolution 26:574-586. 081

Variation in the mitotic chromosome complement is greater within the pocket gopher, Thomomys bottae, than any other recorded species of mammal. This variation involves almost exclusively non-Robertsonian morphological changes and not diploid number. Most populations are polytypic with over 40 different population karyotypes having been recorded, but a few cases of intrapopulation polymorphism are known. The variation is most extensive within and between populations in the Basin and Range Province of the Southwest whereas most populations in coastal and central California are identical, or nearly so. The extensive karyotypic variability is not a function of single causative agents, but rather appears to be dependent upon a suite of highly interrelated selective factors. Historical biogeographic events which provided the means for population isolation under which chromosomal divergence can occur are detailed with selected examples. These events in combination with biological properties of gophers, particularly those centered around their fossorial habitus, are considered largely responsible for the karyotypic diversity.

There is no evidence that this diversity has contributed to reproductive isolation between populations of T. bottae. Rather, it appears to have led to increased population adaptation by modifying linkage groups via redistribution of the genome. The chiasmas localization found in the species aids in tightening linkage groups and reduces genetic variability resulting from segregation and recombination, while at the same time preserves genic heterozygosity. Hence, optimal gene combinations can evolve to meet the highly localized selective parameters under which each population exists. This can be done without sacrificing genetic heterozygosity or forcing reproductive isolation. [Author's summary]

Patton, J.L. and R. E. Dingman 1968. Chromosome studies of pocket gophers, genus Thomomys. I. The specific status of Thomomys umbrinus (Richardson) in Arizona. J. Mammalogy 49(1):1-13. 082

The complexities of morphology and, hence, taxonomy of pocket gophers (genus Thomomys) in southern Arizona are reflected by extreme interpopulation chromosomal variation in both T. bottae (2n=76) and T. umbrinus (2n=78). The variation consists of differing numbers of morphological types of chromosomes for nearly each population karyotype. The known range of variation in either species is less than the amount of difference between the two. A somewhat strict ecological separation exists between T. bottae and T. umbrinus in areas of sympatry or near sympatry, with the former preferring the more friable soils of the valley floors and mountain tops and the latter confined to the indurate soils of the oak zones at intermediate elevations. Chromosomal and ecological concordance support the interpretation that T. bottae and T. umbrinus are distinct species. Limited hybridization between the two species at one locality of sympatric contact, however, is known. [Authors'

Raman, R. and T. Sharma 1972. Similarity in karyotypes of Rattus rattus with 38 chromosomes from India and other parts of the world. Experientia 28(11):1375-1377. 083

The chromosomes of 12 male and 12 female specimens of R. rattus, collected from various locations in India, possessed a diploid complement of 38. Two of the rats had darker underparts than the others; however, their karyotypes did not differ in diploid number. The Indian populations of R. rattus support a concept of chromosomal convergence as a means of evolution. The Indian rats are probably derived from a European ancestor having a diploid number of 42. [Abstract by GLW]

Rausch, R. L. and V. R. Rausch 1972. Observations on chromosomes of Dicrostonyx torquatus stevensoni Nelson, and chromosomal diversity in varying lemmings. Z. Saugetierkunde 37:372-384. 084

The cytogenetic characteristics of the varying lemming, Dicrostonyx torquatus stevensoni, (2n=34), were investigated, and diploid chromosomal numbers were reported for four other nominal subspecies (exsul, nelsoni, richardsoni, and rubricatus) of the torquatus-group in North America. The diploid complements ranged from 30 to 44 chromosomes, and the fundamental number from 50 to 55. Chromosomal ploymorphism was observed in all forms. In cross-breeding experiments, the mating of F_1 progeny was not productive. The findings support the zoogeographic concept that populations of Dicrostonyx became fragmented or displaced southward during Wurm time, with relict stocks persisting in unglaciated refugia or periglacial tundra. Speciation in the isolates led to chromosomal evolution, with the result that populations spreading from refugia in post-glacial time are reproductively isolated. The torquatus-group in North American appears to be a super-species. [Authors' summary]

Rausch, R. L. and V. R. Rausch 1975. Relationships of the red-backed vole, Clethrionomys rutilus (Pallas), in North America: Karyotypes of the subspecies dawsoni and albiventer. Syst. Zool. 24(2):163-170. 085

Cytogenetic comparisons were made of northern red-backed voles of two subspecies, Clethrionomys rutilus dawsoni Merriam and C. r. albiventer Hall and Gilmore, as well as of intergrades of dawsoni X albiventer to the F_{18} generation. The diploid number was 56, and karyotypes were indistinguishable for all animals, with the exception of some individuals of C. r. albiventer (with 2n=55) which were heterozygous for a chromosomal polymorphism evidently resulting from a Robertsonian rearrangement. All species of Clethrionomys for which karyotypes are known have 2n=56, but two groups are distinguishable by the form of the Y-chromosome: in C. rufocanus (Sundevall), C. gapperi (Vigors), and C. occidentalis (Merriam), the Y is acrocentric, whereas in C. glareolus (Schreber) and C. rutilus, it is metacentric. Thus, the karyotypes of dawsoni and albiventer are indistinguishable from that of the Eurasian C. r. mikado (Thomas), and the different forms of the Y-chromosome separate C. rutilus and C. gapperi in North America. These findings further support the concept that C. rutilus is a holarctic species. (Red-backed vole; karyotypes.) [Authors' abstract]

Reig, O. A., J. V. Pincheira, A. O. Spotorno, and P. Waller 1972. New evidence of a 38-chromosome karyotype in South American populations of roof rat Rattus rattus L.(Rodentia, Muridae). Experientia 28(2):225-227. 086

In two populations of Rattus rattus, one from Chile and the other from Venezuela, karyotypes with chromosome complements of 2n=38 were observed in all of the animals studied. Rattus rattus is shown to be highly variable in chromosome number and structure, showing both geographic, and possibly subspecific, multiformity and polymorphism in karyotypes.

The analyses of chromosomes of the South American R. rattus populations suggests that they were derived by means of Robertsonian translocation from a European ancestor having a diploid number of 42. [Abstract by GLW]

Robinson, T. J. and J. D. Skinner 1976. A karyological survey of springbok subspecies. S. African J. Science 72:147-148. 087

Studies of subspecies of springbok (A. marsupialis) indicate that the subspecies are characterized by a monomorpic karyotype throughout their distribution in southern Africa, and their diploid chromosome number 2n=56 (54 autosomes and 2 sex chromosomes). [Abstract by GLW]

Schmidly, D. J. and G. L. Schroeter 1974. Karyotypic variation in Peromyscus boylii (Rodentia: Cricetidae) from Mexico and corresponding taxonomic implications. Syst. Zool. 23:333-342. 088

Nine different karyotypes are evident among samples of six subspecies of Peromyscus boylii (P. b. rowleyi, P. b. spicilegus, P. b. simulus, P. b. levipes, P. b. ambiguus, and P. b. beatae). All specimens have a diploid number of 48; the principal differences are in the numbers of large and medium-sized biarmed autosomes which range from 2-10. Three chromosome races are recognizable in P. boylii; they are distributed parapatrically with respect to one another, and present evidence suggests that limited gene exchange occurs among them. The karyotype for topotypes of P. b. simulus from Nayarit, Mexico, is markedly different from all other forms of P. boylii, suggesting that this taxon is a distinct species. Chromosomal polymorphism of a non-Robertsonian type is seen in certain populations of P. boylii and may be the result of intergradation between the different chromosome races. The polymorphism involves a variable number of large biarmed autosomes with certain individuals in a population possessing a heteromorphic pair of autosomes. The karyotypes of P. oaxacensis and P. evides, both members of the boylii species group, are also described for the first time. [Authors' abstract]

Schroder, J., J. Antoni, and W. Van der Loo 1978. Comparison of the karyotypes in the jack rabbit (Lepus californicus deserticola) and the European hare (Lepus europaeus). Hereditas 89:134-135. 089

The karyotypes of Lepus europeaus (European Hare) and L. californicus deserticola (a subspecies of American jack rabbit) were compared to determine correlation between geographic isolation and karyotypical divergence. Both species possessed a diploid number of 48, and differed mainly in chromosome morphology. The study supports the argument that chromosomal speciation is encouraged by geographic proximity, and that geographically isolated species have no need to develop divergent karyotypes. [Abstract by GLW]

Schroder, J., H. Suomalainen, W. Van Der Loo, and E. Schroder 1978. Karyotypes in lymphocytes of two strains of rabbit, and two species of hare. Hereditas 88:183-188. 090

G-banding of metaphase chromosomes in cultured lymphocytes was used to compare the karyotypes of two strains of domestic rabbit. Oryctolagus cuniculus (NZW and Dutch rabbit) and two species of hare (Lepus europaes and Lepus timidus).

The NZW and the Dutch rabbit had identical karyotypes with 44 chromosomes, as did Lepus europaeus and Lepus timidus with 48 chromosomes.

However, all individual rabbits and hares showed chromosomal rearrangments (e.g., deletions and duplications) in 30-50% of all lymphocytes studied. The significance of the findings are discussed. [Authors' abstract]

Schroder, J. and W. Van Der Loo 1979. Comparison of karyotypes in three species of rabbit: Oryctolagus cuniculus, Sylvilagus nuttallii, and S. Idahoensis. Hereditas 91:27-30. 091

The karyotypes in three species of rabbit (Oryctolagus cuniculus, Sylvilagus nuttallii and S. idahoensis) were compared. The karyotype of Oryctolagus cuniculus was used as a reference. The chromosome number in Oryctolagus cuniculus and Sylvilagus idahoensis is 44, and in S. nuttallii, 42. Four chromosome pairs in Sylvilagus idahoensis and three in S. nuttallii are clearly different from those in Oryctolagus cuniculus, but minor differences can also be found in other chromosomes in these species. A very striking similarity in the karyotypes of Oryctolagus cuniculus and Sylvilagus nuttallii is that they have identical metacentric chromosomes 1, whereas in S. idahoensis this chromosome is represented by two separate chromosome pairs. In spite of this, the karyotypes in the three species have diverged from each other about equally. [Authors' abstract]

Selander, R. K., D. W. Kaufman, R. J. Baker, and S. L. Williams 1974. Genic and chromosomal differentiation in pocket gophers of the Geomys bursarius group. Evolution 28:557-564. 092

The processes of karyotypic and genic differentiation have proceeded independently in the evolution of pocket gophers of the Geomys bursarius group. In the peripheral relict G. tropicalis, a reduction in 2N chromosome number from~70 to 38 was not accompanied by an unusual degree of allelic substitution at structural gene loci. The possibility that a reduction in number of linkage groups and an apparent loss of variability at structural gene loci in G. tropicalis represent adaptation to an unusally uniform environment is discussed. [Authors' summary]

Sen, S. and T. Sharma 1979. Sparse distribution of constitutive heterochromatin and its variation in two species of mongooses (Carnivora) with exact G-band homology. Genetica 50(3):221-226. 093

The diploid chromosome number in two species of mongooses viz., Herpestes auropunctatus and H. edwardsi is 35 in males and 36 in females, since the Y chromosome in the males of these species is translocated onto an autosome. C-banding of these karyotypes reveals that (1) they contain an extremely low amount of C-band positive constitutive heterochromatin (C-heterochromatin); (2) H. edwardsi possesses an increased amount of C-heterochromatin compared to H. auropunctatus which is localized as prominent arms on two pairs of chromosomes; (3) the translocated Y chromosome in both species is not stained differentially by this technique. Hoechst 33258 flourescence does not distinguish any differentially bright heterochromatic region in either of the two genomes. G-banding patterns in the chromosomes of these two species show remarkable similarity. [Authors' abstract]

Sharma, T. and I. K. Gadi 1977. Constitutive heterochromatin variation in two species of rattus with apparently similar karyotypes. Genetica 47(1) 77-80. 094

Rattus blanfordi and R. cutchicus medius both have a chromosome complement of 2n = 36 and all chromosomes except the submetacentric Y of R. blanfordi are acrocentric. The apparently similar karyotypes of the two species, however, show variations in the nature and quantity of C-band-positive constitutive heterochromatin (C-heterochromatin) as revealed by C- and G-banding and Hoechst 33258 fluorescence. R. blanfordi with large-sized X and Y chromosomes and conspicuously larger centromeric heterochromatin in all the autosomes as compared to that of R. cutchicus medius has much more C-heterochromatin in its genome than the latter. The variation in the quantity of C-heterochromatin has been accomplished without altering the morphology of the acrocentric chromosomes unlike other mammals in which variations have been reported to result generally in the addition or deletion of a totally heterochromatic second arm. [Authors' abstract]

Sharma, T. and G. S. Garg 1975. Constitutive heterochromatin and karyotype variation in Indian pygmy mouse, Mus dunni. Genet. Res. 25: 189-191. 095

The Indian pygmy mouse, Mus dunni, exhibits great variation [between separate geographic regions] in the number of chromosome arms while its diploid number of chromosomes remains constant. The variation seems to be due to addition or deletion of C-band positive constitutive heterochromatin in the short arms of autosomes. [Authors' summary]

Sharma, T. and R. Raman 1973. Variation of constitutive heterochromatin in the sex chromosomes of the rodent Bandicota bengalensis bengalensis (Gray). Chromosoma 41:75-84. 096

Bandicota bengalensis bengalensis (Gray) trapped from different localities of India and Nepal exhibited a marked variation in the size and morphology of sex chromosomes. Three types of X's were found; A) simple acrocentric, B) composite subtelocentric and C) composite submetacentric X with their relative sizes 5.9%, 7.5% and 9.6% of the genome respectively. The autosomes remained unaltered. It was shown that this variation in the size of sex chromosomes was caused by deletion of constitutive heterochromatin. The Y chromosome was also found to be variable. Usually a large X was combined with a large Y. The preponderance of homozygotes for each type of X chromosome in populations, suggested that probable role of sex chromosomes heterochromatin in speciation. [Authors' abstract]

Singh, R. P. and D. B. McMillan 1966. Karyotypes of three subspecies of Peromyscus. J. Mammalogy 47(2):261-266. 097

Karyotypes of Peromyscus maniculatus gracilis Le Conte, Peromyscus maniculatus bairdii Hoy and Kennicott, and Peromyscus leucopus noveboracensis (Fischer) from southern Ontario were studied to determine whether or not identification of these animals can be made on a cytological basis. The karyotypes as determined from metaphase plates of bone marrow and newborn splenic tissue confirm the diploid number of 48 in each case as given by Makino (1951) and are sufficiently distinct to permit positive identification of each subspecies. [Authors' abstract]

Sokolov, V. E., V. N. Orlov, G. A. Chudinovskaya, and A. A. Danilkin 1978. Chromosomal differences between two subspecies of roe deer, Capreolus capreolus capreolus L. and C. c. pygargus Pall. Zool. ZH 57(7): 1109-1112. 098

Differences in chromosomes are described between roe deer from 2 populations, C. c. capreolus from the Bryansk District and C. c. pygargus from the South Ural [USSR]. The diploid number is 70 for C. c. capreolus and 74 for C. c. pygargus. Unlike the former the karyotype of the latter has 2 pairs of point-like chromosomes. These differences may be used in studying the evolution of C. capreolus. [Abstract from Biological Abstracts]

Soldatovic, B., B. Djulic, I. Savic, and D. Rimsa 1969. Chromosomes of two species of the genus Apodemus (A. agrarius and A. mystacinus -- Mammalia, Rodentia) from Yugoslavia. Arhiv. Biol. Sci. 21(1-4):27-32. 099

The karyotypes of Apodemus agrarius kahmanni and A. mystacinus epimelas are described. The phenomenon of two different karyotypes in the species A. agrarius from Yugoslavia (form from Bosnia with N. F. = 54, while all other forms from Yugoslavia have N.F. = 56) indicates that this is also a case of chromosome polymorphism, probably a consequence of pericentric inversion. It may be hypothesized that pericentric inversion of a metacentric chromosome gave rise to a pair of small acrocentric chromosomes. This would mean that the Bosnian type had the transformed karyotype. On the other hand, the converse transformation is possible, so it is difficult to say which is the primary form. More detailed phenotype analysis will show whether the A. agrarius from Bosnia represents a separate species or subspecies or whether the chromosome polymorphism should be ascribed only to lability of the karyotype resulting in a balanced translocation. [Abstract by GLW]

Sparkes, R. S. and D. T. Arakaki 1966. Intrasubspecific and intersubspecific chromosomal polymorphism in Peromyscus maniculatus (deer mouse). Cytogenetics 5:411-418. 100

Cytogenetic studies of three subspecies of the deer mouse, Peromyscus, maniculatus rubidus, P. m. gracilis and P. m. bairdii have demonstrated an intra- and intersubspecific chromosomal polymorphism in which the karyotypic patterns vary among individuals of the same and different subspecies while maintaining a diploid number of 48 and a constant karyotype in each animal. Present information suggests that pericentric inversion seems the best explanation for this polymorphism. [Authors' abstract]

Sparkes, R. S. and D. T. Arakaki 1971. Chromosome polymorphism in interbred subspecies of Peromyscus maniculatus (deer mouse). Can. J. Genet. Cytol. 13:277-282. 101

Karyotype analyses of eight animals from an interbreeding colony of three subspecies of Peromyscus maniculatus (P. m. gambelli, P. m. rabidus, and P. m. sonoriensis) demonstrated a chromosomal polymorphism, probably due to pericentric inversions involving at least seven chromosomes. This polymorphism may require consideration in the cytogenetic taxonomy of these animals, and may be related to the widespread distribution of deer mice in North America and their apparent adaptability to many different environments. [Authors' abstract]

Stock, A. D. 1975. Chromosome banding pattern homology and its phylogenetic implications in the bat genera Carollia and Choeroniscus. Cytogenetics and Cell Genetics, 14:34-41. 102

The chromosome banding patterns of the mitotic chromosomes of three species of Carollia and Choeroniscus intermedius was compared.

The G-band patterns of the Carollia species were similar but the C-band (heterochromatin) pattern of C. castanea (Peru) differed. The X-autosome translocation in C. perspicillata and C. brevicauda was compared to the untranslocated homologues in C. castanea (Peru).

The G- and C-banding patterns of Choeroniscus intermedius differed from that of the Carollia species and the placement of these genera into different subfamilies was supported. [Author's abstract]

Thaeler, C. S. Jr. 1968. Karyotypes of sixteen populations of the Thomomys talpoides complex of pocket gophers (Rodentia - Geomyidae). Chromosoma 25:172-183. 103

Chromosome material of mitotic bone marrow cells from 59 individuals representing 16 populations of Thomomys talpoides was studied. These populations were found in southern Wyoming, Colorado, northern New Mexico and northern Arizona. A limited amount of intrapopulation variation in form but not number of chromosomes was found. Eight distinct karyotypes were observed. These can be characterized by the following diploid numbers and fundamental numbers of chromosomes: 40(70), 44(70), 56(70), 60(70), 58(76), 48(78), 56(78) and 46(82). Among the six populations with 48 chromosomes some interpopulation variation was noted. In several instances karyotype differences coincided with populations that co-exist without interbreeding. [Author's abstract]

Thaeler, C. S. Jr. 1974. Four contacts betwen ranges of different chromosome forms of the Thomomys talpoides complex (Rodentia: Geomyidae). System. Zool. 23(3):343-354. 104

Contacts between the ranges of four pairs of different chromosome forms of pocket gophers of the Thomomys talpoides complex were studied in an effort to gain insight into the relationship between karyotype differences and level of evolutionary divergence. All contacts are located in the mountainous region of western Colorado. Three different results were found. At one contact no evidence of hybridization between the two chromosome forms was detected by an examination of karyotypes. At two other contacts limited hybridization occurs between the chromosome forms. The fourth contact studied is a broad zone of intergradation (20 miles or more in width) in which more or less unrestricted interbreeding occurs. A discussion of each contact area is presented and I conclude that frequently, though not always, karyotype differences in pocket gophers are indicative of species-level differences. [Author's abstract]

Tikhonov, V. N. and A. I. Troshina 1974. Identification of chromosomes and their aberrations in karyotypes of subspecies of Sus scrofa L. by differential staining. Doklady Biol. Science 214:45-47. 105

Investigations of the karyotype of four widely separated populations of wild boars showed that the diploid set of chromosomes varies from 36 to 38. Many boars from a central Asian population (24 animals) had 36 chromosomes whereas 2n=37 was found in smaller numbers in that population. No individuals having 2n=36 were found among boars of Far-Eastern, Transcaucasian, and western European populations. All homologous chromosomes of the karyotype could be identified by differential staining. [Abstract by GLW]

Valdez, R., C. F. Nadler, and T. D. Bunch 1978. Evolution of wild sheep in Iran. Evolution 32:56-72. 106

Eight populations of wild sheep (Ovis) throughout Iran were sampled and analyzed for chromosome pattern, horn configuration, pelage characteristics, fetal rates, and serum transferrin types. Individual populations from northwestern Iran, the Zagros Mountains, and Laristan uniformly exhibited a 2N of 54, and sheep from northeastern Iran displayed a 2N of 58. Sheep of the Central Alborz possessed 2N's ranging from 54-58 and were considered hybrids, as were sheep from the Kavir desert and the Kerman region, which had 2N's of 54 and 55.

Examination of pregnant ewes from the eastern region of the Central Alborz hybrid revealed 2N's of 56, 57 and 58. Fetal rates were similar to parental types with 2N's of 54 and 58. Morphological, chromosomal, and transferrin data suggest that Iranian sheep are classified most correctly as semispecies, or alternatively as subspecies, because they readily hybridize.

The Kavir population probably is derived from Central Alborz individuals which became isolated in the Kavir desert. The Esfahan and Laristan populations also may have been derived from isolated hybrid populations although a pure Armenian or urial origin is possible also. All these populations are characterized by homonymous horns, black ruffs and white saddle patches.

A tall vegetation barrier is hypothesized to have originally separated Armenian and urial populations in northern Iran. When this barrier disappeared due to drier climatic conditions, these populations met and hybridized. Populations in southern Iran also became isolated by vegetational barriers. The diverse phenotypic variability of Iranian wild sheep probably evolved within the last 15,000 years through hybridization coupled with founder events. [Authors' summary]

Venegas, W. 1974. Karyotypic variation in Phyllotis micropus micropus Waterhouse (Rodentia, Cricetidae). Bol. Soc. Biol. Concepcion 48:69-76 107

The karyologic results obtained from the study of 5 populations of P. micropus micropus are presented. The specimens were captured with Sherman traps in the provinces of Nuble, Malleco and Aysen [Chile]. Females and males (14) were analyzed cytogenetically using routine techniques and bone marrow cultures. A diploid number of 2n = 32 chromosomes with a N.F. [chromosome arm number] = 34 was found in the specimens of 2 populations from the province of Nuble, while a diploid number of 2n = 34 chromosomes with a N.F. = 36 was found in specimens of one population from the province of Malleco and 2 populations from the province of Aysen. The intrasubspecific karyotypic variability found may indicate a speciation process. [Abstract from Biological Abstracts]

Warner, J. W. 1976. Chromosomal variation in the plains woodrat: Geographical distribution of three chromosomal morphs. Evolution 30(3): 592-598. 108

Four hundred and twenty-eight specimens of Neotoma micropus from throughout the species range were karyotypically analyzed. There was noticeable variation in the occurrence of the three morphs within various populations. However, chi-square tests indicate that they were in a state of equilibrium in each population. Statistical analyses of cranial morphometrics revealed little significant difference among the three morphs based on the variables used. There is evidence that this system conforms to White's model for stasipatric speciation. Also one can speculate that it may eventually fit Brown's model for centrifugal speciation. [Author's summary]

Wentworth, F. A., D. A. Sutton 1969. Chromosomes of the townsend pocket gopher, Thomomys townsendii. Southwestern Naturalist 14(2):157-161. 109

Animals were collected, subjected to in vivo colchicine treatment and red bone marrow cells were stained with giemsa. Photomicrographs and karyograms were prepared for all seven subspecies of the Townsend pocket gopher, Thomomys townsendii. A diploid chromosome number of 76 was found for six subspecies. T. t. bachmani, T. t. elkoensis, T. t. nevadensis, T. t. owyhensis, T. t. relictus and T. t. townsendii. The seventh subspecies, T. t. similis, has a 2n chromosome number of 40 which, along with other unique morphological traits, indicates either confusion with the Thomomys talpoides complex or consideration of taxonomic revision to Thomomys similis. [Authors' abstract]

White, M. J. D. 1978. Chain processes in chromosomal speciation. Syst. Zool. 27(3):285-298. 110

In many groups of animals of restricted vagility very closely related species not only differ in karyotype, but exhibit very extensive differences, due to the establishment of "chains" of several or many structural chromosomal changes. These cases which until recently appeared anomalous or inexplicable, can now be used to interpret a basic feature of the "stasipatric" mode of speciation (parapatric speciation of some authors). It is suggested that an important reason for the establishment of these chromosomal rearrangements is their role in protecting coadapted gene complexes ("area effects") from disruption by introgression from neighboring populations. A model, based on the mouse (Mus musculus) populations of Italy and Switzerland studied by E. Capanna, A. Gropp, and their collaborators, is proposed, it relies on sequential establishment of chromosomal rearrangements, each within the range of the previous one. By this means the genetic isolation of the area population is progressively reinforced. [Author's abstract]

Wroblewski, R. and D. Dziekanowska 1968. Karyology of primates. Prezegl. Zool. 12(2):127-140. 111

A review of chromosome numbers and karyotype data is given for 116 spp. and subspecies of Primates. Analysis of chromosome complements indicate that polyploidy did not play any role in the karyological differentiation of this group. The Robertsonian type of centric fusions and other chromosomal arrangements are considered as possible factors in evolution of Primate karyotypes. A significance of karyological studies for taxonomic and phylogenetic cosiderations is discussed too. [Abstract from Biological Abstracts]

Wurster, D.H. and N.B. Atkin 1972. Muntjac chromosomes: A new karyotype for Muntiacus muntjak. Experientia 28(8):972-973. 112

There are eight listed subspecies of the Indian muntjac (Muntiacus muntjak). The diploid number of chromosomes in M. muntjak vaginalis is 7 in the male and 6 in the female; both sexes carry an X autosome translocation. Tissue culture preparations of a female M. muntjak muntjak show a diploid number of 8 with an X to autosome translocation. A diploid number of 9 would be expected in the male of this subspecies.

The karyotype differences between theses subspecies are pronounced enough that one would predict synaptic incompatibility in meiotic division of a hybrid offspring, thus conferring sterility on this individual. It is possible that a taxonomic revision should be considered and that either subspecies muntjak or subspecies vaginalis should receive full species status. Possible evolutionary significance with other species in the same genus is also discussed. [Abstract by GLW]

Wurster, D. H. and K. Benirschke, 1968. Chromosome studies in the superfamily Bovoidea. Chromosoma 25:152-171. 113

The chromosome morphology of about 50 species of Bovoidea has now been investigated. Although the diploid number varies from 30 to 60 among these species, the fundamental number(NF) varies only (with but three exceptions) from 58 to 62. This indicates an almost exclusive use of the Robertsonian fusion mechanism of karyotype evolution in this group of species which represent 30 different genera. All known cytogenetic information on the Bovoidea has been summarized and a complete bibliography is presented for each species. Karyotypes and data on a number of previously unstudied species are presented. [Authors' abstract]

Yosida, T. H. 1977. Frequencies of chromosome polymorphism in pairs no. 1, 9, and 13 in three geographical variants of black rats, Rattus rattus. Chromosoma 60:391-398. 114

Frequencies of the acrocentric and subtelocentric polymorphism in pairs no. 1, 9 and 13 chromosomes have been examined in 358 black rats, Rattus rattus, distributed over several countries of Asia, Australia and United States. The black rats are divided into three geographical types by the different chromosome numbers, such as Asian (2n=42), Ceylon (2n=40) and Oceanian types (2n=38). Pairs no. 13 polymorphism was found widely in these all types, but the pair no. 1 and 9 polymorphisms were found in only Asian type black rats. In the Asian type rats, however, those distributed in northern India and Pakistan showed always the subtelocentric pairs no. 1 and 9 like as those in Ceylon and Oceanian type black rats. This finding supports that the Ceylon and Oceanian type rats have developed in India or Pakistan from the Asian type. The present study also suggests that inversion of the pair no. 13 could have occurred in earlier period than those of the pairs no. 1 and 9. [Author's abstract]

Yosida, T. H. and K. Amano 1965. Autosomal polymorphism in laboratory bred and wild Norway rats, Rattus norvegicus, found in Misima. Chromosoma 16:658-667. 115

Polymorphism in chromosome pair no. 3 of Rattus norvegicus was found in laboratory strains and wild rats. Some of the animals had a subtelocentric pair no. 3, while others had a telocentric pair no. 3. 14 inbred strains were classified into two types concerning the pair no. 3.

1. YOS-type (characterized by a subtelocentric pair no.3): ACI-, Albany-, Buffalo-, CW-, Fisher-, Long-Evans-, NIG-IV-, Wayne pinkeyed hooded-, WKA- and YOS-strains belong to this type.
2. WIS-type (characterized by a telocentric pair no.3): Donryu-, NIG-III-, W/T- and WIS-strains are included in this type.

F_1 hybrids between YOS- and WIS-strain rats had a heteromorphic pair no.3 consisting of a telocentric and a subtelocentric chromosomes.

Polymorphism in pair no. 3 was also found in 43 wild rats collected in Misima. They were classified into three types concerning pair no. 3. Among 43 rats, 17 were WIS-type, 3 were YOS-type and the remaining 23 were of hybrid-type. [Authors' summary]

Yosida, T. H., H. Kato, K. Tsuchiya and K. Moriwaki 1971. Karyotypes and serum transferrin patterns of hybrids between Asian and Oceanian black rats, Rattus rattus. Chromosoma 34:40-50. 116

Karyotypes and serum transferrin patterns were examined in Asian and Oceanian black rats (R. rattus). Japanese R. r. tanezumi and Malayan R. r. diardii had 2n=42, but Australian and New Guinea R. r. rattus showed 2n=38 chromosomes. F_1 hybrids between Japanese and Australian rats and Malayan and New Guinea rats had 2n=40 chromosomes which consists of the two genomes of both parents. Although various matings betwen the F_1 hybrids were made, only one F_2 male rat with 2n=39 chromosomes was obtained. The F_1 hybrids seem to be semisterile. Parental transferrin phenotypes were TfR in Japanese rats and TfCD in Oceanian rats. F_1 hybrids examined showed TfRD in both male and female and F_2 hybrid had TfR type transferrin. Based on the above investigations, it is suggested that Asian and Oceanian black rats are geographically isolated and evolved different chromosomal and serum transferrin characteristics, but the sexual isolation of the two groups is incomplete at the present time. [Authors' abstract]

Yosida, T. H., H. Kato, K. Tsuchiya, T. Sagai, and K. Moriwaki 1972 Ceylon Population of black rats with 40 diploid chromosomes. Jap. J. Genet. 47(6):451-454. 117

F_1 hybrids between Asian and Oceanian black rats had 40 chromosomes in diploid number, but the karyotype was usually a composite consisting of two genomes of Asian and Oceanian black rats. F_2 rats obtained from F_1 hybrids in the laboratory and in natural population in Eniwetok island had 2n=39. The chromosome number of all Ceylon black rats was 40 and the karyotype was well balanced consisting of all homozygous pairs. The karyotype of the Ceylon black rats with one large metacentric pair developed by Robertsonian fusion of pairs No. 11 and 12 should be a transient type from Asian to Oceanian black rats and by the following Robertsonian fusion of pairs No. 4 and 7 the Oceanian type black rat with 2n=38 could occur somewhere in the Southwest Asia, and then they migrated to Europe as we already suggested (Yosida et al. 1972). [Authors' summary]

Yosida, T. H., H. Kato, K. Tsuchiya, T. Sagai, and K. Moriwaki 1974. Cytogenetical Survey of black rats, Rattus rattus, in southwest and central Asia, with special regard to the evolutional relationship between three geographical types. Chromosoma 45:99-109. 118

A chromosome survey of the black rat, Rattus rattus, was made from animals collected at different localities in Southwest and Central Asia. Asian type black rats (2n=42) were distributed in northern India, northern Pakistan, while the Oceanian type rats (2n=38) were found in southern India, southern Pakistan and Central Asia. A border line of distribution of rats with Asian and Oceanian types can be drawn dividing India and Pakistan into northern and southern parts. A hybrid type betwen Asian and Oceanian types was found in Karachi, Pakistan. Rats with 40 chromosomes, probably a transient type from Asian to Oceanian type, were found in Sri Lanka (Ceylon). It is suggested that these three geographic variants have developed via sequential events of Robertsonian fusion of acrocentric chromosomes in Asian type black rats. This fusion probably took place somewhere in southern India. The Oceanian type black rats that thus developed in southern India migrated widely to the rest of the world through Central Asia and Europe accompanying the movement of mankind. [Authors' abstract]

Yosida, T. H., A. Nakamura, and T. Fukaya 1965. Chromosomal polymorphism in Rattus rattus (L.) collected in Kusudomari and Misima. Chromosoma 16:70-78. 119

Chromosomes of Rattus rattus (L.), collected in Kusudomari (Nagasaki) and Misima (Sizuoka) were examined. The karyotype revealed a remarkable heteromorphism in chromosome no. 1. The homozygotic, i.e., standard type, was characterized by 13 pairs of telocentric and 7 pairs of metacentric chromosomes. Chromosome pair no. 1 was telocentric. X and Y chromosomes were also telocentrics. 18.4 per cent of rats from Kusudomari and 40 per cent from Misima showed heteromorphic pair in chromosome no. 1. One chromosome of the heteromorphic pair is conspicuous by the subtelocentric centromere. Total length of the telocentric chromosome of no. 1 is almost the same as of its subtelocentric partner. These facts indicate that the subtelocentric no. 1 chromosome might have arisen by a centromeric inversion of the telocentric chromosome. Individuals homozygous for the subtelocentric no.1 chromosome could not be found in either population. The difference in the frequency of the dimorphics collected in Kusudomari and Misima was statistically significant. Possible causes of the difference are discussed. [Authors' summary]

Yosida, T. H. and T. Sagai 1972. Banding pattern analysis of polymorphic karyotypes in the black rat by a new differential staining technique. Chromosoma 37:387-394. 120

Polymorphic karyotypes of black rats (Rattus rattus) collected in Japan, Australia and India were analysed by a new differential staining technique by which banding patterns in the metaphase chromosomes are revealed. The technique consists in two steps: immersion of slides in a mixture of 2 X SSC and 0.1% (w/v) SDS (sodium dodecyl sulfate) for a few seconds at room temperature, and staining in Giemsa. By this treatment characteristic banding patterns were obtained in each chromosome pair. From the banding pattern analysis, subtelocentric pairs No. 1 and 9, which are polymorphic in respect to the acrocentrics and the subtelocentrics, were proven to have originated by pericentric inversion in the acrocentrics. The origin of two large metacentrics observed in Australian and Indian black rats was confirmed to have been developed by Robertsonian fusion of the acrocentrics No. 4 and 7 and No. 11 and 12 present in the Asian type black rat. [Authors' abstract]

Yosida, T. H. and T. Sagai 1973. Similarity of Geimsa banding patterns of chromosomes in several species of the genus Rattus. Chromosoma 41:93-101. 121

Geimsa banding patterns of chromosomes in seven Rattus species were compared. Four species (R. rattus tanezumi, R. norvegicus, R. exulans and R. meulleri) had all 2n=42 and their karyotypes and banding patterns were similar, although slight differences were observed. Another subspecies (R. rattus rattus) and two other species (R. fuscipes and R. conatus) had fewer chromosomes than the above species by having large biarmed chromosomes developed probably by Robertsonian fusion. The origin of the arms of biarmed chromosomes was recognized by their characteristic banding patterns. The remaining species, R. sabanus, had a karyotype markedly different from the other species by having two small metacentrics although in the others their number was 7. Banding patterns of the chromosomes in this species, however, were also very similar to those of the other, and therefore the 7 small metacentrics seemed to have orginated by pericentric inversion of small acrocentrics. [Authors' abstract]

Yosida, T. H. and T. Sagai 1975. Variation of C-bands in the chromosomes of several subspecies of Rattus rattus. Chromosoma 50:283-300. 122

All subspecies of black rats (Rattus rattus) used in the present study are characterized by having large and clear C-bands at the centromeric region. The appearance of the bands, however, is different in the subspecies. Chromosome pair No. 1 in Asian type black rats (2n=42), which are characterized by an acrocentric and subtelocentric polymorphism, showed C-band polymorphism. In Philippine rats (R. rattus mindanensis) the pair was subtelocentric with C-bands, but in Malayan black rats (R. rattus diardii) it was usually acrocentric with C-bands. In Hong-Kong (R. rattus flavipectus) and Japanese black rats (R. rattus tanezumi) it was polymorphic with respect to the presence of acrocentrics with C-bands or subtelocentrics without C-bands. The other chromosome pairs showed clear C-bands, but in Hong-Kong black rats the pairs No. 2 and 5 were polymorphic with and without C-bands. In Japanese black rats, 6 chromosome pairs (No. 3, 4, 7, 9, 11 and 13) were polymorphic in regard to presence and absence of C-bands, but the other 5 chromosome pairs (No. 2, 5, 6, 8 and 10) showed always absence of C-bands. Only pair No. 12 usually showed C-bands. C-bands in small metacentric pairs (No. 14 to 20) in Asian type black rats were generally large in size, but those in the Oceanian (2n=38) and Ceylon type black rats (2n=40) were small. In the hybrids between Asian and Oceanian type rats, heteromorphic C-bands, one large and the other small, were observed. Based on the consideration of karyotype evolution in the black rats, the C-band is suggested to have a tendency toward the diminution as far as the related species are concerned. [Authors' abstract]

Yosida. T. H., K. Tsuchiya, H. Imai, and K. Moriwaki 1969. New chromosome types of the black rat, Rattus rattus, collected in Oceania and F_1 hybrids between Japanese and Australian Rats. Jap. J. Genet. 44(2):89-91. 123

A new chromosome type of the black rat, Rattus rattus, was found in an Oceanian population. They showed 38 chromosomes, among which two large metacentric chromosomes were noted. The chromosomes of black rats, Rattus rattus, coming from Japan as well as from many other countries in South East Asia showed 43 chromosomes (Yosida et al. unpublished). If normal segregation of the chromosome types can be obtained in the F_2 progenies, it might be assumed that these two groups in Japan and Oceania are derived from a common ancestor and the process is attributable to a polymorphic chromosome alteration.

Meiotic behaviour of chromosomes in F_1 animals and test crosses are under investigation. [Authors' summary]

Yosida, T. H., K. Tsuchiya, and K. Moriwaki 1971. Karyotypic differences of black rats, Rattus rattus, collected in various localities of east and southeast Asia and Oceania. Chromosoma 33(3):252-267. 124

Karyotypes of several subspecies of black rats, Rattus rattus, collected in different localities of Asia and Oceania were examined with special emphasis on the relationship between the chromosome polymorphism and differentiation of the subspecies. Subspecies of black rats (R. rattus) collected were as follows: tanezumi jalorensis from Japan; flavipectus and sladeni from Hong Kong; diardii from Kuala Lumpur, Malaysia; argentiventer from Kuala Lumpur, and Java and Celebes, Indonesia; mindanensis from Luzon and Mindanao, Phillipines; and rattus from Australia, New Zealand, and New guinea. Subspecies in Formosa, Korea and Thailand were not determined. All black rats collected in the above Asian districts had 42 diploid chromosomes, while those in Oceania had 38. The rats collected in Japan (tanezumi), Korea, Formosa, Thailand and Malaysia (diardii) had A/A No. 1 pair or polymorphic No. 1 (A/A, A/S and S/S) pairs, while those collected in Java and Celebes (argentiventer), Luzon and Mindanao (mindanensis) showed a higher frequency of S/S No 1. pair. From the higher occurrence of No.1 A/A pair of black rats in the Asian continent where the black rats originated, it is suggested that the original type of No. 1 chromosome pair of the black rats is A/A, and a pericentric inversion occurred in the acrocentric No. 1 chromosome and thus rats with subtelocentric No. 1 pair formed.--Black rats with 38 chromosomes were observed in Australia, New Guinea and New Zealand. These karyotypes seem to have developed by Robertsonian fusion of 4 acrocentric pairs (No. 4 and 7, and No. 11 and 12) in black rats of the Asian type. A relationship between body size and chromosome constitution was observed in subspecies of the black rats. [Authors' abstract]

Zartman, D. L. and A. N. Bruere 1974. Giemsa banding of the chromosomes of the domestic sheep (Ovis aries). Can. J. Genet. Cytol. 16:555-564. 125

A Giemsa banding procedure was used to construct a basic G-band idiogram for the domestic sheep. The idiogram is labelled in a systematic manner according to the routine recommended for human chromosomes. This pattern based on NaOH treatment, provides a standard of comparison for further studies on intra- and interspecific chromosome homologies in addition to identification of chromosomal abnormalities.

Late replicating regions of chromosomal DNA were detected with tritiated thymidine. Partial homologies between G-bands and these late replicating areas were found. Previously reported areas of prevalent secondary constrictions were seen to coincide with late replicating, G-positive regions on the metacentric and X chromosomes. [Authors' abstract]

Zimmerman, E. G. and M. R. Lee 1968. Variation in chromosomes of the cotton rat, Sigmodon hispidus. Chromosoma 24:243-250. 126

Chromosomes were analyzed from 38 hispid cotton rats, currently assigned to the species Sigmodon hispidus, from populations in southeastern and western United States. Cotton rats from southeastern United States had a 2N of 52 and an F.N. which varied from 52 to 54. Specimens from Obion County, Tennessee, and Highlands County, Florida, were found to be polymorphic with a varying number of arms on the largest pair of autosomes. Cotton rats form Arizona had a 2N of 22 and an F.N. of 38; each pair of chromosomes is distinguishable, and a numbering system is proposed. The cytological data suggest that cotton rats from the southeastern populations and those from the Arizona populations belong to separate species, though morphological characters do not indicate such a difference. [Authors' abstract]

Zivkovic, S., B. Soldatovic, M. Milosevic, and I. Savic 1968. Analysis of chromosomes of three populations of Citellus citellus from Serbia. Zool. Anz. 181(3/4):181-185. 127

The chromosomes of 3 populations of European suslik from Serbia were studied. The diploid number of chromosomes in somatic cells of described populations is 2n = 40. The morphologically identical chromosome groups were found in all analyzed populations. Morphologic analysis made it possible to differentiate 4 groups of chromosomes by similarity. This classifications [sic.] could be helpful in further morphometric and comparative caryotypic investigation in the genus Citellus and the species Citellus citellus itself. [Abstract from Biological Abstracts]

APPENDIX A

Articles Relating to Cytogenetics of Subspecific Taxa

BADR, F. 0006

BADR, F. M. BADR, R. S.

1970

THE SOMATIC CHROMOSOMES OF A WILD POPULATION OF RATS: NUMERICAL POLYMORPHISM.
CHROMOSOMA 30 : 465- 475

BAKER, R 0007

BAKER, R. J. BLEIER, W. J. ATCHLEY, W. R.

1975

A CONTACT ZONE BETWEEN KARYOTYPICALLY CHARACTERIZED TAXA OF URODERMA BILOBATUM (MAMMALIA: CHIROPTERA)
SYST. ZOOL. 24 (2): 133- 142

BAKER, R 0008

BAKER, R. J. PATTON, J. L.

1967

KARYOTYPES AND KARYOTYPIC VARIATION OF NORTH AMERICAN VESPERTILINOID BATS.
J. MAMMALOGY 48 (2): 270- 286

BAVERSTO 0009

BAVERSTOCK, P. R. WATTS, C. H. S. HOGARTH, J. T.
ROBINSON, A. C. ROBINSON, J. F.

1977

CHROMOSOME EVOLUTION IN AUSTRALIAN RATS II. THE RATTUS GROUP
CHROMOSOMA 61 : 227- 241

BELCHEVA 0010

BELCHEVA, R. G. PESHEV, D. T.

1979

INTERSUBSPECIFIC SEX CHROMOSOME DIFFERENCE IN CITELLUS CITELLUS L. (RODENTIA, SCIURIDAE).
EXPERIENTIA 35 (5): 595- 596

BIANCHI, 0012

BIANCHI, N. O. PAULETE-VANRELL, J. DE VIDAL RIOJA, L.A.

1969

COMPLEMENT WITH 38 CHROMOSOMES IN TWO SOUTH AMERICAN POPULATIONS OF RATTUS RATTUS.
EXPERIENTIA 25 :1111-1112

BUETTNER 0020

BUETTNER-JANUSCH, J.HAMILTON, A. E.

1979

CHROMOSOMES OF LEMURIFORMES: IV. KARYOTYPE EVOLUTION IN LEMUR FULVUS COLLARIS (E. GEOFFROY, 1812).
AM. J. PHYS. ANTHROPOL. 50 (3): 363- 366

CAIRE, W 0027

CAIRE, W. ZIMMERMAN, E. G.

1973

CHROMOSOMAL AND MORPHOLOGICAL VARIATION AND CIRCULAR

OVERLAP IN THE DEER MOUSE, PEROMYSCUS MANICULATUS, IN TEXAS AND OKLAHOMA.
SYST. ZOOL. 24 (1): 89- 95

CAPANNA, 0028

CAPANNA, E. CIVITELLI, M. V. NEZER, R.
1970

THE KARYOTYPE OF THE BLACK RAT (RATTUS RATTUS): ANOTHER POPULATION WITH A 38-CHROMOSOME COMPLEMENT.
38-CHROMOSOME COMPLEMENT.
EXPERIENTIA 26 :422- 425
ARTICLE TRANSLATED FROM ITALIAN.

DAVIS, B 0031

DAVIS, B. L. BAKER, R. J.
1971

CHROMOSOME MORPHOLOGY OF NORTH AMERICAN RATTUS RATTUS (L.) (MURIDAE).
CYTOLOGIA 36 : 417- 420

DEV, V. 0032

DEV, V. G. MILLER, D. A. TANTRAVAHI, R.
SCHRECK, R. R. RODERICK, T. H. ERLANGER, B. F.
MILLER, O. J.
1975

CHROMOSOME MARKERS IN MUS MUSCULUS: DIFFERENCES IN C-BANDING BETWEEN THE SUBSPECIES M. M. MUSCULUS AND M. M. MOLOSSINUS.
CHROMOSOMA 53 : 335- 344

DUFFEY, 0033

DUFFEY, P. A.
1972

CHROMOSOME VARIATION IN PEROMYSCUS: A NEW MECHANISM.
SCIENCE 176 :1333-1334

DUTRILLA 0034

DUTRILLAUX, B. FOSSE, A. M. CHAUVIER, G.
1979

CYTOGENETIC STUDY OF SIx SPECIES OR SUBSPECIES OF MANGABEYS MONKEYS, PAPIINAE CERCOPITHECIDAE.
ANN. GENET. 22 (2): 88- 92
ARTICLE IN FRENCH WITH ENGLISH SUMMARY.

DUTRILLA 0035

DUTRILLAUX, B. RUMPLER, Y.
1977

CHROMOSOMAL EVOLUTION IN MALAGASY LEMURS: II. MEIOSIS IN INTRA- AND INTERSPECIFIC HYBRIDS IN THE GENUS LEMUR.
CYTOGENET. CELL GENET. 18 (4): 197- 211

ELDER, F 0036

ELDER, F. F. B.
1978

CHROMOSOMAL EVOLUTION OF THE COTTON RATS, GENUS SIGMODON (RODENTIA, MURIDAE).

DISS. ABSTR. 39 (5): 2171-B

FRECHETT0039

FRECHETTE, A. G. JALAL, S. M.

1971

KARYOLOGICAL STUDY OF TWO SUBSPECIES OF THE RED BACKED VOLE.
MAMM. CHROM. NEWSL. 12 : 38- 39

GLADKINA0042

GLADKINA, T. S.

1972

GEOGRAPHICAL VARIABILITY OF TWO SUBSPECIES OF COMMON VOLE, (MICROTUS ARVALIS).
ZOOL. ZH 51 (2): 267- 279
ARTICLE IN RUSSIAN WITH ENGLISH SUMMARY.

GREENBAU0044

GREENBAUM, I. F. BAKER, R. J. RAMSEY, P. R.

1978

CHROMOSOMAL EVOLUTION AND THE MODE OF SPECIATION IN THREE SPECIES OF PEROMYSCUS.
EVOLUTION 32 (3): 646- 654

GROPP, A0045

GROPP, A. MARKWONG, A MARSHALL, J. KIM, Y. J.

1972

ROBERTSONIAN CHROMOSOMAL VARIATION IN THE LONGTAILED TREE MOUSE (VANDELEURIA).
Z. ZOOL. SYST. EVOLUTIONSFORSCH 10 (3): 210- 214

GROPP, A0046

GROPP, A. MARSHALL, J. MARKWONG, A.

1973

CHROMOSOMAL FINDINGS IN THE SPINY MICE OF THAILAND (GENUS MUS) AND OCCURRENCE OF A COMPLEX INTRASPECIFIC VARIATION IN M. SHORTRIDGEI.
Z. SAUGETIERKUNDE 38 (3): 159- 168

HSU, T. 0052

HSU, T. C. ARRIGHI, F. E.

1968

CHROMOSOMES OF PEROMYSCUS (RODENTIA, CRICETIDAE) 1. EVOLUTIONARY TRENDS IN 20 SPECIES.
CYTOGENETICS 7 : 417- 446

KATO, H. 0055

KATO, H. TSUCHIYA, K. YOSIDA, T. H.

1974

CONSTITUTIVE HETEROCHROMATIN OF INDIAN MUNTJAC CHROMOSOMES REVEALED BY DNASE TREATMENT AND A C-BANDING TECHNIQUE.
CAN. J. GENET. CYTOL. 16 : 273- 280

KOZLOVSK 0058

KOZLOVSKII, A. I.

1974

KARYOLOGICAL DIFFERENTIATION OF NORTH AMERICAN SUBSPECIES OF HOOFED LEMMINGS.
DOKLADY BIOL. SCIENCE 219 : 499- 502

KOZLOVSKII, A. I. ORLOV, V. N. KOZLOVSK 0059
1971
KARYOLOGICAL EVIDENCE FOR SPECIES INDEPENDENCE OF SOREX ISODON TUROV (SORICIDAE, INSECTIVORA).
ZOOL. ZH. 50 (7):1056-1062

KRAL, B. VON LEHMANN, E. ZEJDA, J. KRAL, B. 0060
1972
THE HYBRIDS OF TWO SUBSPECIES OF THE RED-BACKED VOLE.
ZOOL. LISTY 21 (1): 43- 61
ARTICLE IN GERMAN WITH ENGLISH SUMMARY.

KULIEV, G. N. KULIEV, G. K. RADZHABLI, S. I. KULIEV, 0061
1978
KARYOTYPE DIFFERENCES BETWEEN POPULATIONS OF THE WATER VOLE, ARVICOLA TERRESTRIS (ROUENTIA, CRICETIDAE).
ZOOL. ZH 57 (9):1409-1411

LAKHOTIA, S. C. RAO, S. R. V. JHANWAR, S. C. LAKHOTIA 0062
1973
STUDIES OF RODENT CHROMOSOMES VI. COEXISTENCE OF RATTUS RATTUS WITH 38 AND 42 CHROMOSOMES IN SOUTHWESTERN INDIA.
CYTOLOGIA 38 : 403- 410

LEE, M. R. SCHMIDLY, D. J. HUHEEY, C. C. LEE, M. 0064
1972
CHROMOSOMAL VARIATIONS IN CERTAIN POPULATIONS OF PEROMYSCUS BOYLII AND ITS SYTEMATIC IMPLICATIONS.
J. MAMMALOGY 53 (4): 697- 707

MALYGIN, V. M. MALYGIN, 0066
1970
THE SYSTEMATICS OF THE SUBSPECIES OF THE COMMON FIELD MOUSE.
VESTNIK MOSKOVSKOGO UNIVERSITETA SERIYA V BIOLOGIYA POCHVOVEDENIE 25 (5): 89- 91
ARTICLE TRANSLATED FROM RUSSIAN.

MEIER, M.N. MEIER, M 0072
1968
COMPLEX TAXONOMIC ANALYSIS OF THE SPECIES BASED ON THE STUDY OF COMMON VOLES (GENUS MICROTUS).
ZOOL. ZH 47 (6): 850- 859

MEIER, M.N. ORLOV, V.N. SKHOOL, E.D. MEIER, M 0073

1969
USE OF DATA ON KARYOLOGICAL, PHYSIOLOGICAL AND CYTOPHYSIOLOGICAL ANALYSES FOR ISOLATING A NEW SPECIES OF RODENT (RODENTIA, MAMMALIA).
DOKLADY AKAD. NAUK. SSSR 188 (6):1411-1414

NADLER, 0077
NADLER, C. F. LAY, D. M. HASSINGER, J. D.
1971
CYTOGENETIC ANALYSES OF WILD SHEEP POPULATIONS IN NORTHERN IRAN.
CYTOGENETICS 10 : 137- 152

NELSON-R 0078
NELSON-REES, W. A. KNIAZEFF, A. J. BAKER, R. J.
PATTON, J. L.
1968
INTRASPECIFIC CHROMOSOME VARIATION IN THE BAT, MACROTUS WATERHOUSII GRAY.
J. MAMMALOGY 49 (4): 706- 712

PATTON, 0081
PATTON, J. L.
1972
PATTERNS OF GEOGRAPHIC VARIATION IN KARYOTYPE IN THE POCKET GOPHER, THOMOMYS BOTTAE (EYDOUX AND GERVAIS).
EVOLUTION 26 : 574- 586

RAMAN, R 0083
RAMAN, R. SHARMA, T.
1972
SIMILARITY IN KARYOTYPES OF RATTUS RATTUS WITH 38 CHROMOSOMES FROM INDIA AND OTHER PARTS OF THE WORLD.
EXPERIENTIA 28 :1375-1377

RAUSCH, 0084
RAUSCH, R. L. RAUSCH, V. R.
1972
OBSERVATIONS ON CHROMOSOMES OF DICROSTONYX TORQUATUS STEVENSONI NELSON, AND CHROMOSOMAL DIVERSITY IN VARYING LEMMINGS.
Z. SAUGETIERKUNDE 37 : 372- 384

RAUSCH, 0085
RAUSCH, R. L. RAUSCH, V. R.
1975
RELATIONSHIPS OF THE RED-BACKED VOLE, CLETHRIONOMYS RUTILUS (PALLAS), IN NORTH AMERICA: KARYOTYPES OF THE SUBSPECIES DAWSONI AND ALBIVENTER.
SYST. ZOOL. 24 (2): 163- 170

REIG, O. 0086
REIG, O. A. PINCHEIRA, J. V. SPOTORNO, A. O.
WALLER, P.
1972
NEW EVIDENCE OF A 38-CHROMOSOME KARYOTYPE IN SOUTH AMERICAN POPULATIONS OF ROOF RAT, RATTUS RATTUS L. (RODENTIA,

MURIDAE).
EXPERIENTIA 28 (2): 225- 227

ROBINSON0087

ROBINSON, T. J. SKINNER, J. D.
1976

A KARYOLOGICAL SURVEY OF SPRINGBOK SUBSPECIES.
S. AFRICAN J. SCIENCE 72 : 147- 148.

SCHMIDLY0088

SCHMIDLY, D. J. SCHROETER, G. L.
1974

KARYOTYPIC VARIATION IN PEROMYSCUS BOYLII (RODENTIA: CRICETIDAE) FROM MEXICO AND CORRESPONDING TAXONOMIC IMPLICATION.
SYST. ZOOL. 23 : 333- 342

SHARMA, 0095

SHARMA, T. GARG, G. S.
1975

CONSTITUTIVE HETEROCHROMATIN AND KARYOTYPE VARIATION IN INDIAN PYGMY MOUSE, MUS DUNNI.
GENET. RES. 25 : 189- 191

SINGH, R0097

SINGH, R. P. MCMILLAN, D. B.
1966

KARYOTYPES OF THREE SUBSPECIES OF PEROMYSCUS.
J. MAMMALOGY 47 (2): 261- 266

SOKOLOV, 0098

SOKOLOV, V.E. ORLOV, V. N. CHUDINOVSKAYA, G. A.
DANILKIN, A. A.
1978

CHROMOSOMAL DIFFERENCES BETWEEN TWO SUBSPECIES OF ROE DEER, CAPREOLUS CAPREOLUS CAPREOLUS L. AND C. C. PYGARGUS PALL.
ZOOL. ZH. 57 (7):1109-1112

SOLDATOV0099

SOLDATOVIC, B. DJULIC, B. SAVIC, I.
RIMSA, D.
1969

CHROMOSOMES OF TWO SPECIES OF THE GENUS APODEMUS (A. AGRARIUS AND A. MYSTACINUS - MAMMALIA, RODENTIA) FROM YUGOSLAVIA.
ARHIV. BIOL. SCI. 21 (1): 27- 32

SPARKES, 0100

SPARKES, R. S. ARAKAKI, D. T.
1966

INTRASUBSPECIFIC AND INTERSUBSPECIFIC CHROMOSOMAL POLYMORPHISM IN PEROMYSCUS MANICULATUS (DEER MOUSE).
CYTOGENETICS 5 : 411- 418

SPARKES, 0101

SPARKES, R. S. ARAKAKI, D. T.
1971

CHROMOSOME POLYMORPHISM IN INBRED SUBSPECIES OF PEROMYSCUS MANICULATUS (DEER MOUSE).
CAN. J. GENET. CYTOL. 13 : 277- 282

THAELER, C. S. JR. THAELER,0103

1968

KARYOTYPES OF SIXTEEN POPULATIONS OF THE THOMOMYS TALPOIDES COMPLEX OF POCKET GOPHERS (RODENTIA - GEOMYIDAE).
CHROMOSOMA 25 : 172- 183

THAELER, C. S. JR. THAELER,0104

1974

FOUR CONTACTS BETWEEN RANGES OF DIFFERENT CHROMOSOME FORMS OF THE THOMOMYS TALPOIDES COMPLEX (RODENTIA: GEOMYIDAE).
SYST. ZOOL. 23 (3): 343- 354

TIKHONOV, V. N. TROSHINA, A. I. TIKHONOV0105

1974

IDENTIFICATION OF CHROMOSOMES AND THEIR ABERRATIONS IN KARYOTYPES OF SUBSPECIES OF SUS SCROFA L. BY DIFFERENTIAL STAINING.
DOKLADY BIOL. SCIENCE 214 : 45- 47

VALDEZ, R. NADLER, C. F. BUNCH, T. D. VALDEZ, 0106

1978

EVOLUTION OF WILD SHEEP IN IRAN.
EVOLUTION 32 : 56- 72

VENEGAS, W VENEGAS, 0107

1974

KARYOTYPIC VARIATION IN PHYLLOTIS MICROPUS MICROPUS WATERHOUSE (RODENTIA, CRICETIDAE).
BOL. SOC. BIOL. CONCEPCION 48 : 69- 76

WENTWORTH, F. A. SUTTON, D. A. WENTWORT 0109

1969

CHROMOSOMES OF THE TOWNSEND POCKET GOPHER, THOMOMYS TOWNSENDII.
SOUTHWESTERN NATURALIST 14 (2): 157- 161

WROBLEWSKI, R. DZIEKANOWSKA, D. WROBLEWS 0111

1968

KARYOLOGY OF PRIMATES.
PREZEGL. ZOOL. 12 (2): 127- 140

WURSTER, D. H. ATKIN, N. B. WURSTER, 0112

1972

MUNTJAC CHROMOSOMES: A NEW KARYOTYPE FOR MUNTIACUS MUNTJAK.
EXPERIENTIA 28 (8): 972- 973

YOSIDA, 0114

YOSIDA, T. H.

1977

FREQUENCIES OF CHROMOSOME POLYMORPHISM IN PAIRS NO. 1, 9, AND 13 IN THREE GEOGRAPHICAL VARIANTS OF BALCK RATS, RATTUS RATTUS.

CHROMOSOMA 60 : 391- 398

YOSIDA, 0116

YOSIDA, T. H. KATO, H. TSUCHIYA, K.
MORIWAKI, K.

1971

KARYOTYPES AND SERUM TRANSFERRIN PATTERNS OF HYBRIDS BETWEEN ASIAN AND OCEANIAN BLACK RATS, RATTUS RATTUS.

CHROMOSOMA 34 : 40- 50

YOSIDA, 0117

YOSIDA, T. H. KATO, H. TSUCHIYA, K.
SAGAI, T. MORIWAKI, K.

1972

CEYLON POPULATION OF BLACK RATS WITH 40 DIPLOID CHROMOSOMES.

JAP. J. GENET. 47 (6): 451- 454

YOSIDA, 0118

YOSIDA, T. H. KATO, H. TSUCHIYA, K.
SAGAI, T. MORIWAKI, K.

1974

CYTOGENETICAL SURVEY OF BLACK RATS, RATTUS RATTUS, IN SOUTHWEST AND CENTRAL ASIA, WITH SPECIAL REGARD TO THE EVOLUTIONAL RELATIONSHIP BETWEEN THREE GEOGRAPHICAL TYPES.

CHROMOSOMA 45 : 99- 109

YOSIDA, 0119

YOSIDA, T. H. NAKAMURA, A. FUKAYA, T.

1965

CHROMOSOMAL POLYMORPHISM IN RATTUS RATTUS (L.) COLLECTED IN KUSUDOMARI AND MISIMA.

CHROMOSOMA 16 : 70- 78

YOSIDA, 0120

YOSIDA, T. H. SAGAI, T.

1972

BANDING PATTERN ANALYSIS OF POLYMORPHIC KARYOTYPES IN THE BLACK RAT BY A NEW DIFFERENTIAL STAINING TECHNIQUE.

CHROMOSOMA 37 : 387- 394

YOSIDA, 0122

YOSIDA, T. H. SAGAI, T.

1975

VARIATION OF C-BANDS IN THE CHROMOSOMES OF SEVERAL SUBSPECIES OF RATTUS RATTUS.

CHROMOSOMA 50 : 283- 300

YOSIDA, 0123

YOSIDA, T. H. TSUCHIYA, K. IMAI, H.
MORIWAKI, K.

1969

NEW CHROMOSOME TYPES OF THE BLACK RAT, RATTUS RATTUS, COLLECTED IN OCEANIA AND F1 HYBRIDS BETWEEN JAPANESE AND AUSTRALIAN RATS.
JAP. J. GENET. 44 (2): 89- 91

YOSIDA, 0124

YOSIDA, T. H. TSUCHIYA, K. MORIWAKI, K.

1971

KARYOTYPIC DIFFERENCES OF BLACK RATS, RATTUS RATTUS, COLLECTED IN VARIOUS LOCALITIES OF EAST AND SOUTHEAST ASIA AND OCEANIA.
CHROMOSOMA 33 (3): 252- 267

ZIMMERMA 0126

ZIMMERMAN, E. G. LEE, M. R.

1968

VARIATION IN CHROMOSOMES OF THE COTTON RAT, SIGMODON HISPIDUS.
CHROMOSOMA 24 : 243- 250

APPENDIX B

Articles Relating to Cytogenetic Analysis Used to Substantiate the Existence of a Full Species Where Only a Subspecies was Previously Thought to Exist

ELDER, F 0036

ELDER, F. F. B.

1978

CHROMOSOMAL EVOLUTION OF THE COTTON RATS, GENUS SIGMODON (RODENTIA, MURIDAE).
DISS. ABSTR. 39 (5): 2171-B

HSU, T. 0052

HSU, T. C. ARRIGHI, F. E.

1968

CHROMOSOMES OF PEROMYSCUS (RODENTIA, CRICETIDAE) 1. EVOLUTIONARY TRENDS IN 20 SPECIES.
CYTOGENETICS 7 : 417- 446

KOZLOVSK 0058

KOZLOVSKII, A. I.

1974

KARYOLOGICAL DIFFERENTIATION OF NORTH AMERICAN SUBSPECIES OF HOOFED LEMMINGS.
DOKLADY BIOL. SCIENCE 219 : 499- 502

KOZLOVSK 0059

KOZLOVSKII, A. I. ORLOV, V. N.

1971

KARYOLOGICAL EVIDENCE FOR SPECIES INDEPENDENCE OF SOREX ISODON TUROV (SORICIDAE, INSECTIVORA).
ZOOL. ZH. 50 (7):1056-1062

MALYGIN, 0066

MALYGIN, V. M.

1970

THE SYSTEMATICS OF THE SUBSPECIES OF THE COMMON FIELD MOUSE.
VESTNIK MOSKOVSKOGO UNIVERSITETA
SERIYA V BIOLOGIYA POCHVOVEDENIE 25 (5): 89- 91

MEIER, M 0072

MEIER, M.N.

1968

COMPLEX TAXONOMIC ANALYSIS OF THE SPECIES BASED ON THE STUDY OF COMMON VOLES (GENUS MICROTUS).
ZOOL. ZH 47 (6): 850- 859

MEIER, M 0073

MEIER, M.N. ORLOV, V.N. SKHOOL, E.D.

1969

USE OF DATA ON KARYOLOGICAL, PHYSIOLOGICAL AND CYTOPHYSIOLOGICAL ANALYSES FOR ISOLATING A NEW SPECIES OF RODENT (RODENTIA, MAMMALIA).
DOKLADY AKAD. NAUK. SSSR 168 (6):1411-1414

SOLDATOV 0099

SOLDATOVIC, B. DJULIC, B. SAVIC, I.

RIMSA, D.
1969
CHROMOSOMES OF TWO SPECIES OF THE GENUS APODEMUS (A. AGRARIUS AND A. MYSTACINUS - MAMMALIA, RODENTIA) FROM YUGOSLAVIA.
ARHIV. BIOL. SCI. 21 (1): 27- 32

WURSTER, 0112
WURSTER, D. H. ATKIN, N. B.
1972
MUNTJAC CHROMOSOMES: A NEW KARYOTYPE FOR MUNTIACUS MUNTJAK.
EXPERIENTIA 28 (8): 972- 973

ZIMMERMA0126
ZIMMERMAN, E. G. LEE, M. R.
1968
VARIATION IN CHROMOSOMES OF THE COTTON RAT, SIGMODON HISPIDUS.
CHROMOSOMA 24 : 243- 250

APPENDIX C

Articles Relating to Cytogenetics of Sibling Species

BAVERSTO 0009
BAVERSTOCK, P. R. WATTS, C. H. S. HOGARTH, J. T.

ROBINSON, A. C. ROBINSON, J. F.

1977
CHROMOSOME EVOLUTION IN AUSTRALIAN RATS II. THE RATTUS GROUP
CHROMOSOMA 61 : 227- 241

BENADO, 0011
BENADO, M. AGUILERA, M. REIG, O. A.
AYALA, F. J.

1979
BIOCHEMICAL GENETICS OF CHROMOSOME FORMS OF VENEZUELAN SPINY RATS OF THE PROECHIMYS GUAIRAE AND PROECHIMYS TRINITATIS SUPERSPECIES.
GENETICA 50 (2): 89- 97

GREENBAU 0043
GREENBAUM, I. F. BAKER, R. J. BOWERS, J. H.

1978
CHROMOSOMAL HOMOLOGY AND DIVERGENCE BETWEEN SIBLING SPECIES OF DEER MICE: PEROMYSCUS MANICULATUS AND PEROMYSCUS MELANOTIS (RODENTIA, CRICETIDAE).
EVOLUTION 32 (2): 334- 341

HAFNER, 0047
HAFNER, D. J. HAFNER, J. C. HAFNER, M. S.

1979
SYSTEMATIC STATUS OF KANGAROO MICE, GENUS MICRODIPODOPS: MORPHOMETRIC, CHROMOSOMAL, AND PROTEIN ANALYSES.
J. MAMMALOGY 60 (1): 1- 10

HALKKA, 0049
HALKKA, L. HALKKA, O.

1974
KARYOTYPE Q- AND G-BANDING IN THREE SPECIES OF THE GENUS SOREX.
HEREDITAS 78 (2): 314

KENNERLY 0056
KENNERLY, T. E. JR.

1959
CONTACT BETWEEN THE RANGES OF TWO ALLOPATRIC SPECIES OF POCKET GOPHERS.
EVOLUTION 13 : 247- 263

MALYGIN, 0067
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APPENDIX D

Articles Relating to Cytogenetics of Taxa at Specific (or higher) Levels

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HEREDITAS 64 : 237- 242.

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1974

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HEREDITAS 77 : 1- 36

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CHROMOSOMES TODAY 5 : 323- 329

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EVOLUTION 27 (3): 378- 386

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ZARTMAN, D. L. BRUERE, A. N.
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BRUERE, 0017

BRUERE, A. N. CHAPMAN, H. M. JAINE, P. M.

MORRIS, R. M.

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J. HEREDITY 67 : 149- 154

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BRUERE, A. N. MCLAREN, R. D.

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BRUERE, 0019

BRUERE, A. N. ZARTMAN, D. L. CHAPMAN, H. M.

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CYTOGENET. CELL GENET. 13 : 479- 488

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BUNCH, T. D.

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J. HEREDITY 69 : 77- 80

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J. HEREDITY 67 : 167- 170

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FOREJT, J.

1973

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CHROMOSOMA 43 (2): 187- 201

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1969

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J. REPROD. FERT. 18 : 9- 14

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SCHRODER, J. SUOMALAINEN, H. VAN DER LOO, W.
SCHRODER, E.

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1965

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APPENDIX F

Articles Relating to Individual and Intrapopulation Variability, and Sibling Diversity

ARAKAKI, D. T. VEOMETT, I. SPARKES, R. S. ARAKAKI,0001

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CRAIG-HOLMES, A. P. MOORE, F. B. SHAW, M. W. CRAIG-HO0029

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SCHRODER, E.

KARYOTYPES IN LYMPHOCYTES OF TWO STRAINS OF RABBIT, AND TWO 1978

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HEREDITAS 88 : 183- 188

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SHARMA, T. RAMAN, R.
1973
VARIATION OF CONSTITUTIVE HETEROCHROMATIN IN THE SEX CHROMOSOMES OF THE RODENT BANDICOTA BENGALENSIS BENGALENSIS (GRAY).
CHROMOSOMA 41 : 75- 84

WARNER, 0108

WARNER, J. W.
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EVOLUTION 30 (3): 593- 598

APPENDIX G

Articles Relating to C-Band (Constitutive Heterochromatin) Variability

ARRIGHI, 0005

ARRIGHI, F. E. STOCK, A. D. PATHAK, S.

1974

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CHROMOSOMES TODAY 5 : 323- 329

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AMER. J. HUMAN GENET. 25 : 181- 192

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1971

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SCIENCE 174 : 702- 704

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CHROMOSOMA 43 (2): 187- 201

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1978

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EVOLUTION 32 (3): 646- 654

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HSU, T. C. ARRIGHI, F. E.

1971

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CHROMOSOMA 34 : 243- 253

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JALAL, S. M. CLARK, R. W. HSU, T. C.
PATHAK, S.

1974

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1974

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EXPERIENTIA 30 (1): 90- 91

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1973

CHROMOSOMES OF PEROMYSCUS (RODENTIA, CRICETIDAE) IV. THE ROLE OF HETEROCHROMATIN IN KERYOTYPIC EVOLUTION.
CYTOGENET. CELL GENET. 12 : 315- 326

SEN, S. 0093

SEN, S. SHARMA, T.

1979

SPARSE DISTRIBUTION OF CONSTITUTIVE HETEROCHROMATIN AND ITS VARIATION IN TWO SPECIES OF MONGOOSES (CARNIVORA) WITH EXACT G-BAND HOMOLOGY.
GENETICA 50 (3): 221- 226

SHARMA, 0094

SHARMA, T. GADI, I. K.

1977

CONSTITUTIVE HETEROCHROMATIN VARIATION IN TWO SPECIES OF RATTUS WITH APPARENTLY SIMILAR KARYOTYPES.
GENETICA 47 (1): 77- 80

SHARMA, 0095

SHARMA, T. GARG, G. S.

1975

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GENET. RES. 25 : 189- 191

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1973

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CHROMOSOMA 41 : 75- 84

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1975

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CYTOGENETICS AND CELL GENETICS 14 : 34- 41

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1972

BANDING PATTERN ANALYSIS OF POLYMORPHIC KARYOTYPES IN THE BLACK RAT BY A NEW DIFFERENTIAL STAINING TECHNIQUE.

CHROMOSOMA 37 : 387- 394

YOSIDA, 0122

YOSIDA, T. H. SAGAI, T.

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CHROMOSOMA 50 : 283- 300

APPENDIX H

Articles Relating to Speciation and Chromosomal Evolution

ARNASON, 0003

ARNASON, U.

1972

THE ROLE OF CHROMOSOMAL REARRANGEMENT IN MAMMALIAN SPECIATION WITH SPECIAL REFERENCE TO CETACEA AND PINNIPEDIA.
HEREDITAS 70 (1): 113- 118

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1976

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CYTOGENET. CELL GENET. 17 : 122- 136

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1978

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PATTON, J. L.

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EVOLUTION 32 (3): 646- 654

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LAWLOR, T. E.

1974

CHROMOSOMAL EVOLUTION IN PEROMYSCUS.
EVOLUTION 28 (4): 689- 692

NEVO, E. 0079

NEVO, E. CLEVE, H.

1978

GENETIC DIFFERENTIATION DURING SPECIATION.
NATURE 275 : 125- 126

SCHRODER, J. ANTONI, J. VAN DER LOO, W. SCHRODER 0089

1978

COMPARISONS OF THE KARYOTYPES IN THE JACK RABBIT (LEPUS CALIFORNICUS DESERTICOLA) AND THE EUROPEAN HARE (LEPUS EUROPAEUS).

HEREDITAS 89 : 134- 135

WHITE, M. J. D. WHITE, M 0110

1978

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SYST. ZOOL. 27 (3): 258- 298