WHAT THIS ARTICLE IS ABOUT

Similarities in organisms are commonly interpreted as the result of a common ancestry. Since chromosomes are the carriers of heredity, similarities in chromosomes could have special significance in studying the ancestry and relationships of species. Many studies comparing chromosomal banding patterns have been conducted. Through the use of a special staining technique, chromosomes can be stained to show a pattern of alternating dark and light bands. The detail of the pattern depends on the length of the chromosome at the time it is stained. If sufficient detail is present, each pair of chromosomes in a cell can be distinguished. Chromosomes from different species can be stained and then compared and contrasted. Similarities and differences may be interpreted subsequently as reflecting the degree of relationship.

Although there are some interesting exceptions, comparisons of chromosomal banding patterns are generally consistent with comparisons based on other criteria. Species within a family generally show considerable matching of chromosome banding patterns. The cat, camel, and cow families each have substantial intrafamilial similarities in chromosomal banding patterns. On the other hand, some species have banding patterns which differ greatly from those of other species in the same genus. Similar species with different chromosomal banding patterns are found among certain deer (the muntjacs) and bats (Family Phyllostomidae).

More problematic are the similarities in chromosomal banding patterns among species which are different in structure. Interfamilial chromosomal banding similarities are found among the cats, mongooses, and raccoons; among the cow, deer, and giraffe families; among several families of marsupials; and among several families of primates, including humans. This raises questions about the extent of change which may have occurred in mammals, as well as the relationship of humans to other primates.

Four hypotheses to explain similarities of chromosomal banding are discussed in this paper. Such similarities could be the result of common design, of common ancestry, of chance, or of the action of virus-like agents. The hypothesis that chromosomal similarities could be due to chance seems unreasonable. It seems more likely that virus-like agents would cause differences between karyotypes than that they would change different karyotypes to look similar. Common ancestry appears to be the most likely basis for chromosomal similarities in species classified in the same genus, and for some species classified in different genera. However, to extend this explanation to higher taxonomic categories, in which similarities are of lesser extent and of lower quality does not seem necessary. To a creationist, it seems more probable that chromosomal similarities such as are found
within the artiodactyls, the carnivores, the marsupials or the primates may be the result of common design.

INTRODUCTION

The genetic instructions for an organism are located in the chromosomes of the cells of the organism and are transmitted to the offspring by inheritance. A logical prediction of evolutionary theory is that closely related species should have similar chromosomes. Techniques of chromosome banding have now been available for a long enough period of time that some trends have been discovered, and the results can be examined profitably.

Comparisons of karyotypes (sets of chromosomes) can be based upon differing levels of detail (see White 1978:47). The first comparisons were made on the basis of the number of chromosomes. In some cases the number of one-armed (acrocentric) and two-armed (metacentric) chromosomes were included in the comparison, and the sex chromosomes were identified. Extensive lists of chromosome counts can be found in Matthey (1973a,b) for placental mammals and in Sharman (1973) and Hayman (1977) for marsupials. However, attempts to infer relationships based upon unbanded karyotypes have not been satisfactory (Atchley 1972). Frequently, individual chromosomes could not be identified, making comparisons of uncertain validity. Differences in arm number due to gain or loss of heterochromatin (tightly condensed chromatin, generally considered to have little genetic activity) were not correctly interpreted using conventional staining (Duffy 1972).

The development of banding techniques overcame these difficulties and made comparisons more meaningful. Structural changes in chromosomes (chromosomal rearrangements) can now be identified precisely. However, much remains to be learned about the meaning of banding and the structure of chromatin (the chromosomal material),

FIGURE 1. An example of a chromosome spread showing Giemsa banding. The spread illustrated is from a Columbian ground squirrel (Spermophilus columbianus ruficaudus).
and further developments can be expected to add to the value of comparative karyology. Several methods of chromosomal banding are available, but the most widely used method is G-banding (Giemsa-banding). This technique produces a characteristic pattern of contrasting dark and light transverse bands on the chromosomes (see Figure 1). The banding pattern is different for nearly all species studied, although sometimes the differences are slight. A large number of mammal species have been G-banded, but the number of species remaining to be studied is much larger.

### PURPOSES OF COMPARISONS

#### Homeology

Comparisons of banding patterns often reveal nearly identical patterns in closely related species. The corresponding bands are believed to be homologous, but to allow for minor genetic difference, the term “homeology” is often used (e.g., Dutrillaux, Couturier & Fosse 1980).

Chromosomal similarities have been noted between groups of species in different genera or higher taxonomic categories. A significant degree of homeology has been found among all three families of seals (Arnason 1977). Homeologies at the suborder level have been noted within the primates (e.g., Dutrillaux, Couturier & Fosse 1980). Comparison of cat and human banding patterns (Nash & O’Brien 1982) did not show significant banding homeologies, although their gene mapping studies suggest similar gene arrangements (O’Brien & Nash 1982). Claims of banding homeologies between primates and carnivores by Dutrillaux & Couturier (1983) are of uncertain validity, because the proposed homeologies are based on portions of chromosome arms with a small number of bands involved. Reliable homeologies should include entire arms or be supported by other evidence (see Ponsa et al. 1981).

The actual genetic homology of similar banding patterns is supported by comparative gene mapping. Genes for equivalent enzymes are indeed often present on chromosomes with similar banding patterns in different species (Lalley & McKusick 1985). Genes which are found close together on a chromosome are said to be linked. Groups of genes which are linked in humans are generally also found linked in other species. In fact, gene groupings appear to be similar in many species even when chromosome banding homeology has not been detectable (Nash & O’Brien 1982, Kiel et al. 1985). Several equivalent linkage groups have been found on chromosomes with similar banding patterns in humans and other primates (Lalley & McKusick, loc. cit.). Several linkage groups are also common to human and cat chromosomes; in fact, the similarities in linkage patterns between cats and humans are almost as consistent as between chimpanzees and
humans (O’Brien & Nash 1982), although based on fewer gene loci. Several mouse linkage groups are similar to human linkage groups, if one allows for the correspondence of one two-armed human chromosome with two one-armed mouse chromosomes. Whether the genes controlling such characteristics of organisms as development and morphology are also linked in similar ways in similar species is not known.

**Classification**

Comparative studies of chromosomal banding patterns have been useful in classification. Sibling species are species which appear alike morphologically, but have been discovered to be reproductively isolated. Giemsa-banding is not necessary to detect sibling species, but it can assist in identifying the differences between the species more precisely. Chromosomal sibling species have been discovered within cotton rats (*Sigmodon*; see Elder 1980), grasshopper mice (*Onychomys*; Hinesley 1979), and shrews (*Sorex*; Olert & Schmid 1978).

The use of G-banding has sometimes been helpful in clarifying the taxonomic position of species which do not have clear affinities based on other characters. Chromosomal differences have been used in determining the taxonomic placement of the African rat *Mastomys* (Lee & Martin 1980), the golden mouse (*Ochrotomys*; Engstrom & Bickham 1982), and *Neotomodon alstoni* (Yates, Baker & Barnett 1979). The giant panda, *Ailuropoda*, has been variously classified with the bears, raccoons, or in a family by itself. Although previous researchers were unable to find good banding matches (Wurster-Hill & Bush 1980), a more recent study (O’Brien et al. 1985) identified several banding matches linking the giant panda with the bears. The authors conclude by suggesting the giant panda be classified in a separate subfamily within the bear family Ursidae.

Sometimes chromosomal comparisons give unexpected results. For example, the karyotypes of some South American genera of rodents were more like the karyotypes of wood rats (genus *Neotoma*) a primarily North American genus, than they were like the karyotypes of cotton rats (*Sigmodon*), a primarily South American group (Baker, Koop & Haiduk 1983).

The validity of using chromosomal banding comparisons to assist in determining degree of relatedness was supported in a study by Mascarello, Stock & Pathak (1974). The banding pattern of a species of woodrat (*Neotoma*) was compared with that of six other rodent species, progressively more distantly related taxonomically. The degree of matching was near total for another woodrat species from the same subgenus and showed a general decrease in comparison with species of increasing taxo-
onomic distance. About one-third of the chromosomes matched those of species from other tribes or subfamilies. Comparison with a species of kangaroo rat (*Dipodomys*, different superfamily) revealed no detectable banding homeologies with the woodrat. These results show general agreement with traditional methods of classification.

**Constructing Phylogenies**

Giemsa banding has made possible the identification of specific chromosomes involved in rearrangements (Seabright 1972), permitting one to determine whether similar species possess the same rearrangement. Shared chromosomal rearrangements in similar species are interpreted as evidence of a common ancestor which had the rearrangement (see Rofe 1976). Several species of antelopes which share a Y/autosome translocation provide one such example (Benirschke et al. 1980).

The ability to identify similar banding patterns in different species and to identify chromosomal rearrangements has led to interest in reconstructing the historical sequence of rearrangements which have accompanied speciation in a group of species (see Spotorno 1977). The construction of such “family trees” is based on several assumptions. One assumption is that the ancestral karyotype can be determined with reasonable accuracy. This requires that the species to be compared be chosen carefully (Dutrillaux & Couturier 1983) and that homeologies be accurately identified. Another assumption is that the best tree is one which requires the fewest reversals and convergences (principle of parsimony; see Farris 1978).

The method is not without difficulties. One problem is that reversals and convergences do occur (e.g., see Baker, Barnett & Greenbraum 1979; Baker, Koop & Haiduk 1983; Searle 1984), probably because certain points on a chromosome are more susceptible to breakage than other points (Bush 1981, Nevers & Saedler 1977). Another problem is the possibility of mismatches, especially when only portions of chromosomal arms are involved (see Ponsa et al. 1981). Despite these difficulties, cladograms (“family trees”) based on chromosomal characters are useful in testing for congruence with cladograms based on other data.

Cladograms based on chromosomal characters have been constructed for groups at several taxonomic levels, for example the genus *Peromyscus* (Robbins & Baker 1981), the bovid tribe Tragelephini (Benirschke et al. 1980), and several genera of murid and cricetid rodents (Koop et al. 1984). An especially comprehensive study at the superfamily level has been done for phyllostomoid bats (Patton & Baker 1978). Obviously, such cladograms cannot be more accurate than the identification of banding homeologies.
RESULTS OF COMPARATIVE G-BANDING STUDIES

This section discusses numerous examples of studies in which banding patterns of various species have been compared. It forms the basis for the discussion in the next section (Creationist Viewpoint). Readers not interested in details may skip to the next section, referring to this section only if more details are desired. No attempt is made here to present an exhaustive list of references on G-banding results in mammals. Instead, I will discuss briefly a sample of the literature available, emphasizing studies of special interest or taxonomic breadth. Preference is given to papers which compare the banding patterns among several species or higher categories.

Monotremes

The taxonomic relationships of the egg-laying mammals are somewhat uncertain, as they show some skeletal similarities with reptiles and others with mammals (see Nowak & Paradiso 1983:1). There are three living genera, divided into two families. The anatomical uniqueness of the species is paralleled by the unusual nature of the karyotypes. The platypus has 52 chromosomes in each sex (Bick & Sharman 1975). Like most mammals, males have an XY sex chromosome pair, and females have two X chromosomes. *Tachyglossus*, the more widespread genus of echidna, is the only monotreme for which G-banding has been published (Murtagh 1977). There are 63 chromosomes in the male, which has one Y and two X chromosomes ($X_1X_2Y$). The female has two pairs of X chromosomes ($X_1X_1X_2X_2$) with 64 chromosomes in all. *Zaglossus*, the other genus of echidna, apparently has the same system. Unlike most other mammals, all of the monotreme species studied have unpaired elements at meiosis, which participate in a chain multiple with the sex chromosomes. The three genera of monotremes are karyotypically more similar to each other than to any other mammal.

Marsupials

The marsupials are of special interest because of their unusual characteristics and biogeographic distribution. Chromosome numbers for over 100 species of marsupials are listed by Hayman (1977), and trends analyzed. The chromosome numbers range from 10 to 32, with 14 being the most frequent number, and 22 the next most frequent. The greatest diversity of chromosome number is among the Macropodidae (kangaroos etc.).

*Comparing Australian and American marsupials.* The relationship of Australian marsupials to those from South America is a question of continuing interest. An important interfamilial comparison of G-banding
by Rofe & Hayman (1985) may shed some light on the question. The study included one American species and 14 Australian species, representing four or five superfamilies (depending on the classification scheme). All species had 14 chromosomes, and their banding patterns showed remarkable agreement. These results were interpreted by the author as supporting the common ancestry of both Australian and American marsupials, with the ancestral karyotype being most like the one shared by a wombat (*Vombatus ursinus*), a dormouse possum (*Cercartetus concinnus*), and a bandicoot (*Isoodon obesulus*). Differences between species can be accounted for on the basis of pericentric inversions (an inversion including the centromere) and small variations in heterochromatin. The presumed increase in 2n number from the proposed ancestral number of 14 to as many as 32 is attributed to chromosomal fission.

The South American marsupial *Dromiciops* has sometimes been placed in a family separate from other living species. Its chromosomes have not been G-banded, but they appear to be similar to those of the presumed ancestral marsupial 2n=14 karyotype (see Sharman 1982). Karyotypic similarities have also been reported among several species of American opossums (Yonenaga-Yassuda et al. 1982; Casartelli, Rogatto & Ferrari 1986), and among several species of Australian dasyurid marsupials (Young et al. 1982, Baverstock et al. 1983b, Rofe & Hayman 1985).

**Kangaroos.** The chromosomes of kangaroos and their allies appear to be distinct from those of other marsupials. Rofe (1976) compared the G-bands of ten species of kangaroos and their allies, with 2n ranging from 10 to 22. Numerous chromosome arm homeologies could be identified, suggesting Robertsonian fusion (fusion of two chromosomes by their centromeres) to be the predominant type of chromosome rearrangement. The karyotype of the red-bellied pademelon (*Thylogale billardierii*), with 22 chromosomes, was interpreted as being closest to the ancestral condition for the group. Karyotypes for seven species of kangaroos (*Macropus*) were derivable by various fusions. The banding patterns of the swamp wallaby (*Wallabia bicolor*: 10 chromosomes in males, 11 in females) and the rock wallaby (*Petrogale penicillata*: 22 chromosomes, but a different karyotype) displayed greater divergence from the presumed ancestral state. Pericentric inversions and centric shifts (change in position of the centromere) were proposed to explain the differences.

**Insectivores**

One of the first examples of chromosomal polymorphism to be discovered was the European shrew superspecies, *Sorex araneus*. At least 12 chromosomal forms have been described (see Seale 1984). Differences
can be explained on the basis of Robertsonian fusions involving different acrocentrics of an ancestral karyotype. Chromosome numbers range from 20 to 32. Some hybridization occurs, but partial reproductive isolation exists between some of the races. An X-autosome fusion, giving rise to a sex chromosome system of XX in females and XY, Y, in males, is found in some, but not all of the races (Olert & Schmid 1978).

**Bats**

Bats comprise the second-most-diverse order of mammals. Two suborders are present, the Old World fruit bats and the rest of the bats. Eight species of African fruit bats, representing eight genera, were compared on the basis of their G-bands (Haiduk et al. 1981). In spite of the fact that chromosome numbers ranged only from 34 to 36, substantial differences in banding patterns were detected, requiring at least 34 rearrangements to explain the differences among the eight species. The mechanism for nearly half the rearrangements could not be conclusively identified. This study illustrates that significant karyotypic differences may exist between karyotypes which appear similar superficially.

Most G-banding studies of bats are concerned with the insectivorous and nectar-feeding bats. Patton & Baker (1978) concluded that the ancestral karyotype for the largely tropical American superfamily Phyllostomoidea is most like that of the big-eared bat (*Macrotus waterhousii*). In two different genera, a comparison of banding patterns of two similar species suggested that a total rearrangement of the genome had occurred in one species but not in the other. Another interesting discovery in this study was that the fisherman bat (*Noctilio*), placed in its own family on morphological grounds, has very similar G-banding to that of the mustache bat (*Pteronotus pamellii*), family Mormoopidae. The existence of similar karyotypes in morphologically distinct species and of different karyotypes in morphologically similar species can be interpreted as evidence against the theory that chromosomal rearrangements promote speciation by disruption of genes which regulate development (e.g., Wilson, Sarich & Maxson 1974).

Other good studies of chromosomal banding in bats include those of Haiduk & Baker (1982) on the long-tongued bats (Glossophaginae) and on evening bats by Bickham (1979a,b) and Zima (1982). A summary of the kinds of chromosomal rearrangements proposed in various studies of New World bats was published by Baker & Bickham (1980).

**PRIMATES**

Because of the great interest in their relationship to humans, primates have been the object of special attention in comparative karyology.
Numerous banding homeologies have been claimed for some 60 species of primates, including man (Dutrillaux et al. 1978). They conclude that “it is likely that all the euchromatin [genetically active chromatin] ... is identical in all the species”. This statement, if true, would appear to reduce the significance of chromosomal banding comparisons.

As is often the case, different types of chromosomal rearrangements are typical of different taxonomic groups (karyotypic orthoselection; White 1973). In most lemars Robertsonian rearrangements are the most common type of rearrangement, except for one genus in which tandem fusions are common (Rumpler & Dutrillaux 1976, 1978, 1979; Rumpler et al. 1983b, 1985). If their karyotypes are derived from the presumed ancestral karyotype for the group, Robertsonian rearrangements predominate in the species of Galago, while pericentric inversions are more important in Perodicticus, a loris (Dutrillaux et al. 1982, Rumpler et al. 1983a). Chromosome fissions are reportedly very frequent in the Old World monkeys, but have not been found in the other families. In the apes pericentric inversions are the most common type of rearrangement.

One of the most variable genera karyotypically is the New World owl monkey, Aotus. Nine different karyotypes have been reported, differing by fissions, fusions, and inversions (Ma 1981, Galbreath 1983). The number of sex chromosomes differs among the races. An ancestral karyotype for platyrrhine (New World) monkeys was proposed by Dutrillaux & Couturier (1981). A bibliography of cytogenetic studies in New World primates is available (Mudry de Pargament, Brieux de Salum & Colillas 1984).

Different workers have sometimes obtained different results from study of the same material. This can be illustrated in studies comparing the banding patterns of the grivet (Cercopithecus aethiops) and the rhesus monkey (Macaca mulatta). One pair of investigators (Stock & Hsu 1973) reported complete matching of the euchromatin (genetically active chromatin), with differences explainable as the result of heterochromatin additions or fusions. Another group of investigators (Estop, Garver & Pearson 1978) were unable to match some of the chromosomes in the two species. The claim of nearly complete homeology of banding among the Old World monkeys (Dutrillaux 1979, Dutrillaux et al. 1978) has been questioned by Ponsa et al. (1981), who suggest that the extent of banding homeologies among the primates may have been overstated. They emphasize the need to base homeologies on characteristic banding patterns, not merely short segments, and criticize the construction of karyotypes of hypothetical ancestors as “paper cytology.”
Apes and humans. The chromosomes of the great apes have received a great deal of study, and detailed banding patterns have been published and compared with human banding patterns (Yunis & Prakesh 1982). The similarities between chimpanzee and human chromosomes are very striking. Only ten of the 23 pairs of human chromosomes show banding differences when compared with chimpanzee chromosomes. The banding patterns of nine chromosomes are identical in humans and gorillas. The three species differ in their banding patterns by various inversions and a Robertsonian fusion. The fusion involves chimpanzee chromosomes 12 and 13 as equivalent to human chromosome 2 (see Sun, Sun & Ho 1978a,b). No differences in the gene maps of humans and chimps have yet been noted (Lalley & McKusick 1985). In contrast to the usual phylogeny proposed for the group, it is the human karyotype that is considered to be closest to the ancestral type (Yunis & Prakesh 1982). The karyotypes of chimps and gorillas are more similar to the human karyotype than to that of the orangutan.

Carnivores

Banding similarities among the cat, raccoon and mongoose families were reported by Wurster-Hill & Gray (1975). More recently, attempts have been made to propose an ancestral karyotype for the order Carnivora (Dutrillaux & Couturier 1983, Couturier et al. 1986). This hypothetical karyotype is quite similar to that of the palm civet (Paradoxurus hermaphroditus, family Viverridae). Seal karyotypes show banding similarities with those of the carnivore families, but bears and dogs have karyotypes that are quite different.

The hypothetical ancestral carnivore karyotype (see above paragraph) was compared with the hypothetical ancestral karyotype previously proposed for the New World monkeys (Dutrillaux & Couturier 1981), prosimian primates (Rumpler et al. 1983b) and the squirrels (Petit et al. 1984, cited by Couturier et al. 1986). Although banding homeologies are claimed for significant portions of the karyotype, the method used has been criticized (Ponsa et al. 1981). Dutrillaux & Couturier invoke gene mapping similarities to support their view of actual homology of the chromosomes.

Karyotypically, one of the most homogeneous families known is the cat family (Wurster-Hill & Gray 1973). Mongooses show significant but varying degrees of similarity with cats (Wurster-Hill & Gray 1975). Translocations involving a sex chromosome are known in at least two genera of mongooses (Pathak & Stock 1976, Fredga 1972).
Seals and Their Allies

There are three families of pinnipeds: true (earless) seals, sea lions (eared seals), and the walrus. These families all share considerable banding homeology, with only four different karyotypes known (Arnason 1977). Differences among the karyotypes were not described thoroughly, but at least one fusion is involved. A striking resemblance to certain carnivore karyotypes was reported, especially to the coati mundi karyotype, but it is not clear whether this similarity was based on banding patterns.

Whales

Whales are generally divided into two major groups, toothed whales (Odontoceti) and baleen whales (Mysticeti). Karyotypes of members of both groups are very similar (Arnason 1974, Arnason et al. 1977), except for the sperm whales, which have distinctive karyotypes. Several species have interstitial heterochromatin and similar C-bands. Some homeologies were reported, but differences have not been described.

Odd-toed Ungulates

Horses are the only members of this order for which I have seen comparative G-banding studies. All seven living species of the horse family have been studied (Ryder, Epel & Benirschke 1978). Each species has a different 2n number, ranging from 32 to 66. Only the X chromosome and a single autosome show the same banding pattern in each species. The other chromosomes all show differences, most commonly involving Robertsonian fusions and pericentric inversions. The mechanism for many of the rearrangements is unknown. The two species of horses have similar chromosomal banding patterns, as do the two species of asses. Two of the three species of zebras have similar patterns, but the pattern in Hartman’s zebra is so different that little homeology can be determined in comparisons with the other species.

Even-toed Ungulates

Interfamilial G-band homeologies have been identified (Buckland & Evans 1978) among the cow family (Bovidae), deer family (Cervidae) and the giraffe family (Giraffidae). A hypothesis of chromosomal evolution involving fission has been outlined by Todd (1975) for the order, but our knowledge of this group is still very incomplete.

Camels

Camels have a disjunct distribution, with four species in South America and two species in the Old World. A study comparing banding patterns in two South American species and the Bactrian camel found the G-banding patterns to be indistinguishable (Bunch, Foote &
Maciulis 1985). The distributions of heterochromatin were also indistinguishable, a rather unusual result. The lack of chromosomal divergence despite the geographical isolation is unexpected, and suggests either a very stable karyotype or a relatively short period of isolation, or both.

**Cattle family.** The karyotypes of the various species of sheep and goats are very similar, with differences attributed to fusions (Bunch, Foote & Spillett 1976). Cattle chromosomes show large homeologies with those of sheep and goats (Snedl & Czaker 1974). Buckland & Evans (1978), using the goat karyotype as a standard, found nearly complete agreement in banding patterns among several species of bovids, representing three subfamilies. The goat and the horse-like antelope karyotypes were more similar to each other than either was to the cattle karyotype.

A rearrangement which is shared by several similar species is considered to be a good indicator of common ancestry (Rofe 1976). A Y/autosome translocation is found in several species of African cattle-like antelopes (Benirschke et al. 1980), including the eland and the bongo. Differences among the species appear largely due to Robertsonian fusions, with a few tandem fusions and some other unidentified rearrangements. An X/autosome tandem fusion is found in several species of gazelles (Effron et al. 1976, Benirschke et al. 1984). These examples illustrate variability in species which has probably come about relatively recently.

**Deer family.** One of the most unusual examples of chromosome modification yet discovered is found in the muntjacs, a group of small Asian deer. Two species, the Indian muntjac, *Muntiacus muntjak vaginalis*, and *M. rooseveltorum*, share the distinction of having the lowest 2n number known among mammals, six in the female and 7 in the male (Wurster-Hill & Seidel 1985). The Chinese muntjac, *M. reevesi*, looks very similar but has 2n=46 in both sexes. A comparison of the chromosomes of the Indian and Chinese species (Liming, Yingying & Xingsheng 1980) suggests that essentially the same genetic material is present in each and that the lower number of chromosomes is probably derived by tandem fusion from the 2n=46 karyotype. A fourth species, *M. feae*, has 2n=13 (Soma et al. 1983). Karyotypes of these species illustrate the usefulness of G-banding in comparing karyotypes and show that caution is in order in drawing phylogenetic conclusions based solely on chromosomal data.

**Lagomorphs**

Species from both the pika family (Ochotonidae) and the rabbits and hares (family Leporidae) have been studied. The two families appear to share very little or no detectable banding homeologies (Stock 1976), but extensive chromosomal similarities are present among the leporids. Hares
(Lepus) have similar karyotypes, while cottontails (Sylvilagus) show considerable variation (Robinson, Elder & Chapman 1983a,b, 1984). The ancestral karyotype for the group appears to be like that of the hares. Other genera of rabbits appear to be related karyotypically to the hares (Robinson & Skinner 1983, Robinson 1980, Stock 1976). Many of the differences can be ascribed to Robertsonian rearrangements.

**Rodents**

This is the most diverse order of mammals, and a great amount of cytogenetic study has been done with rodents. However, much more remains to be done. Most comparative studies of rodent G-banding have been done with rats and mice, and many families have not yet been studied. A recent bibliography of rodent karyological studies is available (Jotterand-Bellomo 1984).

The G-banding patterns of thirteen species of ground squirrels (Spermophilus) have been published (Nadler et al. 1973, 1975, 1984), and extensive homeologies determined. An interesting geographical pattern has been discovered in this group. The arctic ground squirrel, *S. parryi*, is found on both sides of the Bering Strait, both populations having identical karyotypes. The arctic ground squirrel populations separate two other species: *S. columbianus* in North America and *S. undulatus* in Siberia. The banding patterns of these two species are identical. The highest 2n numbers in the genus are found in the Asian *S. xanthoprymnus* (2n=42) and the North American *S. vigilis* (2n=46). These two species differ primarily by two fusions. In contrast to the karyotypic variability of the squirrel genus Spermophilus, most chipmunks (genus Tamias), have very similar karyotypes (Nadler et al. 1977).

By far the largest family of mammals is the mouse family, and a large number of chromosomal studies have been conducted among its members. Only a few studies can be described here. All species of white-footed mice (*Peromyscus*) studied so far have 48 chromosomes (Robbins & Baker 1981). The most primitive karyotype was proposed to be that of *P. boylii*. A modified *Peromyscus* karyotype was proposed to be ancestral for the family by Koop et al. (1984). They noted that karyotypic differences may be more extensive among species in a genus than between genera.

One of the most interesting cases of chromosomal speciation is found in the house mouse (*Mus musculus* complex). Chromosome numbers range from 22 to 40, with differences due to Robertsonian rearrangements (Gropp & Winking 1981). Such a situation is called a “Robertsonian fan”. Several other species from the same subgenus share identical banding patterns with *Mus musculus*, but at least some species in other subgenera have
quite different banding patterns (Hsu, Markvong & Marshall 1978). Another Robertsonian fan has been described in the European mole-vole, *Ellobius talpinus* (Lyapunova et al. 1984). Here the 2n number varies from 31 to 54 within a geographic distance of only 150 km. All chromosome numbers from 31 to 54 have been found, indicating extensive introgression.

Several genera of native Australian rodents, representing three tribes, have been studied. Each of the three tribes contains a species with a common banding pattern (Baverstock et al. 1983a). These Australian rats have virtually no banding homeologies with species of *Rattus*, indicating only a distant relationship. One genus (*Zyzomys*) has apparently had its genome completely rearranged.

Banding patterns of ten genera of murid rodents, mostly of African origin, were compared by Viegas-Pequignot et al. (1983), and an ancestral karyotype proposed for the murid rodents. Several examples were noted in which a particular type of rearrangement appears to have accumulated in a particular lineage (karyotypic orthoselection). This ancestral karyotype for murid rodents was compared with that of a South American cricetid, *Akodon arvicoloides* to test for similarities between the two subfamilies (Viegas-Pequignot et al. 1985). About 40% homeology was claimed. It would be interesting to compare the “ancestral” karyotype proposed by these authors with that given by Koop et al. (1984).

South American hystricomorph rodents. Several families of mostly South American rodents are included in the hystricomorphous rodents. Not many studies of G-band comparisons have been published, and fewer yet in English. A review of unbanded karyotypes of hystricomorphs was published by George & Weir (1974). Three species of Caviidae, representing three genera, were compared by Maia (1984). Differences reported were primarily due to heterochromatin content. Chromosomal speciation appears to be taking place among populations of a superspecies of spiny rats (*Proechimys*, Family Echimyidae) in Venezuela (Reig et al. 1980). Chromosome numbers range from 42 to 62. Differences are due to Robertsonian fusions, except for the extreme chromosome numbers, where pericentric inversions are also involved.

Miscellaneous rodent families. Five species of gundis (family Ctenodactylidae), representing four genera, have been shown to have similar chromosomal banding patterns (George 1979a). Differences can be explained by a pericentric inversion, and perhaps several very small translocations. The same author (George 1979b) found very close similarity in the banding patterns of two species of African mole-rats (family Bathyergidae). This contrasts sharply with the variability seen in some other

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families of burrowing rodents and casts doubt on the hypothesis that chromosomal evolution is especially promoted by the kind of social structure found in burrowing rodents (Wilson et al. 1975; see also Gileva 1983).

A CREATIONIST VIEWPOINT

A Challenge for Creationism

Although much remains to be learned about the meaning of chromosomal structure, enough data on chromosomal comparisons have been gathered to raise some important questions for creationists. That changes have occurred in organisms since creation is not in question, but the extent of those changes is uncertain.

Species which are similar morphologically generally have similar karyotypes, although there are significant exceptions (e.g., see Liming, Yingying & Xingsheng 1980). This is quite reasonable if species with similar morphology (e.g., in the same genus) are thought of as being related through common ancestry. The occasional exception merely shows that chromosomes can be extensively rearranged with no significant morphological effect.

More problematic is the finding that species which are quite different morphologically may have similar karyotypes. The chromosomal similarities among many of the Australian marsupials (Rofe & Hayman 1985), between goats and giraffes (Buckland & Evans 1978), between seals and terrestrial carnivores (Arnason 1977) and between humans and the great apes (Yunis & Prakesh 1982) raise some significant questions for creationists. Perhaps the two most important questions are:

1. To what extent has morphological change occurred in mammals, and by what mechanisms? and
2. What is the relationship between humans and apes?

These questions will be amplified below, and then various hypotheses regarding the relationship of chromosomal evidence to these questions will be discussed.

Problem 1. The extent and mechanism of morphological change.
There is circumstantial evidence that mammal species may change significantly in their morphology. This evidence comes from the study of island populations (e.g., Lawlor 1982, Simpson 1956), from the results of selective breeding of domestic animals (e.g., Wayne 1986), from the ability of some animals to hybridize (Van Gelder 1977), and from distributional patterns of living mammals (Darwin 1859). However, there seem to be limits on the amount of morphological change possible (Lester & Bohlin 1984).
If groups such as the Australian marsupial families are considered to share a common ancestry in spite of their diverse morphology, one is challenged to propose some mechanism by which such change could be brought about. The standard neodarwinian gradualistic explanation for morphological change is that small changes arise by mutation and accumulate over time by natural selection to produce large changes (e.g., see Charlesworth et al. 1982). However, the lack of fossil intermediates, or even conceivable intermediate stages, has led many scientists to search for other explanations. Several alternative mechanisms for macroevolutionary changes have been proposed (e.g., Gould 1977; Oster & Alberch 1982; Wilson, Maxson & Sarich 1974; Wright 1982), but none has been satisfactory. The possible role of chromosomal rearrangements in speciation was discussed in a previous article (Gibson 1984).

For creationists, the origin of diversity in mammals is an important question. If enough morphological change has occurred since the Genesis flood to explain the origin of diversity among marsupials, it seems reasonable to think that the same amount of change could also have happened among placental mammals, although placentals as a group do not have such similar chromosomal banding patterns as marsupials. However, in the absence of a plausible genetic mechanism for creating new adaptations, creationists are somewhat skeptical that such changes have occurred, even though there is no scriptural prohibition against large changes in species.

If the marsupials are considered to be unrelated, then one has the problem of explaining why they share so many unique characteristics, including chromosomal similarities and such structural traits as their reproductive anatomy, the presence of epipubic bones, and the inflection of the angular process of the lower jaw. Their geographic distribution is also difficult to explain.

**Problem 2. The relationship of man and the apes.** Questions concerning the origin and nature of man have deep philosophical significance. Evolutionists have long held that humans and apes share a common ancestry, a belief based largely on morphological similarities. Fossil discoveries have not clarified the picture, but seemingly have made it more confused, perhaps due to the subjective nature of interpreting the fossils (Washburn 1973). However, striking similarities have been discovered between apes and humans in their proteins (Bruce & Ayala 1979), their chromosomes (Yunis & Prakesh 1982), and in their DNA (Sibley & Ahlquist 1984).

To say that humans and apes are not related by common descent is to emphasize their difference in anatomy and behavior, and to downgrade the importance of their similarities in anatomy, biochemistry and chromo-
somes. Although the human karyotype is considered to be closest to the ancestral condition for humans and apes (Yunis & Prakesh 1982), I am not aware of any serious examination of the possibility that humans might be ancestral to apes.

**The Meaning of Chromosomal Similarity**

As an explanation for similarities in chromosomal structure, four distinct possibilities come to mind, each presented as a separate hypothesis below.

**Hypothesis 1. Chromosomal similarities are the result of common design.** This would mean that organisms which are similar morphologically were created with similar karyotypes, just as they were created with similar anatomical and biochemical features. If the karyotypes have not undergone much change since creation, we should be able to see the similarities. Whether a karyotype should be shared by all mammals or only by those with some degree of morphological similarities is uncertain.

If a karyotype is shared only by species with similar morphology, one might infer that the structure of the chromosomes is somehow related to the morphology of the organism. It is true that, in general, groups of species with similar G-banding patterns are also similar morphologically. However, it is known that major changes in the karyotype, as shown by G-banding, do not cause morphological change (e.g., see Baker, Bickham & Arnold 1985). It is also known that different types of chromosomal change may be found in groups of species which could plausibly have a common ancestry (e.g., see Koop et al. 1984). These facts cast doubt on any fixed relationship between chromosome morphology and anatomical morphology, although they do not disprove a possible original relationship between them.

There have been some suggestions that karyotypic structure has adaptive significance (Baker et al. 1983, Kiel et al. 1985), but this has not been demonstrated conclusively. It is of interest to note that there is frequently a correlation between anatomical distinctiveness and karyotypic distinctiveness between groups at high taxonomic levels.

**Hypothesis 2. Chromosomal similarities are exclusively the result of common ancestry.** According to this hypothesis, if two species have similar chromosomes (including banding patterns), they are related. This would require that each original species group was created with its own unique karyotype. If this hypothesis is correct, one must accept a common ancestry for apes and humans, for at least the majority of the marsupials, and for cattle, goats, antelope and giraffes. Acceptance of this hypothesis is the basis for phylogenies based on chromosomal similarities.
There are problems with this hypothesis. One is that despite some circumstantial evidence for major morphological change in mammals, no mechanism is known which would account for the kind of changes here suggested. Among the Australian marsupials, for example, there are considerable morphological differences between the wombat, the bandicoot and the “native cat”. A second problem is that in comparing banding patterns which are similar but may not be identical, preconceived ideas of ancestry can bias one’s conclusions (e.g., see above under Primates). If one assumes that two similar species do in fact have a common ancestor, then one is committed to finding a way of matching the banding patterns. In view of the subjectivity involved in matching chromosomal banding patterns, one might wonder about the significance of a 25% or 50% match of banding patterns, especially if no entire arms can be matched.

**Hypothesis 3. Chromosomal similarities are due to random changes which happen to produce the same banding pattern in different species.** This hypothesis implies that each originally created species had a unique karyotype. It also implies that chromosomal similarities have no real significance. If a series of patterns is made by randomly arranging dark and light bands, it is inevitable that some patterns will be repeated by chance. Thus the similarities of chromosome banding in humans and apes and within some other groups could be held to be merely a result of chance.

This hypothesis does not seem reasonable for two reasons. Similar chromosome banding patterns are not found randomly distributed throughout all taxonomic groups, but rather are found in groups which share morphological similarities. This argues strongly against any random cause of the banding patterns. In fact, it is known that breakage points in chromosomes are not random (Jacky, Beek & Sutherland 1983), and so changes in a karyotype will not be random. The phenomenon of “karyotypic orthoselection” also shows that chromosomal changes are non-random. If chromosomes have non-random breakage points, similar (parallel) rearrangements could occur independently in similar karyotypes (see below), but it is unlikely that convergent events would occur in different karyotypes to produce similar results.

**Hypothesis 4. Chromosomal similarities are the result of non-random changes due to viruses or transposable elements.** This hypothesis requires that either 1) karyotypes which were once different have been caused to become similar, or 2) karyotypes which were once similar have been changed in a similar way, due to the action of transposable elements or some similar mechanism.

Transposable elements (TEs) are known to increase the rate of chromosomal rearrangements in a non-random way (Nevers & Saedler
1977). But if the karyotypes were substantially different, there is no reason to expect them to change to be the same, since the insertion sites of TEs appear to be at least partially sequence-dependent (see Inouye, Yuki & Saigo 1984; Shapiro 1979).

Similar (parallel) changes do sometimes occur in similar species, as has been shown in several studies (e.g., Robbins & Baker 1981; Baker, Koop & Haiduk 1983; Baker, Bickham & Arnold 1985; Searle 1984). A common ancestry is plausible in each of these cases, and it is likely that the rather similar species have undergone numerous chromosomal changes during speciation, some of which happened to be the same.

It seems more likely that transposable elements could cause karyotypes which were originally similar to become different. This could occur if different species were infected by different TEs or retroviruses having different effects on the genome (see Rose & Doolittle 1983). It seems possible that different TEs might affect a genome in different ways. As a hypothetical example, it seems possible that the ancestors of oryzomine and peromyscine rodents (groups of rats and mice) could originally have had similar karyotypes when infected by different TEs. The TE(s) infecting the peromyscine lineage might have caused a series of heterochromatin additions and pericentric inversions, while the TE infecting the oryzomine lineage might have caused a series of fusions.

**CONCLUSIONS**

It is possible that chromosomal similarities have different explanations in different groups of animals. It this is true, then one must be cautious in using chromosomal comparisons to determine relationships. Nevertheless, chromosomal data can serve as a useful check on data from other sources.

Hypothesis 3, that chromosomal similarities are due to random chromosomal rearrangements which happen to produce similar banding patterns, is not reasonable, for reasons discussed above. Hypothesis 2, that chromosomal similarities are exclusively the result of common ancestry, does not seem consistent with creation theory and does not seem a necessary conclusion from the scientific data. The fact that very large genomic rearrangement does not seem to affect morphology, and yet animals with different body plans (“Bauplan”) appear to have very different kinds of karyotypes suggests to this writer that some different groups had different starting points and do not share a common ancestry.

Hypotheses 1 and 4 seem consistent with both creation theory and the evidence available. It seems likely that species which were morphologically similar were created with similar chromosomes, reflecting their genetic similarity. It is evident that large changes have occurred in
chromosomes since creation. These changes have often resulted in karyotypic divergence and have contributed to the multiplication of species.

Chromosomal rearrangements seem to occur so frequently that one would expect to find very little banding homeology between species which supposedly diverged long ages ago, such as the marsupials. The existence of numerous banding homeologies can be explained as the result of a common design which has been preserved only because a relatively short time has been available for changes to occur.

How much anatomical change has occurred since creation is still an unanswered question. Chromosomal comparisons suggest that new genera may have arisen since creation, for example among the antelopes which share a Y/autosome translocation (Benirschke et al. 1980). Whether larger changes have occurred cannot be determined from chromosomal studies. At the present time there is no known mechanism by which changes in organisms can take place which are large enough to account for the differences among, for example, the Australian marsupials or the various families of artiodactyls (cattle, giraffes, deer). The absence of fossil evidence linking different groups by a common ancestry, together with the lack of biological evidence of a mechanism for such change, seem consistent with the hypothesis that they have separate ancestries.

LITERATURE CITED


