TAXONOMY OF PRIMATES

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Abstract

The membership criteria for grouping organisms into baramins are not the same, or of the same importance for all researchers. The hybridization criterion for existing animals is the most common and explanatory, because it supposes the integration of practically every criterion proposed by the different authors. Taking the basic criterion of hybridization and getting support from the other criteria, I propose a baraminology for the Primate order.

Introduction

From the original proposal of Marsh (1941) on the denomination of the created types or baramins—(meaning bara: created and min: kind) researchers have prescribed a variety of membership criteria to identify these groups of organisms. The first membership criterion was that of hybridization in 1945 (Marsh, 1976). In 1970, Jones proposed the pattern of behavior as a membership criterion, considering unjustified the criterion of Marsh (Jones, 1982). In 1984, Lester and Bohlin relegated the hybridization criterion to a secondary plane, against other criteria proposed by them. They also proposed a new name for the created types: "prototype," that has not been followed.

The reproductive criterion of hybridization has been considered fundamental, though the support of other criteria proposed by the different authors is still important. In 1990, ReMine proposed his "Discontinuity Systematics" in which hybridization was the basic criterion. Also in 1990, Wise expanded "Discontinuity Systematics" by considering the membership criteria useful for defining a baramin in the context of a young earth, without forgetting hybridization as very important (Wise, 1990, 1992). Marsh had already left clear the moment from which an organismal cross was considered hybridization: "…When the chromosome groups of both parents take part in formation of the early blastomeres of the embryo" (Marsh, 1976, p. 37), that is the moment corresponding to when the maternal genetic control gives way to embryonic genetic control of the development and of the morphology from the DNA of both parents (Marsh, 1976; Scherer, 1994). With the basic criterion of hybridization and, finding support from other criteria, I approach the taxonomy of Primates.

Methods

My review and usage of membership criteria is partial, emphasizing the conflicting points in order to demonstrate that the use of a single criterion alone can produce misleading results, and to illustrate the merit of various criteria relative to the hybridization criterion.

In spite of the difficulties of using these criteria by themselves, I have used them as very helpful references. Only in the case of hybridization has an exhaustive review been made.

When we study the morphologic criterion, we consider continuity of the fossil remains across geological periods, though this is a consideration that needs an eucladistic analysis (Wise, 1992). Only in those cases where we specify a continuity can a monobaramin be identified. For example, *Cebupithecia*, a fossil genus from the Miocene, represents great similarity with the current genus *Pithecia*, and both are considered members of the same monobaramin.

Hybridization records are taken from the research of Gray (1972), and from the *Zoological Record.* The criterion given by Marsh (1976) considers hybridization as a valid indicator, rejecting dubious cases. The list of the species of primates and their taxonomy has been taken from MacDonald (1991), Corbet and Hill (1991), and Aguirre (1995). Even if hybridization has not been observed, it is possible to hypothesize a potential cross on the basis of other hybridizations. If A and B hybridize with C, then A and B belong to the same holobaramin, and can or may hybridize, according to the criteria of Marsh (1976; Scherer, 1994).

Molecular Criterion

Diverse methods, possessing different degrees of precision, define differences between proteins. Electrophoresis techniques give less information than the immunologic and sequence studies. The change of an amino-acid is more easily detected through these last two techniques. Even then, the techniques do not allow investigators to easily differentiate what changes are primitive and which are derivative (Dene, Goodman, and Prychodko, 1977).

A study of 23 different proteins from the Hominoidea superfamily by Bruce and Ayala (1979) places the orangutan closer to the chimpanzee and gorilla than to the Asian gibbons. The orangutan remains at the same distance from man, the chimpanzee, and the gorilla. However, in a study of the sequence of myoglobin, position 23 of the protein chain is occupied by serine, as in all primates with the exception of chimpanzees, gorillas and men. In hominoids position 110 is cysteine, while the orangutan has serine, like Old World monkeys (Romero-Herrera, Lehmann, Castillo, Josey, and Friday, 1976). Not all molecular studies coincide when one attempts the taxonomic placement of the different species of

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living hominoids, but it is clear that the differences correspond to those that exist only at a species level in other taxa (Bruce and Ayala, 1979).

Using the method of Nei and Roychoudhury (1974) for establishing the genetic distance between *Homo* and *Pan*, King and Wilson have found that this distance is D = 0.62, while Bruce and Ayala found that the distance was D = 0.386 (Bruce and Ayala, 1979). The difference between genetic distances was attributed to the different conditions under which the electrophoresis was done (Bruce and Ayala, 1979). Since 18 of the proteins analyzed by both investigation teams were the same, the difference was attributed to the dissimilar conditions under which the electrophoresis was performed. King and Wilson (1975) studied 20 loci; Bruce and Ayala (1979) 22 loci. According to Bruce and Ayala (1979), the marked difference in the genetic distances does not seem justified by the analyzed proteins.

Many biological characteristics can be involved in explaining the differences of genetic distances between species. Some indicated by Avise and Aquadro (1982) are the rate of mutation, chromosome number, and the size of the population or fecundity.

The immunologic analysis of serum is another method to determine the similarities and differences between species. A phenogram made using immunodiffusion analysis between serums of primates shows that Strepsirhini form a group of their own, apart from the rest including *Tarsius*, and within this suborder the differences are quite outstanding.

The differences by immunodiffusion in the family Lorisidae, between its *Loris, Galago,* and *Nycticebus* genera is approximately the same magnitude as the difference between the Catarrhini and Platyrrhini infraorders. The families Cheirogaleidae, Indriidae and Lemuridae, of the Lemuriformes infraorder are very different. The two genera of the family Lorisidae, *Arctocebus* and *Perodicticus* are found at a distance similar to the distance that separates Platyrrhini genera such as *Callicebus* and *Aotes.* Tarsius gives a greater signal by immunodiffusion with Strepsirhini than with Haplorhini, and the amino acids sequence of its hemoglobin and the nucleotides of the β-globin cluster (Koop et al., 1989) also supports a path of proximity between Tarsius and Strepsirhini. The differences between gorilla and man are a little greater than those which separate *Hylobates lar* from *H. syndactylus* (Dene et al., 1977). Therefore it is evident that the differences between proteins and anatomical characteristics, in the compared taxa, have unlike proportions.

On the other hand, sequencing of proteins permits a comparison between species that does not always reflect what one would expect. Although, we may frequently find a certain correspondence between the morphologic difference and the substitution of amino-acids in a protein, it is not always like this. For example, the relaxin hormone differs between the *Balaenoptera acurostrata* and *B. edeni* whales by three residues, while the difference of relaxin between the *B. edeni* and the pig, *Sus scrofa,* is only one residue (Schwabe, Bullesbach, Heyn, and Yoshioka, 1989).

We will not discuss the protein molecular clock, performed from the sequencing of proteins, or from other methods of analysis of proteins, because it is an evolutionist view that links protein variation with geologic time. One will only say that, it has not been possible to establish a satisfactory clock, as Scherer (1990) emphasizes: “It can neither be used as a tool for dating phylogenetic splits nor as reliable supportive evidence for any particular phylogenetic hypothesis.”

The DNA molecule carries the necessary information to synthesize proteins, therefore, its changes can be conveyed to the proteins it will codify.

For this reason, the DNA molecule analysis can avoid some of the problems that may rise in analysis of proteins. Even so, two proteins with the same amino-acid sequence may be codified by genes with dissimilar nucleotides; this is due to degeneracy of the code. Comparative DNA sequencing cannot confirm whether or not a given mutation has always been present, since back mutations are possible. The possibilities include: nucleotide Z $\longrightarrow$ nucleotide X $\longrightarrow$ nucleotide Z, or nucleotide Z $\longrightarrow$ nucleotide X $\longrightarrow$ nucleotide Y $\longrightarrow$ nucleotide Z, or other different substitutions of nucleotides. Hence, when sequences of DNA are compared we may find complications in the interpretation of nucleotide substitutions.

Sibley and Ahlquist (1984) have indicated that even though genes, proteins, or morphologic characters vary with different rates: “If one could obtain average rate value for a large enough sample of proteins, individual DNA sequences, or morphological characters, they too should exhibit an uniform average rate of change.” This average rate may be obtained, at least theoretically, with certain ease, by comparing large DNA molecules, complete genomes, or DNA—DNA hybridization (Sibley and Ahlquist, 1984).

The hybridization of the DNA takes advantage of the property by which the double helix can be separated into two chains and then gathered again. Theoretically, this method permits the global differences between genomes of different species to be assessed by separating the chains from the double helix by heating, and gathering the heterologous chains of the species studied while the temperature descends.

The temperature needed to separate the heterologous chains, is inferior with respect to the homologous chains, due to tile maladjustment between nitrogenous bases that do not hydrogen bond. This heterologous hybridization would permit one to evince the average of the total differences of the genomes, since the number of molecules handled is very high.

However, it is difficult to make the theories coincide with reality, and the same Δt is not always found when we com-

pare the same genomes in different experiments (Dickerman, 1991).

Kouznetsov and Ivanov (1991) have found that mRNA poly (A+), highly homologous in different species of wild forest mice, were carrying information for very different proteins as electromorphs. This indicates that the similarity between these molecules carrying the information does not always mean a similarity in the protein molecules they give place, and this presents more difficulties to the interpretation of nucleic acid and protein variation.

The study of highly repeated DNA sequences has been another way to investigate the relationships between species, but it also has drawbacks. The study of these DNA sequences in the Galaginae subfamily has revealed that their species are found to be very close. The species *Perodicticus potto* belonging to the subfamily Lorisinae presents a pattern of highly repeated DNA sequences very similar to that of the subfamily Galaginae. Both subfamilies, Lorisinae and Galaginae make up the family Lorisidae. The species *Microcebus murinus* belonging to the family Cheirogaleidae, taxonomically close to the family Lorisidae, had considerable differences with the pattern of highly repeated DNA sequences of the family Lorisidae (Crovella, Masters, and Rumpler, 1994).

On the contrary, in the family Lemuridae, each species possesses its own pattern of repeated sequences (Crovella et al., 1994) which hinders the interpretation of the results of greater or smaller similarity without further studies.

On the other hand, we have the relationship between molecular changes and morphological variation. Larson (1989) has suggested that both kinds of change seem to be unrelated. In the class Amphibia, we observe only a few corporal morphological patterns, though their degree of protein variation may be very high. On the contrary, in the class Mammalia ‘we observe a great variety of morphological patterns (horses, bats, dolphins, men, etc.), but their degree of protein variation is inferior to that of the amphibians’ (Larson, 1989). Within the same taxon we also find this maladjustment between morphological and molecular variation. In the genus *Tropheus*, a cichlid fish, the endemic inhabitants of Lake Tanganyika present a great genetic divergence with scarce morphological variation, opposite to what happens with other species of lakes Malawi and Victory (Sturmbauer and Meyer, 1992).

The genetic differences between the chimpanzee and man are scarce, insufficient to separate them beyond the species (King and Wilson, 1975; Bruce and Ayala, 1979). Approximately 99% of the polypeptide sequences of both are equal, whether in sequence analysis or by polypeptide comparison of the reactions between their serums. Comparisons of the DNA through heterologous hybridization chains reveal very small differences. In sister species of *Drosophila* the Δt for the separation of heterologous chains, with respect to the homologous is 3° C. The Δt between mammalian genera is greater, but it is very small between the chimpanzee and man at 1.1° C. However, many hold that the morphological distance, ecological differences and that of behavior locate both chimpanzee and man perfectly into different families (King and Wilson, 1975; Bruce and Ayala, 1979; Harvey and Clutton-Brock, 1985).

The fact that molecular and morphological variations do not happen at the same rate has caused some researchers to conclude that changes in the proteins of different species are not very relevant as an explanation of their morphological or behavioral differences. The relevant molecular differences would have to be due to the differences in genetic regulation. A small change in a regulatory sequence could cause large morphological changes (Wilson, Maxson, and Sarich, 1974a; Wilson, Sarich, and Maxson, 1974b; King and Wilson, 1975).

An experiment by Wilson et al. (1974a), whose goal was to verify this hypothesis, used immunological techniques to analyze proteins of different species of anurans or mammals capable of hybridizing. They supposed a priori that the species capable of crossing have proteins very similar or the same. However, they found that although this was true for mammals the same did not occur with anurans.

From this we might conclude that the compatibilities between the development programs of species are not necessarily reflected by differences in the kinds of proteins that are commonly analyzed. Therefore, the analysis of these proteins can only have a relative worth.

The changes in regulatory systems have been related to the chromosome structure. In mammals there is a greater variability in the chromosomes, as well as in their anatomy, with respect to that found in anurans (Wilson et al., 1974b). In birds a relationship was found between a uniform chromosome structure and a uniform morphology, as it happens with anurans. Also, the potential for interspecific hybridization in birds and frogs is much greater than in mammals. Morphologic change and the loss of the capacity for hybridization may therefore be directly related with the changes in the patterns of gene expression (Prager and Wilson, 1975).

The revision by Dickinson (1991) about genetic regulation between species of the genus *Drosophila*, reveals that there is nothing conclusive. The production of a protein can vary between sister species up to two orders of magnitude.

The study of homeotic genes, directly implicated in the morphologic determination of the animal, might provide evidence for a more direct relation between genes and morphology.

Chromosomes and Species

It is generally accepted that each species possesses a particular karyotype, and that the karyotypical differences between species are proportional to the distances between them. However, it does not seem that this affirmation could

be generalized, which may prevent us from clearly establishing a relationship of proximity between species by studying only the karyotype.

Species of the two genera of the family Camelidae, order Artiodactyla, possess identical karyotypes (Bunch, Foote, and Maciulis, 1985). Hybridization between the species of the New World, (llama, guanaco, alpaca, and vicuna) is possible. The same also happens with the species of the Old World camel Bactrian and dromedary.

The genus *Muntiacus,* of the family Cervidae is, however, highly variable as far as karyotype is concerned. The bottom most diploid number found in Mammals is six chromosomes for the female of the *Muntiacus muntjak* and seven chromosomes for the male. The species *Muntiacus reevesi* possesses 2n = 46 chromosomes, but both species hybridize (Yang, Carter, Shi, and Ferguson-Smith, 1995).

The chromosomal differences between both species do not alter their function, neither their structure, nor their genetics. Dutrillaux exposes the case of a human patient with just one chromosome resulting from the fusion of 46 (Dutrillaux, 1979).

In the family Cercopithecidae the karyotypical differences are due largely to chromosomal fissions and fusions. The chromosome number in the genera *Papio, Macaca, Cercocebus* and *Cynopithecus* is 42 compared to 70 of the genus *Cercopithecus* (Dutrillaux, 1979; Dutrillaux, Biemont, Viegas-Pequinot, and Laurent, 1979), with which all hybridize. All these genera could be a superspecies, that would comprise an important morphological diversity, in contrast to what occurs with other groups of Primates with variable karyotypes, and greater anatomical uniformity.

In the family Callitrichidae, *Cebuella pygmea* possesses a karyotype much closer to *Callithrix jachus* than the latter to *Callithrix emiliae,* which is indicative of the proximity of both genera : *Cebuella* and *Callithrix.*

Microcebus, Cheirogaleus, and *Allocebus,* of the family Cheirogaleidae possess a very similar karyotype. The genus *Phaner,* presents, however, the karyotype with greater differences with respect to other genera of the family Cheirogaleidae (Rumpler et al., 1995).

The banding of the chromosomes in Pongidae and man reveals a high degree of identity, 18 of 33 chromosomes pairs are practically indistinguishable between them, and the rest possess very limited variations. (Yunis and Prakash, 1982). In the family Lemuridae, however, two subspecies, *Lemur fulvus collaris* and *Lemur fulvus albocollaris* differ by eight Robertsonian translocations, and still hybridize (Dutrillaux, 1979). In *Drosophila,* sister species with homosequential polytenes cannot hybridize (Dutrillaux, 1979).

The hylobatid karyotype is radically different from the rest of Primates with a diploid number of 38, 44, 50 and 52 chromosomes. By chromosome banding greater differences are found between the different species (Koehler, Arnold, Weinberg, Tofanelli, and Stanyon, 1995). Their morphology remains similar (Figure 1), which is opposite to what occurs in Cercopithecidae.

Hybridization techniques *in situ* between DNA libraries and chromosomes are another complement to the chromosomal analysis. This technique reveals a very high molecular correspondence between chromosomes of Cercopithecidae and those of man (Wiemberg, Stanyon, Jouch, and Cremer, 1992), opposite to what occurs upon comparing Hylobatidae with man (Koehler et al., 1995). This allows us to doubt whether there is enough proximity between gibbons and humans to include them in the same superfamily, Hominoidea.

The Morphologic Criterion

The cranium is the bony structure most used in anatomical comparison between vertebrates, and therefore their taxonomy. The motive is the complex interaction between the bones that compose it and the soft tissues with which they interact, generally very sensitive, brain and organs of the senses among others. This motivates its stability, especially in the base of the cranium (Enlow, 1992). Dentition also presents a special stability.

In the order Primates, the auditory bulla formed by the petrosal and the ectotympanic, the rounded form of the promontory, the loss of the medial branch of the artery internal carotid, and the formation of a bony channel for the lateral branch of the same are considered as apomorphic (i.e., derived) features of the basicranium (Aguirre, 1995).

To establish the classification we use mainly the bony structure in the otic region, the tracings of its circulatory net in the basicranium, and the nasal bone fundamentally (Aguirre, 1995).

According to these characteristics, the animals with the greatest similarities would be found within the order Carnivore (Aguirre, 1995). It becomes evident that few anatomical characteristics cannot be used as the only differentiation criterion.

Characteristics of the postcranial skeleton and even of the soft tissues help define the differences between species or superior taxa.

The origin of the order Primates is not justified by the fossil record as descendant of some less specialized mammal, nor that man emerged by evolution from some type of monkey, as pointed out by Cheek (1981).

The Plesiadapiformes group, which many consider small Primates, includes exclusively Paleocene fossils. Their incorporation among Primates is due to certain trends in the dentition and the otic region. However, they present dental adjustments more characteristic to other orders, as Insectivora, Rodentia, and even with the family Carpolestidae, within the Marsupials (Aguirre, 1995).

The ocular orbits of these animals are not closed and remain located on the side. The incisors are separated by a wide diastema of the premolar and molar teeth. They do not

present opposable thumbs, have claws, and furthermore their crania are flattened (Fleagle, 1988). It has been suggested that they present a greater similarity with the Dermoptera order mostly on the basis of recent fossil finds involving hard bones (Aguirre, 1995).

After the anatomical relationships are established, the Plesiadapiformes are found estranged of the rest of the Primates even in their basicranial circulatory pattern (Szalay, 1975). Neither can we find intermediate stratomorphs to join the Plesiadapiformes with some taxon of the Primates (Fleagle, 1988). Hence, we prefer to leave them out of the order Primates, and not to consider them in our classification.

In the suborder Strepsirhini are grouped an extinct infraorder, the Adapiformes, and the infraorder Lemuriformes. The Adapiformes have only one family, belonging to the Eocene. The Lemuriformes have current representatives, with continuity from the Miocene. The fossil record presents a discontinuity between Adapiformes and Lemuriformes.

The Adapiformes are grouped into one isolated family, Adapidae. The Lemuriformes includes eight families. Three of them are already extinct. The Lorisidae, with current representatives, has continuity back to the beginning of the Miocene (Aguirre, 1995).

The suborder Haplorhini includes the Primates with an independent ear opening of the bulla, the thickening of the stapedial branch of the internal carotid artery, a replacement of the rhinarium of the Strepsirhini by a pilose nose, and an increase in the cerebral volume and cranial capacity. In this suborder three infraorders are differentiated: Tarsiiformes, Platyrrhini and Catarrhini. The Tarsiiformes are grouped into two families, Omomyidae, extinct and with continuity throughout Eocene and beginning of the Oligocene, and Tarsiidae, with only one current representative and without continuity with the known fossil record (Aguirre, l995).

The infraorder Platyrrhini groups the South American monkeys into two families. The first is Cebidae, which channels to its current representatives with fossil specimens until the Oligocene. The fossils of the genus *Dolichocebus* of the Oligocene, *Neosaimiri* and *Saimiri bernensis* present great similarity with the genera *Cebus* and *Saimiri* (Delson and Rosenberger, 1984; Fleagle, 1988). *Cebupithecia,* of the Miocene, is very similar to the current genus *Pithecia* (Fleagle, 1988). *Aotus dindensis* of the Miocene is almost identical to representatives of the current genera *Aotus* (Fleagle, 1988), and *Stirtonia,* of the Miocene, possesses many of the characters of the current genera *Alouatta* (Fleagle, 1988). *Tremacebus* of the Oligocene presents a great similarity with *Callicebus* and current *Aotus* (Fleagle, 1988), and a close proximity to the current *Aotus* for Delson and Rosenberger (1984).

Recently a very complete skeleton of a *Protopithecus* has been found which was a giant primate of the Pleistocene. The preliminary investigations on this fossil reveal that the cranium is very similar to the *Alouatta* genus, and its postcranial skeleton to the genera *Ateles, Brachyteles,* and *Lagothrix* (Hartwig and Cartelle, 1996). This may mean that all these genera are part of a single holobaramin, and that they emerged as variations of *Protopithecus.*

A genus, *Branisella,* appears isolated in the Oligocene without clear relationships with the rest of monkeys in the New World. A second family of Platyrrhini, Callitrichidae contains only current representatives of great anatomical uniformity, and has been called "Anatomical Complex of the Marmoset" (Delson and Rosenberger, 1984). Additionally *Cebuella* and *Callithrix,* belonging to the family Callitrichidae share a particular physiological attribute: intrauterine placental anastomoses formation between heterosexual twins (Benirschke, Anderson, and Brownhill, 1962). One must emphasize that the remains of Platyrrhini do not occupy more than a "shoe box" (Fleagle, 1988).

The infraorder Catarrhini groups all the European, Asian and African monkeys. In the early Egyptian Oligocene, begins the fossil record of the greatly diverse Catarrhini, all belonging to the family Parapithecidae. Another two extinct families, Oreopithecidae and Pliopithecidae are located in the Miocene. The family Cercopithecidae is currently very diversified, with continuity until the Miocene. In this family two subfamilies are differentiated, Colobinae and Cercopithecinae. These may correspond to two different monobaramins, although we cannot determine whether they belong to a single holobaramin. The fossils attributed to the subfamily Colobinae are not very similar to the current representatives, opposite to what occurs with the fossils that are attributed to the subfamily Cercopithecinae (Fleagle, 1988). Some authors have emphasized the great similarity between the remains attributed to extinct *Macaca* and current representatives of this same genera, to the extent of being practically indistinguishable in many cases (Delson and Rosenberger, 1984; Fleagle, 1988).

The fossil remains assigned to the genera *Papio, Cercocebus* and *Theropithecus,* all belonging to the subfamily Cercopithecinae, also present a close similitude with current representatives of these same genera, but present greater anatomical specialization (Fleagle, 1988). This family Cercopithecidae presents some additional difficulties involving the identification of the fossil remains. To determine which subfamily the taxa belong to, the current representatives are compared by characters of their soft tissues, such as the stomach or the bags of the cheeks. Unfortunately, these characters cannot be recognized, at least with ease, in the fossils.

The family Hylobatidae descends with continuity from Miocene representatives, if the fossils of *Dendropithecus* are accepted as hylobatids (Aguirre, 1995). Similarly, the family Pongidae, whose most ancient representative would be *Proconsul* descends from the Miocene.

The case of the hominids deserves an independent mention, because it is a group that we consider polybaraminic.

In the order Primates, the only occasion we can use the Scriptures as a baraminologic membership criterion is to differentiate man from the rest of the biota. Man was created on the sixth day (Genesis 1:26, 27) independently of the rest of the animals. Are the Australopithecus, *H. habilis* and *H. erectus* part of that sixth day of the creation?

When the first fossil of *Australopithecus africanus* was discovered, the child Taung, Dart (1925) saw in him anatomical characters more advanced than those of Primates, and considered it an intermediate in the evolution towards man. However, not everyone found those characteristics superior to those of monkeys (Keith, Smith, Woodward and Duckworth, 1925). Not until the 1950's were the Australopithecines considered by a majority as evolutionary intermediate towards man. Around this time the Piltdown man was discovered to be a fraud. Broom found indications in postcranial remains of *Australopithecus,* that these would have been bipeds (Verhaegen, 1994).

The Piltdown fraud showed a simian dentition and jaw and a human brain; the Taung child showed the opposite. When the evidence vanished for the man from Piltdown, *Australopithecus* had the road free as intermediate in human evolution (Verhaegen, 1994). However, Verhaegen (1994) considers the placement of the *Australopithecus* in the base of the human evolutionary line as nothing more than a prejudice. Bipedalism does not guarantee human affinity, although all and only humans are bipeds at present. After an examination of Australopithecine anatomy Verhaegen (1994) located their origin with the current anthropomorphs. The common ancestor of humans and anthropomorphs would have been more similar to both than they are to each other. Whether this idea is right or wrong will not be analyzed here, but with the Scriptural basis we consider that the Australopithecines are monkeys with greater or smaller degree of bipedalism (Mehlert, 1996).

Gibson considers that the anthropomorphs may possibly be degenerated forms of humans (Gibson, 1986). We do not share this opinion because it has not been possible to find out whether human sexual cells interact with those of anthropomorphs (Bedford, 1981), and it has never been demonstrated that these and man may have hybridized (Marsh, 1973). We also do not believe that *Homo habilis* presents human characteristics in its anatomy or behavior (Lubenow, 1992; García-Pozuelo-Ramos, 1993; Verhaegen, 1994).

Homo erectus presents every human characteristic. Anatomically they seem capable of speech, possess bipedalism and human corporal proportions, and have a brain of the size and structure of human beings. Furthermore it has been demonstrated that they are stewards and handlers of human instruments, in addition to using fire (Lubenow, 1992; García-Pozuelo-Ramos, 1993).

It does seem that there are degeneracy signs in *H. erectus,* but as a result of natural variation in humans, accepted by most creationists. The Neanderthals do not deserve greater commentary; they are human. From all of this we conclude that *H. erectus, H. sapiens neandertalensis* and *H. sapiens sapiens* certify a holobaramin (Figure 2).

We consider *H. habilis* and *Australopithecus* to be a unique monobaramin (Figure 3) (Lubenow, 1992; García-Pozuelo-Ramos, 1993; Verhaegen, 1994) in which a great variability is presented, with differentiation into robust and gracile forms. The Australopithecines may form a monobaramin near the anthropomorphs, though this must be confirmed.

Chromosomal and protein comparisons, would group *Pan* and *Gorilla* into the same monobaramin. However, with these criteria alone, man would form part of the same monobaramin though the anatomical differences, ecological differences, and behavioral differences have determined that man be classified in a different family.

The analysis of Primate fossils that are presently known to date could increase the number of families and subfamilies of the order Primates to double those existing. Broadly speaking, we consider the subfamily or in some cases the family as equivalent to a holobaramin, (to consider the different membership criterion and Figure 4), and we believe this is a conservative measure. The fossils indicate that the Primates gather an intrabaraminic diversification, but that the number of holobaramins has not had to surpass more than 30.

The Hybridization Criterion

The most determinant criterion to establish the ownership to a holobaramin is that of hybridization. However, we cannot use hybridization with fossils. The importance of the hybridization criterion comes from the fact that it compels a biochemistry compatibility, chromosomal, morphological, etc. that is manifested in a correct development. Simply put it integrates all other affiliation criteria.

Proposed by Marsh (1941), this criterion goes beyond the mere ovum/sperm interaction, since this can occur between very different species and without genetic relationship. The hamster oocyte permits in its interior the entry of sperms of many species of mammals, included marsupials, and even fowl (Samour, Moore, and Smith, 1986). After the introduction of human sperm in an egg of a hamster, free of the zona pellucida, it is possible to transform chromatin from human sperm into first-cleavage mitotic chromosomes that can be karyotyped (Brandriff and Gordon, 1989). However, all these gametic interactions between different animals only reflect the existence of common mechanisms of superficial interaction. The information carried by the DNA of both gametes to form the new being does not behave as a whole. The human sperm is capable of joining to the covers of the gibbon ovum, though it does not interact with the ova of sub-hominoids such as *Macaca* or *Papio* or of other mammals (Bedford, 1977).

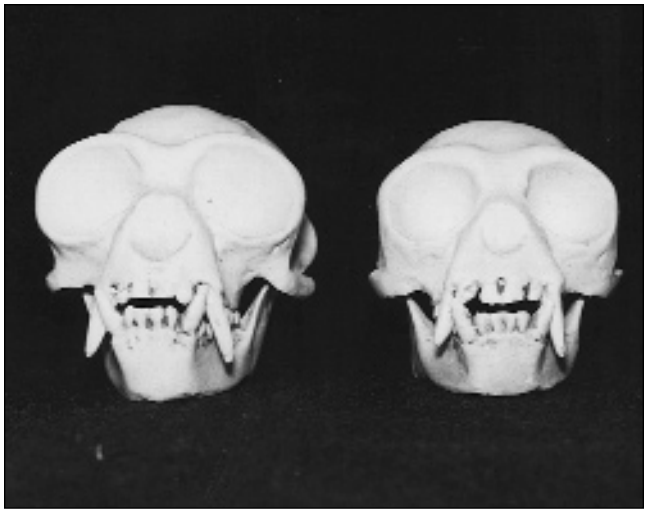

Figure 1. Skulls (casts) of *Hylobates syndactylus* male (left) and *Hylobates lar* female (right). The differences do not go beyond those inherent of sexual dimorphism in other species.

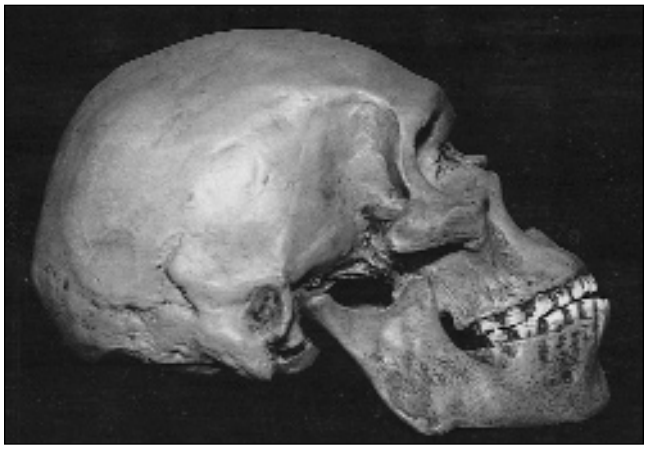

Figure 2a. Skull (cast) of present Australian aborigine, *H. sapiens sapiens.* b. Skull (cast) of *H. sapiens neandertalensis,* La Ferrassie I. c. Skull (cast) of *H. erectus* KNM-ER 3733. All of these *Homo* share morphologic and behavioral characteristics that allows us to group them as humans.

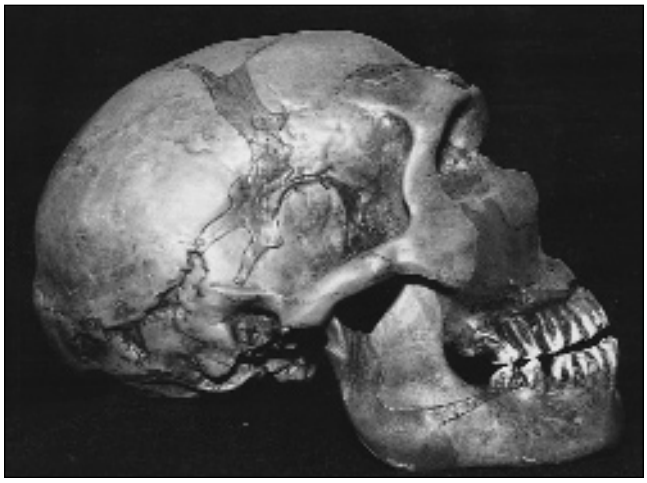

Figure 2b. See caption 2a.

Figure 2c. See caption 2a.

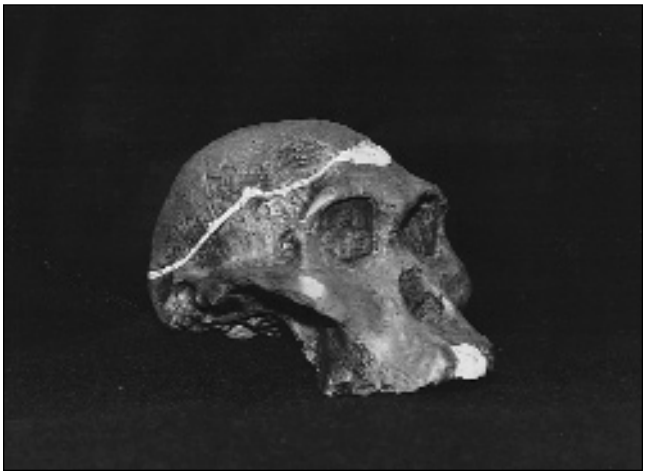

Figure 3a. Skull (cast) of *A. africanus,* Sts 5. b. Skull (cast) of *H. habilis,* O.H.24. The similar morphologic characteristics allows us to place them in the same monobaramin.

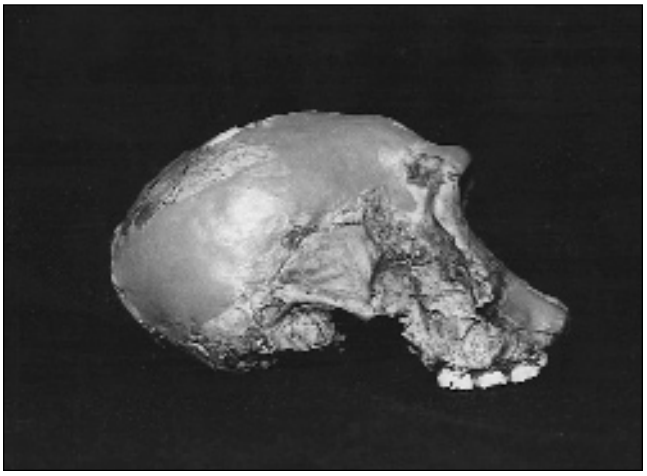

Figure 3b. See caption 3a.

ORDER PRIMATES (182 species)*

SUBORDER STREPSIRHINI0
+INFRAORDER ADAPIFORMES
+FAMILY Adapidae
INFRAORDER LEMURIFORMES
+FAMILY Megaladapidae
+FAMILY Palaeopropitacidae
+FAMILY Archaeolemuridae
FAMILY Lorisidae
Subfamily Lorisinae
Subfamily Galaginae (M)
FAMILY Daubentonidae (unique specie)
FAMILY Indriidae
FAMILY Lemuridae
Subfamily Lemurinae
Subfamily Lepilemurinae
Subfamily Hapalemurinae
FAMILY Cheirogaleidae (C)
SUBORDER HAPLORHINI
INFRAORDER TARSIIFORMES
+FAMILY Omomyidae
FAMILY Tarsiidae (Three species in one genus)
INFRAORDER PLATYRRHINI
FAMILY Cebidae
FAMILY Callitrichidae (c)[a]
INFRAORDER CATARRHINI
+FAMILY Parapithecidae
+FAMILY Oreopithecidae
+FAMILY Pliopithecidae
FAMILY Cercopithecidae
Subfamily Cercopithecinae (H)
Subfamily Colobinae
FAMILY Hylobatidae (H)
FAMILY Pongidae (M,C)
FAMILY Hominidae (S)

Bold words belongs to monobaramin or holobaramin.
* MacDonald,1991.
\+ Extinct taxon.
M Monobaramin by molecular criterion.
C Monobaramin by chromosomal criterion.
[a] "Marmoset Anatomical Complex" Morphological unity.
H Monobaramin by hybridization criterion.
S Holobaramin by Scriptural criterion.

Figure 4.

The order Primates groups 12 families with current representatives (MacDonald, 1991), and eight extinct families (Aguirre, 1995). The *Lemur* genus is the only member of the family Lemuridae known to hybridize because no data is available for the other two genera (Gray, 1972; Warter and Rumpler, 1985). We have found no hybridization data for the families Cheirogaleidae, Indriidae, Daubentonidae, Lorisidae and Tarsiidae. In the family Callitrichidae there are five genera (MacDonald, 1991), of which two, *Callithrix* and *Saguinus* possess species that hybridize within the genus, but not between genera (Gray, 1972). In the family Cebidae, with 11 genera, four hybridize between species of the same genus, including *Cebus, Pithecia, Chiropotes* and *Ateles* (Gray, 1972; Rossan and Baerg, 1976).

The family Cercopithecidae includes 14 genera. Hybridization occurs between species of different genera, and thus we can establish a continuous line between *Cercopithecus, Macaca, Theropithecus, Allenopithecus, Erithrocebus, Papio* and *Cercocebus.* In the genus *Semnopithecus* there is hybridization between species within the genus. In the subfamily Cercopitecinae all the genera hybridize mutually or through third parties, except the genus *Miopithecus,* of which there have been no reported cases of hybridization. (Gray, 1972; Matsubayashi, Hirai, Watanabe, Ohkura and Nozawa, 1978; Ledbetter, Grant, and Kuehl, 1979; Muleris, Gautier, Lombard, and Dutrillaux, 1985).

In the family Hylobatidae, all the current representatives hybridize mutually (Gray, 1972; Shafer and Myers, 1976; Wolkin and Myers, 1980). In the Pongidae hybridization has only been reported between the two representatives of the *Pan* genus (Vervaecke and Elsacker, 1992).

Conclusions

We have analyzed the data available in the fields of molecular biology, anatomy, and physiology to attempt to determine the discontinuities between different holobaramins of the order Primates. We have emphasized the difficulties of using only one criterion. In addition to the methodological difficulties and those of interpretation, the studies that have been accomplished up until now are based on the continuity prejudice of the theory of evolution. This forces us to design some experiments or to think over observations with the purpose of getting some objective results.

With the available data, it is difficult to offer a definitive baraminology in this mammalian order, though some preliminary results are given that permit a program of systematic investigation of the discontinuities (Figure 4). It is necessary to generate a eucladistic reappraisal (Wise, 1992) of the order Primates to assure the anatomical relationships, but we believe the number of holobaramins has not surpassed more than 30, if they correspond with families or subfamilies. At least, it seems we can deduce this from the analysis we have presented. However, if the proposal of Wise (1992), that there may be three or four holobaramins for each order is generalizable, then the holobaramins of the order Primates would correspond approximately to the taxon infraorder.

Since hybridization is the more reliable criterion, efforts should he centered in the search of species capable of hybridization following the criterion of Marsh (1976). The hybridizations will serve to calibrate the rest of the membership criteria. Once the molecular, chromosomal, anatomical, or other kind of membership criteria variations are established for a holobaramin, we can compare these variations with other species whose ability for hybridization has not

been determined. The comparison has to be done using statistical methods (Wise, 1992). The greatest variability found in the characters studied, we think, should be considered as the most reliable reference. Thus, we think that the morphologic variability in the sub-family Cercopithecinae is a better calibrated reference than the reference of morphologic variation in the family Hylobatidae.

Later, we will have to determine the taxa to which a calibrated membership criterion can be applied. The morphologic variability in Cercopithecinae could serve as a reference to determine other holobaramins. In any case, a single membership criterion, other than the hybridization criterion, may not be enough to reliably establish monobaraminic continuity.

Investigation of the hybridization criterion must be a high priority, although it will evidently be costly. To optimize resources, the most fruitful options need to be found, as Wise (1995) has indicated for the field of transitional forms in the fossil record, and their utilization for establishment of continuity lines.

In the research of discontinuity by hybridization, investigation is needed to find the continuity or discontinuity between genera of the subfamily Colobinae, and between this subfamily and its sister Cercopithecinae, which can be considered a monobaramin (Hartwig-Scherer, 1993).

In the suborder Strepsirhini, information is needed about the unity or disunity between the representatives of the family Lorisidae and its relationship to the family Cheirogaleidae, and in addition the relationships of these two families with the family Lemuridae. In the suborder Haplorhini, the relationships between the genera of the family Cebidae and of this family with Callitrichidae need to be investigated.

In the family Pongidae one must establish the relationships between its three anthropomorphic genera.

It is also necessary to find the relationship between New World Primates and Old World Primates. It seems reasonable that New World Primates would diversify from one or several populations of the Old World. Another possibility is that the ancestors of New World Primates, survivors of the Flood settled exclusively in the land colonized and that now corresponds with the American continent.

We do not discount the idea that hybridization capacity between members of a same holobaramin is lost with time. However, with well-calibrated accessory criteria the determination of holobaramins should be possible, something that still seems precipitate in the order Primates. What seems impossible is that those species belonging to different holobaramins could hybridize. As outlined by Marsh (1981), if God creates separately, He would have done so that discontinuity continues to exist

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