Evidence for a Holobaraminic Origin of the Cats

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Abstract

The baraminology of living cats has been investigated using recently described quantitative methods. A variety of characters including ecological, morphological, chromosomal, and molecular data were used to characterize 17 cat species, the spotted hyaena, and the meerkat. Application of phenetic and cladistic clustering algorithms defined three subgroups of cats, which are: the genera *Panthera* plus *Neofelis*, *Acionyx* plus *Puma*, and *Felis* plus allied genera. Quantitative analyses suggested that the three cat subgroups each form a monobaramin. Hybridization records suggesting a potential for gene flow between two of the monobaramins, plus extensive phenetic overlap between all three of the monobaramins suggested all felids could be lumped into a single monobaramin. Statistically significant gaps between the cat and outgroup taxa suggested these species were apobaraminic. Monobaraminic continuity within the cats and apobaraminic discontinuity between the cat and outgroup taxa leads to the hypothesis of a single Felid holobaramin.

Introduction

Subfamilial relationships within the cat family Felidae have not been firmly established. O'Brien et al. (1987) note that cats have been classified into as few as two genera and as many as 20. Such a biosystematic conundrum may be due, in part, to the search for natural groups within a macroevolutionary framework. Baraminology is a creationist biosystematics that seeks to establish the identity of specially created groups of organisms called baramins. As the basic unit of biological creation, the baramin is hypothesized to represent the true natural group which biosystematists seek. The goal of this paper is to provide new insights into the systematics of living cats using recently described quantitative methods in baraminology (Robinson and Cavanaugh, 1998). Several ongoing questions are addressed including the reliability of different criteria for identifying holobaramins, and the interpretation of homoplasy within a creationist context.

Materials and Methods

Data Acquisition and Analysis

We selected 287 polymorphic characters (Appendix I) representing 17 cat species, the spotted hyaena, and the meerkat (Table I). The hyaena and meerkat were selected as outgroups because they are members of the same superfamily, the Aeluroidea, to which cats belong. We classified the data into four general criteria including ecological, morphological, chromosomal, and molecular characters. The complete data matrix is available upon request. Baraminic distance, the proportion of mismatched characters between two species, was used as a measure of resemblance. A panel of diagnostic statistics were used to describe the relevance (*A*), diversity (*C* and d_{avg}), and signal (*S1*) within the data set (Robinson and Cavanaugh, 1998).

Table I. List of species included in this study.

Taxon	Common Name	Code
Superfamily Aeluroidea		
Family Felidae		
Panthera leo	lion	Ple
Panthera tigris	tiger	Pti
Panthera pardus	leopard	Ppa
Panthera onca	jaguar	Pon
Panthera uncia	snow leopard	Pun
Neofelis nebulosa	clouded leopard	Nne
Pardofelis marmorata	marbled cat	Pma
Lynx rufus	bobcat	Lru
Lynx canadensis	Canadien lynx	Lca
Caracal caracal	caracal	Cca
Leptailurus serval	serval	Lse
Prionailurus bengalensis	leopard cat	Pbe
Profelis aurata	African golden cat	Pau
Profelis temmincki	Asian golden cat	Pte
Acionyx jubatus	cheetah	Aju
Puma concolor	cougar	Pco
Leopardus pardalis	ocelot	Lpa
Family Hyaenidae		
Crocuta crocuta	spotted hyaena	Ccr
Family Viverridae		
Suricata suricatta	meerkat	Ssu

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Baraminic distances and most of the diagnostic statistics were calculated with a Macintosh computer program developed by the first author. The MANTEL 3.0 program of the R package (Legendre and Vaudor, 1991) was used to calculate the criterial correlations, and to estimate their significance using Mantel's test. The Bonferroni correction was used to establish a significance level ($P = 0.0002$ in this study) for evaluating the criterial correlations. The CLUSTAL W program (Thompson, Higgins, and Gibson, 1994) was used to align the DNA sequences, and to calculate uncorrected transitional and transversional sequence differences as described previously (Robinson, 1997). The DATA DESK 3.0 statistical package (Odesta Corporation, Northbrook, Illinois) was used for the organismal correlation analyses. A neighbor-joining (Saitou and Nei, 1987) dendrogram based on baraminic distances was generated using the NEIGHBOR program of the PHYLIP 3.54 computer package (Felsenstein, 1989). Cladograms were generated using the PAUP 3.1.1 computer program (Swofford, 1993) treating all characters as unordered and unweighted. A 50% majority rule consensus tree was constructed using the heuristic search option, random addition of taxa, MAXTREES set to 100, and TBR branch swapping parameters. Both the phenetic and cladistic dendrograms were evaluated statistically with 200 bootstrap iterations.

Scriptural Considerations

While the acts of biological creation recorded in the Scriptures form the philosophical basis of baraminology (that creation of different taxa precludes their evolutionary continuity), the Scriptures may seldom affect the routine work of identifying and classifying baramins. A recent study concluded that although the Hebrew word *min* may be a word of biological origin, and may have a basic meaning of division, its relationship to the creationist term baramin is unclear (Williams, 1997). The word *min* is not used with specific reference to cats. There are, however, other passages of Scripture that may be relevant to cat baraminology.

The Hebrew word *namer*, meaning spotted, has been translated as leopard and cheetah because both species have spotted coats. Based on behavioral clues such as the propensity to ambush rather than chase prey (Jeremiah 5:6, Hosea 13:7) we suggest *namer* refers to the leopard, *Panthera pardus*. Isaiah 11:6-9 describes a herbivorous Garden of Eden environment with lions and leopards (Hebrew *namer*) present. The coexistence of multiple cat species in the original Garden would support a hypothesis of polybaraminic cat origins; specifically a separate origin for congeneric cat species. We suggest this passage reflects Garden of Eden conditions not organisms since the only humans in the Garden were Adam and Eve, and other humans are mentioned in the Isaiah 11 record. Furthermore, the context is a prophetic statement of the conditions of the earth as restored by the Messiah, the Branch from Jesse. Jeremiah 13:23 also provides an interesting comment relevant to cat baraminology, "Can the Ethiopian change his skin or the leopard its spots? Neither can you do good who are accustomed to doing evil." This rhetorical question suggests the individual leopard cannot change genetically inherited traits. However, variation in human characters can occur through generations as indicated by Acts 17:26. We suggest the Jeremiah 13 passage likewise allows for variation in cats to be expressed through generations.

Results

Evaluation of Criteria

The combined data set was applicable to an average of 97.3% of the species (Table II). The more relevant criteria tended to contain more characters. For example, there were no missing data among the 199 molecular characters whereas the ten chromosomal characters were only applicable to an average of 83.7% of the species. The organisms differed on average among 27.5% of their characters with a 22.2% probability of a mismatch at the average character. An inverse relationship was found between the number characters and diversity of a given criterion. For example, the probability of a mismatch between two species ranged from 54.7% with the ecological characters to 19.3% with the molecular characters. The combined data set plus the morphological, chromosomal, and molecular criteria considered separately contained a statistically significant level of baraminic signal. These data suggested a heterogenous assemblage of organisms was sampled. In contrast to the results reported for Catarrhine primates (Robinson and Cavanaugh, 1998) there was no association between many of the

Table II. Summary of data used to characterize the felids and aeluroid outgroups.

Criteria	No. of Characters	Diagnostic Statistics A	C	d_{avg}	S1
Combined	287	0.973	0.222	0.275	314.403***
Ecological	8	0.842	0.547	0.553	62.800
Morphological	70	0.932	0.255	0.324	258.571***
Chromosomal	10	0.837	0.307	0.411	122.583*
Molecular	199	1.000	0.193	0.249	190.524**

* $P<0.05$
** $P<0.005$
*** $P<0.0005$

criteria (Table III). Only the baraminic distances calculated from morphological and molecular data were significantly correlated.

A variety of techniques exist for assessing biosystematic relationships at the level of genes and proteins. The use of mitochondrial DNA (mtDNA) has received increased attention because several of its properties are uniquely suited for studies of phylogeny (Avise, et al., 1987). For example, in many organisms the mitochondrion is maternally inherited and not subject to the scrambling effects of recombination. Genetic differences in mitochondrial genes are therefore largely the result of mutation. Closer inspection has re-

Table III. Product-moment correlation matrix of baraminic distances calculated for each pair of criteria.

	Eco	Mor	Chr	Mol
Ecological	–			
Morphological	0.527	–		
Chromosomal	0.419	0.602	–	
Molecular	0.468	0.786*	0.627	–

*$P < 0.0002$

vealed a certain type of nucleotide substitution called transitions are more frequent between taxonomically similar organisms (Holmquist, 1983). These mutations result when purines are substituted by other purines or pyrimidines are substituted by other pyrimidines. Transversional substitutions predominate between divergent taxa. Such substitutions represent the replacement of purines for pyrimidines and vice versa, which is an exchange of structurally different molecules. A study of turtle mtDNA has suggested substitutional patterns might provide useful data for baraminologists by reflecting a process of limited variation (Robinson, 1997). In this survey we examined portions of both 12S-rRNA and cytochrome *b* mitochondrial genes for substitutional patterns (Figure 1). The cat-hyaena comparisons slightly overlapped for the 12S-rRNA gene, whereas both outgroups were separated from cats by a transversional gap for the cytochrome *b* gene.

Cluster Analyses

The phenetic and cladistic dendrograms were notably congruent (Figure 2). Although the phenetic dendrogram was more highly resolved, no topological discrepancies were observed. While the separate baraminic membership criteria were not significantly associated with each other (Table III), they did not significantly conflict since both the phenetic and cladistic analyses based on the combined data set were able to resolve three major subgroups with confidence. Subgroup A was composed of the large cats and received 96% and 85% bootstrap support in the respective cluster analyses. The intermediate-sized cheetah and cougar formed subgroup B with 76% and 81% bootstrap support respectively. Subgroup C was represented by the seven small cat genera, although these species did not form a single bootstrap supported cluster. Groups such as the ocelot plus leopard cat, African golden cat plus caracal, and the lynxes received moderate to strong bootstrap support in one or both analyses. The outgroup taxa formed subgroup D, and their separation from the cats was fully corroborated with 100% bootstrap support in both cluster analyses.

Baraminic Distance Variation Analyses

In general, intragroup versus intergroup comparisons can be made by estimating 95% confidence intervals around average baraminic distances. Overlapping intragroup and intergroup confidence intervals would suggest there is no statistically significant difference in the baraminic distance variation of the groups being compared. The average baraminic distance within group X would not differ significantly from the average baraminic distance between groups X and Y, which would suggest groups X and Y may be monobaraminically related. On the other hand, non-overlapping confidence intervals would suggest the range of baraminic distance variation is significantly different. In this case, the average baraminic distance within group X would be significantly lower than the distance between groups X and Y, and may be diagnostic of an apobaraminic division separating groups X and Y (Robinson and Cavanaugh, 1998).

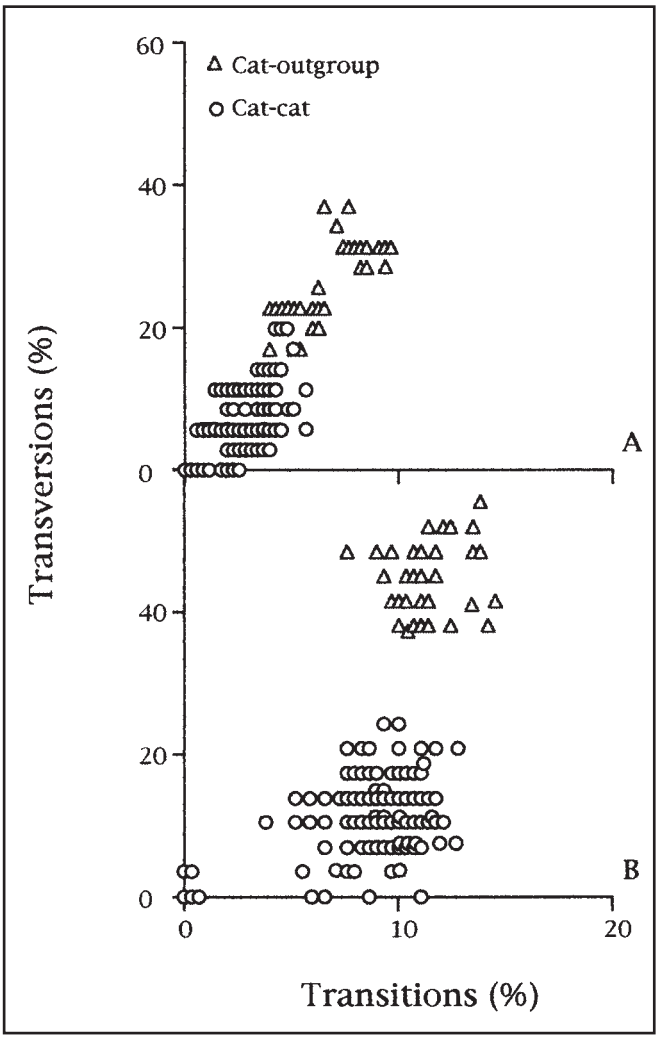

Figure 1. Transition versus transversion sequence differences for 12S-rRNA (A) and cytochrome *b* (B) genes.

In this study, baraminic distances ranged from 1.5% between the two lynx species, to 58.8% between the lion and meerkat (Table IV). Based on the combined data set, the average baraminic distance of cat species within a genus did not differ significantly from that found within the phenetically and cladistically defined subgroups (Table V). The same pattern was found with each criterion considered separately except with the chromosomal data. Baraminic distance variation within a given cat subgroup was therefore

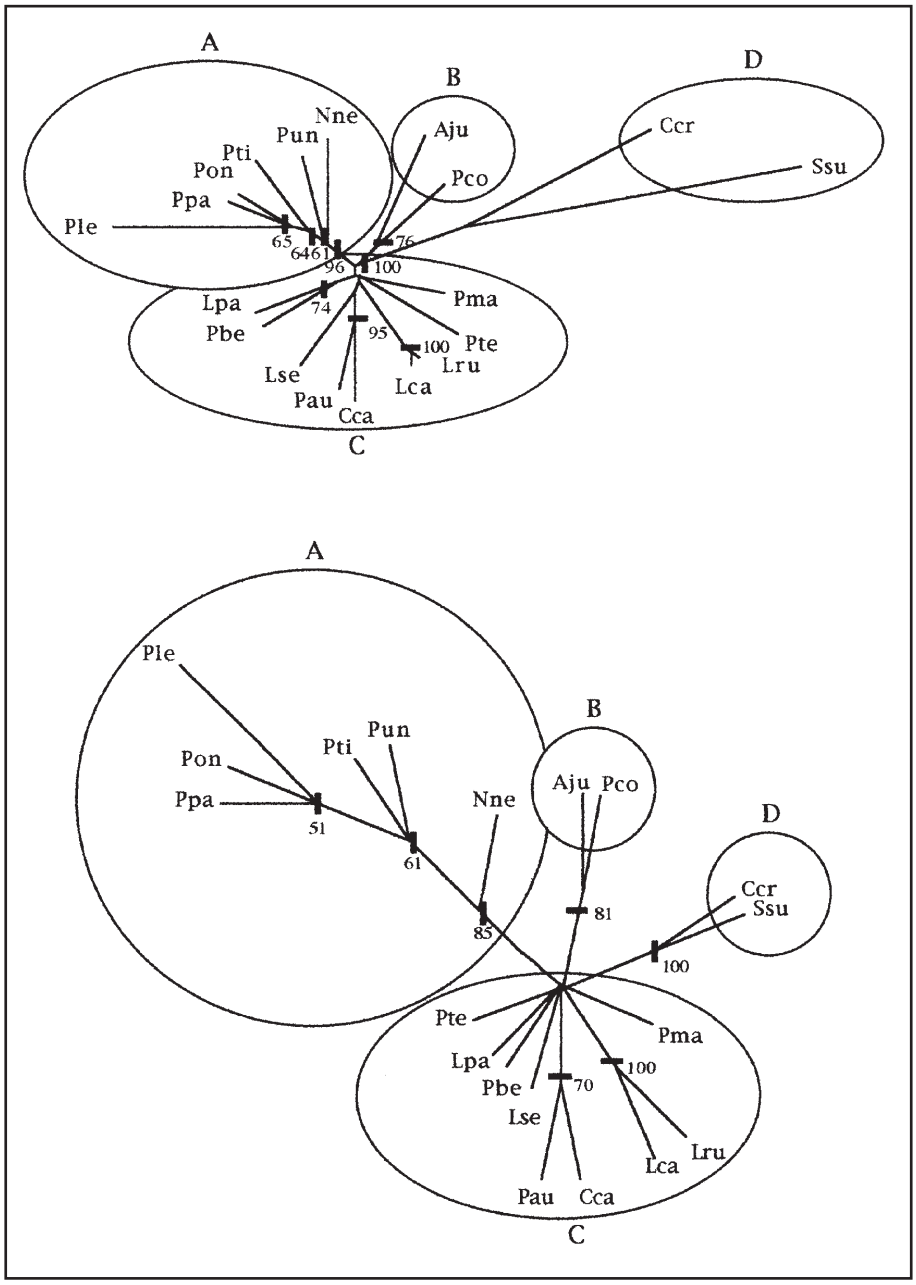

Figure 2. Unrooted neighbor-joining (upper) and cladistic (lower) dendrograms. The branch lengths are proportional to baraminic distances in the neighbor-joining dendrogram. Bootstrap values supporting branches with at least 50% confidence are numbered and highlighted. Four major subgroups labelled A-D have been marked with ellipses.

equivalent to the baraminic distance variation within a genus. Such data support a classification of three cat genera corresponding to *Panthera* (subgroup A), *Acionyx* (subgroup B), and *Felis* (subgroup C). Also based on the combined data set, a statistically significant gap of 4.2% was found between the average intrasubgroup and intersubgroup baraminic distance. This distinction of subgroups was supported by all criteria except the chromosomal data.

For two reasons, we do not interpret the gap of 4.2% as evidence that cats are apobaraminic. First, the short internal branches and long terminal branches depicted in the phenetic dendrogram (Figure 2) suggested deep divisions were present within the Felidae family. This type of taxonomic structure is expected to reveal some degree of discontinuity between the different cat subgroups. Second, a small gap of 4.2% could be within the range of experimental error. Note that, in a previous study, the gaps based on morphological and ecological baraminic distances which separated humans from nonhuman primates were 20.4% and 45.7% respectively (Robinson and Cavanaugh, 1998). A gap of this size, 16.5%, was found between the average intersubgroup and cat-outgroup baraminic distance, based on the combined data set (Table V). The separation of cats from outgroups was further supported by all of the criteria.

Organismal Correlation Analyses

Correlation analyses of baraminic distance sets can be used to identify two species as monobaraminic or apobaraminic. A positive correlation between all of the baraminic distances of two organisms (less the zero distance between the organism and itself) indicates the two organisms have equivalent sets of baraminic distances, and suggests the organisms may be monobaraminic. In contrast, a negative correlation between the baraminic distances of two organisms may mark these organisms as apobaraminic because their baraminic distance sets are antithetical (Robinson and Cavanaugh, 1998).

We have used previously a graphical method for summarizing the numerous correlation analyses that can be made when different taxonomic groups and different baraminic membership criteria are examined (Robinson and Cavanaugh, 1998). Figure 3 summarizes 20 such analyses for the present study. Correlation coefficients noted on the right side of a graph are positive and may identify monobaramins, whereas correlation coefficients noted on the left side of a graph are negative and may identify apobaramins. Statistically speaking, correlation coefficients that could be obtained by random data lie in the middle of a graph; the baraminic relationships inferred by these comparisons are statistically unresolved. However, for unresolved comparisons a trend towards the right or left side of a graph hints at the baraminic relationship that might be sup-

Table IV. Baraminic distance matrix listing the proportion (lower diagonal) and number (upper diagonal) of character mismatches.

	Ple	Pti	Ppa	Pon	Pun	Nne	Pma	Lru	Lca
Ple	–	70/287	62/287	62/287	74/279	86/278	81/273	102/286	89/269
Pti	0.244	–	49/287	44/287	53/279	55/278	57/273	70/286	57/269
Ppa	0.216	0.171	–	34/287	41/279	57/278	57/273	70/286	56/269
Pon	0.216	0.153	0.119	–	40/279	61/278	58/273	71/286	58/269
Pun	0.265	0.190	0.147	0.143	–	51/275	60/271	62/279	52/264
Nne	0.309	0.198	0.205	0.219	0.185	–	58/272	65/277	58/26
Pma	0.297	0.209	0.209	0.213	0.221	0.213	–	42/273	42/263
Lru	0.357	0.245	0.245	0.248	0.222	0.235	0.154	–	4/269
Lca	0.331	0.212	0.208	0.216	0.197	0.219	0.160	0.015	–
Cca	0.364	0.283	0.265	0.254	0.261	0.261	0.205	0.194	0.182
Lse	0.343	0.261	0.247	0.226	0.235	0.261	0.177	0.166	0.168
Pbe	0.327	0.278	0.264	0.257	0.250	0.236	0.167	0.184	0.192
Pau	0.337	0.239	0.232	0.235	0.244	0.261	0.185	0.207	0.216
Pte	0.351	0.235	0.239	0.235	0.218	0.242	0.168	0.188	0.192
Aju	0.339	0.276	0.280	0.262	0.229	0.291	0.223	0.239	0.209
Pco	0.322	0.241	0.234	0.231	0.245	0.256	0.191	0.225	0.208
Lpa	0.352	0.244	0.226	0.247	0.229	0.219	0.183	0.196	0.186
Ccr	0.453	0.379	0.398	0.359	0.406	0.429	0.406	0.418	0.392
Ssu	0.588	0.525	0.510	0.510	0.512	0.547	0.496	0.490	0.490

Cca	Lse	Pbe	Pau	Pte	Aju	Pco	Lpa	Ccr	Ssu
103/283	97/283	93/284	93/276	97/276	97/286	92/286	101/287	116/256	150/255
80/283	74/283	79/284	66/276	65/276	79/286	69/286	70/287	97/256	134/255
75/283	70/283	75/284	64/276	66/276	80/286	67/286	65/287	102/256	130/255
72/283	64/283	73/284	65/276	65/276	75/286	66/286	71/287	92/256	130/255
72/276	65/277	69/276	66/270	59/271	64/279	68/278	64/279	101/249	127/248
72/276	72/276	65/275	71/272	66/273	81/278	71/277	61/278	106/247	135/247
56/273	48/272	45/270	50/270	45/268	61/273	52/272	50/273	99/244	121/244
55/283	47/283	52/283	57/276	52/276	68/285	64/285	56/286	107/256	125/255
49/269	45/267	51/266	57/264	51/265	56/268	56/269	50/269	96/245	120/245
–	54/281	61/280	40/276	62/275	78/282	68/282	61/283	104/254	127/254
0.192	–	51/280	50/275	56/275	75/283	63/282	54/283	105/254	123/254
0.218	0.182	–	58/276	57/276	70/283	53/283	44/284	102/253	117/252
0.145	0.182	0.210	–	61/274	78/276	68/275	58/276	96/247	114/247
0.226	0.204	0.207	0.223	–	70/276	61/276	54/276	101/246	125/246
0.277	0.265	0.247	0.283	0.254	–	58/285	73/286	103/255	128/254
0.241	0.223	0.187	0.247	0.221	0.203	–	57/286	106/255	132/254
0.216	0.191	0.155	0.210	0.196	0.255	0.199	–	100/256	122/255
0.409	0.413	0.403	0.389	0.411	0.404	0.416	0.391	–	124/255
0.500	0.484	0.464	0.462	0.508	0.504	0.520	0.478	0.486	–

ported if more powerful data were available (Robinson and Cavanaugh, 1998).

The aeluroid correlation analyses provided evidence for both monobaraminic continuity uniting cats, and an apobaraminic division separating cats from outgroups. Thus, by definition these data identified a Felid holobaramin. Of all the aeluroid graphs presented in Figure 3 (Panels A, E, I, M, Q) a total of 850 correlation coefficients were noted (171 correlations per criteria, x 5 criteria, –5 correlations between the outgroups themselves). Most of the cat-cat correlations were skewed towards the right (633 positive, 47 negative), whereas most of the cat-outgroup correlations were skewed towards the left (19 positive, 151 negative). A majority (64.8%) of the aeluroid correlations were statistically significant. Note the distinct bimodal distribution obtained from the correlations based on the combined (panel A), morphological (panel I), and molecular (panel Q) data. This pattern was not as obvious in the ecological (panel E) and chromosomal (panel M) data.

The felid correlation analyses further supported the unity of the three cat subgroups. Of the felid graphs presented in Figure 3 (Panels B, F, J, N, R) a total of 680 correlation coefficients were noted (136 correlations per criteria, x 5 criteria). Most of the intrasubgroup cat correlations were skewed

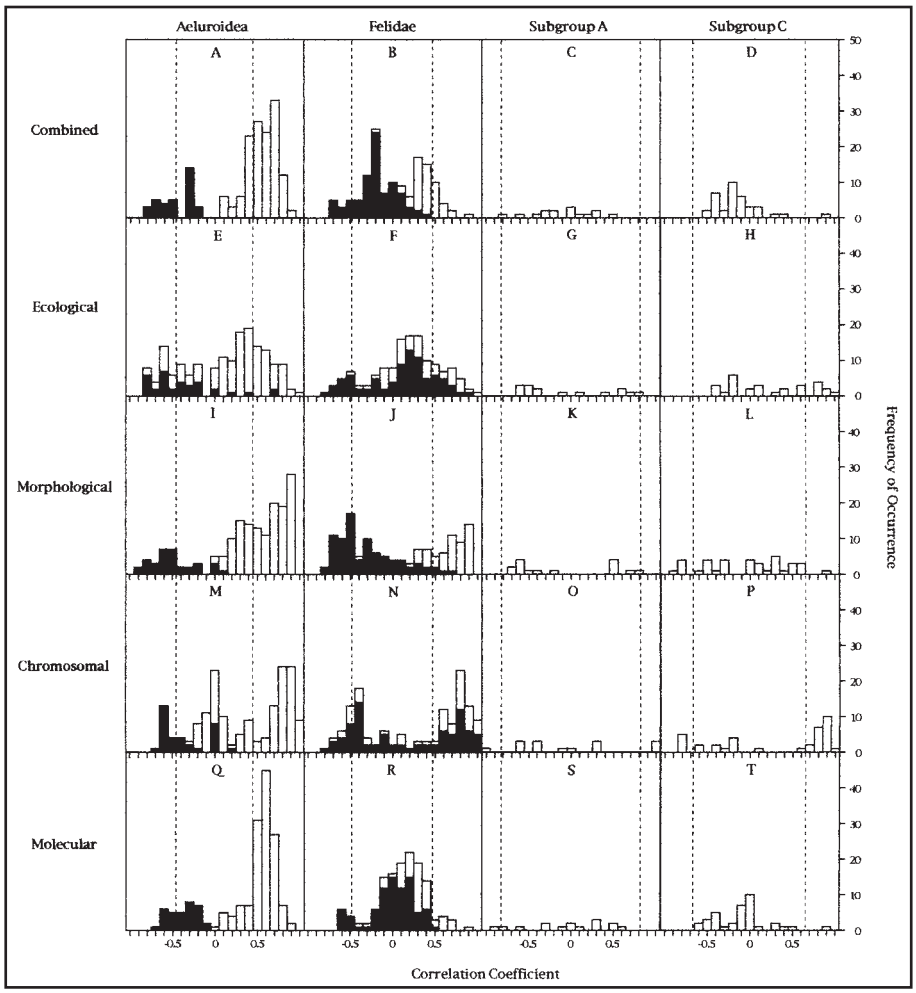

Figure 3. Exhaustive summary of the organismal correlation analyses based on different groups of taxa and different data sets. The dotted lines represent critical values for a 95% probability that the correlation is not zero (the values are: Aeluroidea ±0.455, Felidae ±0.482, Subgroup A ±0.811, Subgroup C ±0.666). In the Aeluroidea graphs, black bars denote cat-outgroup comparisons, and white bars represent cat-cat comparisons. In the Felidae graphs, black bars denote intersubgroup comparisons, and white bars represent intrasubgroup comparisons.

towards the right (229 positive, 31 negative). However, the intersubgroup cat correlations were distributed evenly in the right and left directions (199 positive, 221 negative). The resolution of the felid correlations was poor because only 36.2% of the correlations were statistically significant.

A couple of points can be made from the correlation analyses of subgroups A and C in Figure 3 (Panels C, G, K, O, S and D, H, L, P, T respectively). These data sets were relatively small and represented comparisons among very similar species. The correlations are almost completely unresolved as only 9.3% and 24.4% of the correlations for subgroups A and C respectively were statistically significant. Moreover, these data detected negative correlations between species that are capable of hybridizing and producing fertile offspring; certainly not apobaraminic species. Our results showed that the greatest resolution was obtained with the largest data set (the aeluroids). As successively smaller data sets were examined more similar species were compared and the resolution diminished.

Hybridograms

The potential for interspecific hybridization provides an important data set for elucidating monobaramins. Five species included in this survey are known to hybridize: *Panthera leo* x *Panthera tigris*, *Panthera pardus*, *Panthera onca*; *Panthera tigris* x *Panthera pardus*; *Panthera pardus* x *Panthera onca*, *Puma concolor*; *Panthera onca* x *Puma concolor* (Gray, 1972; Van Gelder, 1977). Gene flow is also possible between *Lynx rufus* and *Prionailurus bengalensis* since both species are known to cross with *Felis domesticus* (Gray, 1972). Mapping the information obtained from the quantitative analyses onto a matrix of hybridization data (here called a hybridogram) resulted in a useful graphical method for identifying monobaramins (Figure 4). Eleven cat species contained pairwise

Table V. Comparisons of intragroup with intergroup baraminic distance variation.

	Average Baraminic Distance (±95% C.I.)			
Criteria	Cat Species Within Genera	Cats Within Subgroups	Cats Between Subgroups	Cats Versus Outgroups
Combined	0.175 (0.218, 0.132)	0.193 (0.201, 0.185)	0.252 (0.261, 0.243)	0.455 (0.484, 0.426)
Ecological	0.477 (0.629, 0.325)	0.391 (0.483, 0.299)	0.546 (0.598, 0.494)	0.789 (0.850, 0.728)
Morphological	0.145 (0.190, 0.100)	0.164 (0.183, 0.145)	0.306 (0.321, 0.291)	0.611 (0.653, 0.569)
Chromosomal	0.094 (0.183, 0.005)	0.298 (0.378, 0.218)	0.336 (0.389, 0.283)	0.831 (0.880, 0.782)
Molecular	0.178 (0.231, 0.125)	0.192 (0.203, 0.181)	0.221 (0.231, 0.211)	0.405 (0.421, 0.389)
n	12	40	84	34

Note: Subgroups are defined in Figure 2.

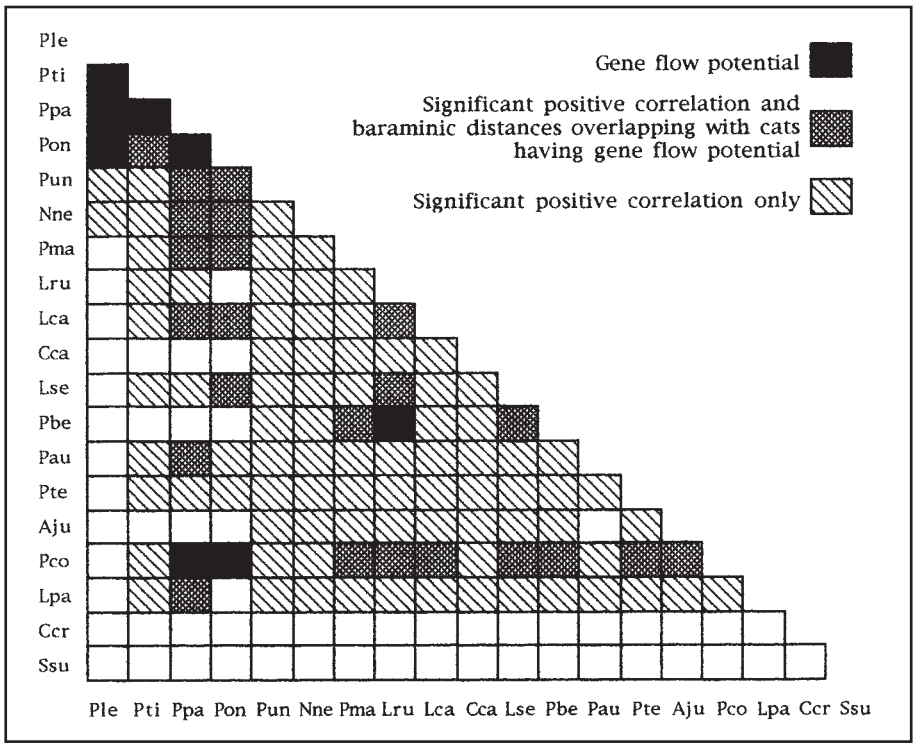

Figure 4. Hybridogram characterizing a single cat monobaramin on the basis of gene flow potential, overlap in pairwise baraminic distances, and significantly positive organismal correlations.

baraminic distances (the values tabulated in Table IV, not the confidence intervals estimated in Table V) that overlapped with those of hybridizing cats. The organismal correlations based on the combined aeluroid data set (Figure 3A) was more inclusive and grouped nearly all cats into a single monobaramin. All cat species within the range of baraminic distances of cats capable of gene flow were also significantly and positively correlated. There was no overlap of cats with outgroups.

Eaton (1974) noted that *Acionyx jubatus* displays an aggressive rather than copulative behavior towards dummies of *Panthera pardus*. Thus, a possible lack of gene flow between these species may partially explain the lack of correlation between their characters. Aggressive behavior may also partially explain the observation that large cats tended to be uncorrelated with the intermediate and smaller species. Indeed, based on the combined aeluroid data set 96% of the unresolved organismal correlations were comparisons of large cats with smaller species. The clouded and snow leopards being the smallest of the large cats provided an exception. The baraminic distances of these two species were correlated with the baraminic distances of the small cats, and aligned more closely on the dendrograms.

Evaluation of the Homoplasy Criterion

Characters that occur in disjoint branches of a cladogram are defined as homoplasies. Homoplasies could be potentially the result of a separate creative act by the Creator, parallel evolution, an error in diagnosing the character, an event that transfers the character between different lineages, or an event that expresses the character from a previously unexpressed state.

Roughly half of the characters included in this study were homoplasious for the Aeluroidea and Felidae (Table VI). With the exception of the ecological criterion the amount of homoplasy among the felids was slightly higher than among all aeluroids considered together. The amount of homoplasy within subgroup C was roughly twice as high as that found within subgroup A. Homoplasy indices were relatively high in this study. All carnivorans share a certain number of characters that allows them to fulfill their predatory function. Crompton (1993) noted that 15 of 19 chromosomes present in the Felidae are also present in the Hyaenidae and Viverridae. This much shared genomic information might lead to a number of different homoplasies. Furthermore, we know that the biology of carnivorous baramins has been altered at some point in their natural history (see Lambert, 1983; Stambaugh, 1991). It is tempting to speculate that this alteration either distributed new information for carnivoran characters across different carnivoran baramins or regulated the expression of already present carnivoran characters in a similar manner.

In a previous study the relationship between baraminic distance and homoplasy was relatively uniform; as the phenetic distance between two species increased so did the number of homoplasies (Robinson and Cavanaugh, 1998).

Table VI. Comparisons of homoplasy within the Aeluroidea, Felidae, and two felid subgroups.

	Aeluroidea		Felidae		Subgroup A		Subgroup C	
Criteria	Length	H.I.	Length	H.I.	Length	H.I.	Length	H.I.
Combined	737	0.488	562	0.505	192	0.214	256	0.387
Ecological	50	0.540	42	0.500	13	0.154	13	0.231
Morphological	187	0.476	147	0.490	40	0.025	52	0.442
Chromosomal	37	0.514	31	0.613	4	0.000	15	0.267
Molecular	503	0.527	385	0.558	130	0.254	176	0.392

Note: Subgroups are defined in Figure 2. Length refers to the total number of character changes required by the indicated cladogram and H.I. represents the homoplasy Index. The Felidae, Subgroup A, and Subgroup C values were obtained by pruning the necessary taxa from the five Aeluroidea cladograms.

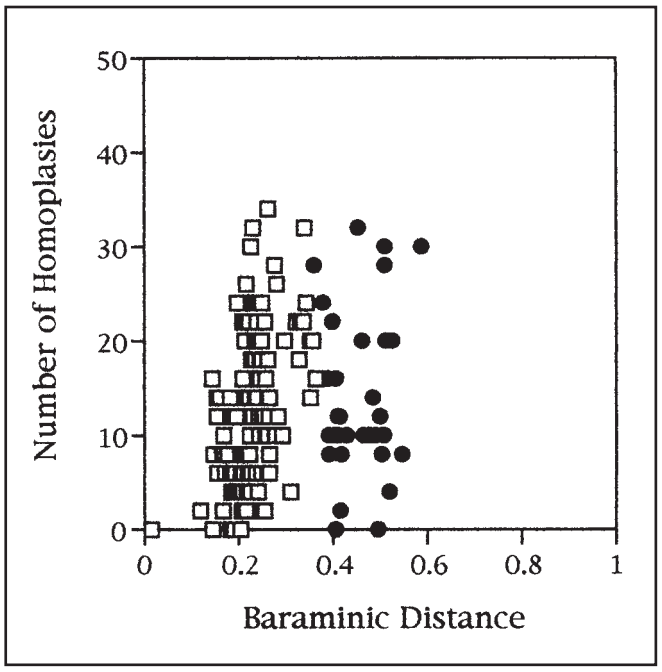

Figure 5. Plot of pairwise baraminic distances versus the number of pairwise homoplasies detected in the cladistic analysis. Black circles denote cat-outgroup comparisons, and white squares represent cat-cat comparisons.

In the present study the relationship between baraminic distance and homoplasy was spurious (Figure 5). The outgroups were phenetically distant from the cats, but the number of homoplasies shared between cats and outgroups was of the same magnitude as those shared between different cat species. Future studies of different taxonomic groups, especially carnivorans, are needed to help explain these observations.

Discussion

Baraminology of the Cats

Evidence for three major cat monobaramins has been presented. The cluster analyses suggested that the Felidae was composed of three major subgroups, although only two of these received bootstrap support. The baraminic distance variation and organismal correlation analyses confirmed the distinction of these groups. More importantly, the extensive overlap between subgroups as illustrated in the hybridogram strongly suggested all cats could be lumped into a larger monobaramin. Simpson (1945) classified living cats into the same three subgroups, although he placed the cougar into the genus *Felis* rather than *Acionyx*. It is encouraging to note that baraminology can yield practical classifications that have some conventional support.

In order to identify a group as a holobaramin it is necessary to identify both monobaraminic relationships uniting the group and apobaraminic divisions separating the group from other species. The clear separation of cats from outgroups in the cluster analyses, large gaps in the baraminic distance variation of cats from different subgroups versus cats and outgroups, and predominantly negative correlation coefficients between cats and outgroups in the organismal correlation analyses all indicated the cats were distinct from the selected outgroups. Since the Hyaenidae and Viverridae resemble the Felidae more closely than other living families, comparisons of cats with additional carnivore families would be expected to yield even larger biological discontinuities. Mehlert (1995) noted that fossil evidence for a macroevolutionary relationship uniting cats and other carnivores was lacking. Despite a century of research into the evolution of cats, no common ancestor uniting cats and other carnivores has been established (Hunt, 1987). The living cat family can therefore be confidently defined as a holobaramin, which is composed of phylogenetically related species and fully surrounded by a phyletic division (Figure 6).

The unity of large cats was one notable finding of this study. The lion was the most divergent cat and shared statistically significant similarities only with the other large cats. Species within a monobaraminic group that are difficult, if not impossible, to classify because of conflicting characters have been called aberrant (Scherer, 1993). *Neofelis nebulosa* is such an aberrant species whose taxonomic affinity traditionally has been puzzling. The current survey consistently placed the clouded leopard basally within the *Panthera* monobaramin. Werdelin (1983) demonstrated the clouded leopard was intermediate between the large and small cats for a variety of skull and dentition characters. The upper canine teeth of the clouded leopard were further noted to be similar in size to saber-toothed specimens. Incidently, molecular evidence has allied the saber-toothed cat near the *Panthera* subgroup (Janczewski, Yuhki, Gilbert, Jefferson, and O'Brien, 1992), possibly within the range of sequence variation of hybridizing species. These data would challenge Mehlert's (1995) contention that saber-toothed cats form a separate holobaramin, although a study should be conducted to formally test his hypothesis.

An accurate understanding of the potential for variability within the *Acionyx* monobaramin might be crucial to its preservation because the cheetah and cougar are endangered in all or parts of their range. Moderate bootstrap support in both the phenetic and cladistic cluster analyses indicated these species may form a natural group, a hypothesis strengthened by molecular (O'Brien et al., 1987; Collier and O'Brien, 1985) and morphological (see data of Herrington in Salles, 1992) evidence not included in this study. The *Felis trumani* specimen of North America has been offered as an intermediate between the cheetah and cougar (Adams, 1979). Cheetah fossils are also found among the lowest strata known for modern cats. It is therefore possible that the lineage leading to the cheetah and cougar represents an early monobaraminic radiation within the Felid holobaramin.

The high degree of morphological specialization exhibited by the cheetah has led systematists to postulate an early origin for this species. As noted by Scherer (1993) the process of specialization indicates the descendant population

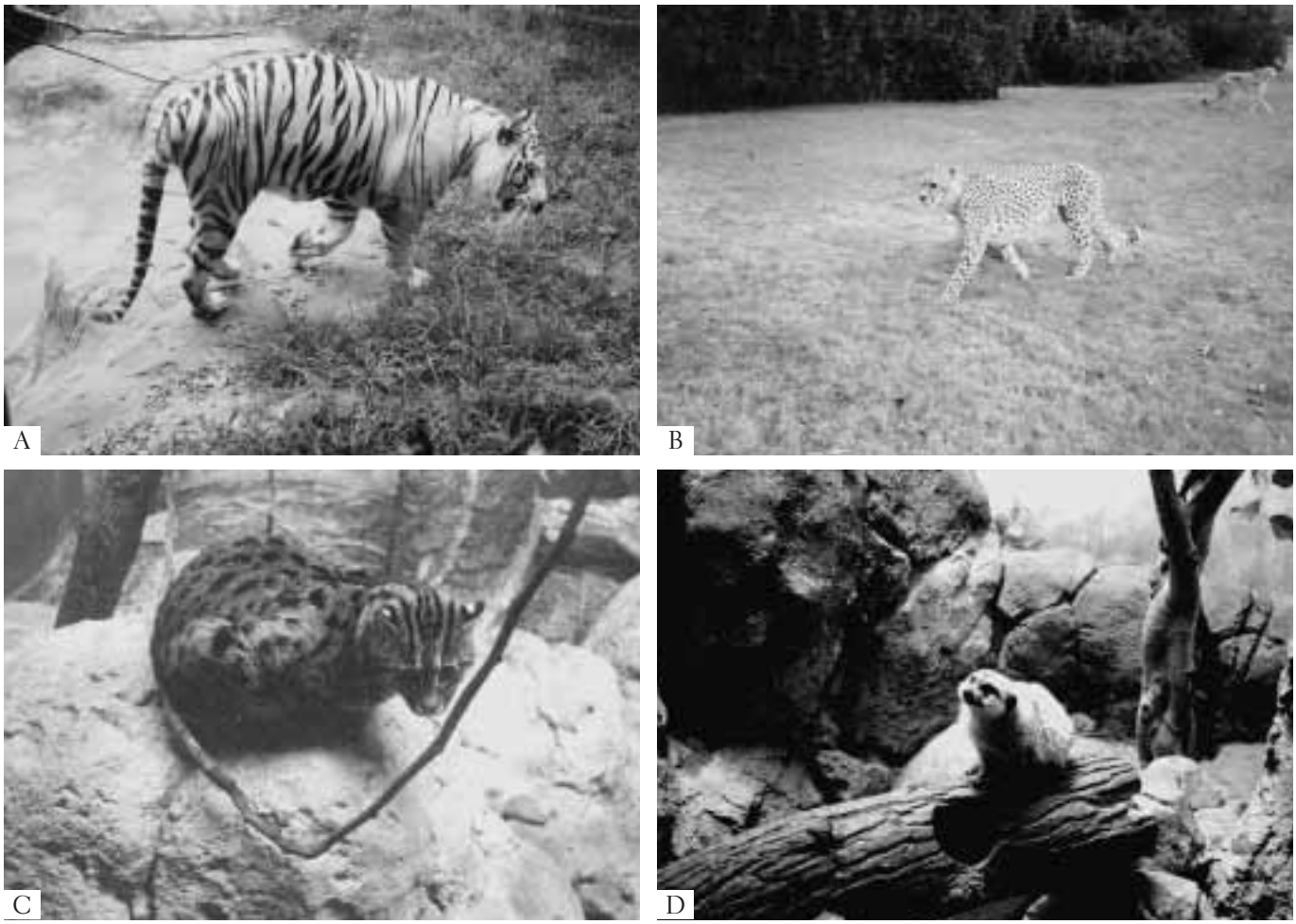

Figure 6. Representative members of the Felid holobaramin and an aeluroid outgroup. The white bengal tiger (*A*) is classified along with other large cats into the *Panthera* monobaramin. The cheetah (*B*) is one of two living species within the *Acionyx* monobaramin. The fishing cat (*C*), *Prionailurus viverrina*, was not included in this study but is expected to be classified along with the leopard cat, *Prionailurus bengalensis*, into the *Felis* monobaramin. The meerkat (*D*), *Suricata suricatta*, was suggested to be unrelated to the cats. (Photographs by D. A. Robinson)

has lost variation potential when compared to the ancestral population. Indeed, modern cheetahs are noted for being genetically depauperate (O'Brien, Wildt, Goldman, Merril, and Bush, 1983), suggesting the variation potential within this species has been diminished. Aggressive behavior (Eaton, 1974) and the propensity to inbreed (O'Brien, et al., 1983) may prevent the cheetah from hybridizing with other cat species (and thus tapping into a potentially rich pool of genetic information). The cougar qualifies as another aberrant species because it is morphologically similar to the small cats, yet produces viable offspring with the large cats (Van Gelder, 1977). This observation alone strongly supports the unity of all three felid subgroups.

The classification of small cats traditionally has proved enigmatic as witnessed by a profusion of generic names. Although the current survey was unable to resolve many of the relationships within this monobaramin, two pairs of taxa were supported in both the phenetic and cladistic cluster analyses; the African golden cat plus the caracal, and the two lynxes. The Asian golden cat and the caracal are especially aberrant species that have been classified into a variety of genera. It is possible the data failed to support a particular arrangement of species within the *Felis* monobaramin because rapid microevolution has led to a tangled network of characters. The short internal branches and long terminal branches depicted in the phenetic dendrogram are supportive of this hypothesis.

Hybridization among a genetically rich ancestral population might promote such a burst of speciation (Scherer, 1993; Fehrer, 1996). Moreover, some characters of small cats may be better explained as a result of historical hybridization rather than selective pressure leading to the independent evolution of these characters. For example, both the caracal and the lynxes display conspicuous ear tufts, a character without any obvious selective advantage. Perhaps the relatively more gentle behavior of small cats has provided an increased opportunity for hybridization, and thus higher frequencies of character exchange. As rather weak support for this hypothesis we note that Gray (1972) recorded six species of small cats that hybridize, but only four

and one species respectively among the large and medium cats. Further support could be taken from the observation that the homoplasy indices for subgroup C were roughly twice as large as the homoplasy indices for subgroup A.

Two major radiations are often hypothesized to have occurred within the *Felis* monobaramin; one leading to a domestic cat lineage, the other leading to an ocelot lineage. It is noted that the domestic cats contain specific endogenous retroviral sequences within their genomes, an inheritable feature not present in other cat species. Ocelots, on the other hand, have a unique diploid number of 36 and a restricted South American distribution (O'Brien, 1986; Wayne, Benveniste, Janczewski and O'Brien, 1989).

Reliability of Criteria

In a previous study the ecological and morphological data were the most reliable for distinguishing humans from nonhuman primates (Robinson and Cavanaugh, 1998). In the present study the ecological data were the least reliable criterion, both in terms of overall resolving power and in specific terms of being able to distinguish cats from the aeluroid outgroups. Ecology may be an especially unstable baraminic membership criterion within carnivorous taxa such as the Aeluroidea. Support for this hypothesis comes from the observation that the criterial diversity of ecological characters was nearly twice as high as in other criteria, its baraminic signal was not statistically significant, plus ecology was the most homoplasious criterion among aeluroids. Moreover, only eight ecological characters (most of which were originally continuous variables) were sampled in this study, versus 18 in the previous study (Robinson and Cavanaugh, 1998).

The chromosomal data proved yet again to be a weak data set as witnessed by a low (but statistically significant) baraminic signal and relatively poor separation of distributions in the organismal correlation analyses. There may be simply too few chromosomal characters which can be collected to make a reliable chromosomal criterion. Chromosomal characters are often combined into morphological data sets in conventional biosystematics.

Our results have suggested that morphological and molecular characters could be of great value in baraminology research. The baraminic signal of these criteria was highly significant, and the organismal correlations based on these criteria produced a distinct and highly resolved pattern separating cats from outgroups. More detailed analyses of the molecular data suggested that non-protein coding genes may not be generally useful for examining discontinuity in terms of transition and transversion substitutional patterns. These data also confirmed previous observations that substantial levels of variation in non-protein coding genes often occur among taxonomic units higher than the holobaramin (Robinson, 1997; Robinson and Cavanaugh, 1998). Thus, non-protein coding genes may not be properly calibrated for identifying holobaramins. Future studies should examine the sequences of other molecules to determine the extent of these generalizations.

Epilogue

As suggested in a previous study (Robinson and Cavanaugh, 1998) the proper selection of characters may be the most important factor in baraminology studies. We have dealt pragmatically with character selection, mostly seeking to maximize criterial relevance (A). In other words, we selected characters that were available for a majority of the species included in the study, regardless of its historical use in the systematics of primates or cats. Some characters possibly should have been removed from our studies because of logical correlations such as the presence or absence of folivory and the percent foliage in the diet. Another reason for our pragmatic selection of characters is that we are neither primate nor cat experts. In order for baraminology to become a productive scientific discipline, it is necessary for numerous biologists in diverse subdisciplines to gain a curiosity about the baraminology of their particular organism of expertise. What is their natural history? What does their origin and microevolution suggest about other aspects of their biology? Nearly every biologist is an expert on some organism, and is therefore most qualified to decide which characters are taxonomically important for that organism. Finally, we can justify the relatively pragmatic selection of characters in our studies by pointing out that our main goal has been to introduce new tools for baraminology. If these methods were successful with pragmatically selected data, then it is possible they may perform even better with more carefully selected data.

We note that characters are given weight merely by their inclusion in a study. Natural weighting schemes, however, are not appreciated by all biosystematists. Sneath and Sokal (1973) present compelling arguments for not artificially weighting characters unless one has good reason to do so. Guidelines for weighting characters phenetically and cladistically have been published, and their use in studies of baraminology should be examined. We have presented a simple weighting scheme (Robinson and Cavanaugh, 1998). It might be useful for future studies to examine the effects of weighting transversional nucleotide substitutions higher than transitions. The predicted effect would be to highlight phylogenetic gaps because these mismatches tend to predominate between proposed apobaraminic species (this study and Robinson, 1997). Transversions are often weighted in conventional systematics because it is assumed these mutations accumulate more slowly.

We have classified biological characters into very broad baraminic membership criteria. Future studies might benefit from classifying characters into narrower criteria. For example, the ecological criterion might be separated into ethological (behavioral) and life history characters. Morphological characters might be divided into major anatomical systems (Wise, 1992). Molecular characters might be separated into protein and non-protein genes. A narrower categorization of characters may be important because different subsets of criteria will probably have different reliabilities for inferring baraminic relationships in different groups of organisms. For example, the morphology of mouthparts are

important taxonomic characters in the larvae of aquatic insects in the family Chironomidae, but are not as important for turtle taxonomy. Two cautions are advised when classifying characters into different baraminic membership criteria.

(1) It is possible to classify characters into too narrow a baraminic membership criterion, such that the data set is too weak to support any particular hypothesis. We believe that considering single characters such as the trophic status or habit of organisms as separate baraminic membership criteria is an example of a weak data set (and can lead to confusion, see Wise, 1992; Robinson, 1997; Robinson and Cavanaugh, 1998). In the context of quantitative baraminology, there is no real estimate on the minimum number of characters that should be used to form the basis of a reliable measure of resemblance. Sneath and Sokal (1973) have arbitrarily suggested 60 characters. The ecological criterion that separated humans from nonhuman primates was composed of only 18 characters. However, the more characters the better, as more information gives a more complete description of the species, and thus a better estimate of the differences between species.

(2) Our classification of characters into different criteria has been a largely subjective process. There is a school of thought in conventional biosystematics that argues that different classes of phylogenetic evidence do not exist, but are merely artifacts of tradition and technology (Miyamoto and Fitch, 1995). For example, molecular data are only separated from morphological data because the techniques for collecting and analyzing this data are more recent. At first glance, there is no rational basis for separating the data and attaching special importance to one or the other data sets. The decision to combine or separate data sets is often resolved by testing for a so-called process partition. A process partition is a division of characters into subsets that are subject to different evolutionary forces (Bull et al., 1993). The generation of conflicting but statistically supported dendrograms are grounds for separating the data sets. Otherwise, it is suggested that the data sets be combined and analyzed together.

Returning to the relevance of this issue for baraminology, if different data sets seem more useful for detecting phylogenetic discontinuity, then we need some rational basis for claiming that their evidence is superior to evidence that may not support phylogenetic discontinuity. For example, why was the ecological criterion reliable and the molecular criterion unreliable for distinguishing humans from nonhuman primates (Robinson and Cavanaugh, 1998), whereas the opposite result was found with cats and aeluroid outgroups? With primates the Scriptural criterion was used to interpret the different data sets. We suggested that the ecological and morphological criteria were most reliable simply because they most efficiently distinguished humans from nonhuman primates. These data sets were also the most highly correlated (Robinson and Cavanaugh, 1998). With cats there was no Scriptural criterion available for interpreting the results. We concluded, however, that the morphological and molecular criteria were more reliable because they had the greatest resolving power. Interestingly, these two criteria provided the only correlated data sets. Will the most reliable criteria always be the most highly correlated? Data sets that yield congruent dendrograms would also be expected to yield significant criterial correlations. Thus, it is possible that the most reliable criteria for detecting phylogenetic discontinuity will be the ones that present no demonstrable process partition. In other words, the natural history of the most baraminically informative characters may be subject to the same microevolutionary forces. These issues raise fundamental questions about the nature of the holobaramin and the characters that can be used to identify them. We hope that baraminologists will give these questions thoughtful attention.

Appendix I

Ecological characters: activity pattern, vegetation, zonation, diet, social behavior, litter size, gestation length, age of maturity (Gittleman, 1985; 1986a; 1986b; 1991)

Morphological characters: body weight, body length, brain weight, birth weight, olfactory bulb height, olfactory bulb width, olfactory bulb length, anterior dentary, lower third deciduous premolar-second posterior accessory cusp, upper third premolar-parastyle, upper fourth premolar-protocone, upper canine-dorsoventral length, upper canine-lingual ridge, relative position of foramen rotundum to basicranial plane, external pterygoid fossa, palatine bones, occipital condyles, subarcuate fossa, internal auditory meatus-marginal surface, longitudinal ridge of auditory meatus, malleus-processus brevis, incus-inferior head with malleus, groove for stylomastoid foramen, frontal sinus-relative position on the skull, anterodorsal frontal sinus cavity, first caudal ethmoturbinate scroll-posterior position, frontal sinus volume, frontal bone-outer surface depression, frontal bone-lateral expansion, frontonasal region-dorsal profile, frontonasal region-dorsoventral compression, frontonasal region-ridge, rostral constriction, infraorbital foramen, maxilla expansion over infraorbital foramen, jugal and frontal postorbital processes, jugal anterior process, hyoid apparatus, fibula head, tendon for extensor digitorium longus, olecranon of ulna, caudal vertebrae, shape of ear, pencil hair of ear, interdigital webs of hind foot, digit tips of fore and hind feet, growth of neck fur, pupils, tongue, anterior palatine foramina, relative size of palatine, alisphenoid canal, auditory bulla-posterior carotid canal, external auditory meatal tube, caudal entotympanic, paraoccipital process, processus gracilis of malleus, major a2 arterial shunt, major a4 arterial shunt, major anastomosis Y, course of internal carotid, P1, p1, p2, M1, M2, m1, m2, hallux, anal glands (Salles, 1992; Wozencraft, 1989)

Chromosomal characters: diploid number, fundamental number, morphology of metacentric, acrocentric, and Y chromosomes, banding patterns of chromosomes B4, D2, E4, F1, and C3 (Modi and O'Brien, 1988; Wurster and Benirschke, 1968)

Molecular characters: 124 polymorphic sites for cytochrome *b*, 75 polymorphic sites for 12S-rRNA (Janczewski, Modi, Stephens, and O'Brien, 1995; Masuda, Yoshida, Shinyashiki and Bando, 1994).

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CRSQ - Creation Research Society Quarterly
Mol. Biol. Evol. - Molecular Biology and Evolution

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Book Review

A *Biologist Examines the Book of Mormon* by Thomas D. S. Key. 1995
Utah Missions, P.O. Box 348, Marlow, OK 73055. 1995. 59 pages. $6 postpaid. (Paperback)
Reviewed by George F. Howe*

A copy of this book was given to me by my friend Edmund Gruss who is an historical researcher and an author of many books on Mormonism and on the Jehovah's Witness movement. The name Thomas D. S. Key immediately caught my eye because when I was a beginning instructor in biology, I received a beneficial boost in my own burgeoning creation studies from a fine chapter written about 40 years ago by this same author (Key, 1959, pp. 11-52) in a symposium volume which some readers may still remember—*Evolution and Christian Thought Today*.

But Key's 1995 book is not about creation or evolution. It is worth reviewing here, however, because most creationists like to check statements from the Bible and other religious writings against the facts of science. The Bible emerges from such comparisons smelling like a proverbial rose. Not so, says T. D. S. Key, with *The Book of Mormon*. Key raises no objections to the concept of miracles as such, but he has located many apparent scientific blunders in the discussions of both ordinary and miraculous events. He has not intended, he says, to offend Mormons (pp. 4-6) but wants to shed light on possible scientific discrepancies.

Key has organized his many arguments into 19 scientific sections which are arranged alphabetically from "Anatomical Problems" to "Zoological Problems," with "Geological Problems" somewhere in the middle. One of the anatomical glitches he reports is in *Mosiah* 3:7 (which Mormons date at about 124 B.C.). In a reference to Jesus' sufferings, it says that "…blood cometh from every pore…" (p. 6); but skin pores were not described or even discovered, writes Key, until after microscopes were developed—many centuries later.

Flax is mentioned as being present in the Americas (I *Nephi* 13:7 refers to linen, an indirect but definite involvement of flax because linen is made only from processed flax stems), but native Americans had neither flax nor linen (p. 13). Under "Anthropological Problems" (p. 9) he notes that *The Book of Mormon* treats dark skin pigmentation as a definite curse while it can, in many climates, be a physiological blessing. A few of the other questions analyzed include: (1) whether or not Native Americans are descended from middle-eastern Hebrews, (2) did the animals called "cureloms" or "cummoms" have real counterparts in natural history, and (3) did horses exist in pre-Columbian America?

This brief but lucid book contains cartoons illustrating various purported errors. It concludes with Key's personal Christian testimony and a direct comparison between the Bible and Mormonism regarding the subject of eternal life. This booklet will interest all readers who want to discover whether or not the revered writings of Mormonism are replete with scientific errors. Key concludes that *The Book of Mormon* is "…definitely not fact but clearly fiction" (p. 56).

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