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Mitochondrial DNA Analysis of Three Terrestrial Mammal Baramins (Equidae, Felidae, and Canidae) Implies an Accelerated Mutation Rate Near the Time of the Flood

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MITOCHONDRIAL DNA ANALYSIS OF THREE TERRESTRIAL MAMMAL BARAMINS (EQUIDAE, FELIDAE, AND CANIDAE) IMPLIES AN ACCELERATED MUTATION RATE NEAR THE TIME OF THE FLOOD

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ABSTRACT

If modern species descended from "two of every kind" aboard Noah's Ark, as creationists commonly assert, then intrabaraminic diversification and speciation must have been extremely rapid. Although there has been limited creationist research on the genetic component of the speciation mechanism, a simple means of gaining insight into possible molecular mechanisms related to speciation is to evaluate the molecular diversity of known baramins, especially those with ancient DNA (aDNA) sequences recovered from extinct taxa, which can give us a window to the genetic diversity of a baramin soon after the Flood. Here, published mitochondrial DNA sequences from members of three baramins (Equidae, Felidae, and Canidae) are evaluated. For each group, the results show that the diversity of the aDNA sequences fall within the range of modern sequences, thus implying that the modern sequence diversity must have already been established by the time the fossils were formed soon after the Flood. Comparisons to outgroups also indicate that transversion substitutions might be a means of distinguishing different baramins.

INTRODUCTION

Creationists generally accept the idea of speciation as long as it occurs within the bounds of the created kind or baramin (Wood, 2008; Brand, 2009; Lightner, *et al*., 2011). Furthermore, creationists commonly assert that the "two of every kind" aboard Noah's Ark represented two of each baramin, from which all modern species of each terrestrial created kind have descended (e.g., Lightner, *et al*., 2011). Thus, the diversity of modern equid or canid species is attributed to equid and canid ancestors who survived the Flood aboard the Ark. Speciation among plants and marine creatures is also likely, but the ancestry of such is less clear, since we do not know how many individuals of each baramin survived the Flood. For example, Wood (2002a) argued that all grasses were members of the same kind, but he also suggested that modern grass species might not share a common ancestor at the Flood.

By assuming the common ancestry of terrestrial mammal species belonging to a single baramin, Wood (2002b) concluded that intrabaraminic speciation and diversification must have been extremely rapid, although it should be noted that rapid speciation may apply only to speciose baramins (see Wood, 2011). There has been limited research on the genetic component of this

speciation. Lightner (2008a, 2009a) has implicated directed, nonrandom mutations in the origin of novel traits, and Wood (2003), Borger (2009a, 2009b), and Shan (2009) proposed speculative models involving transposable elements and genomic rearrangements. Though all of these models have attractive features, it is unclear whether any one of them can account for the full range of genomic modifications observed in species of a baramin.

An obvious means of studying potential molecular mechanisms of speciation is to evaluate the molecular diversity of members of known baramins. Lightner has followed this approach, surveying chromosomal and sequence diversity within bovids (Lightner, 2008a), canids (Lightner, 2009b), and cercopithecids (Lightner, 2009a). One drawback to comparative studies of extant sequences is a lack of time calibration. Archaeological remains and ancient artwork can only give us a very crude estimate of when a particular species originated. With extant sequences, we do not know for certain when genomic or sequences mutations occurred. We could assume a molecular clock (constant changes over time), but whether such an assumption is warranted is a matter of debate (Scherer, 1989; Mills, 1994; Pulquério and Nichols, 2007).

One possible method of assessing sequence diversity in the past is to extract and sequence ancient DNA (aDNA), especially from extinct taxa that are predicted to be part of a known baramin. Ancient DNA comes with its own set of experimental difficulties that hinder purification, amplification, and sequencing (e.g., Gilbert, *et al*., 2005; Carter, 2009; Criswell, 2009; Green, *et al*., 2009). Although there are methods to overcome some of these difficulties, not all aDNA sequencing studies are performed to the same level of quality. In using aDNA sequences, then, we must be cautious and draw tentative conclusions. Nevertheless, aDNA can give us some insight into the genetic diversity of a baramin soon after the Flood, thus allowing us to evaluate mutation rates qualitatively without necessarily assuming a molecular clock.

Previously, I examined complete aDNA mitochondrial genomes from extinct hominids (Wood, 2012) and concluded that there must have been a short burst of single nucleotide mutations around the time of the Flood or before. To expand those results, I here examine published mitochondrial DNA sequences of three well established baramins: Equidae, Felidae, and Canidae. As terrestrial baramins, we may hypothesize that they have descended from a single pair preserved by Noah on the Ark. Consequently, any mitochondrial sequence variability must be attributed to real mutations instead of allelic diversity preserved from before the Flood (barring the *ad hoc* assumption that the female of each pair was heteroplasmic).

To prevent arguments over the precise membership of the baramins, I chose three mammal families that have been analyzed by creationists using multiple lines of evidence. Robinson and Cavanaugh (1998) evaluated the felids in one of their first papers on statistical baraminology, and Crompton and Winkler (2006) and Pendragon and Winkler (2011) summarized the most recent information on felid hybrids. Both analyses agreed that the felids constituted a baramin. Hybridization of extant horses was summarized by Stein-Cadenbach (1993), and later fossil equids were analyzed using statistical baraminology by Cavanaugh, *et al*. (2003). The baraminic status of family Equidae was supported by both studies. Finally, the hybridization of canids has been reviewed by Siegler (1974), Crompton (1993), and Pendragon (2011). Each author classified Canidae as a baramin. Thus, with hybridization and other lines of evidence, the baraminic status of each of these families would appear to be as firmly established as any

baramin could be.

Barnett, *et al*. (2005) sequenced aDNA from three extinct felids: *Smilodon*, *Homotherium*, and *Miracinonyx*. In contrast to a previous report of *Smilodon* DNA from Janczewski, *et al*. (1992) that indicated *Smilodon* DNA was similar to modern big cat sequences, Barnett, *et al*.'s results supported the separation of *Smilodon* and *Homotherium* into a separate subfamily Machairodontinae. Orlando, *et al*. (2003, 2008, 2009) have published numerous studies of aDNA from fossil equid specimens. Surprisingly, despite being classified in a separate genus, *Hippidion* consistently clusters as a sister taxon to *Equus caballus* in phylogenetic analyses. Their results were independently confirmed by the analysis of *Hippidion* aDNA by Weinstock, *et al*. (2005). For canids, aDNA has been sequenced by Germonpre, *et al*. (2009) and Horsburgh (2008). In particular, Germonpre, *et al*. (2009) analyzed numerous specimens from across Eurasia, some as much as 31,000 years old according to conventional dating. Much more recent aDNA canid sequences were reported by Leonard, *et al*. (2002). All aDNA from felid, canid, and equid specimens were mitochondrial DNA.

METHODS

All aDNA sequences were obtained from GenBank (Table 1). Alignments were generated automatically using CLUSTALW as implemented in MEGA 5 (Tamura, *et al*., 2011). MEGA was also used to calculated single nucleotide differences (SNDs) for all sequence pairs. For the felids, I analyzed a 287-nucleotide alignment of cytochrome *b* sequences that included sequences from seventeen extant felids from nine genera, three extinct felids (*Homotherium serum*, *Smilodon populator*, and *Miracinonyx trumani*), and four outgroup taxa (*Suricata*, *Herpestes*, *Fossa*, and *Crocuta*). The three aDNA sequences came from fossils that are at least 10,000 years old by conventional dating.

For the equids, I analyzed a 423-nucleotide alignment of the mitochondrial control region that included sequences from seven extant equids, 30 fossil and subfossil equids, and two outgroups (*Diceros* and *Dicerorhinus*). The aDNA sequences came from some recently extinct specimens (*Equus capensis*) as well as true fossils as old as 53,000 by conventional dating. The fossil sources of aDNA also included fourteen specimens referred to several species of the South American horse genus *Hippidion* (Table 1).

For the canids, I analyzed a 493-nucleotide alignment of a fragment of the mitochondrial control region from twelve extant canids, the recently extinct Ezo wolf (*Canis lupus hattai*), and one outgroup (*Ursus arctos*). Since the only aDNA sequence in this set came from a recent specimen, a second 58-nucleotide alignment of the most variable part of the control region in canids was also examined. This alignment included sixteen canid sequences, seven of which were aDNA sequences from *Canis lupus*. The aDNA sequences came from specimens at least 13,000 years old by conventional dating (Stiller et al., 2006).

Some disagreement among creationists over the Flood/post-Flood boundary still continues today (Whitmore and Garner, 2008; Oard, 2010a, 2010b). In each of these baramins, however, the fossil remains from which the aDNA sequences were obtained were Upper Pleistocene, and thus post-Flood by any definition of the post-Flood/Flood boundary. To obtain more precise age

estimates, I converted the radiocarbon dates of nine *Equus* and three *Canis* species to calendar dates based on Brown's (2006) general calibration formula (Table 2). The conversion formula used here is where *C* is radiocarbon years before present, *T* is calendar years before present, and the date of the Flood was set at 4400 years before present according to the Masoretic chronology.

$$C = T + 8300 \ln\left(\frac{1}{1 - 0.997 \exp(-0.007475(4400 - T))}\right)$$

RESULTS

I used Brown's (2006) recalibration to estimate possible post-Flood dates for twelve of the fossil specimens used in this study that were dated by radiocarbon dating. The radiocarbon dates for these specimens ranged from 12,510 to 53,100 years old. Recalibration with a Flood date of 4400 years before present resulted in dates that ranged from 4338 years before present to the Flood year itself. Though these estimates cannot be taken as absolutely correct, they do confirm that the specimens used for aDNA extraction and sequencing are close in time to the date of the Flood.

For the felid cytochrome *b* sequences excluding aDNA sequences, the number of single nucleotide differences (SNDs) from felid-felid comparisons (2-46 SNDs) overlapped significantly with those of felid-outgroup comparisons (35-56 SNDs) when total differences were counted. For transitions only, a similar overlap was seen when felid-felid (2-41 SNDs) and felid-outgroup (21-43 SNDs) SNDs were compared. In contrast, when transversions alone were evaluated, a distinction between felid-felid (0-9 SNDs) and felid-outgroup comparisons (11-19 SNDs) was observed (Figure 1).

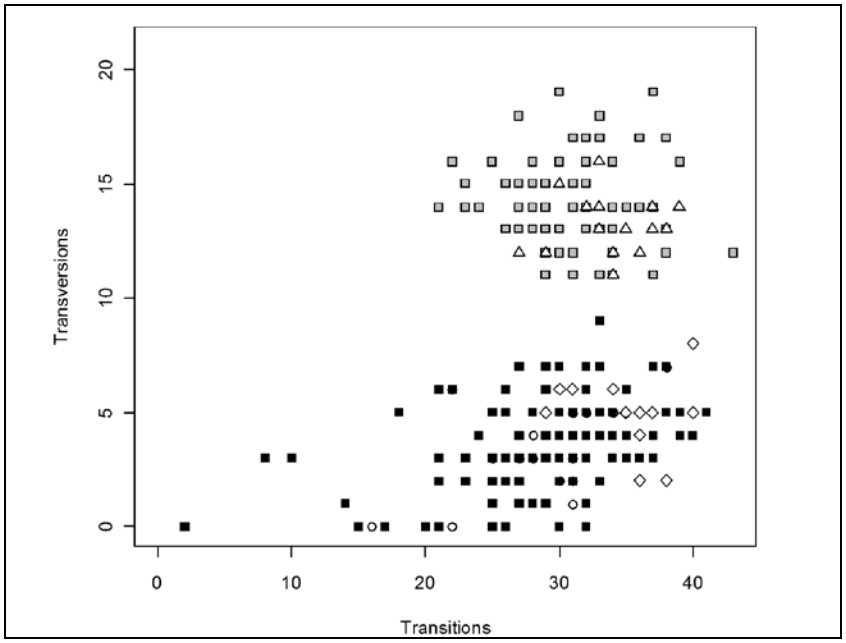

Figure 1. Transitions and transversions from an alignment of twenty felid and four outgroup mitochondrial cytochrome *b* sequences. There were 287 positions in the final alignment. Extant felid-felid comparisons are shown as filled squares, and extant felid-outgroup comparisons are shown as grey squares. Open symbols represent felid-felid comparisons with aDNA sequences. *Miracinonyx* is represented by a circle; *Smilodon* is represented by a diamond; and *Homotherium* is represented by a triangle.

SNDs for aDNA sequences from *Smilodon* and *Miracinonyx* compared to extant felids fell within the range of modern felid-felid comparisons. *Smilodon*-felid SNDs ranged from 34 to 48 for all differences, 29-40 for transitions only, and 2-8 for transversions only. *Smilodon*-outgroup SNDs ranged from 40 to 48 for all differences, 28-37 for transitions, and 9-13 for transversions. *Miracinonyx*-felid SNDs ranged from 16 to 45 for all differences, 16-38 for transitions, and 0-7 for transversions. *Miracinonyx*-outgroup SNDs ranged from 38 to 49 for all differences, 24-36 for transitions, and 11-14 for transversions. As with extant felids, *Miracinonyx* and *Smilodon* could be distinguished from non-felid outgroups only by reference to transversion SNDs.

In contrast to *Miracinonyx* and *Smilodon*, the aDNA sequence from the scimitar cat *Homotherium* resembled non-felid outgroups more than other felids. Total *Homotherium*-felid SNDs were 39-53, and transition SNDs were 27-39. Transversion SNDs for *Homotherium*-felid comparisons were 11-16. *Homotherium*-outgroup SNDs were 41-54 for all differences, 27-39 for transitions, and 14-21 for transversions. Thus, while extant felids, *Smilodon*, and *Miracinonyx* can be distinguished from non-felids based on their transversion SNDs, *Homotherium* cannot (Figure 1).

As with the felids, extant equids and non-equids could not be distinguished based on just transition SNDs. For extant *Equus* species, equid-equid transition SNDs were 0-26, and equid-outgroup transition SNDs were 20-26. Nevertheless, extant equid-equid comparisons differed

from equid-outgroup comparisons in both transversions (0-5 vs. 17-22) and total SNDs (5-29 vs. 37-45) (Figure 2).

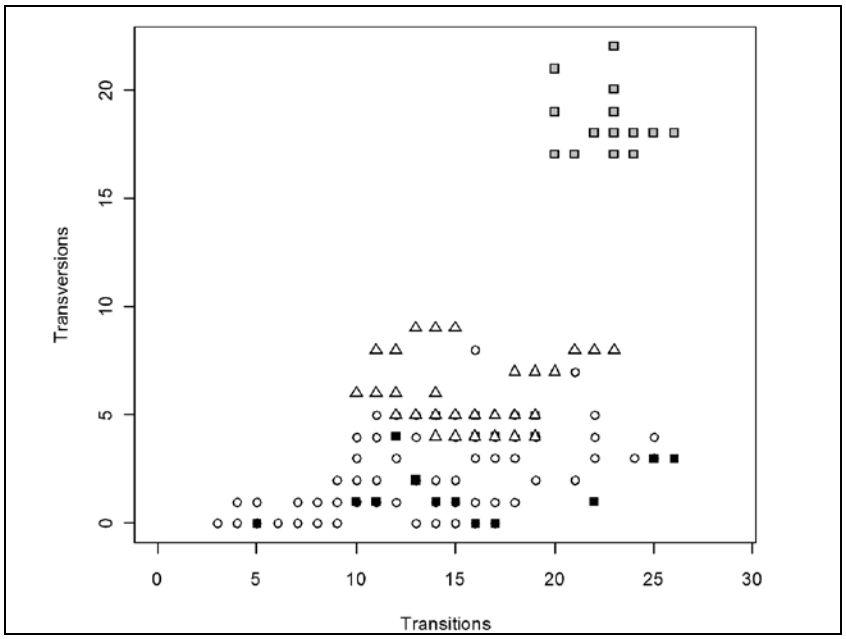

Figure 2. Transitions and transversions from an alignment of thirty equid and two outgroup mitochondrial control region sequences. There were 423 positions in the final alignment. Extant equid-equid comparisons are shown as filled squares, and extant equid-outgroup comparisons are shown as grey squares. Open symbols represent equid-equid comparisons with aDNA sequences. Fossil *Equus* is represented by a circle, and *Hippidion* is represented by a triangle.

All aDNA sequences from *Equus* and *Hippidion* had transversions and total SNDs within the range of modern *Equus* sequences. For extinct vs. extant equid-equid comparisions, total SNDs were 3-29, and transversion SNDs were 0-8. Extinct equids differed from outgroups by 36-47 total SNDs and 16-22 transversion SNDs. For extant equids compared to *Hippidion*, total SNDs were 16-31, and transversion SNDs were 4-9. *Hippidion*-outgroup total SNDs were 43-47, and transversion SNDs were 19-22. Thus, equids are easily distinguishable from non-equids based on their transversion and total SNDs in the mitochondrial control region, regardless of whether the equid sequence is of ancient or modern origin.

Unlike the previous groups, extant canids could be distinguished from non-canids by transition, transversion, and total SNDs (Figure 3). For extant sequences only, canid-canid total SNDs were 0-62, transitions were 0-39, and transversions were 0-31. Canid-outgroup total SNDs were 98-108, transitions were 44-56, and transversions were 51-59. The aDNA sequence from the recently extinct *Canis lupus hattai* fell within the range of modern canid-canid comparisons. *C. l. hattai* and the extant canids differed by 2-54 SNDs for all differences, 2-28 transition SNDs, and 0-28 transversion SNDs. *C. l. hattai* and the outgroup *Ursus arctos* differed by 99 total SNDs, 47 transition SNDs, and 52 transversion SNDs.

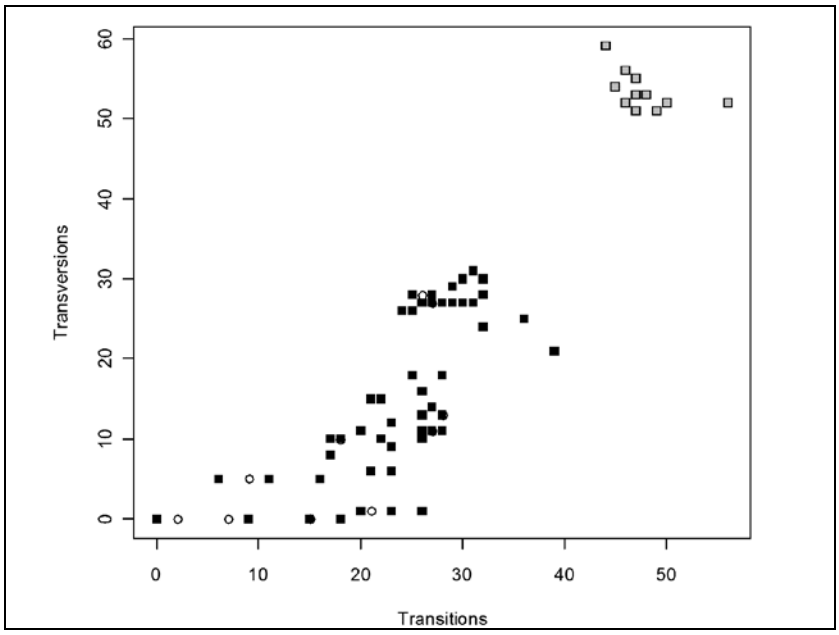

Figure 3. Transitions and transversions from an alignment of thirteen canid and one outgroup mitochondrial control region sequences. There were 493 positions in the final alignment. Extant canid-canid comparisons are shown as filled squares, and extant canid-outgroup comparisons are shown as grey squares. Open circles represent canid-canid comparisons with the aDNA sequence from *Canis lupus hattai*.

A shorter alignment was also examined in order to include aDNA sequences from Pleistocene wolf specimens. The ancient and recent canid sequences differed by a median of 7 total SNDs (range: 1-15), 5 transition SNDs (range: 1-12), and 1 transversion SND (range: 0-4). Recent sequences compared to other recent sequences differed by a median of 8 total SNDs (range: 3-15), 6 transition SNDs (range: 2-12), and 2 transversion SNDs (range: 0-5). Thus, the ancient sequences were well within the range of the variability of recent sequences.

DISCUSSION

Recalibration of radiocarbon dates to calendar dates is still an imprecise science due to a number of factors that must be assumed or modeled, such as equilibrium between the production and decay of radiocarbon, the date of the Flood, and the possibility of nonconstant decay rates. The recent discovery of measurable residual radiocarbon in specimens that are supposedly “too old” to date reminds us that important discoveries can still be made in this field (e.g., Giem, 2001; Baumgardner, 2003). Nevertheless, given that the rationale of this study depends on placing fossil remains within some kind of post-Flood chronology, even imprecise recalibrations can be informative.

The recalibration used here places twelve of the specimens within seven decades of the Flood, but four of those specimens were dated to the Flood itself. Since the Upper Pleistocene is unquestionably post-Flood, the recalibration used here cannot be precisely correct, but the relative dating reaffirms the assumption that these fossil remains represent lineages that existed in the first few centuries after the Flood. These aDNA sequences can therefore give us a window

into the genetic status of baramins immediately following the Flood. For each baramin evaluated here, the results show that the diversity of most aDNA sequences fall within the range of modern sequences.

When compared to outgroup sequences, however, all three baramins evaluated here could be distinguished by nonoverlapping distributions of transversions. Intrabaraminic comparisons invariably had fewer transversion SNDs than interbaraminic comparisons. The significance of this pattern is especially significant in the case the scimitar cat *Homotherium*. If the *Homotherium* sequence is not a contaminant or damaged, the results here suggest that *Homotherium* is not a felid. Traditionally, saber-toothed and scimitar-toothed cats are separated from extant cats into their own felid subfamily Machairodontinae (McKenna and Bell, 1997). Machairodontines are in turn classified into tribes Smilodontini and Machairodontini (to which *Homotherium* is assigned). In the history of classification, there has been no doubt that *Homotherium* is a felid, thus warranting further inspection of the *Homotherium* mtDNA here analyzed. Additional aDNA sequences from *Homotherium* and other machairodontinans should be sought to verify or falsify the existing *Homotherium* sequence.

Aside from the anomaly of the *Homotherium* transversions, all other species could be readily distinguished from outgroup taxa by the distribution of transversions. In a previous analysis of ancient hominin mitochondrial genomes, Wood (2012) noted that the ratio of transversions to transitions was significantly higher for human-animal comparisons than for comparisons of humans to humans, humans to Neandertals, or humans to Denisovans. The present results further suggest that transversion substitutions might be useful in delineating baramins from DNA sequence data.

If we accept that the species of each of these baramins descended from common ancestral pairs that survived the Flood aboard the Ark (since they are biblically unclean), the similarity of aDNA from Pleistocene specimens to modern mitochondrial DNA implies a rapid sequence diversification from the time of the Flood to the time the fossils were formed. Since then, DNA divergence has been low, since these ancient sequences closely resemble their extant counterparts. Thus, these results imply a period of rapid genetic divergence after the Flood that quickly decreased to the low mutation rates characteristic of the present.

Alternatively, these results could be interpreted as the result of heteroplasmy in the animals aboard the Ark, wherein different mtDNA types were sorted into different lineages in a mechanism analogous to Tinkle's (1967) theory of heterozygous creation. If correct, the different mtDNA types would be relicts of pre-Flood diversity or were generated during the Flood itself. Despite being a somewhat *ad hoc* explanation, this hypothesis could be tested by evaluating the relationships implied by morphological vs. molecular similarity. In this model, there would be no expectation that the mtDNA similarities would reflect morphological similarity, since mtDNA types would be sorted randomly into different lineages. Since the broad intrabaraminic relationships inferred from morphology do reflect mtDNA similarity, this relict mtDNA hypothesis can be ruled out, and instead, the hypothesis of rapid mtDNA divergence is supported.

As noted previously, creationists have proposed various speculative models for the generation of

genetic and phenotypic diversity within created kinds after the Flood. Based on data from the Bible and baramin studies, Wood (2002) argued that post-Flood diversification must have been rapid. This study provides additional evidence that rapid divergence also included mitochondrial DNA sequence diversity.

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APPENDIX

Table 1. DNA sequences used in this study. Specimens dated by radiocarbon are noted with an asterisk.

Taxon	Conventional Age	Accession #
Felidae cytochrome *b*		
Acinonyx jubatus	extant	AY463959
Catopuma temminckii	extant	FJ594957
Felis catus	extant	AB004238
Felis silvestris	extant	EF689045
Lynx Canadensis	extant	AY598475
Lynx pardinus	extant	EF689047
Lynx rufus	extant	GU175436
Neofelis nebulosa	extant	NC_008450
Panthera leo	extant	AF384815
Panthera onca	extant	HM107682
Panthera pardus	extant	EF551002
Panthera tigris	extant	AF053025
Prionailurus bengalensis	extant	AB210233
Prionailurus iriomotensis	extant	AB210228
Prionailurus planiceps	extant	FJ594958
Prionailurus viverrinus	extant	AB210239
Puma concolor	extant	AY598487
Uncia uncia	extant	NC_010638
Homotherium serum	>10,000 YBP	DQ097176
Smilodon populator	>10,000 YBP	DQ097174
Miracinonyx trumani	>10,000 YBP	DQ097175
Suricata suricatta (outgroup)	extant	AF522346
Herpestes edwardsii (outgroup)	extant	DQ519052
Fossa fossana (outgroup)	extant	AF511062
Crocuta crocuta (outgroup)	extant	DQ157555
Equidae mitochondrial control region		

Equus asinus	extant	NC_001788
Equus burchelli	extant	AF220921
Equus caballus	extant	NC_001640
Equus capensis	recent	GQ324605
Equus capensis	recent	GQ324603
Equus capensis	148 YBP	GQ324604
Equus grevyi	extant	AF220930
Equus hemionus	extant	AF220936
Equus kiang	extant	AY569542
Equus neogeus	>10,000 YBP	EU030680
Equus przewalskii	extant	AF055878
Equus sp. AA26819	12,510 YBP*	DQ007555
Equus sp. CMN49368	43,900 YBP*	DQ007557
Equus sp. IEM_200_483	27,500 YBP*	DQ007552
Equus sp. KU62158	unknown	DQ007569
Equus sp. LACM109/150807	13,070 YBP*	DQ007570
Equus sp. LLO-2009a	unknown	GQ324606
Equus sp. P94.1.415	unknown	DQ007559
Equus sp. PET09	12,545 YBP*	DQ007558
Equus sp. PIN3659_6	53,100 YBP*	DQ007553
Equus sp. SMNS	12,550 YBP*	DQ007556
Equus sp. YG109.7	>47,000 YBP*	DQ007568
Equus sp. YG130.3	46,600 YBP*	DQ007567
Equus zebra	extant	AF220931
Hippidion devillei	23,250 YBP	GQ324598
Hippidion devillei	23,250 YBP	GQ324599
Hippidion devillei	23,250 YBP	GQ324600
Hippidion devillei	23,250 YBP	GQ324601
Hippidion saldiasi	unknown	EU030679
Hippidion saldiasi	10,000-13,000 YBP	GQ324593
Hippidion saldiasi	10,000-13,000 YBP	GQ324594

Hippidion saldiasi	10,000-13,000 YBP	GQ324595
Hippidion saldiasi	10,000-13,000 YBP	GQ324596
Hippidion saldiasi	10,000-13,000 YBP	GQ324597
Hippidion sp. CDM28/6c-780	unknown	DQ007560
Hippidion sp. CLV	unknown	DQ007563
Hippidion sp. MLP6-272	unknown	DQ007562
Hippidion sp. TA14001	unknown	DQ007564
Diceros bicornis (outgroup)	extant	FJ905814
Dicerorhinus sumatrensis (outgroup)	extant	FJ905816
Canidae mitochondrial control region		
Alopex lagopus beringensis	extant	DQ630747
Canis lupus chanco	extant	NC_010340
Canis lupus familiaris	extant	NC_002008
Canis lupus hattai	recent	AB500701
Canis lupus laniger	extant	NC_011218
Canis lupus lupus	extant	NC_009686
Canis latrans	extant	NC_008093
Cuon alpinus	extant	NC_013445
Dusicyon thous	extant	EF194191
Nyctereutes procyonoides	extant	NC_013700
Pseudalopex gymnocercus	extant	EF107034
Pseudalopex vetulus	extant	EF107033
Urocyon cinereoargenteus	extant	GU903034
Vulpes vulpes	extant	NC_008434
Ursus arctos (outgroup)	extant	AB013060
Canidae mitochondrial control region		
Canis lupus	21,810 YBP*	DQ852650
Canis lupus	“Late Glacial”	DQ852644
Canis lupus	“Late Glacial”	DQ852645
Canis lupus	“Pleniglacial”	DQ852646
Canis lupus	“Pleniglacial”	DQ852647

Canis lupus	13,681 YBP*	DQ852648
Canis lupus	24,780 YBP*	DQ852649
Canis lupus familiaris	extant	NC_002008
Canis simensis	extant	HQ845261
Canis latrans	extant	EF508154
Canis lupus hattai	recent	AB500701
Canis himalayensis	extant	AY289995
Canis indica	extant	AY289984
Lycaon pictus	extant	AF335732
Dusicyon thous	extant	EF194191
Pseudalopex vetulus	extant	EF107032

Table 2. Radiocarbon dates recalibrated to calendar dates

Taxon	**Accession #**	**Radiocarbon date (YBP)**	**Calendar date (YBP)**
Equus sp. AA26819	DQ007555	12,510	4338
Equus sp. PET09	DQ007558	12,545	4338
Equus sp. SMNS	DQ007556	12,550	4338
Equus sp. LACM109/150807	DQ007570	13,070	4343
Canis lupus	DQ852648	13,681	4348
Canis lupus	DQ852650	21,810	4383
Canis lupus	DQ852649	24,780	4388
Equus sp. IEM_200_483	DQ007552	27,500	4392
Equus sp. CMN49368	DQ007557	43,900	Flood
Equus sp. YG130.3	DQ007567	46,600	Flood
Equus sp. YG109.7	DQ007568	>47,000	Flood
Equus sp. PIN3659_6	DQ007553	53,100	Flood