



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

Todd Charles Wood, Core Academy of Science, Dayton, TN 37321

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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 sequence 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 calculate 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).

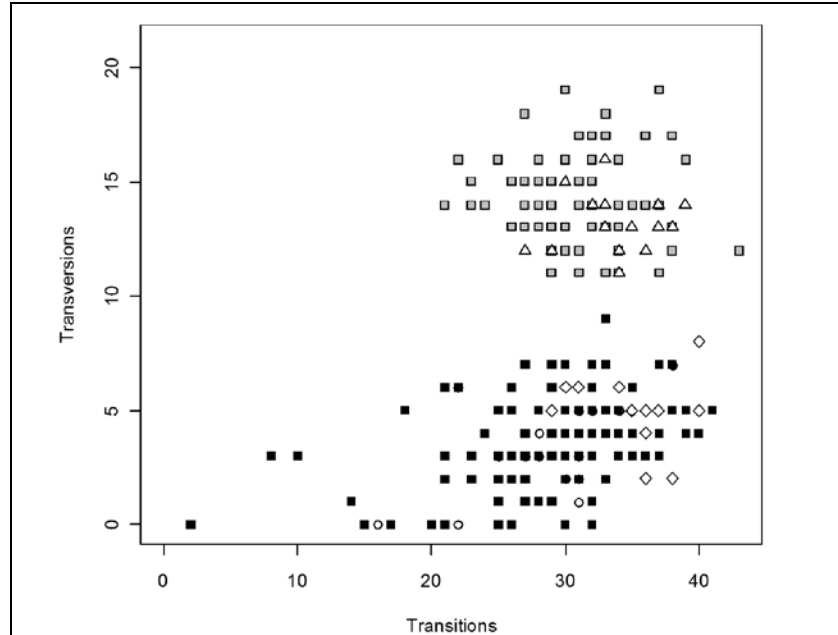


Figure 1. Transitions and transversions from an alignment of twenty felid and four outgroup mitochondrial cytochrome *b* sequences. There were 287 positions in the final alignment. Extant felid-felid comparisons are shown as filled squares, and extant felid-outgroup comparisons are shown as grey squares. 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).

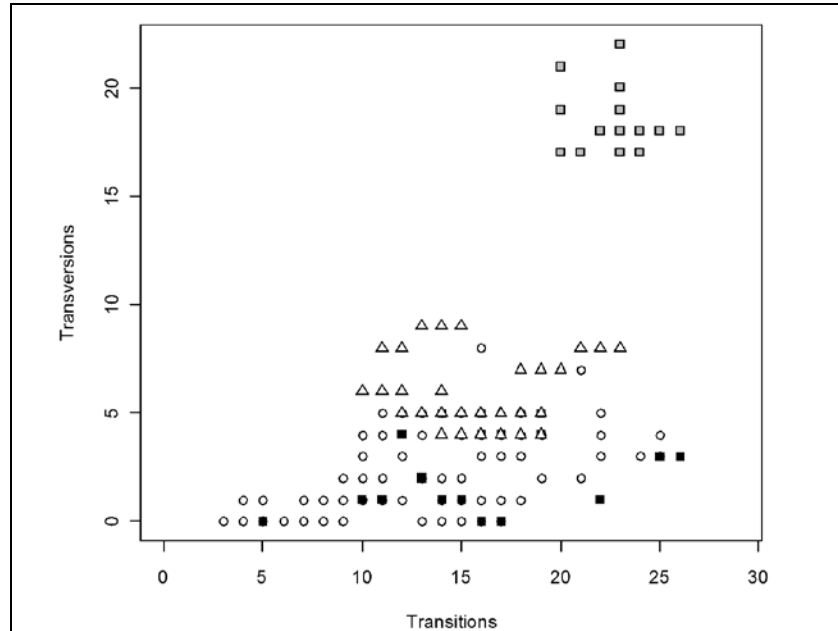


Figure 2. Transitions and transversions from an alignment of thirty equid and two outgroup mitochondrial control region sequences. There were 423 positions in the final alignment. Extant equid-equid comparisons are shown as filled squares, and extant equid-outgroup comparisons are shown as grey squares. 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 comparisons, 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.

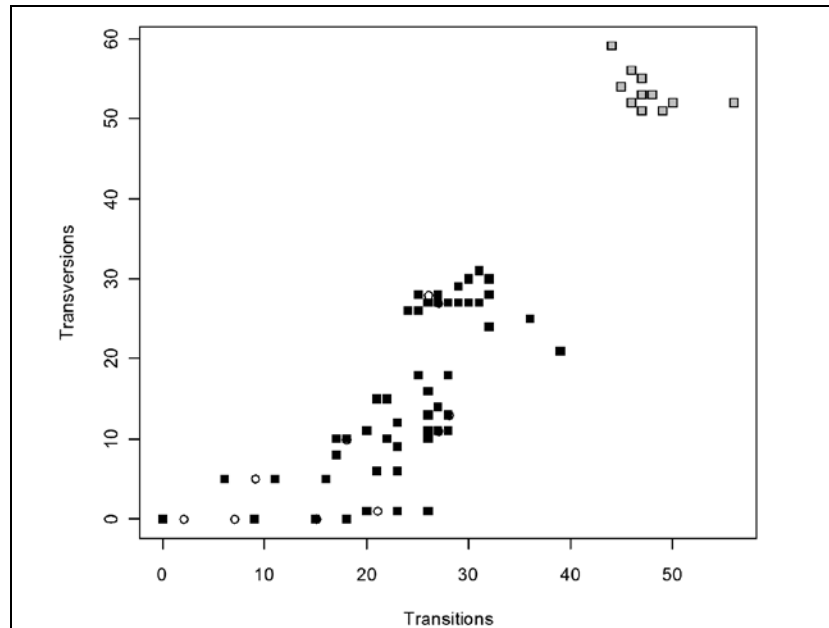


Figure 3. Transitions and transversions from an alignment of thirteen canid and one outgroup mitochondrial control region sequences. There were 493 positions in the final alignment. Extant canid-canid comparisons are shown as filled squares, and extant canid-outgroup comparisons are shown as grey squares. 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., Giam, 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 <i>b</i>		
<i>Acinonyx jubatus</i>	extant	AY463959
<i>Catopuma temminckii</i>	extant	FJ594957
<i>Felis catus</i>	extant	AB004238
<i>Felis silvestris</i>	extant	EF689045
<i>Lynx Canadensis</i>	extant	AY598475
<i>Lynx pardinus</i>	extant	EF689047
<i>Lynx rufus</i>	extant	GU175436
<i>Neofelis nebulosa</i>	extant	NC_008450
<i>Panthera leo</i>	extant	AF384815
<i>Panthera onca</i>	extant	HM107682
<i>Panthera pardus</i>	extant	EF551002
<i>Panthera tigris</i>	extant	AF053025
<i>Prionailurus bengalensis</i>	extant	AB210233
<i>Prionailurus iriomotensis</i>	extant	AB210228
<i>Prionailurus planiceps</i>	extant	FJ594958
<i>Prionailurus viverrinus</i>	extant	AB210239
<i>Puma concolor</i>	extant	AY598487
<i>Uncia uncia</i>	extant	NC_010638
<i>Homotherium serum</i>	>10,000 YBP	DQ097176
<i>Smilodon populator</i>	>10,000 YBP	DQ097174
<i>Miracinonyx trumani</i>	>10,000 YBP	DQ097175
<i>Suricata suricatta</i> (outgroup)	extant	AF522346
<i>Herpestes edwardsii</i> (outgroup)	extant	DQ519052
<i>Fossa fossana</i> (outgroup)	extant	AF511062
<i>Crocuta crocuta</i> (outgroup)	extant	DQ157555
Equidae mitochondrial control region		

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

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

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

Table 2. Radiocarbon dates recalibrated to calendar dates

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