

# Implications of Creation Biology for a Neogene-Quaternary Flood/Post-Flood Boundary

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## Abstract

While several current Flood models posit an Upper Cenozoic Flood/Post-Flood Boundary, none of them adequately address the serious problem that they engender regarding biblical kinds and their relationship to the Genesis narrative. Genesis 7 lays a constraint on the development of Flood models—only one pair of every terrestrial unclean kind was taken into the Ark. One recent Flood model places the boundary between the Neogene and Quaternary. This puts multiple genera within a terrestrial unclean kind on both sides of the boundary, contravening the traditional understanding of the biblical kind. This paper lays out the issue and examines possible alternative solutions, but concludes that the Neogene-Quaternary boundary is not viable within a biblical framework.

**Keywords:** baramin, biostratigraphy, carnivores, creation biology, fossils, Genesis, kinds, lizards, Neogene, Flood/post-Flood boundary, Quaternary, reptiles, snakes

## Introduction

Several individuals have posited the Upper Cenozoic for the Flood/post-Flood boundary over the years (for example, Holt 1996; Oard 2008–2020). The recently published Clarey Flood Model suggests that the boundary generally separates the Neogene and Quaternary, or Pliocene from Pleistocene strata (Clarey 2020; Hebert 2020a). Such boundaries have considerable biological implications within a creation science framework, which are not fully addressed (or perhaps even recognized) by upper boundary proponents.

Placing the Flood/post-Flood boundary between the Neogene and Quaternary directly affects how a fundamental unit in creation biology, the kind, is interpreted. The Creation account in Genesis tells us that God originally organized plants and animals within “kinds” (Genesis 1). God created all biological life ‘according to their kinds’ (NIV). The phrase is repeated ten times in Genesis 1, verses 11, 12, 21, 24, and 25. Plants were created “bearing seed” or “bearing fruit” and God blessed animal life to increase and fill the earth. Creation biologists refer to these as the original created kinds (for example, Ahlquist and Lightner 2019). Wise (1990) denoted the original created individuals as each kind’s archaebaramin, and defined a baramin as comprising an archaebaramin and all its descendants. Wood et al. (2003) formalized the baramin concept to focus, not on ancestry, but on biological character space. In doing so, they argued that the biblical word for kind, *mîn*, in Genesis 1 is “not directly linked with reproduction but with creation,” and made the leap to *mîn* having no link to reproducing ‘after their kinds.’ Wood (2018) repeats this argument. Future research should reexamine this question, as it deserves robust

analysis. An argument against direct connection is not an argument against any connection. There is a distinct pattern in the structure of Genesis 1 that deserves further attention.

Regardless, creation biology has traditionally assumed that one created kind does not hybridize with another (Garner 2009). Not every species within a kind can hybridize with another species, but if two species can hybridize, they have traditionally been considered to be within the same kind. Wise (2020) has suggested, based on hybridization reports in fish, that this may not apply to all vertebrates. “Distant hybridization” at or above the family level has also been reported in marine invertebrates and in a few amphibians (Zhang et al. 2014), however caution is warranted before accepting all such claims, as taxonomic misidentification or lack of genetic evidence may muddy the issue.

Baraminology uses similarity and discontinuity between organisms, using a wide range of character traits, to determine holobaramins. A holobaramin is a group of species “discontinuous with all other organisms and within which each individual shares continuity with at least one other member of the group” (Wood and Murray 2003). On a practical level, the holobaramin is “all members of a specific created kind; in other words, the whole baramin” (Lightner et al. 2011).

For many organisms, the holobaramin appears comparable to the family level in the Linnaean system of classification (Wood 2008; Wood 2009), but there are exceptions where a kind may be more or less inclusive (Wise 2009; Wood 2009). For example, the family Felidae is made up of very different felines ranging from cougar and tigers to lynx and ocelots. Members of different species and genera

(even subfamilies) of living felines are capable of hybridization (Pendragon and Winkler 2011), but no feline has been recorded to hybridize with members of the canine or ursine kinds. Lightner (2012) considered the Felidae a strong candidate for a holobaramin due to hybridization data and a strong cognitum, though based on his post-Flood continuity criterion, Wise (2009) suggested the suborder Feliformia could be a holobaramin. Thompson and Wood (2018) used statistical baraminology techniques to conclude that the Felidae is likely a holobaramin.

The Genesis narrative of the global flood (Genesis 6–8) also refers to animal kinds. Pairs of every terrestrial animal and flying creature were taken into the Ark, “every wild animal,” “all livestock,” “every creature that moves along the ground,” and “every bird,” “according to its kind” (Genesis 7:14, NIV). While clean animals and birds were taken aboard in sevens or pairs of seven (Genesis 7:2–3), only one pair of every unclean terrestrial kind was given passage on the Ark and opportunity to establish a new population in the post-Flood world. Traditionally, the Ark kind has been equated with the created kind. Certainly, similarity in ethnozoological nomenclature between Genesis 1 and the Flood account suggest little if any distinction. [Created kinds are objectively real, in that they are distinct, unrelated lineages. They are also ethnozoological, in that anyone, not just biologists, can categorize, compile, and divide kinds by perceived similarities and differences. Genesis incorporates ethnozoological categories (Atran 1990; Berlin 1992) such as “livestock,” “wild animals,” “birds,” “creatures that move along the ground,” and “great creatures of the sea.”]

The pairing of unclean kinds is significant to the development of Flood models. Because only one pair from each unclean terrestrial kind survived the Flood, there are constraints on how we can interpret the fossil record in a way that makes sense of the biblical narrative.

The majority of recognizable holobaramins (determined from hybridization reports, statistical baraminology, and other studies [Ahlquist and Lightner 2019]) are made up of multiple genera and species (e.g. Doran et al. 2018; Hennigan 2014b; Hennigan 2015; Lightner 2012; Lightner 2013; Thompson and Wood 2018; Wood 2016). Kinds are capable of extensive physiological, morphological, and behavioral adaptations. There is no reason to expect that post-Flood descendants of a single surviving pair on the Ark would diversify into exactly the same variations as those found before the Flood. The post-Flood world offered new climates, new landscapes, and new ecological relationships. The idea that a single pair would produce exact replicas from a pre-Flood world lacks foundation.

The data, however, clearly shows that multiple genera and species from within the same unclean terrestrial kinds are found on both sides of a Neogene-Quaternary Flood/post-Flood boundary. Data has been presented previously (Arment 2014, 2020b; Ross 2012), but additional evidence will be shown here to augment the point.

## Methodology

Three sets of data are presented here. For all sets, only unclean terrestrial animals are considered, based on the premise (Genesis 7:2) that only one pair of each such kind survived on the Ark. The purpose of these datasets is to demonstrate the extent of boundary-crossing of such genera, and the incompatible nature of such with the traditional understanding of creation biology.

Table 1 collects locality data on three monobaramins with extant genera found in the same fossil sites below the Neogene-Quaternary boundary in North America. A monobaramin is “a group of known organisms that share continuity, without regard to discontinuity with other organisms” (Wood et al. 2003). So, each genus within a monobaramin is included in the baramin, but the baramin may include additional genera not addressed in these monobaramins. Here, each monobaramin includes genera capable of hybridizing with another genus within that monobaramin. As noted in Arment (2014), formations with such fossil associations should be considered post-Flood within traditionally understood creation biology.

The first group, a colubrid snake monobaramin, includes New World ratsnakes (*Pantherophis*), kingsnakes and milksnakes (*Lampropeltis*), and bullsnakes, gopher snakes, and pine snakes (*Pituophis*). Intergeneric hybrids are well established within this monobaramin (Arment 2020a; Fankhauser and Cumming 2008; Hennigan 2005; Hennigan 2019; LeClere et al. 2012).

The second group noted is a viperid snake monobaramin that includes the North American pit vipers *Crotalus*, *Sistrurus*, and *Agkistrodon*. The rattlesnake genera *Crotalus* and *Sistrurus* have produced a recognizable hybrid (Bailey 1942; Hennigan 2019), while details on a *Crotalus* × *Agkistrodon* (copperhead) hybrid were recently described (Arment 2020a).

The third group is a canid monobaramin, including *Canis*, *Vulpes*, and *Urocyon*. In 1973, a female red fox (*Vulpes*) gave birth to two cubs sired by a male coyote (*Canis*) at the Cohanzick Zoo in Bridgeton, New Jersey, though neither survived the first week (Anonymous 1973; Loane 1973; Van Gelder 1977). These hybrids indicate that *Vulpes* and *Canis* species are in the same kind. There is one record of a red fox-

grey fox (*Vulpes-Urocyon*) hybrid, though it is based on notes taken by a fur-trader who recognized that the skin showed a split of characteristics between the two species (Bezdek 1944). While anecdotal, it is reasonable to assume that grey foxes and red foxes are within the same created kind, and the creationist literature reflects this (Lightner 2012; Pendragon 2011; Siegler 1974).

Table 2 shows genera of herpetofauna that fulfilled the requirements of being a) extant and endemic to North America, b) found in the fossil record only in North America, and c) found in the fossil record below the Neogene-Quaternary boundary. Two endemic snake genera, *Nerodia* and *Pantherophis*, were excluded due to similarity to Old World genera. The number of genera listed can be used to calculate the likelihood of all genera being found on only one continent both in Flood deposits and after the Flood (Arment 2020b). Creation researcher Paul Garner (pers. comm.) has noted that such boundary-spanning taxa would not necessarily be returning to the continent where their pre-Flood ancestors lived, but simply to where they were buried, as Flood transport likely would have moved the remains considerable distances from their original territories. Assuming six continents (Antarctica excluded), the probability calculation is  $(1/6)^x$  where  $x$  is the number of species considered.

Table 3 compiles terrestrial carnivore genera found on both sides of the Neogene-Quaternary boundary. Some genera are extinct and only represented above the Neogene-Quaternary boundary by Pleistocene remains. This table shows the extent of boundary crossing within a single order (Carnivora), excluding aquatic genera, around the world. Multiple boundary-crossing genera within a single family suggests that either each of those genera are separate Ark kinds (even if they are capable of intergeneric hybridization), or the Neogene-Quaternary boundary is not the Flood/post-Flood boundary.

## Results

Table 1 shows 44 distinct monobaraminic associations of extant genera capable of hybridization found at thirty-eight North American locations below the Neogene-Quaternary boundary. These include both Pliocene and Miocene fossil sites. This is only a small subset of possible monobaraminic groupings, and if indicative of what we can expect by looking at fossil sites around the world, is a significant challenge for Neogene-Quaternary boundary proponents.

Table 2 shows 15 snake genera, 12 lizard genera, and two terrestrial chelonian genera were found to fulfill all three requirements. The likelihood of all twenty-nine genera being found on only one continent both in Flood deposits and after the Flood

is:  $(1/6)^{29} = 2.71 \times 10^{-23}$ . This result shows it is highly improbable that all twenty-nine genera would be found only on the North American continent, both extant and in Flood deposits. These results add to the evidence provided with the same calculation using the marsupials of Australia and South America (Arment 2020b), and can certainly be used with other organisms fossilized in Cenozoic layers around the world.

Table 3 shows ten families of carnivores around the world were found to have 73 genera on both sides of the Neogene-Quaternary boundary. Nine of these families had multiple genera on both sides. At least three families (Canidae, Felidae, and Ursidae) have extant boundary-crossing genera that are known to hybridize with other genera (Hennigan 2010; Lightner 2012; Van Gelder 1977).

## Discussion

Each table of data presented here shows a different facet of the same problem: there are far too many genera from terrestrial unclean kinds found on both sides of a Neogene-Quaternary boundary for that location to be a viable answer to the Flood/post-Flood boundary question if the Ark kind is typically at or near the family level and/or if hybridization is evidence for inclusion in the same kind.

Not only has this issue been inadequately addressed by upper boundary proponents, in some cases it has been outright ignored. In a critique of Arment (2020b), Heerema (2020) offered not a single response to the fact that an upper boundary necessitates a far greater number of Ark kinds than there are created kinds. He claimed that “the Bible is the authority on which we must build our thinking,” yet ignored Genesis 7:2—only one pair of every unclean kind was taken onto the Ark. Instead, Heerema simply used the opportunity to promote his own Flood model. Oard (2015), in response to Arment (2014), did not address the evidence (the presence of monobaraminic associations in specific fossil deposits), instead casting aspersions on the accuracy of osteological identification. Given that all data presented here is at the genus level, and covers a wide range of fossils worldwide, that simply is not a reasonable response. Clarey (2020) brought up the marsupial problem, noting the study by Ross (2012), but argued for a one-in-five chance for kangaroos returning to Australia in a post-Flood “sweepstakes” model. Obviously, that is an untenable solution (Arment 2020b), and peculiar because there is no indication that Clarey recognizes that kangaroos (Family Macropodidae), given his proposed boundary, would include sixteen separate genus-specific Ark kinds! This clearly illustrates a disconnect in the thinking of upper boundary proponents. Clarey (2020) stated, “Fossil evidence is





**Table 2.** Extant and endemic North American herpetogaua that cross the Neogene-Quaternary boundary.

	Miocene	Pliocene	Pleistocene	Holocene	Reference
<b>Snakes</b>					
<i>Agkistrodon</i>	X	X	X	X	Holman 2000
<i>Arizona</i>	X		X	X	Holman 2000
<i>Carphophis</i>		X	X	X	Holman 2000; Jurestovsky 2016
<i>Charina</i>	X		X	X	Holman 2000
<i>Coluber</i>	X	X	X	X	Holman 2000
<i>Diadophis</i>	X		X	X	Holman 2000
<i>Gyalopion</i>		X	X	X	Holman 2000; Jurestovsky 2016
<i>Heterodon</i>	X	X	X	X	Holman 2000
<i>Pituophis</i>	X	X	X	X	Holman 2000
<i>Regina</i>		X	X	X	Holman 2000
<i>Rhinocheilus</i>		X	X	X	Holman 2000
<i>Salvadora</i>	X		X	X	Holman 2000
<i>Sistrurus</i>	X	X	X	X	Holman 2000; Parmley and Holman 2007
<i>Storeria</i>		X	X	X	Holman 2000
<i>Thamnophis</i>	X	X	X	X	Holman 2000
<b>Lizards</b>					
<i>Anniella</i>	X	X	X	X	Bell, Mead, and Fay 1995
<i>Callisaurus</i>	X		X	X	Mead 2005; Scarpetta 2019
<i>Crotaphytus</i>		X	X	X	Hollenshead and Mead 2006; Mead 2005
<i>Dipsosaurus</i>		X		X	Hulse 1992
<i>Elgaria</i>	X		X	X	Scarpetta 2018; Wake and Roeder 2009
<i>Gambelia</i>		X		X	Hollenshead and Mead 2006
<i>Gerrhonotus</i>	X		X	X	Robinson and Van Devender 1973; Springer et al. 2009
<i>Heloderma</i>	X	X	X	X	Mead 2005; Mead et al. 2012
<i>Phrynosoma</i>	X	X	X	X	Oelrich 1954; Van Devender and Eshelman 1979
<i>Sceloporus</i>	X		X	X	Mead 2005; Scarpetta 2019
<i>Uma</i>	X			X	Scarpetta 2019
<i>Uta</i>	X		X	X	Mead 2005; Scarpetta 2019
<b>Chelonians</b>					
<i>Gopherus</i>	X	X	X	X	Franz and Quitmyer 2005; Reynoso and Montellano-Ballesteros 2004
<i>Terrapene</i>	X	X	X	X	Holman and Fritz 2005

all about the probabilities and nothing more.” Even if this claim were true, if the calculations are done correctly, the probabilities certainly do not favor the upper boundary proponent (Arment 2020b; table 2). But fossil patterns in biogeography and biostratigraphy are also important evidence, from the Great American Biotic Interchange to the Bering Land Bridge Theory.

A recent summary of alleged Neogene-Quaternary boundary evidence (Tomkins and Clarey 2020) not only fails to acknowledge the issues brought up by numerous previous papers, but repeatedly engages in the logical fallacy of affirming the consequent in the assertions proffered. For example, they state,

“Most of these fossilized mammals would have been living at higher, more temperate elevations than the dinosaurs and thus would have been buried in the uppermost Flood layers of the Cenozoic—which is exactly where we find them.” This fallacy simply ignores other possible explanations for the phenomenon of the diversity of fossil mammals in the Upper Cenozoic.

While these upper boundary proponents may not be seriously grappling with the issue, there are other creation researchers who are considering the implications of boundary position on creation biology. After some discussion with other researchers (for example, Jean Lightner, pers. comm.), only a few

**Table 3.** Terrestrial carnivores (worldwide) that cross the Neogene-Quaternary Boundary.

	Miocene	Pliocene	Pleistocene	Holocene	References
<b>Canidae</b>					
<i>Canis</i>	X	X	X	X	Sotnikova and Rook 2010; Tedford, Wang, and Taylor 2009; Wang and Tedford 2007
<i>Cerdocyon</i>		X	X	X	Tedford, Wang, and Taylor 2009
<i>Chrysocyon</i>		X	X	X	Tedford, Wang, and Taylor 2009
† <i>Dusicyon</i>		X	X	X	Ramirez and Prevosti 2014
<i>Lycalopex</i>		X	X	X	Lucherini and Vidal 2008; Ramirez and Prevosti 2014
<i>Lycaon</i>		X	X	X	Hartstone-Rose et al. 2010
<i>Nyctereutes</i>		X	X	X	Lucenti 2017; Wang and Tedford 2007
<i>Otocyon</i>		X	X	X	Clark Jr. 2005
<i>Urocyon</i>		X	X	X	Bozarth et al. 2011; Tedford, Wang, and Taylor 2009; Wang and Tedford 2007
<i>Vulpes</i>	X	X	X	X	De Bonis et al. 2007; Tedford, Wang, and Taylor 2009; Wang and Tedford 2007;
<b>Felidae</b>					
<i>Acinonyx</i>		X	X	X	Avery 2019; Cherin et al. 2014
<i>Caracal</i>		X	X	X	Avery 2019; Werdelin et al. 2010
† <i>Dinofelis</i>	X	X	X		Geraads 2004; Jiangzuo, Sun, and Flynn 2020; Morales, Pickford, and Soria 2005
<i>Felis</i>		X	X	X	Geraads and Peigné 2016; Morales, Pickford, and Soria 2005; Palombo and Valli 2003–2004
<i>Herpailurus</i>		X	X	X	Bravo-Cuevas et al. 2016; Chimento, Derguy, and Hemmer 2014
† <i>Homotherium</i>		X	X		Antón et al. 2014; Avery 2019
<i>Leptailurus</i>		X	X	X	Avery 2019
<i>Lynx</i>		X	X	X	Rothwell 2003; Werdelin et al. 2010
† <i>Megantereon</i>		X	X		Palmqvist et al. 2007; Zhu et al. 2014
† <i>Metailurus</i>	X	X	X		Jiangzuo, Sun, and Flynn 2020; Morales, Pickford, and Soria 2005
† <i>Miracinonyx</i>		X	X		Van Valkenburgh, Grady, and Kurtén 1990
<i>Panthera</i>	X	X	X	X	Avery 2019; Tseng et al. 2014; Werdelin et al. 2010
<i>Puma</i>		X	X	X	Chimento and Dondas 2018; Ercoli et al. 2019; Hemmer, Kahlke, and Vekua 2004
<b>Herpestidae</b>					
<i>Atilax</i>	X		X	X	Cohen, O'Regan, and Steininger 2019; Peigné et al. 2005
<i>Cynictis</i>		X	X	X	Avery 2019
<i>Galerella</i>	X		X	X	Cohen, O'Regan, and Steininger 2019; Peigné et al. 2005
<i>Helogale</i>		X	X	X	Assefa, Yirga, and Reed 2008; WoldeGabriel et al. 1994
<i>Herpestes</i>	X	X	X	X	Cohen, O'Regan, and Steininger 2019; Geraads 2006; Peigné et al. 2005
<i>Icheumia</i>	X	X	X	X	Cohen, O'Regan, and Steininger 2019; Geraads 2006; Peigné et al. 2005
<i>Mungos</i>		X	X	X	Cohen, O'Regan, and Steininger 2019; Kovarovic, Andrews, and Aiello 2002
<b>Hyaenidae</b>					
† <i>Chasmaporthetes</i>	X	X	X		De Bonis et al. 2010; Tseng, Zazula, and Werdelin 2019; Turner, Antón, and Werdelin 2008
<i>Crocuta</i>		X	X	X	Turner, Antón, and Werdelin 2008; Werdelin and Lewis 2008
<i>Hyaena</i>		X	X	X	Kuhn, Werdelin, and Steininger 2017; Werdelin and Lewis 2008
† <i>Pachycrocuta</i>		X	X		Mazza 2006; Turner, Antón, and Werdelin 2008
† <i>Pliocrocuta</i>		X	X		Turner, Antón, and Werdelin 2008
<i>Proteles</i>		X	X	X	Koehler and Richardson 1990; Kuhn, Werdelin, and Steininger 2017

	Miocene	Pliocene	Pleistocene	Holocene	References
<b>Mephitidae</b>					
<i>Conepatus</i>		X	X	X	Wang, Carranza-Castañeda, and Gómez 2014
<i>Mephitis</i>		X	X	X	Wang, Carranza-Castañeda, and Gómez 2014; Wang, Whistler, and Takeuchi 2005
<i>Spilogale</i>		X	X	X	Wang, Carranza-Castañeda, and Gómez 2014; Wang, Whistler, and Takeuchi 2005
<b>Mustelidae</b>					
† <i>Eirictis</i>		X	X		Lucenti 2018
† <i>Enhydriodon</i>	X	X	X		Geraads et al. 2011; Morales, Pickford, and Soria 2005; Willemsen 1992
<i>Galictis</i>		X	X	X	Rodrigues, Avilla, and De Azevedo 2016
<i>Gulo</i>		X	X	X	Samuels, Bredehoeft, and Wallace 2018
<i>Hydrictis</i>		X		X	Werdelin, Lewis, and Haile-Selassie 2014
<i>Lontra</i>		X	X	X	Prassack 2016
<i>Lutra</i>	X	X	X	X	Geraads et al. 2015; Hung and Law 2016
† <i>Martellictis</i>		X	X		Lucenti 2018
<i>Martes</i>	X	X	X	X	Koufos 2011; Stone and Cook 2002
<i>Meles</i>		X	X	X	Jiangzuo et al. 2018; Madurell-Malapeira et al. 2011
<i>Mellivora</i>		X	X	X	De Bonis et al. 2009
<i>Mustela</i>	X	X	X	X	Harding and Smith 2009
† <i>Pannonictis</i>		X	X		Lucenti 2018
<i>Pekania</i>	X	X	X	X	Samuels and Cavin 2013
† <i>Satherium</i>		X	X		Hulbert Jr. 2010; Willemsen 1992
† <i>Sivaonyx</i>	X	X	X		Grohé et al. 2013; Morales, Pickford, and Soria 2005
<i>Taxidea</i>		X	X	X	Carranza-Castañeda et al. 2013; McDonald 2002
† <i>Trigonictis</i>		X	X		Skinner and Hibbard 1972
<i>Vormela</i>		X	X	X	Spassov 2001
<b>Nandiniidae</b>					
<i>Nandinia</i>	X			X	Morales, Pickford, and Soria 2005
<b>Procyonidae</b>					
<i>Bassariscus</i>	X	X	X	X	Baskin 2003, 2004; Gustafson 2015; Koepfli et al. 2007
† <i>Cyonasua</i>	X	X	X		Engelman and Croft 2019
<i>Nasua</i>		X	X	X	Koepfli et al. 2007
<i>Procyon</i>	X	X	X	X	Arata and Hutchison 1964; Koepfli et al. 2007
<b>Ursidae</b>					
† <i>Agriotherium</i>	X	X	X		Salesa et al. 2011; Samuels, Meachen-Samuels, and Gensler 2009
<i>Ailuropoda</i>		X	X	X	Jin et al. 2007; Salesa et al. 2011
† <i>Arctodus</i>		X	X		Schubert et al. 2010
† <i>Arctotherium</i>		X	X		Soibelzon et al. 2008
† <i>Protarctos</i>		X	X		Wang et al. 2017
<i>Tremarctos</i>		X	X	X	Schubert et al. 2010
<i>Ursus</i>		X	X	X	Rustioni and Mazza 1993
<b>Viverridae</b>					
<i>Civettictis</i>		X	X	X	Ray 1995; Werdelin and Lewis 2000; Werdelin, Lewis, and Haile-Selassie 2014
<i>Genetta</i>	X	X	X	X	Larivière and Calzada 2001; Morales, Pickford, and Soria 2005; Werdelin, Lewis, and Haile-Selassie 2014
<i>Viverra</i>	X	X	X	X	Ray 1995; Rook and Martínez-Navarro 2004; Liu et al. 2010; Avery 2019

† = Extinct taxon



arguments that might benefit the Upper Cenozoic boundary proponent could be mustered:

(A) The kinds brought into the Ark were not the created kinds, but divisions (arbitrary or not) of the created kinds. This would increase the number of Ark kinds, allowing more genera within the same created kind to survive the Flood. The Ark kinds would be potentially capable of hybridizing with certain other Ark kinds. For example, there may have been an original created feline kind, which diversified before the Flood, leading to multiple feline pairings (a panther pair, a small cat pair, a cheetah-like pair, a sabre-tooth cat pair, etc.) surviving on the Ark. Or perhaps the Ark kind was typically at the genus level, and each feline genus was paired separately on the Ark. But, in some cases, it might need to be at the species level. The extant (and distinctive) North American endemic snake species *Lampropeltis getula* (common king snake) and *Lampropeltis triangulum* (milk snake) are both found in Pliocene and Miocene deposits (Holman 2000). Was a pair of each on the Ark?

(B) The Ark kinds, generally referable to the family level, upon embarking into the post-Flood world, engaged in both rapid speciation and hyper-convergence on pre-Flood forms, disregarding adaptation to a new world to simply reproduce a range of exact pre-Flood morphologies. In other words, a single pair of the kangaroo kind (Family Macropodidae) emerged from the Ark, and its descendants made their way back to Australia, only to diversify into the exact sixteen genus-specific morphologies found in the uppermost Flood layers in Australia (but not the additional morphologies found in lower layers). These rapid changes would have taken place in a few hundred years or so. The irony here is that many of those who support an Upper Cenozoic Flood boundary refer to lower Flood boundary proponents as hyper-evolutionists (Clarey 2020) or “Young Earth Evolutionists” (Hebert 2020b).

(C) Many “Miocene” and “Pliocene” fossils are in incorrectly identified fossil strata. Essentially, this argues for paleontological gerrymandering. The Upper Cenozoic boundary proponent would simply decide which fossils they think are actually post-Flood in order to compatibilize their argument. Mike Oard, for example, has suggested (pers. comm., reviewing an early draft of Arment (2020b)) that Australian fossils recorded from Miocene and Pliocene strata may be better characterized as Pleistocene, arguing that the age of those fossils was pushed back primarily due to alleged ‘primitive’ characteristics requiring an earlier evolutionary position. Of course, that does not explain the South American marsupial fossils presented in Arment (2020b), or the fossils presented in this paper.

(D) Anatomical differences between genera are too slight, too confusing, or too variable to be useful in accurate identification, and we cannot assume that Neogene and Quaternary fossils that appear to be the same genus, actually are. Of course, none of the studies that have tested the Neogene-Quaternary boundary are based on only a handful of specimens. The idea that osteological identification is inadequate at the genus-level for so many vertebrates around the world, with a multitude of specimens and fossil sites, has no rational basis. For this paper, I have specifically attempted to derive fossil data from up-to-date papers and reviews to minimize issues with fossil identification.

The biostratigraphic data tables presented here allow us to examine these alternative arguments closer.

Were there more Ark kinds than created kinds? While it may be tempting to jump into a Hebrew word study for “kind” to wrangle a few more passengers on the Ark, we are not simply talking about a few extra kinds. While Woodmorappe (1996) calculated his feasibility study on the Ark based on nearly 16,000 individual animals, his decision to use genus-level numbers was made to make the problem more challenging to bolster his defense against anti-creationists. He noted that the likely estimate of Ark inhabitants was closer to 2,000 animals. Recent estimates of Ark kinds number at 196 extant bird kinds (Lightner 2013), up to 300 extant and fossil mammal kinds (Lightner 2012), 101 extant reptile kinds (Hennigan 2014a, 2014b; Hennigan 2015), and 248 extant and fossil amphibian kinds (Hennigan 2013a, 2013b; Ross 2014a). Doran et al. (2018) noted 27 potential dinosaur holobaramins. This is not an exhaustive list of Ark kinds, but it provides insight into the effective group size necessary to rescue the genetic potential of the created kinds and deliver them to a new world. We know that an Ark pair would be capable of family-level diversification after the Flood (Jeanson 2017), so an obligatory genus-level Ark kind has no biological justification. We also see (table 2) that the more kinds there are on the Ark, the greater the number of genera found both extant on a single continent and buried in Flood deposits on that same continent—a highly improbable correlation. Any attempt to make the Ark kinds mean something different from created kinds must be carefully weighed for its implications, not simply used as a rescue device for a Flood model.

Was there a hyper-convergent evolution of Ark kinds to pre-Flood forms in the post-Flood world? Despite Heerema’s (2020) complaints, the majority of creation scientists hold to distinct continental differences between the pre-Flood and post-Flood worlds. Even the Clarey (2020) Flood Model suggests

a pre-Flood Pangaea-like continental configuration. That, and what we know about the vast variety of extinct plants and animals in the fossil record, means there were significant differences in climate, habitat, and ecological networks. We know that the pre-Flood earth “was full of violence” (Genesis 6:11, NIV), and that God regretted creating not just humanity, but “the animals, the birds and the creatures that move along the ground” (Genesis 6:7, NIV). That is a very different world from the one the Ark kinds encountered after the Flood. This period, sometimes termed the Arphaxadian epoch after Noah’s grandson (Wise 2002), would have offered the Ark kinds opportunities to adapt in new ways. Clearly God created the original kinds with the ability to diversify into distinctive and fascinating morphologies. There is no biological (or theological) foundation to argue that such diversification after the Flood was constrained by pre-Flood phenotypes. Proponents also face the improbability of so many genera being found on a single continent after the Flood, while their counterpart fossil “twins” are buried in Flood deposits on that same continent (table 2).

Are fossil strata often identified incorrectly? Table 1 and table 2 note fossils from Miocene and Pliocene deposits from across North America, as did Ross’s (2012) study on North American mammal genera. Table 3 notes fossils from Miocene and Pliocene deposits from around the world. It is unlikely that the upper boundary proponent will be able to explain all of these as misidentified Pleistocene deposits. This argument seems entirely ad hoc, intended to protect a pet model from contrary data. Sedimentary identification isn’t changed on paleontological whims, and is not based on the fossils under discussion here. Rather, paleontologists examine palynoflora, foraminifera, macroinvertebrates, and other fossils of that nature. The biostratigraphy of many Australian fossil assemblages (Arment 2020b) is based on radiometry, magnetostratigraphy, and correlating foraminifera and pollens (Black et al. 2012; Long et al. 2002; Woodhead et al. 2016), not simply on whether various marsupial fossils were “primitive” or “advanced.” Anyone who argues that these deposits are incorrectly assigned should be able to demonstrate in detail that the data that is actually used to identify those sediments is flawed.

Is it impossible to accurately distinguish fossils at a generic level? Ross (2014b) responded to a similar argument, which bears repeating: “My own experiences with fossil collections and evolutionary paleontologists over the past 20 years provide no sympathy for...unrestrained skepticism of their work. So unless and until [he] can provide specific, character-based, morphological reasons for his assertions of gross fossil misidentification, the

multitude of fossil occurrences incongruent with his proposed geological model should make us reassess the model, not the fossils.”

## Conclusion

There do not appear to be any arguments that can explain worldwide Cenozoic fossil data and trends from a Neogene-Quaternary Flood/post-Flood boundary perspective. If upper boundary proponents truly believe such an argument can be made, that should be their priority if they wish to sway those who hold to competing models.

Table 1 shows that there are (at least) 44 monobaraminic associations of extant genera at 38 North American Miocene and Pliocene fossil sites, which should only be possible with post-Flood fossil sites. Table 2 presents data that follow the calculation methods from Arment (2020b), illustrating the incredibly low probability that all of those genera would be found on only one continent both extant and in Flood deposits. Table 3 shows the extensive Neogene-Quaternary boundary-crossing (73 genera in only 10 families) found in terrestrial carnivore families all over the world, indicating that this is not a problem limited to one continent.

When we hold that the Genesis Flood narrative is historically true, that only a single pair of every unclean terrestrial animal kind survived on the Ark to establish a new population, this sets up very clear constraints. The Flood/post-Flood boundary should not be placed between the Neogene and Quaternary.

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