

To the Ark, and Back Again? Using the Marsupial Fossil Record to Investigate the Post-Flood Boundary: A Reply

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Abstract

Nathan Mogk (2025) has attempted to solve the Australian marsupial problem for Upper Cenozoic Flood Boundary models with a naturalistic framework. In commenting on the high improbability that so many marsupials would end up in the same remote location on the fossil bones of their direct ancestors, Mogk asserts that there are biogeographic parameters that would render Ark marsupials interdependent as they migrated into the post-Flood world. This, he believes, would greatly increase the probability that they would end up together in the same region. This reply considers Mogk's claims and how well they fit with what is known regarding ecological relationships and the geographic pathways necessary for a mass migration of marsupials. Mogk's assumption of interdependency is rejected, as it is biologically inadequate. Unless a better argument emerges, Upper Cenozoic Flood Boundary proponents must continue to argue for biblically unrecorded divine intervention to explain the Australian marsupial problem. Lower Cenozoic Flood Boundary proponents may continue to investigate that issue through natural post-Flood dispersal and diversification mechanisms.

Keywords: biogeography, biostratigraphy, competition, dispersal, Flood models, marsupials, placental mammals, predation, symbiosis

Introduction

In setting up the presentation for his calculations, Nathan Mogk (2025) claims that my paper “contains a major statistical error,” or an “unwarranted assumption of statistical independence.” He claims that this is “without justification and contrary to current biogeographic knowledge,” and that I “should supply the biological justification for his chosen statistical model.” The irony here is that Mogk offers no justification for assuming that there is interdependency. When I first received notice that Mogk had sent in this reply to my paper, I saw that it lacked supporting data, biogeographical or otherwise, for presuming that any marsupials must have migrated together from the Ark to Australia. There was only a single biogeography paper used as a reference. I sent it back, asking that he offer something to substantiate his claim. As can be seen in his published reply, no such support is given. Instead, Mogk (2025) proffers a litany of terminology. A list of biogeographic phrases does not in and of itself support the concept that up to hundreds of marsupials must have migrated en masse from the Ark to Australia in his Flood model—a Marsupial Mass Migration theory that must be held by all Upper Cenozoic Flood Boundary models. In fact, there is nothing in Mogk's list to support the idea that any two different species of marsupials must have traveled together.

Mogk's assumption of interdependency is simply the result of poor reasoning:

(1) Within an Upper Cenozoic Flood Boundary model, an improbable number of marsupials

ended up in Australia living exactly where their pre-Flood ancestors were buried.

- (2) It is excessively improbable that so many marsupials did so independently.
- (3) Mogk assumes an Upper Cenozoic Flood Boundary model is true.
- (4) Therefore, the marsupials must have traveled interdependently.

What Interdependency?

We can look at the different ways in which supposed interdependency would develop, and evaluate them as potential justification for Mogk's (2025) argument. On the biological side, ecological relationships that affect interdependency between organisms include symbiotic relationships, predator-prey relationships, and competition.

Symbiosis in vertebrates primarily deals with parasitism (not applicable here), mutualism (where both species benefit from a relationship of close association), or commensalism (where one species benefits, while the other species does not benefit but is not harmed by such a relationship). As one example, a South America opossum, *Dromiciops gliroides*, feeds on insects and fruits, preferentially berries from a mistletoe, *Tristerix corymbosus*; the mistletoe berry seeds are exclusively dispersed through the opossum's ingestion and defecation (Rodríguez-Cabal, Aizen, and Novaro 2007). This mutualism benefits the opossum with edible berries, and the mistletoe with seed dispersal. The relationship is obligate for the mistletoe, but only facultative for the

opossum. This mutual relationship is clearly a post-Flood adaptation, otherwise the mistletoe's ancestors would have died out long before any marsupial arrived in South America.

There are no recognized forms of symbiosis between different marsupial species. No marsupial species directly benefits from being in an obligate ecological relationship with any other marsupial species. Many marsupials are kept in captivity for both conservation and educational purposes, as well as for pets (wallabies, kangaroos, sugar gliders, the Virginia opossum, various South American possums), and they do perfectly well on their own or in single-species groups. The Virginia opossum has extensively expanded its natural range in North America since the late Pleistocene, reaching Ohio by the 1600s (McManus 1974). Its ongoing expansion into western and northeastern states is of great interest to wildlife biologists, but it has expanded its range without the benefit of any other marsupials in the United States. Opossums do benefit from human activity, but that is not going to help Mogk's (2025) case. A number of Australasian marsupials have been anthropogenically introduced, independently, in different locations around the world, several of which have established themselves in free-ranging populations (Gilmore 1977). Just as one example, a rock wallaby population on O'ahu, Hawaii, is descended from a single pair that escaped in 1916 (Maynes 1989).

What about predator-prey relationships? This also is a dead end for Mogk's (2025) theorizing. While there are marsupial carnivores, there is nothing inherent in their biology that would maintain an obligate association with other marsupials. Tasmanian devils can capture mammalian prey in size up to a wallaby, but prefer small mammals, birds, fish, insects, or carrion (Pemberton et al. 2008). They are no respecter of person when it comes to marsupial or placental prey. Quolls feed on small marsupials and placentals, birds, reptiles, and invertebrates (Glen and Dickman 2008). Thylacine diet is primarily reconstructed based on skeletal remains, and *Thylacinus* were likely carnivores in a similar trophic niche as the coyote (Jones and Stoddart 1998). Most earlier thylacines were smaller-bodied and had dentition for smaller vertebrates or invertebrates (Rovinsky, Evans, and Adams 2019). *Thylacoleo* was the largest marsupial carnivore (Nedin 1991), with large incisors, a massive bite force (Wroe, McHenry, and Thomason 2005), and each forearm armed with a large, retractable claw on a semi-opposable thumb possibly used, there is some debate, for slashing and disemboweling large prey (Figueiridio, Martín-Serra, and Janis 2016). One Pleistocene bone bed in Lancefield, Victoria, includes a number of megafaunal bones, including the large

kangaroo *Macropus titan*, with cut marks that are best attributed to *Thylacoleo* tooth marks (Horton and Wright 1981). It likely preyed or scavenged on the large megafaunal species of its time, marsupials and others like the avian *Genyornis* or the emus. Not a single one of these predators required marsupial prey. *Thylacoleo* was not skulking behind a herd of herbivorous marsupials as they traveled through Asia, ignoring all the tasty placental mammals.

Competition is the next ecological relationship, and it is no wonder that Mogk (2025) does not refer to it. It is no friend to the Upper Cenozoic Flood Boundary models. Competition does not bring species together, but drives them apart. Competition for resources would be one of the primary reasons that species began to spread out from the Ark. This would also be one of the driving forces in adaptation to new niches. Of course, with the Upper Cenozoic Flood Boundary models, there would already be species with prior morphological and physiological adaptations leaving the Ark, but without a niche at hand to fill. That would leave them less capable of surviving long enough to find the correct niche. With Lower Cenozoic Flood Boundary models, animals would expand their range, migrate as necessary, and adapt to fill available niches as they disperse and diversify.

While we recognize now that Australia was the final destination for most, not all, Australidelphian marsupials, we cannot focus on that continent as some sort of marsupial magnet. All animals that left the Ark immediately found themselves in roughly the same ecological habitats. From there, they dispersed, and the route of dispersion to Australia would have provided the same ecological parameters to all of the marsupials (vegetation, geology, landscape, climate). It would be beyond silly to argue that the different marsupials used a multitude of different routes to Australia. There is no such route within Asia that can be identified as either placental-resistant, or marsupial-centric. Wherever marsupials could go, so could placental mammals. This is particularly problematic, for example, with the modern koala, *Phascolarctos*, which requires eucalyptus leaves—one of the few marsupial species that actually shows interdependency. There is no pathway of eucalypt trees from the Middle East to Australia. Not surprisingly, Oard (2022) asserted that koalas may not have eaten eucalyptus at the time of the Ark, but this ignores the anatomical evidence. Miocene and Pliocene koala genera demonstrate cranial and dental transitions towards fibrous, tough leaf mastication (Black 2016; Louys et al. 2009), and all *Phascolarctos* fossils, a genus that crosses the Plio-Pleistocene boundary, demonstrate the features necessary for a eucalypt diet (Price et al. 2009). There is no difference

in that respect with the modern koala, *Phascolarctos cinereus*, and its sedentary, leaf-chewing lifestyle.

There are only two possible dispersion scenarios from Asia to Australia within an Upper Cenozoic Flood Boundary model: a land bridge, or a sweepstakes route. A land bridge can be an open corridor that allows all species through, or a filter bridge that blocks certain species (Simpson 1940). Clearly, an open corridor from Asia to Australia is not an option for any Flood model—the lack of Australian placental mammals larger than a rodent is clear evidence against that. In order for us to consider a filter bridge from Asia to Australia, there must be some way to filter out placental terrestrial mammals while allowing marsupials through. There are no such ecological variables known to do that. Wherever marsupials thrive, so do placental mammals. This is especially true in Australia itself. When placental mammals were anthropogenically introduced (dingoes, rabbits, hares, foxes, camels, deer, various livestock), they quickly spread throughout a range of habitats, making pests of themselves and often outcompeting native marsupial species. There is nothing inherently marsupial-centric about Australia's various ecological habitats. Marsupials inhabit deserts, rain forests, temperate forests, grasslands, wetlands, etc. Placental mammals inhabit the very same habitats, when they are given opportunity. There are no environmental conditions in Australia that would attract marsupials while repelling placental mammals.

A sweepstakes route is no better, as it is essentially a probability-driven route. A sweepstakes route is decidedly not a filter bridge. Marsupials do have an advantage over some, not all, placentals in that they have a low metabolism, which could benefit long-distance rafting dispersal. But, with an Upper Cenozoic Flood Boundary model, we are not talking about a handful of species. Quaternary Australian marsupials, extant and fossil, range in size from shrew- and mouse-like, to rabbit- or squirrel-sized, from little rat-kangaroos to giant kangaroos reaching over six feet in height, teddy-bear-sized koalas to the 4-meter-long, multi-ton *Diprotodon*. There are sand-swimmers, burrow-diggers, tree-dwellers, saltational leapers, gliders, and waddlers—some nocturnal, some diurnal. Some are herbivorous, others omnivorous, insectivorous, or carnivorous—some very dangerous, like the marsupial lion, *Thylacoleo*. With an Upper Cenozoic Flood Boundary, specifically the Plio-Pleistocene boundary, as I have noted previously (Arment 2022), there are too many genera within families crossing, for the biblical Ark kind to be anything higher than the genus. Anything higher (family-level, for example) would require some form of magical morphological

convergence in offspring towards highest-strata fossil forms (Arment 2024c) that is unacceptable to reason. So, beyond merely those Australian genera that show up below and above the Plio-Pleistocene boundary, most if not all other Australasian genera found in the Pleistocene would have had to take that sweepstakes route. It is incredibly unlikely that new genera would immediately diverge upon ancestors reaching Australia, without leaving transitional evidence. Evidence of genus-developing transitions can be readily found below the Pleistocene, such as the stepwise morphocline of molar topography in phascolarctids (Crichton et al. 2023), but rarely during the Pleistocene. This means at least 82 marsupial genera (Arment 2020a) with distinctly different ecological requirements and behaviors, made their way to Australasia unaccompanied by placental mammals, outside of murine rodents and a few bats. That is unacceptable for a sweepstakes route.

All of this informs us that there is no justification from ecological relationships or physical environments for a Marsupial Mass Migration from the Ark, marching to a promised land Down Under.

The Flat Pleistocene Model

I should note that the situation is even worse when we consider Mike Oard's (2022) asynchronous Flood model, which essentially flattens Australian depositional strata so that much of what is considered Oligocene to Pliocene in Australia is now part of his Pleistocene. Oard argues that marsupial fossils at Riversleigh, "dated as Pleistocene in the early 1900s" were pushed by paleontologists "back to the late Oligocene" due to primitive features. That misrepresents interpretation of Riversleigh fossils—there are, in fact, separate and distinctive faunal assemblages at Riversleigh representing the Oligocene-Miocene, Pliocene, Pleistocene, and Holocene (Archer et al. 1989).

Oard's (2022) dismissal of biocorrelation is without merit. Biocorrelation is simply recognizing patterns in fossil species presence or absence, species abundance, transitional morphologies, and biozone differences between different fossil strata. Biochronology, or piecing together faunal succession through fossil assemblages, is another important tool. Marsupial fossils are not the only fossils in Australia used for biocorrelation. Bat fossils, for example, can also be used, as with the molossid bat genus *Hydromops* from Oligocene-Miocene Riversleigh correlating with *Hydromops* in Middle Miocene Thailand or Early-Middle Miocene Europe (Hand et al. 1997). The bat genus *Hipposideros* (subgenus *Brachhipposideros*) is found in both Middle Miocene Riversleigh and Miocene Europe (Sigé et

al. 1982). Beyond Riversleigh, there are hundreds of fossil sites throughout Australia with all manner of Cenozoic fossils that are used to show environmental and biological change. Oard (2022) believes that marsupials “arrived early in the Ice Age” to Australia, “rapidly from Ararat to the Indian Ocean,” migrating together (“or those going elsewhere died without leaving a fossil trace”), but does not seem to recognize just how large a problem this is. At least 81 genera of marsupials (see table 1) are found from Oligocene to Pleistocene strata in Australasia, all of which had to arrive independently. There is no reasonable natural explanation for this, a direct migration of widely different marsupial animals using an infinitesimally-low-probability sweepstakes route, that somehow didn’t allow for placental mammal accompaniment. Oard (2022) recognizes this, arguing that “God was possibly directing their dispersal.” This has become something of a trend, with Taylor (2023) also arguing that there are no natural explanations for the marsupial arrival to Australia, so all post-Flood biogeography must be put down to God’s direct intervention.

A significant problem with Oard’s methodology is that he is simply moving the goalpost as he flattens so much of Australian stratigraphy into a Pleistocene layer. If we have to change our understanding of a serious conrainicator to an Upper Cenozoic Flood Boundary model in the Australian stratigraphic record to fit Oard’s beliefs, what happens when we see the same conrainicators elsewhere around the planet?

More Boundary Crossing

Oard (2022) and Mogk (2025) both seem to think that this is simply an Australian marsupial issue. Not true. Within the Upper Cenozoic Flood Boundary models, many other mammals are also found on a single continent after the Flood, the same continent on which their supposed pre-Flood ancestors of the same genus are all buried. As it happens, I had already charted Cenozoic mammal genera for another project (Arment 2024c), so I could easily pull out genera from around the world that cross the Plio-Pleistocene boundary and are found on both sides on a single continent. (See table 2.) These are primarily from the Paleobiology Database, Arment (2020a), with an update on marsupials from Fabian et al. (2023). These groups, by continent,

include all mammals, so the Australian group here includes marsupials, placental bats, and terrestrial monotremes.

There are 96 endemic boundary crossers for Africa, 35 endemic boundary crossers for Asia, 66 endemic boundary crossers for Australia, 30 endemic boundary crossers for Europe, 60 endemic boundary crossers for North America, and 55 endemic boundary crossers for South America. This means there are at least 342 genera around the world that meet the boundary-crossing criteria above. More importantly, there is not a single piece of evidence that any of these genera would have been dependent upon any other genus leaving the Ark. Similarities in diet or climatic adaptability are not interdependencies. This is a phenomenally poor position for the Upper Cenozoic Flood Boundary proponent to be in.

It also begs another question. If it is just random chance that positions a genus solely above its ancestors of the same genus, on the same continent, then we should also see many other genera solely on a single continent after the Flood, while all their pre-Flood buried ancestors of the same genera are solely on a different continent. Where are all those genera? They are very, very rare.

Rather, it is much more common to find genera which are found only on one continent in Neogene deposits and on that same continent and a very close portion of an adjacent continent in the Quaternary. For example, the hartebeest, *Alcelaphus buselaphus*, is a monospecific genus found only in African deposits below the Pleistocene, and is primarily in Africa to the present day, but with a recently extinct subspecies that ranged into the Sinai Peninsula and Israel until extirpated. Many other genera are found in South America below and above the Plio-Pleistocene boundary, but might range up into Central America or southern Mexico in the Quaternary. (I have removed two genera from the 2020 South American marsupial list that do so.) These genera, commonly encountered, are not included in my calculations, but they also support the concept of endemic radiation in the post-Flood landscape rather than yo-yoing to and from the Ark, before and after the Flood.

Back to Interdependency

When I stated (Arment 2020a, 4), “Either marsupials had certain characteristics that allowed

Table 1. Eight-one Australian marsupial genera from Oligocene to Pleistocene strata.

Acrobates, Aepyprymnus, Ailurops, Antechinomys, Antechinus, Baringa, Bettongia, Bohra, Borungaboodie, Burramys, Caloprymnus, Cercartetus, Chaeropus, Congruus, Dactylopsila, Darcus, Dasycercus, Dasyuroides, Dasyurus, Dendrolagus, Diprotodon, Dorcopsis, Dorcopsulus, Euowenia, Euryzygoma, Hulitherium, Hypsiprymnodon, Invictokoala, Isoodon, Lagorchestes, Lagostrophus, Lasiorhinus, Lemdubuoryctes, Macropus, Macrotis, Maokopia, Metasthenurus, Microperoryctes, Myoictis, Myrmecobius, Ningai, Nototherium, Onychogalea, Palorchestes, Perameles, Petauroides, Petaurus, Petrogale, Petropseudes, Phalanger, Phascogale, Phascolarctos, Phascolonus, Planigale, Potorous, Prionotemnus, Procoptodon, Propleopus, Protymnodon, Pseudocheirus, Pseudochirops, Pseudokoala, Ramasayia, Sarcophilus, Silvaroo, Simosthenurus, Sminthopsis, Sthenomerus, Sthenurus, Synaptodon, Tarsipes, Thylacinus, Thylacoleo, Thylogale, Trichosurus, Troposodon, Vombatus, Wallabia, Warendja, Wyulda, Zygomaturus

Table 2. Continentally-endemic Pliocene-Pleistocene boundary crossing genera (342 genera in total).**A) Africa (96 genera)**

Aepyceros, Aethomys, Anomalurus, Atilax, Australopithecus, Bathyergus, Beatragus, Cephalophus, Cercocebus, Cercopithecoides, Cercopithecus, Chlorocebus, Chlorotalpa, Chrysospalax, Civettictis, Colobus, Connochaetes, Cryptomys, Cynictis, Damaliscus, Dasymys, Dendrohyrax, Desmodillus, Dinopithecus, Eidolon, Elephantulus, Eudorcas, Eurygnathohippus, Galago, Galagoides, Genetta, Gerontochoerus, Gorgopithecus, Graphiurus, Helogale, Heterocephalus, Heterohyrax, Hippotragus, Hylochoerus, Ictonyx, Kobus, Lemniscomys, Leptailurus, Loxodonta, Lupulella, Macroscelides, Madoqua, Makapania, Malacothrix, Mastomys, Megalotragus, Menelikia, Mesochoreus, Metridiochoerus, Mungos, Mystromys, Nandinia, Nanger, Notochoerus, Numidocapra, Nyanzachoerus, Okapia, Omochoerus, Oreotragus, Otocyon, Otomys, Paracolobus, Paranthropus, Parapapio, Paraxerus, Parmularius, Pedetes, Pelea, Phacochoerus, Poecilogale, Praomys, Pronolagus, Proteles, Pseudocivetta, Raphicerus, Rhabdomys, Rhinocolobus, Rhynchocyon, Saccostomus, Serengetilagus, Soromandrillus, Steatomys, Syncerus, Tachyoryctes, Taurotragus, Thallomys, Theropithecus, Thryonomys, Ugandax, Zelotomys, Zenkerella

B) Asia (35 genera)

Ailuropoda, Anourosorex, Brachyrhizomys, Callosciurus, Caprolagus, Celebochoerus, Dremomys, Elaphurus, Elasmotherium, Gigantopithecus, Hemibos, Hylomys, Ia, Metacervulus, Murina, Nestoritherium, Platacanthomys, Praesinomegaceros, Procapra, Prosiphneus, Pseudois, Ptilocercus, Rhizomys, Rucervus, Rusa, Simatherium, Sinicuon, Sinomammut, Sinomastodon, Sinomegaceros, Spirocerus, Styloidipus, Tarsius, Tupaia, Typhlomys

C) Australia (66 genera)

Acrobates, Aepyprymnus, Antechinus, Baringa, Bettongia, Bohra, Burramys, Cercartetus, Chaeropus, Dactylopsila, Darcus, Dasycercus, Dasyuroides, Dasyurus, Dendrolagus, Distoechurus, Dorcopsis, Euowenia, Euryzygoma, Hypsiprymnodon, Isoodon, Lagostrophus, Lasiorhinus, Macroderma, Macropus, Megalibgwilia, Myoictis, Nototherium, Onychogalea, Palorchestes, Perameles, Petauroides, Petaurus, Petrogale, Petropseudes, Pewelagus, Phalanger, Phascolarctos, Phascolonus, Planigale, Potorous, Prionotomus, Propleopus, Protomodon, Pseudantechinus, Pseudochairus, Pseudochirops, Pseudokoala, Ramsayia, Rhinonictis, Sarcophilus, Silvaroo, Simosthenurus, Sminthopsis, Sminthozapus, Sthenurus, Thylacinus, Thylacoleo, Thylogale, Trichosurus, Troposodon, Vombatus, Wallabia, Wyulda, Zaglossus, Zygomaticus

D) Europe (30 genera)

Arvernoceros, Asoriculus, Baranogale, Blarinoides, Castillomys, Deinsdorfia, Dinaromys, Drepanosorex, Estramomys, Galemys, Gallogoral, Geotrypus, Hesperidoceras, Hypnomys, Kislangia, Lagotherium, Maltamys, Martellictis, Myotragus, Nesiotites, Palerinaeus, Pliotragus, Procarnptoceras, Rhinocricetus, Stephanomys, Sulimskia, Trilophomys, Tyrrhenoglis, Ursulus, Xenictis

E) North America (60 genera)

Aluralagus, Ammospermophilus, Antilocapra, Antrozous, Apelops, Arctodus, Aztlanolagus, Baiomys, Bassariscus, Bensonomys, Blancocamelus, Blarina, Camelops, Capricamelus, Capromeryx, Castoroides, Cordimus, Cratogeomys, Cynomys, Dipodomys, Erethizon, Geomys, Gigantocamelus, Guildayomys, Hibbardomys, Hodomys, Lasionycteris, Megalonyx, Megatylopus, Mephitis, Microdipodops, Miracinonyx, Neotamias, Neotoma, Nerterogeomys, Notiosorex, Notolagus, Ondatra, Onychomys, Orthogeomys, Otospermophilus, Paramylodon, Pekania, Perognathus, Peromyscus, Petauristodon, Phenacomys, Prodipodomys, Rhynchotherium, Satherium, Scalopus, Scapanus, Spilogale, Stockoceros, Taxidea, Tetrameryx, Thomomys, Titanotylopus, Trigonictis, Zapus

F) South America (55 genera)

Abrocoma, Actenomys, Antifer, Aotus, Auliscomys, Bolivartherium, Catonyx, Cavia, Cebuella, Chaetophractus, Chapalmalania, Chorobates, Clyomys, Dolicavia, Dolichotis, Duscycyon, Eumysops, Eutatus, Falcontoxodon, Graomys, Lagostomus, Lama, Lestodon, Lutreolina, Lycalopex, Macrauchenia, Megalonychops, Mesotherium, Microcavia, Myocastor, Neosclerocalyptus, Neuryurus, Notiomastodon, Olympicomys, Oxydontherium, Paedotherium, Palaeocavia, Panochthus, Paramyocastor, Pediolagus, Philander, Phyllomys, Pithanotomys, Proechimys, Reithrodontomys, Scapteromys, Tetrastylus, Thylamys, Thyroptera, Toxodon, Tremacyllus, Trigodonops, Windhausenia, Xotodon, Zaedyus

them to take greater advantage of such a migration, or there was a barrier to placental mammalian migration that had little effect on marsupials”, that was not a contradiction of my “chosen assumption of statistical independence,” as Mogk (2025) asserts, but a challenge to critics to come up with a valid justification when they make any such speculation. Mogk clearly has not done so. A list of biogeographic terminology is not itself a coherent defense justifying such a peculiar argument. Listing is not demonstrating.

Mogk (2025) also errs when he looks at what he considers my preferred boundary. He makes the unwarranted assumption that I necessarily equate families with kinds despite my discussion of the various high and low estimates. As we clearly see in post-Flood diversification patterns (for example, lemurs, sloths, caviomorph rodents [Arment 2023a, 2023b]), that would be an incorrect position to take. Many, perhaps most, recent Cenozoic mammals, including marsupials, are part of multi-familial baraminic lineages. It is likely that none of the

modern Australidelphian marsupial genera were represented on the Ark—it is likely that many of the families were not, either, being post-Flood divergent branches off the original baraminic lineage. Their diversification from within one or a handful of baraminic lineages began in South America, after rafting the Atlantic. Along with other groups, like ratites and aquatic platypuses (Arment 2024a, 2024b), their lineages extended across Antarctica, before arriving in Australia—a practically unfilled continent perfect for the extensive radiation into modern families, ‘filling the Earth,’ as God directed (Arment 2020a). Further to Mogk’s (2025) claim, I do not have a ‘preferred’ boundary. I believe the evidence clearly discounts an Upper Cenozoic Flood/post-Flood Boundary, and is thus somewhere in the Lower Cenozoic; it may in some, many, or all places be at or near the K-Pg boundary, but I believe a great deal of work is required before we determine exactly how and where that upper Flood boundary appears in the fossil record.

While we are on the subject, I think it is worth briefly mentioning one other argument that has been made against Lower Cenozoic Flood Boundary models: the idea that during the Paleogene, the Middle East was still underwater. Many attempts to locate the resting place of the Ark seem to rely on regional folklore which certainly point to areas that would still have been under water in the Paleocene and Eocene. One brief but interesting suggestion (Humphreys 2011) points to the Zagros Mountains extending into southern Iran. Some of that region does not appear to have been flooded during the early Paleogene (Scotese 2014), suggesting it may have emerged early from Floodwaters. The centralized location, though surrounded by water, would have provided more opportunities for smaller terrestrial mammals to immediately begin moving out of the area via rafting or swimming, especially if the water was filled with Flood debris. Larger animals could take advantage of land bridges that formed later, or swim shallows as water retreated. Most Paleocene mammal fossils were, in fact, smaller. The largest would have included certain cow-sized pantodonts, but those appear to have diverged from much smaller relatives, such as the dog-sized *Bemalambda*.

Summary

The Marsupial Mass Migration theory is not creation science; it is creation fantasy. Mogk's (2025) calculations are meant to impress, but are built on a foundation of sand that is swept away by the basic principles of biogeography.

There are no obligate commensal ecological connections between any marsupials.

There is nothing about Australia alone that fulfills an obligate ecological requirement for any of the marsupials.

There is no migration pathway between Asia and Australia that would act as a bridge (or a lottery route) for marsupials and also a blockade for placentals.

A marsupial migration pathway would have to offer specific constraining ecological parameters directly from the Ark all the way to Australia—that does not and did not exist.

The scope of the problem is not limited to marsupials. It is a placental issue as well. In fact, it is not even limited to mammals (Arment 2020b).

Marsupial mass migration from the Ark is based on the idea that God had to directly intervene and move various animals from the Ark to the far reaches of the earth. Within an Upper Cenozoic Flood Boundary model, that is the only feasible way to explain Quaternary conditions. Mogk's (2025) calculations attempt to create a natural framework for Australian marsupial migration, but are clearly unable to support it biologically. This leads to two conclusions:

- (1) If the marsupial migration was natural, Mogk's premise of interdependency is inadequate.
- (2) If the marsupial migration was miraculous, Mogk's calculations are irrelevant.

Not every baraminic lineage survived after leaving the Ark, which would be confounding if divine direction was the post-Flood mandate. Most Cenozoic mammal genera, which would have had to have been on the Ark within an Upper Cenozoic Flood Boundary model, never appear above the Plio-Pleistocene boundary. More than 60% of all Cenozoic mammal families disappear before the Pleistocene (Arment 2024c).

While God did bring animals to the Ark, it is clear from the fossil record that post-Flood dispersal and diversification by baraminic kinds played out according to natural principles, just as climatic and geological forces played out after the Flood according to natural principles. The biogeographic quandaries produced by an Upper Cenozoic Flood Boundary are greatly diminished when we recognize that a Lower Cenozoic Flood Boundary is far more reasonable for Flood models. That does not mean we have all the answers, but it is far more biblically consistent, allowing the Ark kinds to refer to actual baraminic lineages, rather than pairs of every genus within every created kind. It allows for natural migration in post-Ark dispersal and extensive diversification within baraminic lineages as they encounter new landscapes and changing climatic conditions. Creationists do not need to invent miracles for every immediate problem, when the Bible does not specify divine intervention. Sometimes we need to just step back and readjust our perspective.

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