

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

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Abstract

There is no debate as contentious as the post-Flood boundary issue within creation science. Given that testing theories is as important as developing them, this paper offers a method to test the placement of a post-Flood boundary at different points in the stratigraphic record. Marsupial fossil presence in strata below and above a suggested post-Flood boundary can be used to calculate the likelihood of those genera being found on a single continent (notably Australia or South America) both before and after the Flood. These calculations suggest that post-Flood boundary placements in the Cenozoic, within the continents noted, face a difficult challenge. Other fossil groups with high continental endemism may be similarly useful in this type of calculation. This paper's results have implications for post-Flood biogeographic modeling.

Keywords: Post-Flood boundary, marsupials, fossil record, biostratigraphy, Australia, South America

Introduction

The placement of the Flood/post-Flood boundary in the fossil record is arguably one of the more important questions yet to reach consensus in creation science. Its placement affects how we view the geological and paleontological records, the limits and diversification of biological kinds, and the ecological and biogeographical differences between the pre- and post-Flood worlds.

Historically, creationists have suggested placement of the post-Flood boundary anywhere from the Hadean to within the Pleistocene (Holt 1996; Wise 2006). Today there are two primary camps, with late post-Flood boundary proponents typically placing the boundary within the Cenozoic, somewhere above the Oligocene-Miocene boundary (Oard 2008-2020), while early post-Flood boundary proponents place the boundary at or near the Cretaceous-Paleogene boundary (Austin et al. 1994; Whitmore and Wise 2008). Within each camp are researchers who may differ on exactly where the post-Flood boundary is placed, or even whether the boundary can be applied to exactly the same position within strata around the world (Oard 2010; Walker 2014a, 2014b; Whitmore 2006).

It can be readily determined that if the post-Flood boundary is found in later strata (for example, between the Pliocene and Pleistocene), this means that some organisms with limited biogeographical ranges (both in modern times and as seen in the fossil record) would have been living in a certain geographical region before the Flood, then upon disembarking the Ark, migrated directly back to the same region, leaving little or no trace anywhere else in the world. Take, for example, the thylacine or 'marsupial wolf' (*Thylacinus*), driven extinct in 1936 (Long et al. 2002), fossils of which can be found in Australia in Pleistocene, Pliocene, and Miocene strata (Long et al. 2002). If Miocene thylacine fossils were deposited as part of the last stage of the Flood, these animals, known only to have existed in pre-Flood Australia (however that continent was then situated), migrated to the Ark, in which they survived the Flood, then returned to post-Flood Australia. (Obviously, this scenario doesn't imply a single pair made the entire round trip.)

This scenario is problematic (and not surprisingly, the target of skeptics [Moore 2004; Siemens 1992]). It is unlikely that the modern continent of Australia (or any other continent) was isolated as such before the Flood. Rather, all continents are believed to have been attached together as part of a much larger supercontinent (Snelling 2009). Given the vast changes in continental position due to the break-up of the pre-Flood supercontinent during the Flood, it seems unlikely that these (and other) marsupials would have specifically sought out their ancestral homeland in such a difficult-to-reach location. Invoking an innate homing beacon or divine guidance would be untestable and, in the latter case, simply God-of-the-gaps theorizing. Certainly, there is no reason to think that this geographic area would share some environmental condition both pre- and post-Flood, obligatory for marsupial survival. After all, South America has its own marsupials, and many closely related metatherian groups are found in the fossil record on other continents. (Widescale anthropogenic introductions [Woodmorappe 1990]

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can also be discounted as more imaginative than realistic, given the complete lack of evidence of human presence in the same strata as marsupials' earliest appearance on either continent.)

Could it just have been the luck of the draw? At a 2018 International Conference on Creationism panel discussion, Dr. Tim Clarey, a late post-Flood boundary proponent, proposed that the probability of an organism returning to its original home region after the Flood was simply one out of the number of continents available (though he suggested five). If we follow this reasoning (and correct the number of continents to six, assuming Antarctica isn't included), thylacines had one out of six chances to end up back in Australia. The problem with this assertion is that that probability calculation $(1/_{6})$ only applies when a single species is considered. When multiple species are considered, the correct probability calculation is $(1/6)^x$ where x is the number of species considered. This means that the probability of multiple species finding their way back to the very same continent from which they started gets much smaller as more species are considered.

Marsupials are extraordinarily useful in this sort of calculation, due to their high level of continental endemism. Thus, we can place a post-Flood boundary at different positions in the stratigraphic record to calculate the probability of multiple marsupials returning to the same location in which their pre-Flood ancestors allegedly lived.

Marsupials

Marsupials are famously distinguished by their reproduction, with their young born immature and helpless. Most female marsupials have a brood pouch, or marsupium. Dental characteristics and other morphological traits also serve to distinguish marsupials from placental mammals and monotremes (Dawson et al. 1989). Living marsupials (and most fossil marsupials) are split between the superorder Australidelphia (most orders found in Australia, but also includes the South American icrobiotherians) and several orders found primarily in South America. The latter groups used to be considered part of superorder Ameridelphia, but that is now considered a paraphyletic taxon (Eldridge et al. 2019).

Marsupials are metatherians, which include a number of other marsupial-like groups now extinct (such as the South American sparassodonts, some species of which were convergently similar to sabertooth cats). Some of these have been included within the Marsupialia in the past, but are now considered distinct enough to simply be sister groups within the Metatheria. These include species from continents in North America, Asia, and Africa which have elicited comment in popular creationist literature of marsupial fossils in those regions, but which are now considered non-marsupial metatherians such as herpetotheriids, pediomyids, and peradectids (Eldridge et al. 2019; Goin et al. 2016). (Attempts to compare kangaroos to the herpetotheriids *Herpetotherium* of North America or *Peratherium* of Europe and Africa, or to the peradectid *Siamoperadectes* of Asia, would be like comparing distinctly different placental mammals such as cats to elephants. They do not share a relationship within the same biblical kind.)

Methodology

Two hundred and ninety-four genera of marsupials (extant and extinct) were charted and marked to show presence in any given epoch according to data within the Paleobiology Database (via the Fossilworks portal, initially examined 10/22/2018) and other published sources (see figs. 1 through 14). For the purpose of this paper, genus is used rather than species because the genus is more taxonomically stable and is more consistently recognizable in the fossil record. This conservative approach best fends off arguments that species are arbitrarily defined. Genera are sorted by family, though organization of higher taxa often varies by author (Case, Goin, and Woodburne 2005; Eldridge et al. 2019; Goin et al. 2016; Long et al. 2002); those debates are irrelevant to the purpose of this paper. We simply need to know whether a given genus is found in strata on both sides of a theorized post-Flood boundary. (Similarly, there may be some debate over whether certain genera should be classified as marsupials or nonmarsupial metatherians. Again, that is irrelevant to this calculation as the methods employed here are not dependent upon the correctness of higher-level taxonomic assignments. It may be used with any group of fossil genera, including groups of unrelated taxa.)

While it is true that the biblical kind is likely at (or above) the level of the family, this calculation would not be more effective or relevant if the family is used instead of the genus. The focus of the calculation is not on the kind, but on units within the kind which appear to be the same both before and after a proposed post-Flood boundary. If multiple genera within the same family on the same continent are found together in adjacent fossil strata (strata that are separated by a proposed post-Flood boundary), then either the genera form separate kinds (a problematic scenario) or the boundary line is incorrectly placed. If the family level is used, however, records may cover multiple genera occurring in adjacent strata without overlap (whether sister groups or ancestor-descendent pairs), which do little to inform us as to the likelihood of any alleged post-Flood boundary placement.

On the other hand, species could be used as the unit in future calculations, and would conceivably increase the number of strata-crossing records. This would simply require a rigorous determination that fossil records are correctly identified to species level. One additional objection that may be raised is that the strata on one continent may not be equivalent to

another (i.e. Oligocene strata in North America may not have been created at the same time as Oligocene strata in Australia). Ross (2014a) responded to similar claims about long-distance biostratigraphic correlations, noting that they are created through "observable patterns of fossils and rocks" based on "observable, verifiable field data." However, we can include calculations here on a 'per continent' basis along with an encompassing global calculation.

Results

Evaluating Late Post-Flood Boundaries

Three possible placements for a late post-Flood boundary are between (A) the Oligocene and Miocene, (B) the Miocene and Pliocene, and (C) the Pliocene and Pleistocene. Forty-six marsupial genera are found on both sides of an Oligocene-Miocene Flood boundary within a single continent. Thirty-one marsupial genera are found on both sides of a Miocene-Pliocene Flood boundary within a single continent. Sixty-one genera are found on both sides of a Pliocene-Pleistocene Flood boundary within a single continent. Didelphis (which includes the Virginia opossum) crosses both Miocene-Pliocene and Pliocene-Pleistocene boundaries, but is the only extant marsupial now native to two continents, so was not included on either list. (For the purpose of this methodology, 'Australia' includes Australasian islands: New Guinea, New Caledonia, and Indonesia.)

Marsupial genera crossing the Oligocene-Miocene boundary include Abderites, Balbaroo, Barguru, Bematherium, Bulungamaya, Bulungu, Burramys, Cercartetus. Clenia, Cookeroo. Dactylopsila, Djilgaringa, Ekaltadeta, Ektopodon, Eomicrobiotherium, Galadi. Galanarla, Ganawamaya, Gumardee, Ilaria, Litokoala, Madju, Marlu, Microbiotherium, Muramura, Nambaroo, Neohelos, Ngapakaldia, Nimiokoala, Onirocuscus, Palaeopotorous, Palaeothentes, Paljara, Parabderites, Perikoala, Pildra, Proargyrolagus, Propalorchestes, Pseudochirops, Silvabestius, Trelewthentes, Wabularoo, Wakaleo, Wururoo, and Yarala.

Marsupial genera crossing the Miocene-Pliocene boundary include Argyrolagus, Bettongia, Burramys, Cercartetus, Chironectes, Dactylopsila, Ektopodon, Hyperdidelphys, Hypsiprymnodon, Kolopsis, Lasiorhinus, Lutreolina, Marmosa, Microtragulus, Muramura, Onirocuscus, Paljara, Palorchestes, Perikoala, Philander, Pildra, Pliolestes, Pseudochirops, Pseudokoala, Sparassocynus, Thylacinus, Thylacoleo, Thylamys, Trichosurus, Wyulda, and Zygomaturus.

Marsupial genera crossing the Pliocene-Pleistocene boundary include Aepyprymnus, Antechinus, Baringa, Bettongia, Bohra, Burramys, Cercartetus, Chaeropus, Chironectes, Dactylopsila, Darcius, Dasycercus, Dasyuroides, Dasyurus. Dendrolagus, Dorcopsis, Euowenia, Euryzygoma, Hypsiprymnodon, Isoodon, Lasiorhinus, Lutreolina, Macropus, Marmosa, Myoictis, Nototherium, Onychogalea, Palorchestes, Perameles, Petauroides, Petaurus, Petrogale, Petropseudes, Phalanger, Phascolarctos, Phascolonus, Philander, Planigale, Potorous, Prionotemnus, Propleopus, Protemnodon, Pseudocheirus, Pseudochirops, Pseudokoala. Ramasayia, Sarcophilus, Silvaroo, Simosthenurus, Sminthopsis, Sthenurus, Thylacinus, Thylacoleo, Thylamys, Thylogale, Trichosurus, Troposodon, Vombatus, Wallabia, Wyulda, and Zygomaturus.

Using this data, we can simply calculate the probability of marsupial genera from a single pre-Flood geological region returning after the Flood to the very same location, whichever boundary placement is used. Technically, there are seven continents in the post-Flood world, and marsupial fossils have been found in Antarctica. As most early post-Flood boundary proponents agree, however, that Antarctica was covered in ice sometime within the post-Flood stage when Miocene deposits were made, Antarctica would only be relevant for earlier strata considerations. We can remove Antarctica from consideration and use $(1/6)^x$.

For the Oligocene-Miocene boundary:

Combined probability: $({}^{1}/_{6})^{46}=1.6\times10^{-36}$ South America only: $({}^{1}/_{6})^{8}=5.95\times10^{-7}$ Australia only: $({}^{1}/_{6})^{38}=2.69\times10^{-30}$

For the Miocene-Pliocene boundary: Combined probability: $(^{1}/_{6})^{^{31}}=7.54\times10^{^{25}}$ South America only: $(^{1}/_{6})^{^{9}}=9.92\times10^{^{8}}$ Australia only: $(^{1}/_{6})^{^{22}}=7.6\times10^{^{18}}$

For the Pliocene-Pleistocene boundary: Combined probability: $(^{1}/_{6})^{61}=3.41\times10^{-48}$ South America only: $(^{1}/_{6})^{4}=7.72\times10^{-4}$ Australia only: $(^{1}/_{6})^{57}=4.42\times10^{-45}$

These calculations clearly show that late post-Flood boundary proponents have a serious challenge in the fossil record. The fact that these crossovers widely occur on two separate continents is evidence against complaints that it may only be an artifact of Australian Flood Geology.

To go back to our original example, is it likely that *Thylacinus*, along with so many other marsupials, was found in one specific geographic area before

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the Flood, survived on the Ark, and then made its way back to that very same region (leaving no trace elsewhere), now split off as the continent of Australia? (Or for others, South America?) It's not only unlikely, it is highly improbable.

Evaluating Early Post-Flood Boundaries

The method in this paper provides a way to test early post-Flood boundaries as readily as late post-Flood boundaries (though we can use all seven continents). While there are numerous Cretaceous metatherians, none of these are currently accepted within the Infraclass Marsupialia (Eldridge et al. 2019). So, if the K/T boundary is postulated as recording the end of the final stage of the Flood, there is no data here that contradicts that.

Only two genera surveyed in this paper (*Bardalestes* and *Riolestes*) cross the Paleocene-Eocene boundary on a single continent, both in South America ($[^{1}/_{7}]^{2}$ =.02). (*Woodburnodon* is found in South America in the Paleocene, and Antarctica in the Eocene.) Five genera cross the Eocene-Oligocene boundary on a single continent; again, all five in South America ($[^{1}/_{7}]^{5}$ =5.95×10⁻⁵).

Future studies should examine a wider range of metatherians from these periods. This will likely work better with South American metatherians. As Eldridge et al. (2019) notes, "Particularly frustrating is the near total lack of Australian fossil sites [with the exception of the Eocene Murgon fossil site] preserving mammals from the early Paleogene, as this is the period during which the Australian marsupial radiation probably began to diverge."

Discussion

Does this calculation overexaggerate the improbability of a Cenozoic post-Flood boundary in Australia or South America? If anything, this is a conservative measure. After all, this is not a marsupial-specific argument. There are other fossil groups which would likely pair well with calculation. Non-marsupial metatherians, this monotremes, camelids, South American primates, caviomorphs, xenarthrans, and meridiungulates all show high levels of continental endemism. Any additional records showing the presence of a genus on a single continent on both sides of a postulated post-Flood boundary would serve as further evidence of low probability that such a boundary is correctly placed.

This study raises questions that may be fruitful for further research:

How many marsupials kinds are there? Creationist research on the subject is not extensive. Lightner (2012) listed hybridization reports that could be found, and generally placed the level of kind at the family (but noted that for marsupials, "it appears that it could even be above this level.") Wise (2009) suggested there could be 1 to 5 kinds within the Australidelphia, and 6–11 within the 'Ameridelphia.' (Both of his groupings appear to have been calculated with what are now considered non-marsupial metatherians.) Thompson and Wood (2018) used statistical baraminology to evaluate a selection of Cenozoic mammals. Among marsupials examined, they identified the Palorchestidae, Hypsiprymnodontidae, Macropodidae, Pseudocheirinae, and Phascolarctidae as holobaramins. (Species within a holobaramin share common ancestry and share no common ancestry with other species (Wood and Murray 2003).)

Figs. 1–14 show 44 families of marsupials (along with additional unplaced genera). If the biblical kind is at the level of family, then there are, at a minimum, 44 marsupial kinds. If kinds are more inclusive (at the level of order or suborder), then there might be as few as 8 kinds. If the kind is constricted to the level of genus, then there would be 294 marsupial kinds, which is clearly untenable.

If there are only a few marsupial kinds, then it is clear that the rate and diversification of post-Flood speciation was very high. If there are more marsupial kinds, then the question as to why marsupials saturated the Australian faunal migration is raised. Either marsupials had certain characteristics that allowed them to take greater advantage of such a migration, or there was a barrier to placental mammalian migration that had little effect on marsupials. (Simpson (1940) referred to such selective passages as 'filter-bridges,' as opposed to open corridors or 'sweepstakes routes' like rafting.) For rapid diversification, creationists have a viable genetic answer within the post-Flood period (Jeanson 2017), which fits well with an early post-Flood boundary. (While Jeanson focuses on speciation within families, his application of heterozygosity as key to speciation is not inherently limited to the family level. As post-Flood populations migrated away from the Ark, speciation through shifting population sizes and inbreeding led to increased homozygosity, resulting in new genera and new species, but also a decline in the rate of speciation within each new species.)

Late post-Flood boundary proponents have a problem, however. If multiple genera within the same family are crossing the post-Flood boundary, then we have to conclude that each of those genera constitute their own biblical kind. This is because there would only be one pair of each marsupial kind on the Ark (being 'unclean' animals). We can see, for example, that within the family Dasyuridae (which includes quolls, marsupial mice, and the Tasmanian devil), there are eight genera found on both sides of **Table 1**. Order Argyrolagoidea (Families Argyrolagidae, Groeberiidae, Patagoniidae). Data from the Paleobiology Database via Fossilworks gateway (http://fossilworks.org/) and additional material (Eldridge et al. 2019). Some researchers suggest placing the Argyrolagidae in the Polydolopimorphia or the Paucituberculata (Eldgridge et al. 2019). Chimento, Agnolin, and Novas (2015) proposed that *Groeberia* and *Patagonia* were late surviving gondwanatherians, but recent analysis retains them in the Marsupialia (Beck 2017; Eldridge et al. 2019). Zimicz and Goin (2020) noted that cladistic analysis clustered *Groeberia* near vombatiform diprotodontians. SA=South America.

	Cre	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Family Argyrolagidae								
Anargyrolagus					SA			
Argyrolagus					SA	SA		
Hondalagus					SA			
Klohnia				SA				
Microtragulus					SA	SA		
Proargyrolagus				SA	SA			
Family Groeberiidae								
Groeberia			SA					
Family Patagoniidae								
Patagonia					SA			

the Pliocene/Pleistocene boundary (in fact all eight survive today). It would be absurd to argue that all eight of these genera (and a few others) were living as part of the same biblical kind before the Flood, with only one representative pair of the kind surviving on the Ark, which then returned to Australia to diversify into exactly the same genera as found before the Flood like some sort of biological memory foam. So, the late Flood-boundary proponent is stuck: either each genus is its own biblical kind (contrary to what most creation biologists would accept), or they have to discard parts of the stratigraphic record as incorrectly identified in order to fit the data to their model.

Early post-Flood boundary proponents still have questions to consider. If the marsupial fossil record is only found in post-Flood strata, does this infer that all marsupials today must have diversified from a single ancestral pair from the Ark? That seems unlikely, stretching the marsupial kind to encompass the entire infraclass. If there are multiple kinds, how did they end up only in South America/Australia?

How did marsupials reach South America? Oceanic dispersal likely played a part in the introduction of several animal groups to South America from Africa: South American tortoises, *Chelonoidis*, are most closely related to African hingeback tortoises, *Kinixys* (Le et al. 2006); the oldest New World monkey fossil, an Eocene primate from Peru, *Perupithecus*, resembles Eocene anthropoids in Africa (Bond et al. 2015); South American amphisbaenids (burrowing, legless reptiles) likely arrived via transatlantic dispersal on floating islands (Vidal et al. 2007); weakflying hoatzins have fossil relatives in the African Miocene and European Eocene (Mayr, Alvarenga, and Mourer-Chauviré 2011; Mayr and de Pietri 2014), suggesting a westward transatlantic dispersion.

Founder species utilizing oceanic dispersal are usually small to medium-sized (de Queiroz 2005; Diamond 1987; Houle 1998), diversifying into larger species. (Most large marsupials do have smaller kin.) This is an area which may be guite fruitful for creation biologists and geologists; secular research has suggested that transatlantic rafting for Paleogene species may have been greatly aided by favorable winds and currents (Houle 1999). Of course, a post-Flood model would include vast amounts of floating debris rafts (Oard 2014; Wise and Croxton 2003; Wood and Murray 2003), which could be favorable to larger species in transatlantic dispersal. Ongoing secular discussion has debated whether flightless phorusrhacoid birds dispersed from Africa to South America, or vice versa (Angst et al. 2013; Mourer-Chauviré et al. 2011). Within a creation model, oceanic dispersal of this avian kind from Africa to both Europe and South America fits well with an early post-Flood boundary.

Did Antarctica have a role in post-Flood marsupial migration? The creationist literature skews towards marsupial migration to Australia via an Asian land bridge with a separate route for South American marsupials (e.g. Johnson 2012; Morris 1976; Snelling 2009; though Wood and Murray (2003) suggested independent dispersion via post-Flood rafting could explain marsupial colonization patterns), but an Antarctic connection between South America and **Table 2.** Order Didelphimorphia (Families Caroloameghiniidae, Sparassocynidae, Didelphidae), asterisk indicates extant genera. Data from the Paleobiology Database via Fossilworks gateway and additional material (Abello et al. 2015; Beck and Taglioretti 2019; Cozzuol et al. 2006; Eldridge et al. 2019; Marshall 1977; Solari 2005). SA=South America; NA=North America.

	Cre	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Family Caroloameghiniidae								
Canchadelphys				SA				
Caroloameghinia			SA					
Procaroloameghinia		SA						
Family Sparassocynidae								
Hesperocynus					SA			
Sparassocynus					SA	SA		
Family Didelphidae								
Caluromys*								SA
Caluromysiops*								SA
Chacodelphys*								SA
Chironectes*					SA	SA	SA	SA
Cryptonanus*								SA
Didelphis*					SA	SA	SA/NA	SA/NA
Glironia*								SA
Gracilinanus*							SA	SA
Hyladelphys*								SA
Hyperdidelphys					SA	SA		
Incadelphys		SA						
Lestodelphys*							SA	SA
Lutreolina*					SA	SA	SA	SA
Marmosa*					SA	SA	SA	SA
Marmosops*								SA
Metachirus*								SA
Mizquedelphys		SA						
Monodelphis*							SA	SA
Philander*					SA			SA
Sairadelphys							SA	
Szalinia		SA						
Thylamys*					SA	SA	SA	SA
Thylophorops						SA		
Tiulordia		SA						
Tlacuatzin*								SA
Zygolestes					SA			

Australia may be an alternative solution (though would have had to occur within a relatively brief period after the Flood). Several other Eocene metatherians are known from Antarctica (e.g., *Derorhynchus*, *Xenostylus*, *Polydolops*, *Antarctodolops*). There is one Paleocene-Eocene marsupial genus, *Chulpasia*,

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Table 3. Order Paucituberculata (Families Abderitidae, Caenolestidae, Palaeothentidae, Pichipilidae, *incertae sedis*), asterisk indicates extant genera. Data from the Paleobiology Database via Fossilworks gateway and additional material (Abello 2007; Bown and Fleagle 1993; Eldridge et al. 2019; Engelman et al. 2017). SA=South America; AU=Australia.

	Cre	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Family Abderitidae								
Abderites				SA	SA			
Parabderites				SA	SA			
Pitheculites					SA			
Family Caenolestidae								
Caenolestes*								SA
Caenolestoides					SA			
Gaimanlestes					SA			
Lestoros*								SA
Perulestes			SA	SA				
Pliolestes					SA	SA		
Progarzonia			SA					
Rhyncholestes*								SA
Stilotherium					SA			
Family Palaeothentidae								
Acdestis					SA			
Acdestoides					SA			
Acdestodon					SA			
Antawallathentes					SA			
Carlothentes				SA				
Chimeralestes					SA			
Hondathentes					SA			
Palaeothentes				SA	SA			
Pilchenia				SA				
Propalaeothentes					SA			
Sasawatsu			SA	SA				
Titanothentes					SA			
Trelewthentes				SA	SA			
Family Pichipilidae								
Phonocdromus					SA			
Pichipilus					SA			
Quirogalestes			SA					
Paucituberculata, incertae sedis								
Bardalestes		SA	SA					
Chulpasia			SA/AU					
Evolestes				SA				
Fieratherium				SA				
Riolestes		SA	SA					

found in both Australia and South America, providing a direct link between those two continents. Eocene fossils referable to (or very closely related to) the Diprotodontia have been found in Patagonia (Lorente et al. 2016). Beck (2012) discussed an unnamed Eocene taxon in Australia that exhibited 'Ameridelphian'

Table 4. Order Microbiotheria (Families Microbiotheriidae, Woodburnodontidae), Order Notoryctemorphia (Family Notoryctidae), and Order Yalkaparidontia (Family Yalkaparidontidae), asterisk indicates extant genera. Data from the Paleobiology Database via Fossilworks gateway and additional material (Gelfo et al. 2019). The placement of *Khasia* and *Mirandatherium* within the Microbiotheriidae has been questioned; they may be metatherians outside the Marsupialia (Beck et al. 2008; Eldridge et al. 2019). SA=South America; ANT=Antarctica; AUS=Australia.

	Cre	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Family Microbiotheriidae								
Clenia				SA	SA			
Dromiciops*								SA
Eomicrobiotherium			SA	SA	SA			
Ideodelphys			SA					
Khasia		SA						
Kirutherium			SA	SA				
Marambiotherium			ANT					
Microbiotherium			SA	SA	SA			
Mirandatherium		SA						
Oligobiotherium				SA				
Pachybiotherium				SA				
Pitheculus				SA				
Family Woodburnodontidae								
Woodburnodon		SA	ANT					
Family Notoryctidae								
Naraboryctes					AUS			
Notoryctes*								AUS
Family Yalkaparidontidae								
Yalkaparidon					AUS			

traits. Clues are found beyond marsupials, as well. A fossil platypus tooth found in Paleocene strata in Patagonia suggests a biogeographical connection (Pascual et al. 1992). Bourdon, de Ricqles, and Cubo (2009) noted morphological evidence for a clade comprising South American rheas and Australian emus and cassowaries, and pointed out the existence of an Eocene ratite on Seymour Island, Antarctica.

Once marsupials arrived in South America, could Antarctica have provided a bridge to Australia before freezing over? Within the secular model, Australia and New Guinea separated from Antarctica during the Eocene (approx. 40Ma), while South America became separated from Antarctica by the opening of the Drake Passage (estimates have ranged between 17 and 49Ma (Scher and Martin 2006)). The opening of the Drake Passage (likely aided by the opening of additional seaways around the continent (Lawver, Gahagan, and Dalziel 2011)) allowed the formation of the Antarctic Circumpolar Current which contributed to rapidly decreasing temperatures on the continent (Livermore et al. 2005). Semipermanent ice sheets began forming on the continent near the Eocene-Oligocene boundary (Ivany et al. 2006; Zachos, Breza, and Wise 1992). This secular model offers the possibility of millions of years for marsupials to travel from South America to Australia. For a creationist, however, holding to an early post-Flood boundary, there would likely only be a few hundred years available between the end of the Flood and the complete isolation of Antarctica. So is this Antarctic bridgeway plausible?

One factor that has to be considered is how quickly a species can spread over a continent in the absence of predators. The fastest known example is the rabbit, with 13 wild rabbits introduced onto a Victoria, Australia, estate in 1859. By 1866, hunters on the estate had killed 14,000 rabbits. Rabbits reached New South Wales by 1880, Queensland by 1886, and Western Australia by 1894. Over 2/3 of Australia was colonized by rabbits within fifty years of their release (National Museum of Australia n.d.). Whether early marsupials could have spread that quickly is unknown, but with regard to modern species, Gilmore (1977) noted, "certain marsupials [such as the brush-tailed possum] have proved themselves **Table 5.** Order Peramelemorphia (*incertae sedis*, Families Chaeropodidae, Peramelidae, Thylacomyidae, Yaralidae), asterisk indicates extant genera. Data from the Paleobiology Database via Fossilworks gateway and additional material (Gurovich et al. 2014; Kear, Aplin, and Westerman 2016; Travouillon 2016; Travouillon et al. 2017; Travouillon et al. 2017). AUS or AU=Australia; NG=New Guinea; IND=Indonesia.

	Cre	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Peramelemorphia, incertae sedis								
Bulungu				AUS	AUS			
Galadi				AUS	AUS			
Kutjamarcoot					AUS			
Lemdubuoryctes							IND	IND
Madju				AUS	AUS			
Family Chaeropodidae								
Chaeropus						AUS	AUS	AUS
Family Peramelidae								
Crash					AUS			
Echymipera*								AU/NG
Isoodon*						AUS	AUS	AU/NG
Microperoryctes*							NG	NG
Perameles*						AUS	AUS	AUS
Peroryctes*								NG
Rhynchomeles*								NG
Silvicultor						AUS		
Family Thylacomydiae								
Ischnodon						AUS		
Liyamayi					AUS			
Macrotis*							AUS	AUS
Family Yaralidae								
Yarala				AUS	AUS			

to be capable of not only holding their own, but also rapidly extending their range when introduced into a new environment."

If the marsupial fossil record is essentially post-Flood, what can we determine from the differences between Australia and South America? Many South American marsupials (a few, such as the Didelphidae, excepted) disappeared, along with other metatherians, shortly after the Miocene, while Australian marsupials continued to thrive and diversify. One factor may have been increased competition with new species as North and South America finally connected (Marshall 1988).

What else might we learn from the biostratigraphic record? Creationists should look more closely at developing arguments that utilize the fossil record in testable ways. Ross (2012, 2014a, 2014b) and Arment (2014) demonstrate two such objective methods, using the fossil record to distinguish between pre-Flood and post-Flood strata. Brand and Chadwick (2016) noted that high percentages of paleogeographic regional endemism in mammalian families, particularly in South America and Australia, suggest that all or most Cenozoic fossils were formed after the Flood. Wise (2008, 2009, 2015) introduced a technique (the Post-Flood Continuity Criterion) which examines the size of the biblical kind and notes patterns in the fossil record (disparity of kinds and diversity within kinds) that add to our understanding of the post-Flood boundary. Wood and Cavanaugh (2003) likewise proposed 'biological trajectories' as one means of identifying baraminic lineages. Tomkins and Clarey (2019) attempted to use Cenozoic whale fossils to contend for a late post-Flood boundary, though nothing in their results actually rules out an earlier boundary (particularly as their mapping emphasizes coastal fossilization within a post-Flood continental landscape). There are doubtless many additional testable arguments to be raised and debated.

Table 6. Order Dasyuromorphia (*incertae sedis*, Families Myrmecobiidae, Malleodectidae, Thylacinidae), asterisk indicates extant genera. Data from the Paleobiology Database via Fossilworks gateway and additional material (Archer et al. 2016b; Plane 1976; Rovinsky, Evans, and Adams 2019; Wroe 2003). Eldridge et al. (2019) noted that *Badjcinus* has been classified as ?Thylacinidae in one recent analysis. AUS or AU=Australia; NG=New Guinea.

	Cel	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Dasyuromorphia, incertae sedis								
Apoktesis				AUS				
Dasylurinja				AUS				
Joculusium					AUS			
Mayigriphus					AUS			
Mutpuracinus					AUS			
Wakamatha					AUS			
Family Myrmecobiidae								
Myrmecobius*							AUS	AUS
Family Malleodectidae								
Malleodectes					AUS			
Family Thylacinidae								
Badjcinus				AUS				
Maximucinus					AUS			
Muribacinus					AUS			
Ngamalacinus					AUS			
Nimbacinus					AUS			
Thylacinus					AUS	AU/NG	AUS	AU/NG
Tyarrpecinus					AUS			
Wabulacinus								

Table 7. Order Dasyuromorphia (Family Dasyuridae), asterisk indicates extant genera. Data from the Paleobiology Database via Fossilworks gateway and additional material (Archer et al. 2016; Wroe 2003). AUS or AU=Australia; NG=New Guinea.

	Cre	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Family Dasyuridae								
Antechinomys*							AUS	AUS
Antechinus*						AUS	AUS	AU/NG
Archerium						AUS		
Barinya					AUS			
Dasycercus*						AUS	AUS	AUS
Dasykaluta*								AUS
Dasyuroides*						AUS	AUS	AUS
Dasyurus*						AUS	AUS	AUS
Ganbulanyi					AUS			
Glaucodon						AUS		
Micromurexia*								NG
Murexechinus*								NG
Murexia*								NG
Myoictis*						NG		NG
Neophascogale*								NG
Ningaui*							AUS	AUS
Paramurexia*								NG
Parantechinus*								AUS
Phascogale*							AUS	AUS
Phascolosorex*								NG
Phascomurexia*								NG
Planigale*						AUS	AUS	AU/NG
Pseudantechinus*								AUS
Sarcophilus*						AUS	AUS	AUS
Sminthopsis*						AUS	AUS	AU/NG
Whollydooleya					AUS			

Table 8. Order Diprotodontia, Suborder Vombatiformes (Families Diprotodontidae, Ilariidae, Maradidae, Palorchestidae). Data from the Paleobiology Database via Fossilworks gateway. AUS or AU=Australia; NG=New Guinea; NC=New Caledonia.

	Cre	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Famly Diprotodontidae								
Alkwertatherium					AUS			
Bematherium				AUS	AUS			
Diprotodon							AUS	
Euowenia						AUS	AUS	
Euryzygoma						AUS	AUS	
Hulitherium							NG	
Kolopsis					AUS	NG		
Kolopsoides						NG		
Maokopia							NG	
Meniscolophus						AUS		
Neohelos				AUS	AUS			
Nototherium						NG	AU/NG	
Plaisiodon					AUS			
Pyramios					AUS			
Raemeotherium				AUS				
Silvabestius				AUS	AUS			
Sthenomerus							AUS	
Zygomaturus					AUS	AU/NC	AU/NG	
Family Ilariidae								
Ilaria				AUS	AUS			
Kuterintja				AUS				
Nimbadon					AUS			
Family Maradidae								
Marada				AUS				
Family Palorchestidae								
Ngapakaldia				AUS	AUS			
Palorchestes				-	AUS	AUS	AUS	
Pitikantia				AUS	-		-	
Propalorchestes				AUS	AUS			

Table 9. Order Diprotodontia, Suborder Vombatiformes (Families Phascolarctidae, Thylacoleonidae, Vombatidae, Wynyardiidae), asterisk indicates extant genera. Data from the Paleobiology Database via Fossilworks gateway and additional material (Black 2016; Brewer et al. 2015; Gillespie, Archer, and Hand 2017; Gillespie, Archer, and Hand 2020). AUS=Australia.

	Cre	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Family Phascolarctidae								
Invictokoala							AUS	
Koobor						AUS		
Litokoala				AUS	AUS			
Madakoala				AUS				
Nimiokoala				AUS	AUS			
Perikoala				AUS	AUS	AUS		
Phascolarctos*						AUS	AUS	AUS
Priscakoala					AUS			
Stelakoala					AUS			
Family Thylacoleonidae								
Lekaneleo				AUS	AUS			
Microleo					AUS			
Thylacoleo					AUS	AUS	AUS	
Wakaleo				AUS	AUS			
Family Vombatidae								
Lasiorhinus*					AUS	AUS	AUS	AUS
Nimbavombatus					AUS			
Phascolonus						AUS	AUS	
Ramasayia						AUS	AUS	
Rhizophascolonus					AUS			
Vombatus*						AUS	AUS	AUS
Warendja							AUS	
Family Wynyardiidae								
Muramura				AUS	AUS	AUS		
Namilamadeta				AUS				
Wynyardia					AUS			

Table 10. Order Diprotodontia, Suborder Phalangeriformes (Families Acrobatidae, Burramyidae, Ektopodontidae, Miminipossumidae, Miralinidae), asterisk indicates extant genera. Data from the Paleobiology Database via Fossilworks gateway and additional material (Archer et al. 2018, 2019; Schwartz 2006; Rich et al. 2006). AUS=Australia; NG=New Guinea.

	Cre	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Family Acrobatidae								
Acrobates*							AUS	AUS
Distoechurus*								NG
Family Burramyidae								
Burramys*				AUS	AUS	AUS	AUS	AUS
Cercartetus*				AUS	AUS	AUS	AUS	AUS
Family Ektopodontidae								
Chunia				AUS				
Darcius						AUS	AUS	
Ektopodon				AUS	AUS	AUS		
Family Miminipossumidae								
Miminipossum					AUS			
Family Miralinidae								
Barguru				AUS	AUS			
Durudawiri					AUS			
Miralina				AUS				

Table 11. Order Diprotodontia, Suborder Phalangeriformes (Families Petauridae, Phalangeridae, Pilkipildridae, Pseudocheiridae, Tarsipedidae), asterisk indicates extant genera. Data from the Paleobiology Database via Fossilworks gateway and additional material (Brumm et al. 2018; Case, Meredith, and Person 2009; Crosby 2007; Leavesley 2005). AUS or AU=Australia; NG=New Guinea; IND or IN=Indonesia.

	Cre	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Family Petauridae								
Dactylopsila*				AUS	AUS			NG
Gymnobelideus*								AUS
Petaurus*						AUS	AUS	AU/NG
Family Phalangeridae								
Ailurops*							IND	IND
Eocuscus				AUS				
Onirocuscus				AUS	AUS	AUS		
Phalanger*						AUS	NG	NG/IND
Spilocuscus*								AU/NG/IN
Strigocuscus*								AUS
Trichosurus*					AUS	AUS	AUS	AUS
Wyulda*					AUS			AUS
Family Pilkipildridae								
Djilgaringa				AUS	AUS			
Pilkipildra				AUS				
Family Pseudocheiridae								
Gawinga					AUS			
Hemibelideus*								AUS
Marlu				AUS	AUS			
Paljara				AUS	AUS	AUS		
Petauroides*						AUS	AUS	AU/NG
Petropseudes*						AUS		AUS
Pildra				AUS	AUS	AUS		
Pseudocheirus*						AUS	AUS	AUS
Pseudochirops*				AUS	AUS	AUS		AUS
Pseudochirulus*								AUS
Pseudokoala*					AUS	AUS	AUS	
Family Tarsipedidae								
Tarsipes*							AUS	AUS

Table 12. Order Diprotodontia, Suborder Macropodiformes (Family Macropodidae), asterisk indicates extant genera. Data from the Paleobiology Database via Fossilworks gateway and additional material (Flannery, Archer, and Plane 1982; Mountain 1991; Prideaux and Warburton 2009). Eldridge et al. (2019) noted that the affinities of bulungamyines (such as *Bulungamaya* and *Cookeroo*) are uncertain. AUS or AU=Australia; NG=New Guinea.

	Cre	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Family Macropodidae								
Archaeosimos						AUS		
Baringa						AUS	AUS	
Bohra						AUS	AUS	
Bulungamaya				AUS	AUS			
Congruus							AUS	
Cookeroo				AUS	AUS			
Dendrolagus*						AUS	NG	AU/NO
Dorcopsis*						AU/NG		NG
Dorcopsoides					AUS			
Dorcopsulus*							NG	NG
Ganguroo					AUS			
Hadronomas					AUS			
Kurrabi						AUS		
Lagorchestes*							AUS	AU/NO
Lagostrophus*						AUS		AUS
Macropus*						AUS	AUS	AU/NO
Metasthenurus							AUS	
Onychogalea*						AUS	AUS	AUS
Petrogale*						AUS	AUS	AUS
Prionotemnus						AUS	AUS	
Procoptodon							AUS	
Protemnodon						AU/NG	AU/NG	
Rhizosthenurus						AUS		
Setonix*								AUS
Silvaroo						AUS	AUS	
Simosthenurus						AUS	AUS	
Sthenurus						AUS	AUS	
Synaptodon							AUS	
Thylogale*						AUS	AU/NG	AU/NO
Troposodon						AUS	AUS	
Wabularoo				AUS	AUS			
Wallabia*						AUS	AUS	AUS
Wanburoo					AUS			
Watutia						NG		

Table 13. Order Diprotodontia, Suborder Macropodiformes (Families Balbaridae, Hypsiprymnodontidae, Potoroidae) and Order Diprotodontia (*incertae sedis*), asterisk indicates extant genera. Data from the Paleobiology Database via Fossilworks gateway and additional material (Arena et al. 2014; den Boer and Kear 2018; Flannery, Archer, and Plane 1982; Flannery and Rich 1986; Schwartz and Megirian 2004; Wroe 2003). Louys and Price (2015) noted that *Brachalletes* had been placed in both Macropodidae and Diprotodontidae, but they considered it a species inquirenda. AUS = Australia.

	Cre	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Family Balbaridae								
Balbaroo				AUS	AUS			
Galanarla				AUS	AUS			
Ganawamaya				AUS	AUS			
Nambaroo				AUS	AUS			
Wururoo				AUS	AUS			
Family Hypsiprymnodontidae								
Ekaltadeta				AUS	AUS			
Hypsiprymnodon*					AUS	AUS		AUS
Jackmahoneyi						AUS		
Propleopus						AUS	AUS	
Family Potoroidae								
Aepyprymnus*						AUS	AUS	AUS
Bettongia*					AUS		AUS	AUS
Borungaboodie							AUS	
Caloprymnus*							AUS	AUS
Gumardee				AUS	AUS			
Milliyowi						AUS		
Ngamaroo				AUS				
Palaeopotorous				AUS	AUS			
Potorous*						AUS	AUS	AUS
Purtia				AUS				
Wakiewakie					AUS			
Diprotodontia, <i>incertae sedis</i>								
Brachalletes						AUS		

Table 14. Infraclass Marsupialia (*incertae sedis*) and Superorder Australidelphia (*incertae sedis*). Data from the Paleobiology Database via Fossilworks gateway and additional material (Eldridge et al. 2019). *Djarthia* is recognized as Australia's oldest fossil marsupial (Beck et al. 2008). Eldridge et al. (2019) noted that *Ankotarinja* and *Keeuna*, previously considered members of Dasyuromorphia, form a clade with *Djarthia*. Sigé et al. (2009) referred *Thylacotinga* and *Chulpasia* to the same sub-family, within the Polydolopimorphia, while Eldridge et al. (2019) noted that higher-level relationships are still in doubt. AUS=Australia.

	Cre	Pal	Eo	Oli	Mio	Plio	Plei	Holo
Marsupialia, <i>incertae sedis</i>								
Numbigilga						AUS		
Thylacotinga			AUS					
Yingabalanara					AUS			
Australidelphia, incertae sedis								
Ankotarinja				AUS				
Djarthia			AUS					
Keeuna				AUS				

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