How has the biogeography of Gondwanan mammal clades varied across deep time?

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Declaration

I declare that the work presented in this thesis is wholly my own work, except where otherwise stated. The views and opinions expressed herein are mine and not necessarily those of any other person or body unless so attributed.

Jack McMinn, October 2024

Abstract

My thesis concerns the changing biogeography of terrestrial therian mammals in South America, Antarctica and Australia, focussing on the Palaeogene Period [66-23.03 Ma] to the present day. During much of the Palaeogene, South America and Australia were joined to Antarctica to form the supercontinent Gondwana, with dispersal opportunities between these continents likely resulting in the present-day geographical distributions of different Gondwanan therian clades. Across three data chapters, I examine the abiotic and biotic factors thought to have influenced Palaeogene therian biogeography, thereby predicting dispersal dynamics previously obscured by the limitations of the Gondwanan fossil record. For my first study, I modelled the present-day climatic tolerances of Gondwanan therian family-level groups, projecting said tolerances onto Palaeogene palaeoclimate reconstructions to visualise the abiotically suitable area in Antarctica for these groups over millions of years. Eomarsupialia (Australian marsupials), Paucituberculata (shrew opossums) and Microbiotheria (*monito del monte*) had large suitable regions in Antarctica during the Danian [66-61.6 Ma], meaning that stem members of these groups may have been able to travel between South America and Australia during this time. The second study focussed on quantifying the ecological roles of Gondwanan terrestrial therians to test for biotic niche change across the Palaeogene and up to the present day. Biotic niches were estimated using a combination of diet and body mass for every Palaeogene and present-day terrestrial therian genus in South America, Antarctica and Australia. The collective biotic attributes of Metatheria and Eutheria changed between the five time intervals I considered, thereby showing little broad-scale niche conservatism from the Palaeogene to the present day in South America and Australia. My analyses did show potential evidence for niche stasis between early [56-47.8 Ma] and late Eocene time intervals [47.8-33.9 Ma] in Antarctica, but these results are likely affected by small sample sizes. In my third and final study, I tested the longevity of the apparent ecological relationships between Microbiotheria and the temperature rainforest plant species the clade relies upon for food and shelter in the present day. The extent of abiotic niche overlap was used

as a proxy for the magnitude of potential ecological interactions, measured in environmental space, and in geographical space when projecting models onto Palaeogene Antarctica. Contrary to previous work, little support was found for significant co-evolution between microbiotheres and plant species (especially the mistletoe *Tristerix*), suggesting that these relationships may have had little effect on trans-Gondwanan dispersal of metatherians. My multidisciplinary analyses emphasise that Gondwanan therian clades, historically depicted by Western science as 'living fossils', have undergone significant ecological and biogeographical change since the Palaeogene, eventually producing some of the most important global hotspots for present-day mammal diversity.

An Acknowledgement

This thesis concerns the analysis of fossil and living animals found in South America and Australia. I acknowledge the Traditional Owners, Custodians and indigenous peoples who populate the continents my research relies upon. I pay my respect to Indigenous Elders past, present and emerging. The sovereignty of the indigenous peoples of South America and Australia has never been ceded, and these lands and their associated waterways remain justly theirs, as they have for tens of thousands of years. The colonial structures and policies ingrained in modern South American and Australian culture continue to facilitate acts of violence and dispossession against indigenous peoples. Indeed, my own extended family has been a participant in this – men named McMinn have claimed lagoons in Larrakia Country/Darwin, and raised buildings on native land in Kaurna Country/Adelaide. I recognise the efforts of indigenous peoples past and present to dismantle these colonial structures, and hope that they find justice, agency and peace as soon as possible.

Yet blaming these atrocities purely on the governments in South America and Australia is over-simplistic. The United Kingdom, the United States, France, Germany and other Western countries all actively encourage crimes committed against indigenous peoples, and monetarily benefit from doing so. This extends to the University of Oxford and the Natural History Museum, the two institutions under which I have worked for the past four years. The foundations of Western academia and science are built from the illegal seizing of indigenous property, land and bodies - both the University and Museum retain thousands of remains from indigenous humans, along with artefacts and objects (both natural and manmade) stolen from native land.

Though pipelines to reconciliation and repatriation have been introduced, the reliance on colonial structures still persists in these places. In May 2023, the Natural History Museum hosted an evening dinner for ‘National Conservatism’, a thinktank promoting anti-immigration policy which disproportionately and violently affects indigenous refugees. In May 2024, student protesters

established encampments in Oxford, asking the University to divest from companies complicit in the ongoing Palestinian massacre. The University responded via siege, sealing its own students inside the protest area with tall steel fencing. Eventually, a University-mandated bulldozer was sent to destroy the encampment all together – it was filmed crushing a symbolic punnet of strawberry plants (a crop long associated with indigenous Palestine) beneath its enormous wheels.

This acknowledgement is part of the continuing peaceful protest.

Personal Thanks

I would like to first thank my supervisors Professors Erin Saupe and Anjali Goswami. These past four years have been a rollercoaster (and I appreciate that the speed of my writing has left much to be desired!) but your contributions, advice, and kindness have been invaluable. I first applied to this DPhil project for the academic year beginning 2019 – when I was unsuccessful, Erin reached out to me and encouraged me to try again the following year. I'm so glad that I did, and without Erin's continued encouragement and patience for nearly half a decade, this DPhil would simply not exist. Anjali's support has also helped immeasurably, and our conversations in the office (and the pub) shaped and consolidated the core ideas for what I wanted this thesis to be, as well as what I wanted to do with my life after it was all done. Her influence has also resulted in many amazing opportunities to discuss my work at conferences and meet other incredible people. In short, my work has been made so much better because of you both and all you have done, and I cannot express my gratitude adequately.

Next, a shout out to the entire collective of the Saupe and Goswami Labs, and the wider palaeontology communities of Oxford and London – all of you are wonderful friends. Victoria Forth and the team at the Doctoral Training Centre have also done (and continue to do!) a fantastic job at managing the NERC DTP programme, as well as sorting out every inane question I've emailed their way – their efforts were an anchor throughout the pandemic years of this DPhil and I don't know where I'd be without them. I also must thank St Cross College's kind and supportive porters, and my college tutor Professor Blanca Rodriguez – along with Dr Alex Farnsworth, who graciously provided his palaeoclimate maps and associated expertise, and Dr Robin Beck, who sent some great resources my way.

Thanks to Mum and Dad and Issey of course, and to James and Fanny for being there when this whole journey began, and to Hollie, Pete, Stef and Yuri for being the first friends I made in Oxford, and to Absana and all the other music/comedy folks for being friends I made at a

somewhat later date. Thanks to the teeming diversity of animal life across the planet Earth, without whom it would be a lot more difficult to bump up this DPhil's wordcount.

A very esoteric thanks to former Beatle Ringo Starr. When experimenting with the earliest lines of code for this project, I named a variable after the marsupial clade Didelphimorphia – 'diddy' for short. In the next iteration of the code, I changed this to 'dingo' for the sake of differentiating it from my previous efforts, and subsequently to 'ringo'. Sure enough, the so-called 'Ringo code' ended up being vitally important in almost all of my analyses, and I used it pretty consistently for three years. So, um, thanks, Sir Richard.

Finally, it's generally a tradition to end the 'personal thanks' section of a doctoral thesis with the author crediting their romantic partner. I would never stoop to something so obvious. Kelsey, you already know the extent to which I love and adore you, and how much I owe you not only for supporting me throughout this DPhil but for improving my life and happiness as much as you have. Therefore, I see no reason to stroke your ego any further in the dreg-pages of some shabby DPhil. Deal with it, my darling.

“Fire is nothing, just clean up. When you burn, new grass coming up. That means good animal soon, might be goanna, possum, wallaby. Burn him off, new grass coming up, new life all over."

- Bill "Big Bill" Neidjie, Gaagudju elder and traditional owner of the Bunitj estate, Australia.

"*Back then long time ago when grass was green*

Woke up in a daze

Arrived like strangers in the night…

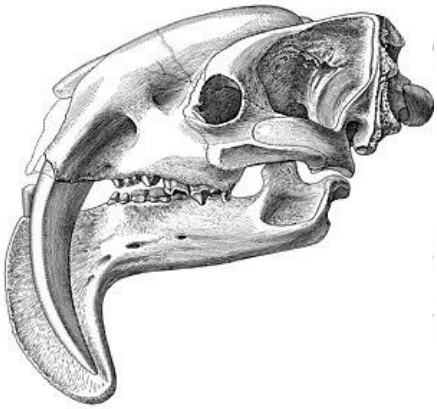
The microscopes that magnified the tears

Studied warts and all

Still the life flowed on and on…

Long time ago when we was fab."

- verses 1 and 3, and chorus, from 'When We Was Fab' by George Harrison and Jeff Lynne [BMG Publishing, 1987], Oxfordshire.



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Chapter 1 – Introduction to Gondwanan mammal biogeography

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ABSTRACT

South America and Australia, which were once part of the southern supercontinent Gondwana, are known for their present-day mammal diversity and multiple endemic clades, yet many uncertainties remain regarding the evolutionary origins and biogeographical history of mammals in these continents, in large part due to the limitations of the fossil record. Here I summarise the existing consensus on Gondwanan mammal ecology and evolution, focussing on the origination, diversification, and dispersal of therian groups across the Palaeogene [66-23.03 Ma], and the ambiguities that remain in our understanding of these hypothesized events. I discuss how my doctoral work offers alternative approaches to working around said ambiguities, largely involving therian abiotic and biotic niches. My thesis chapters collectively demonstrate how palaeontological analysis can co-opt multiple novel methodologies to interrogate ecological and evolutionary narratives across deep time, while additionally proposing potential trajectories for future research and analysis.

A REVIEW OF GONDWANAN MAMMAL ECOLOGY AND EVOLUTION

Global mammal diversity

Predictions as to the timing of the origination of Mammalia, the crown group of Synapsida, vary considerably between studies, but almost certainly occurred within the Triassic [251.9-201.4 Ma] or Jurassic Periods [201.4-145 Ma] (Luo, Gatesy et al. 2015, Irisarri, Baurain et al. 2017, Álvarez-Carretero, Tamuri et al. 2022, Velazco, Buczek et al. 2022, Yu, Wang et al. 2023). The clade includes three extant groups: Monotremata (Flannery, Rich et al. 2022), Metatheria, and Eutheria. Metatheria and Eutheria are sister groups, and together form the clade Theria, which first appeared in the Jurassic or Cretaceous Periods [145-66 Ma] (King and Beck 2020, Álvarez-Carretero, Tamuri et al. 2022, Velazco, Buczek et al. 2022, Beck 2023). The extant crown clades within Metatheria and Eutheria – Marsupialia and Placentalia, respectively – originated in the Cretaceous or early Palaeogene Periods [66-47.8 Ma] (Archibald and Deutschman 2001, O'Leary, Bloch et al. 2013, Esselstyn, Oliveros et al. 2017, Álvarez-Carretero, Tamuri et al. 2022, Velazco, Buczek et al. 2022, Beck 2023). The Cretaceous-Palaeogene extinction event ~66 Ma, which saw the extinction of the non-avian dinosaurs with the beginning of the Cenozoic Era [66-0 Ma] (**Figure 1.1**), initiated an episode of rapid mammal diversification globally (Archibald and Deutschman 2001, Meredith, Janečka et al. 2011, Grossnickle and Newham 2016, Lyson, Miller et al. 2019, Bertrand, Shelley et al. 2022, Goswami, Noirault et al. 2022), and, in the present day, Mammalia is found on every continent on Earth, with five species of Monotremata (platypuses and echidnas), almost 400 species of Marsupialia, and over 6,100 species of Placentalia (Burgin, Colella et al. 2018). Thousands of extinct mammal taxa have also been described from the fossil record, including stem therians, non-placental eutherians, and non-marsupial metatherians.

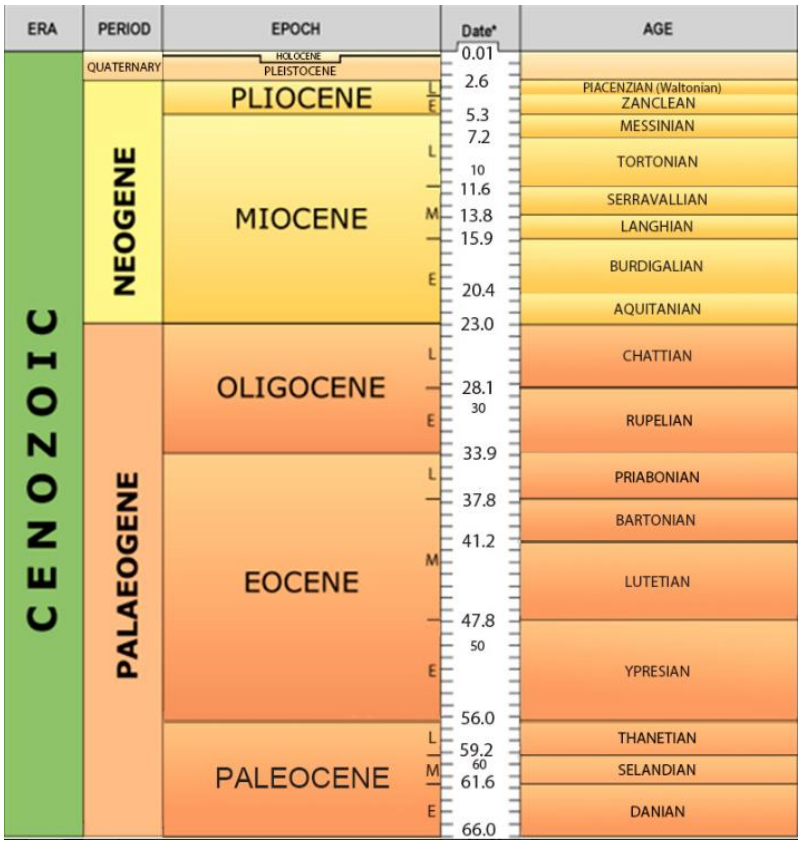

Figure 1.1. The BGS geological timescale of the Cenozoic Era [66-0 Ma] - this thesis focusses particularly on the Palaeogene Period [66-23.03 Ma] and its component epochs and ages. BGS ©UKRI. The inclusion of this illustration is non-commercial and thus usable within this context (https://www.bgs.ac.uk/bgs-intellectual-property-rights/using-bgs-copyright-material/).

Marsupialia presently consists of Eomarsupialia (marsupials associated with Australia, New Guinea, and Indonesia), along with three American family-level clades: Didelphidae (opossums, the crown group of Didelphimorphia), Caenolestidae (shrew opossums, the crown group of Paucituberculata), and Microbiotheriidae (*monito del monte*, the crown group of Microbiotheria) (Wilson and Reeder 2005). Didelphidae and Caenolestidae are paraphyletically known as 'Ameridelphia', and Eomarsupialia and Microbiotheriidae as Australidelphia. Placentalia presently consists of four superorders: Euarchontaglires (primates, tree-shrews, flying lemurs, rodents and lagomorphs), Laurasiatheria (carnivorans, ungulates, bats, pangolins and insectivores), Afrotheria (elephants, sea-cows, hyraxes, aardvarks and afroinsectivores), and Xenarthra (sloths, armadillos and anteaters). Euarchontaglires and Laurasiatheria together form the clade Boreoeutheria, and

Afrotheria and Xenarthra are collectively known as Atlantogenata (Foley, Mason et al. 2023) (***Figure 1.2***).

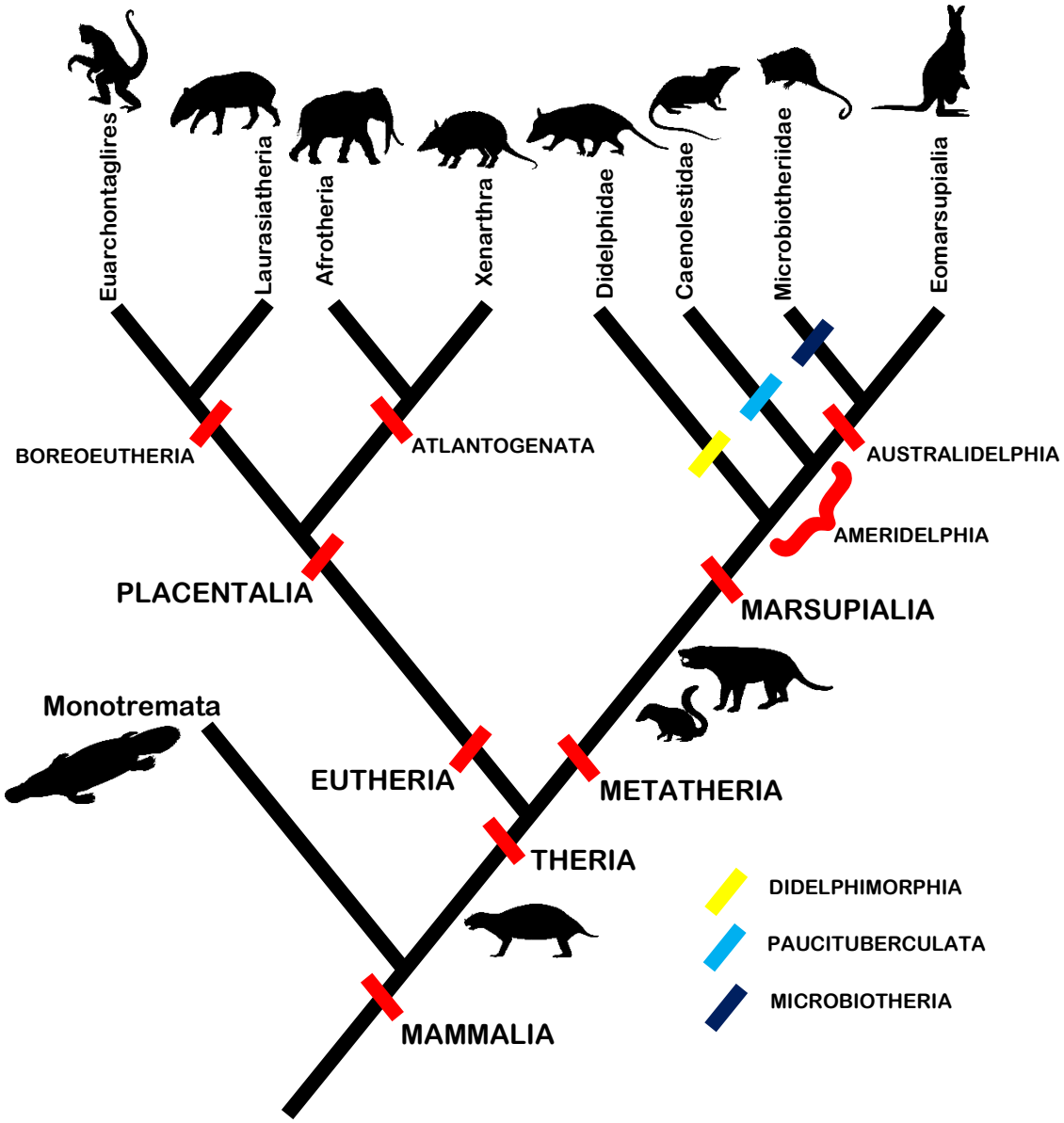

Figure 1.2. The relationships among Mammalia (Eldridge, Beck et al. 2019, Foley, Mason et al. 2023). Near the root of Mammalia is the gondwanathere *Adalatherium,* a stem therian genus. Near the root of Metatheria are *Pediomys* and the sparassodont *Arminiheringia*, two non-marsupial metatherian genera. Caenolestidae and Microbiotheriidae silhouettes by Sarah Werning, and *Adalatherium* silhouette by Scott Hartman (vectorised by William Gearty), on Phylopic (CC 3.0 Unported).

Gondwanan continents and biota

The mammal biota of South America and Australia is known for its great diversity. The Neotropics, which encompass South America, Central America, and the Caribbean, presently harbour over 1,600 mammal species, the most of any biogeographical region – even when regions' mammal species counts are ranked relative to their geographical areas, the Neotropics are still ranked third, with Oceania (which includes Australia) at second (the Indo-Malayan region is first) (Burgin, Colella et al. 2018). South America and Australia are also known for their multiple endemic clades, some of which have proliferated on the two continents since perhaps the Cretaceous-Palaeogene extinction event (Gaudin and Croft 2015, Beck 2017, Eldridge, Beck et al. 2019, Beck, Voss et al. 2022, Foley, Mason et al. 2023). Understanding the biogeographical context of such diversity, across the past 66 million years and beyond, is thus of significant interest for mammalogists, as well as biodiversity and evolutionary scientists in general.

At the time of the Cretaceous-Palaeogene extinction event, South America, Australia and Antarctica were continuous, forming the last remnant of Gondwana, a supercontinent which comprised much of the Southern Hemisphere (***Figure 1.3***) (Reguero and Goin 2021). India had also been part of this landmass, but broke off in phases throughout the Cretaceous, first separating from Antarctica and Australia 130-120 Ma, then from Madagascar ~90 Ma (Prasad and Parmar 2022). Africa, another former Gondwanan continent, had separated from South America ~95-110 Ma to form the South Atlantic Ocean, potentially resulting in the vicariance of therian populations and the later phylogenetic divergence of Afrotheria and Xenarthra (clades associated with Africa and South America respectively) (Tarver, Dos Reis et al. 2016, Scotese 2021, Foley, Mason et al. 2023).

Figure 1.3. The Gondwanan supercontinent circa the Cretaceous-Palaeogene boundary 66 Ma. Adapted from Figure 1 in Kielan-Jaworowska et al. (2007), licensed under the Creative Commons Attribution 4.0 International license.

The final break-up of South America, Antarctica, and Australia probably occurred during the Palaeogene, though the exact timings are poorly constrained. Although Reguero et al. (2014, 2021) suggest that the isthmus connecting South America and Antarctica was already covered by a shallow epicontinental sea ~55 Ma, estimates for tectonic separation (which resulted in the Drake Passage and Scotia Arc) range from the Eocene [56-33.9 Ma] to early Miocene Periods [23.03-15 Ma] (Hodel, Grespan et al. 2021, Reguero and Goin 2021, van de Lagemaat, Swart et al. 2021, Martos and Catalán 2024). The formation and deepening of the Drake Passage is commonly associated with the formation of the Antarctic Circumpolar Current and Antarctica's transition to 'icehouse' conditions at the Priabonian-Rupelian boundary ~33.9 Ma (Sijp and England 2004, Lauretano, Kennedy-Asser et al. 2021, Huang, Steel et al. 2022, Martos and Catalán 2024), but some climate and ocean current modelling disputes this narrative (Zhong-Shi, Qing et al. 2010, Hodel, Grespan et al. 2021, Vincze, Bozóki et al. 2021, Munday, Sauermilch et al. 2024). In contrast, the timing for the opening and deepening of the Tasmanian Seaway between Antarctica

and Australia is better constrained to around the Priabonian-Rupelian boundary (Scher, Whittaker et al. 2015, Evangelinos, Escutia et al. 2022, Munday, Sauermilch et al. 2024). With the final break-up of Gondwana began the so-called 'Splendid Isolation' of its continents (Simpson 1961, Simpson 1980) - the geographical insularity of South America and Australia across millions of years, which resulted in much of their unique modern flora and fauna.

Although isolated for millions of years, South America, Antarctica, and Australia still share a 'pan-Gondwanan biota', a collection of extant or extinct taxa shared between two or three of these continents on account of their former proximity. These include the southern beech *Nothofagus* (Veblen, Hill et al. 1996), the tree fern family Dicksoniaceae (Noben, Kessler et al. 2017), the ectomycorrhizal fungus *Amanita* (Truong, Sánchez-Ramírez et al. 2017), the extinct horned turtle family Meiolaniidae (Brown and Moll 2019), and the extinct predatory bird family Phorusrhacidae (Acosta Hospitaleche and Jones 2024). Many mammal groups are also shared between the former Gondwanan continents. Gondwanatheria and Meridiolestida, for instance, are two stem-therian groups known from the fossil record of both South America and Antarctica (Goin, Tejedor et al. 2012, Hoffmann, Beck et al. 2020, Martinelli, Soto-Acuña et al. 2021). Gondwanatheres and meridiolestids both persisted through the Cretaceous and Palaeogene Periods, with one genus from the latter clade (the fossorial invertivore *Necrolestes*) surviving in South America until the early Miocene, making it the last surviving stem therian globally (Chimento, Agnolin et al. 2012, Rougier, Wible et al. 2012, Wible and Rougier 2017). Monotremata is another example of a pan-Gondwanan mammal group. Although most of its fossil and extant diversity is known from Australia and New Guinea (Flannery, Rich et al. 2022, Flannery, McCurry et al. 2024), the platypus species *Patagorhynchus pascuali* and *Monotrematum sudamericanum* are South American representatives from the Cretaceous and Palaeocene [66-56 Ma], respectively (Pascual, Archer et al. 1992, Chimento, Agnolín et al. 2023). Perhaps the most unusual non-therian mammal in Gondwana is the so-called 'St Bathans mammal' from the early Miocene of Aotearoa/New

Zealand - the only extinct or extant terrestrial mammal endemic to the islands, yet only known from taxonomically ambiguous jaw and femoral fragments (Worthy, Tennyson et al. 2006).

Therian evolution in South America

The South American therian fossil record is spatio-temporally patchy and unevenly sampled, especially in comparison to the extensive historical fossil collection in Europe and North America (Kidwell and Holland 2002, Vilhena and Smith 2013). This scarce fossil record has made it difficult to infer macroevolutionary and biogeographical trends across deep time (Nilsson, Churakov et al. 2010, Bennett, Upchurch et al. 2018, Beck, Voss et al. 2022). However, based on available evidence, it is thought that early therians dispersed into South America from North America at the end of the Cretaceous (Beck 2017, Reguero and Goin 2021), an event possibly enabled by the extinction of previously dominating Gondwanan non-therian mammals (Brocklehurst, Panciroli et al. 2021). However, the fact that Cretaceous eutherian fossils have been described in both India and Madagascar suggests that therians were already established in Gondwana before this time period (Averianov and Archibald 2003, Rana and Wilson 2003, Prasad, Verma et al. 2010, Goswami, Prasad et al. 2011). The earliest recorded therian species in South America is *Patagomaia chainko*. Although its identity as either a metatherian or eutherian is currently ambiguous, the taxon is the largest known mammal before the Cretaceous-Palaeogene extinction event, at ~14 kg (Chimento, Agnolín et al. 2024).

Metatheria may have originated in North America (Crespo and Goin 2019) – the clade's earliest known unambiguous fossil is a lower molar from the early Cretaceous of Montana [107-104 Ma] (Cifelli and Davis 2015, Beck, Voss et al. 2022), while the morphological and taxonomic diversity of Metatheria appears to have exceeded that of Eutheria in North America throughout the Cretaceous (Williamson, Brusatte et al. 2014, Bennett, Upchurch et al. 2018). Not surprisingly then, many of the earliest South American therians to originate from North America were metatherians, as seen in Palaeocene deposits in Bolivia and Argentina (Goin, Pascual et al. 2006,

Goin, Woodburne et al. 2016, Defler 2019, Ladevèze, Selva et al. 2020). The rapidity of metatherian diversification in South America from the Cretaceous-Palaeogene boundary to the Ypresian Age [56-47.8 Ma] (Bennett, Upchurch et al. 2018) is sometimes considered as evidence that metatherians were well established on the continent before the dispersal event from North America (Defler 2019). One of the earliest non-marsupial metatherian orders in South America was the faunivorous Sparassodonta, a group which survived until the Pliocene [5.3-2.6 Ma] (De Muizon, Ladevèze et al. 2018), and ranged from the 250g mesocarnivore *Allqokirus australis* (Zimicz 2012, Beck 2023) to the 200kg apex predator *Proborhyaena gigantea* (Zimicz 2012, Prevosti and Forasiepi 2018). Polydolopimorphia, which also first appeared in the Palaeocene, was similarly speciose (though its taxonomic relationship with other metatherian clades is debatable) (Beck 2023) – representatives of this order vary in diet from invertivory to frugivory (Zimicz 2012, Zimicz 2014), and in locomotion from scansoriality to bipedal saltation (Croft 2016, Abello and Candela 2020) (see Chapter 3).

The crown group Marsupialia appears to have originated in South America, in all likelihood post-dating the North American metatherian dispersal (Beck 2017, Eldridge, Beck et al. 2019, Beck, Voss et al. 2022). Identifying fossil taxa from Didelphimorphia, Paucituberculata, and Microbiotheria (the most basal marsupial groups) is complicated by the fact that these groups retain many dental and skeletal plesiomorphies also seen in non-marsupial metatherian clades (Ladevèze, Selva et al. 2020, Beck, Voss et al. 2022), including herpetotheriids, derorhynchids and pucadelphids (Case, Goin et al. 2005, Sánchez-Villagra, Ladevèze et al. 2007). For instance, while the extinct invertivorous *Khasia cordillerensis* is often considered a member of Microbiotheria (Marshall and DeMuizon 1988, Zimicz 2012), which would make it the only described Palaeocene marsupial, it has also been diagnosed as a relative of the North American metatherian *Pediomys* (Szalay 1994, Beck, Voss et al. 2022, Beck 2023).

The earliest uncontroversial marsupial remains in South America, dating to the Ypresian, are the fossil molars of paucituberculates and microbiotheres (Goin, Candela et al. 2009, Tejedor, Goin et al. 2009). These two groups in the present day consist only of invertivores weighing less than 50 g (Wilman, Belmaker et al. 2014), but had greater ecological diversity during the Eocene and Oligocene [33.9-23.03 Ma], largely driven by the extinct sister clades of Caenolestidae and Microbiotheriidae - Palaeothentoidea and Woodburnodontidae, respectively, which both included larger-bodied herbivorous taxa (Goin, Zimicz et al. 2007, Zimicz 2012, Abello, Toledo et al. 2020, Beck 2023). In contrast, the fossil record of uncontroversial didelphimorphs begins as late as the Miocene with early representatives of Didelphidae (Eldridge, Beck et al. 2019, Beck, Voss et al. 2022), although phylogenetic analysis and biogeographical modelling indicates that this crown clade first appeared in Amazonian forests during the Eocene or Oligocene (Mitchell, Pratt et al. 2014, Castro, Dahur et al. 2021, Beck, Voss et al. 2022). Some didelphid taxa have since dispersed from South America into North America, the most prolific of these being the genus *Didelphis,* which entered North America ~0.8 Ma and has undergone rapid range expansion within the United States and Canada over the last 200 years (Woodburne 2010, Walsh and Tucker 2018, Wait and Ahlers 2020).

Terrestrial South American placentals during the Palaeogene fall into two main taxonomic categories – xenarthrans and SANUs (South American Native Ungulates). Xenarthra has a limited fossil record over this time period. A key characteristic of this superorder is reduced or absent dentition (possibly due to ancestral myrmecophagy) (Vizcaíno 2009, Gaudin and Croft 2015), and molars are the most consistently fossilised parts in the mammal skeletal system (Gingerich 1974, Gingerich 1977). Thus, while some molecular evidence indicates that xenarthrans originated in the Palaeocene (Foley, Mason et al. 2023), the oldest fossil evidence are isolated armadillo osteoderms and limb bones from Ypresian deposits in south-eastern Brazil (Oliveira and Bergqvist 1998, Bergqvist, Abrantes et al. 2004, Gaudin and Croft 2015). The earliest known sloth genus *Pseudoglyptodon* first appeared in the late Eocene [47.8-33.9 Ma] and survived until the end of

the Palaeogene (McKenna, Wyss et al. 2006, Pujos and De Iuliis 2007). The anteater fossil record begins after the Palaeogene, in the early Miocene (Gaudin and Branham 1998). Similarly to Didelphidae, modern sloths, armadillos and anteaters have all successfully dispersed northwards into the North American continent, as did extinct xenarthrans such as 'ground sloths' (a polyphyletic category of often large terrestrial sloths), glyptodonts (large-bodied herbivorous armadillos), and pampatheres (stem armadillo grazers) (Shaw and McDonald 1987, Vizcaíno, De Iuliis et al. 1998, McDonald 2005, Woodburne 2010, Mitchell, Scanferla et al. 2016, McDonald and Carranza-Castañeda 2017).

The term 'SANU' describes a collective of five extinct herbivorous 'ungulate' orders (along with multiple smaller clades) which persisted in South America across almost the entire Cenozoic (Croft, Gelfo et al. 2020). The group's taxonomic position within Placentalia is unclear, as is whether it represents a single monophyletic group or multiple independent radiations. Molecular analyses of preserved collagen and a near-complete mitochondrial genome indicate that at least two SANU orders, Notoungulata and Litopterna, were stem representatives of Perissodactyla (an ungulate clade which presently consists of horses, rhinos and tapirs) (Buckley 2015, Westbury, Baleka et al. 2017). The SANU collective includes a range of omnivore-herbivores, folivores, and grazers, variably converging on the *Bauplans* of rodents, elephants, eomarsupials, and other hoofstock. The largest SANUs, members of the orders Astrapotheria and Pyrotheria, may have weighed over 3000 kg (Croft 2016, Croft, Gelfo et al. 2020). Despite such diversity, only a single SANU taxon, the ~1500 kg notoungulate genus *Mixotoxodon* (MacFadden 2005), is known to have dispersed into North America (Lundelius Jr, Bryant et al. 2013).

South America's 'Splendid Isolation' after final Gondwanan break-up was by no means absolute. For instance, caviomorphs and anthropoids (New World rodents and monkeys, respectively) both arrived via oceanic dispersal from Africa in the late Eocene or Oligocene (Antoine, Marivaux et al. 2012, Croft 2016, Löwenberg-Neto 2024). South American caviomorphs appear to have been

derived from a single dispersal event, while at least four separate anthropoid clades dispersed across the Atlantic (including the one extant group Platyrrhini) (Marivaux, Negri et al. 2023). Both caviomorphs and platyrrhines saw notable morphological diversification during the Miocene, with Caviomorpha undergoing additional pulses of diversification in the Oligocene (Álvarez, Arévalo et al. 2017, Rocatti, Aristide et al. 2017, Defler 2019, Álvarez, Ercoli et al. 2021).

Arguably the most significant interruption to South America's biogeographical insularity was the 'Great American Biotic Interchange' (GABI), which began ~10 Ma after the collision of South America with North America (Webb and Stehli 1985, Woodburne 2010, Croft 2016). The event was plausibly enhanced by global cooling trends, which reduced sea levels and transformed Central America (part of North America) into a sizeable land bridge (Bacon, Molnar et al. 2016, Freitas-Oliveira, Lima-Ribeiro et al. 2024). The previously discussed northward dispersal of didelphids, xenarthrans, and SANUs were components of the interchange, as were dispersals of platyrrhines and caviomorphs into North America, but these are greatly exceeded in scale by the southward dispersal of North American therian taxa, including carnivorans (cats, dogs, bears, raccoons, skunks and mustelids), ungulates (camelids, deer, peccaries, horses and tapirs), rabbits, shrews, and stem elephants (Croft 2016). As was the case with the initial Cretaceous therian dispersal from North America, the mass dispersal of therians into South America during the GABI was probably enabled by the high extinction rate of South American mammals at that time (Carrillo, Faurby et al. 2020). The GABI was a major component in producing the therian communities which existed in South America just before the arrival of humans ~25,000 years ago (Pansani, Pobiner et al. 2023) (and, later, their domesticated Eurasian mammals).

Therian evolution in Antarctica and Australia

The Antarctic ice cap covers the vast majority of the Antarctic continent in the present day, limiting outcrop exposure. As a result, the terrestrial therian fossil record is spatially restricted to the Eocene deposits of Seymour/Marambio Island, adjacent to the northern tip of the Antarctic

Peninsula (Gelfo, Goin et al. 2019). Given these sites' spatial proximity to South America, the presence of South American therian clades, including microbiotheres, polydolopimorphs, litopterns, astrapotheres, and possible xenarthrans, is unsurprising (Gelfo, Goin et al. 2019). The Antarctic representatives of these groups are all either small invertivores and frugivores, or larger-bodied terrestrial browsers (Gelfo, Goin et al. 2019) – ecological roles which reflect the dense *Nothofagus* temperate rainforest biome that covered Antarctica during the Cretaceous and early Palaeogene (Reguero, Marenssi et al. 2002, Francis, Ashworth et al. 2008, Bowman, Francis et al. 2014, Macphail, Carpenter et al. 2022, Thompson, Salzmann et al. 2022)**.** The lack of carnivorous mammal remains may be an artefact of reduced sampling (Gelfo, Goin et al. 2019), or an indication that predacious roles were filled by other clades in Antarctica. Eocene fossils of mammalivorous birds have been found in Seymour/Marambio Island, including falconids and the aforementioned giant phorusrhacids (Tambussi, Noriega et al. 1995, Acosta Hospitaleche and Jones 2024). In the present day, Antarctica is populated only by marine mammals in the clades Pinnipeda (seals, sea lions and walruses) and Cetacea (toothed and baleen whales).

Australia, too, has a patchy Palaeogene fossil record, likely obscuring the timing of the continent's earliest therians. Four distinct Australian localities harbour Cretaceous mammal remains, but none have any evidence of Theria (Beck 2017, Flannery, McCurry et al. 2024). The oldest known therian-bearing deposit on the continent is thus the Ypresian [~54.6 Ma] Murgon Fossil Site in Wakka Wakka Country/south-eastern Queensland, thought to represent a low-energy freshwater depositional environment (Godthelp, Archer et al. 1992, Salisbury and Willis 1996). The animal fossils discovered at the locality, collectively named the Tingamarra Local Fauna, include cranial and tarsal elements from *Djarthia murgonensis,* a ~40 g invertivore considered the earliest described australidelphian (though not an eomarsupial) (Godthelp, Wroe et al. 1999, Beck, Godthelp et al. 2008, Beck 2013). Other Tingamarra therians include *Chulpasia*, a metatherian genus with potential Ypresian fossils from South America (Crochet and Sigé 1993, Sigé, Archer et al. 2009), and the 'condylarth' *Tingamarra* (Long 2002, Beck 2017), which, while not yet formally

described, may be the only non-volant Australian eutherian until the arrival of rodents from Asia ~10 Ma (Breed and Ford 2007, Rowe, Reno et al. 2008).

The next oldest Australian deposits with mammal fossils have been dated to the late Oligocene (a gap of ~30 million years), and include Etadunna, Wipajri, and Namba Formation outcrops across south-eastern Australia (Woodburne, MacFadden et al. 1994, Megirian, Prideaux et al. 2010). Arguably the most famous set of Oligocene fossil sites is the Riversleigh World Heritage Area in Boodjamulla Country/north-western Queensland, which consists of over 200 localities representing four temporally successive 'faunal zones' across the Oligocene and Miocene (Archer, Arena et al. 2006, Travouillon, Legendre et al. 2009, Travouillon, Escarguel et al. 2011). The Riversleigh sites represent a forested environment (Guerin and Hill 2006, Travouillon, Legendre et al. 2009) occupied by some of the earliest members of many extant eomarsupial clades, including Phascolarctidae (koalas), Macropodidae (kangaroos and wallabies), Vombatidae (wombats), Dasyuridae (marsupial carnivores), and the possum families Petauridae and Phalangeridae (Archer, Arena et al. 2006, Travouillon, Escarguel et al. 2011). The pygmy possum genera *Burramys* and *Cercartetus*, fossils of which are recorded at multiple Riversleigh sites, persist in Australia in the present day (Osborne and Christidis 2002, Archer, Bates et al. 2019). Conversely, some marsupial clades present at Riversleigh became extinct during Australia's megafaunal extinction event in the Pleistocene [2.6-0.012 Ma], including Diprotodontidae ('giant wombats'), Ektopodontidae (marsupial rodents), Palorchestidae (marsupial tapirs), and Thylacoleonidae (marsupial lions) (Archer, Arena et al. 2006, Travouillon, Escarguel et al. 2011, Black, Archer et al. 2012). These extinctions were likely initiated by the arrival of modern humans in Australia ~65,000 years ago (Malaspinas, Westaway et al. 2016, Clarkson, Jacobs et al. 2017), with later extinctions of the families Thylacinidae (thylacines) and Chaeropodidae (pig-footed bandicoots) caused by the historical invasion of European settlers and their livestock (Travouillon 2016, Carlson, Bond et al. 2018).

The earliest Australian therians probably originated from South America, dispersing between the continents via Antarctica before final Gondwanan break-up. However, the specific biogeographical history is presently unclear (Godthelp, Wroe et al. 1999, Beck, Godthelp et al. 2008, Nilsson, Churakov et al. 2010, Goin, Woodburne et al. 2016, Beck 2017, Reguero and Goin 2021). One indication of potential dispersal dynamics may be the discovery of Australian taxa at South American fossil sites. Lorente et al. (2016), for example, described possible eomarsupial tarsal elements at the Eocene locality of La Barda, Argentina, while phylogenetic analysis suggests that the South American gondwanathere species *Groeberia minoprioi* may instead be a member of Vombatiformes (an eomarsupial suborder which includes Vombatidae, Phascolarctidae and many extinct families) (Zimicz and Goin 2020). The remains of South American marsupials may have also been found as part of Australia's Tingamarra Local Fauna. The isolated marsupial calcaneus specimen '*QM F30060*' is grouped within Paucituberculata in Bayesian phylogenies (though this observation is not repeated in phylogenies constructed under the assumption of maximum parsimony) (Beck 2012), and Archer, Arena et al. (1999) mention the presence of undescribed microbiothere fossils at the Murgon site.

DISCUSSION AND THESIS SCOPE

Our understanding of Gondwanan mammal evolution is rife with uncertainty. Many details concerning the origination, proliferation, and dispersal of eutherian and metatherian clades across South America, Australia, and Antarctica remain obscured. The Palaeogene, in particular, appears to be a significant time period for the establishment of therian biogeographical patterns still evident in the present day, such as the endemism of Ameridelphia and Xenarthra to South America, and Eomarsupialia to Australia. Yet, it is difficult to derive valid ecological narratives from direct surveys of fossil occurrences, which consist of limited samples of taxa at a coarse spatio-temporal resolution that are often taxonomically ambiguous and known only from fragmentary remains. Alternative methodologies less coupled to these restrictions are necessary to test hypotheses of Gondwanan therian biogeography across deep time.

Throughout the three ensuing chapters, I quantify the abiotic and biotic niches of terrestrial Gondwanan therians to test for continent-level ecological change over the Palaeogene and up to the present day. Abiotic, or beta, niches describe a taxon's tolerance to non-biological ecosystem components (e.g. temperature and precipitation), which roughly align with G. Evelyn Hutchinson's original 1957 definition of 'environmental niche' (Vandermeer 1972, Colwell and Rangel 2009). This definition also corresponds with the concept of the 'fundamental niche', a hypothetical *n*-dimensional hypervolume in environmental space, which most organisms rarely 'fill' completely, given restrictions imposed by the physical and biological environment (the niche fraction that an organism has 'filled' is called a 'realised niche') (Austin 1999, Kearney and Porter 2004, Munguía, Townsend Peterson et al. 2008, Soberón and Nakamura 2009, Barve, Barve et al. 2011). Biotic, or alpha, niches describe the collection of traits observable in a taxon's anatomy, behaviour, and life history which contribute to its role within an ecosystem (e.g. body mass and diet) (Cirtwill, Stouffer et al. 2015, Saban, Qu et al. 2023). Abiotic and biotic niches inform species' distributions in geographical space, as well as taxon origination and extinction (Pearman, Guisan et al. 2008, Rabosky and Hurlbert 2015, Chiarenza, Mannion et al. 2019, Raia, Mondanaro et al. 2020, Barreto, Lim et al. 2023), and so are invaluable for analysing historical biogeography.

Crucially, niche analysis methodologies do not necessarily require fossil occurrence data to provide potential insight into the ecology of extinct Gondwanan therians. In this thesis, I model the abiotic niches of only extant taxa and use these to infer past dynamics. More specifically, abiotic niches are modelled by extracting climatic data associated with where a taxon occurs, and statistically comparing these data to climatic information extracted across an appropriate background or 'calibration region' - the null hypothesis being that the taxon could occur across the geographical extent of the calibration region, were it not for its abiotic tolerances limiting it to its observed range (Merow, Smith et al. 2013). This methodology is called 'ecological niche modelling' (Peterson 2001). The validity of a modelled abiotic niche is thus affected by the extent to which the taxon's occurrence localities reflect the totality of its abiotic tolerances, and

whether the chosen calibration region reflects the implicit null hypothesis. Fossil occurrence localities and reconstructed palaeoclimatic conditions can be used to assess a clade's abiotic niche across deep time (Myers, Stigall et al. 2015, Chiarenza, Mannion et al. 2019), yet this methodology is built around a great number of assumptions. Niches derived from a limited fossil record risk being excessively extrapolative, while the geographical restriction of extinct occurrences to outcrop localities limits sample size and makes it difficult to deduce where the taxon was truly absent, let alone where the boundaries of a reasonable calibration region would extend across continents across deep time (given that this thesis's research questions concern the prediction of dispersal, it is somewhat circular to use, in our modelling, calibration regions themselves estimated from our taxa's expected ability to disperse). Reconstructing palaeoclimatic conditions also comes with limitations, with significant uncertainties in the value of and interactions between environmental variables over extended timeframes (Braconnot, Harrison et al. 2012, Huntley 2012). These uncertainties are often minimally recorded in existing publications (Jonkers, Cartapanis et al. 2020).

Many of these issues affect the quantification of ecological niches of living taxa to a lesser degree (though any consideration of abiotic environments across deep time involves the limitations and uncertainties of palaeoclimatic reconstructions). Thus, I have chosen in this thesis to use present-day abiotic niches to represent the tolerances of Gondwanan clades across the Palaeogene, an approach which assumes that clades have conserved their abiotic niches from the Cretaceous-Palaeogene boundary to the present day (Cooper, Jetz et al. 2010). This approach most closely follows Saupe, Farnsworth et al. (2019), who used the climatic tolerances of living tropical birds to estimate the latitudinal distribution of abiotically suitable regions for these clades across deep time.

In contrast to my approach with abiotic niches, I consider the biotic niches of both extinct and extant taxa, as even a single fragmentary fossil can often allow for assessment of some biotic

traits, such as approximate body mass and diet. However, using the quantified attributes of a small sample of fossils to represent a biotic niche may risk misrepresenting the true variation within the taxon. Binning biotic traits (e.g. classifying body masses and diets into weight classes and dietary categories respectively) and adjusting how biotic niches are represented in analyses may partially account for such uncertainty.

In Chapter 2, I model suitable abiotic regions for extant therian clades across Antarctica during the Palaeogene, to test hypotheses of dispersal between South America and Australia. The aforementioned potential presence of Australian fossil taxa in South America, and vice versa, implies complex therian dispersal across Palaeogene Gondwana, prior to the final break-up of the supercontinent. I tested two hypotheses: (i) that modern therian biogeography was established by a single dispersal of ancestral eomarsupials from South America to Australia (Nilsson, Churakov et al. 2010, Goin, Woodburne et al. 2016, Beck 2017, Reguero and Goin 2021), or (ii) that modern therian biogeography was established by a more complex dispersal scenario involving multiple groups (Archer, Arena et al. 1999, Beck, Godthelp et al. 2008, Beck 2012, Eldridge, Beck et al. 2019). I modelled the abiotic niches of extant family-level groups within Marsupialia and Xenarthra, the two extant therian clades which may have also been present in Gondwana since the Palaeocene Epoch, and projected said niches onto palaeoclimate reconstructions, to quantify the area of abiotically suitable regions in Antarctica during six different Palaeogene ages. These suitable regions may correspond to clades' predicted distribution, assuming equivalent niche filling to the present day. My results support a complex therian dispersal scenario during the Danian [66-61.6 Ma] at the beginning of the Palaeocene. Abiotically suitable regions, however, still existed in Antarctica for many potentially dispersing marsupial clades after Gondwanan breakup. Many clades with traits suited for polar regions also see a distinctive 'corridor' of abiotic suitability along the Antarctic Pacific coast during the Palaeogene - a potential dispersal route, potentially complemented by oceanic dispersal via the Ross Sea oceanic gyre (Kennedy, Farnsworth et al. 2015, Zhang, Huck et al. 2020). Statistical

comparisons between the spatial distribution of abiotically suitable regions and known fossil localities, however, suggest limited niche conservatism in both Marsupialia and Xenarthra, undermining a key assumption of this approach – but this assessment in turn is built around its own set of assumptions.

Biotic, rather than abiotic, niches are explored in Chapter 3, for metatherians and eutherians in South America, Antarctica, and Australia. I classify every described Palaeogene and extant Gondwanan terrestrial therian genus by weight class and dietary category, bin them into one of five discrete time intervals, and compare the time intervals using two dissimilarity metrics - thereby adapting the methodology of Cribb et al. (2023) to measure biotic niche change across the Palaeogene and present day. I find that the collective biotic niches of both Gondwanan metatherians and eutherians changed significantly between time intervals, often aligning with global-scale mammal evolutionary trajectories in spite of the continents' 'Splendid Isolation' (Raia, Carotenuto et al. 2012, Lovegrove and Mowoe 2013, Saarinen 2019, Huang, Saarinen et al. 2022), which again suggests a lack of niche conservatism. An exception is Antarctica, which showed little turnover across the Eocene in terms of therian genera or represented biotic niches (though the sample size of Antarctic genera is extremely limited). My analyses also tentatively suggest that geologically older South American metatherians had more similar biotic niches to extant American marsupials, which may inform both groups' capacity for inter-continental dispersal (Beck 2017, Walsh and Tucker 2018, Wait and Ahlers 2020, Reguero and Goin 2021). However, this observation is only seen in one of the two dissimilarity metrics, and its validity is questionable.

My abiotic and biotic niche analyses largely consider therian clades as independent ecological entities, yet biogeographical patterns are also informed by interactions with other organisms (Alexander, Diez et al. 2015, Cazelles, Mouquet et al. 2016, Thuiller, Calderón-Sanou et al. 2024). As a case study of these dynamics, Chapter 4 concentrates on the interactions between the

marsupial clade Microbiotheria and associated plant species. *Dromiciops,* the only living microbiothere genus, lives in 'Valdivian' temperate rainforest (Hershkovitz 1999) and maintains ecological relationships with multiple species of plant, possibly the result of respective co-evolution (Rageot 1979, Amico and Aizen 2000, Cortés, Franco et al. 2011, Fontúrbel, Franco et al. 2022). The Palaeogene microbiothere fossil record includes remains from South America, Antarctica, and possibly Australia (Marshall 1982, Marshall and DeMuizon 1988, Archer, Arena et al. 1999, Eldridge, Beck et al. 2019, Gelfo, Goin et al. 2019), which were at the time largely covered by polar forests markedly similar to *Dromiciops* habitat (Reguero, Marenssi et al. 2002, Francis, Ashworth et al. 2008, Bowman, Francis et al. 2014, Macphail, Carpenter et al. 2022, Thompson, Salzmann et al. 2022). Thus, it has been suggested that microbiothere-plant interactions have existed since the Palaeogene, and may have influenced trans-Antarctic dispersal. To test this, I adapt the methodologies used in Chapter 2 to measure the area of abiotically suitable regions in Palaeogene Antarctica for microbiotheres and Valdivian plants, and then compared the spatial overlap between these areas as a proxy for the strength of the ecological relationship. My findings imply that, whilst microbiotheres and Valdivian plants have similar abiotic niches, their ecological association during the Palaeogene was not as strong as it appears to be in the present day. Perhaps most significantly, the relationship between microbiotheres and Gondwanan mistletoes (for which *Dromiciops* presently acts as a key seed disperser) does not appear to have co-evolved across deep time (Watson 2020, Fontúrbel, Franco et al. 2022)**,** but instead may be an example of 'ecological fitting'—two taxa with coincidentally corresponding ecological roles encountering one another by chance and subsequently establishing an ecological relationship (Janzen 1985).

My three thesis data chapters cover three important aspects of biogeographical consideration – abiotic tolerances, biotic traits and ecological interactions – all while demonstrating examples of analytical pipelines with wider applicability in palaeontology and beyond, as well as providing extensive resources for future research. Even beyond the uncertainties of the fossil record,

Gondwanan mammal biogeography remains a complex topic, and my results consistently support more complicated hypotheses of dispersal, niche change, and biotic interaction. New fossil discoveries in South America, Australia, and Antarctica, along with updated taxonomic descriptions of existing fossil material, will help to elucidate these evolutionary and ecological narratives, and likely demonstrate further the capacity of mammals to rapidly adapt in former Gondwanan continents and beyond.

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Chapter 2 – On the absence of armadillos in Australia: Ecological niche modelling of mammalian dispersal across Palaeogene Gondwana

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ABSTRACT

Two extant mammalian clades, marsupials and xenarthrans (sloths, armadillos, and anteaters), evolved as endemic Gondwanan groups in the Palaeogene [66-23.03 Ma], a period during which South America, Antarctica, and Australia formed a single supercontinent. The present distributions of these groups suggest a straightforward biogeographical narrative of trans-Antarctic mammal dispersal – that is, basal members of the Australian marsupial clade Eomarsupialia underwent a single 'dispersal' from South America to Australia through Antarctica, while xenarthrans and other placentals, such as the South American Native Ungulates (SANUs), remained restricted to South America. However, fossil evidence suggests that other groups of American marsupials may have also dispersed between South America and Australia. The multiple possible dispersal events for marsupials, but not of contemporaneous South American placentals, raises the question of whether there were abiotic barriers to dispersal for some groups but not others. Here we use ecological niche modelling to test two hypotheses of differential dispersal opportunity for extant marsupial and xenarthran family-level groups. We project estimates of climatic tolerances for multiple clades onto reconstructed Palaeogene climatic landscapes. We then test whether clades hypothesised to have dispersed via Antarctica had significantly more suitable and contiguous areas in the Palaeogene of Antarctica than hypothesised non-dispersers. Our results indicate that, while eomarsupials had significantly greater areas of suitable conditions than other groups [$p < 0.025$] during the Early Oligocene Rupelian Age [33.9-27.82 Ma], Eomarsupialia + Microbiotheriidae + Caenolestidae (all marsupial

groups with fossil evidence for trans-Antarctic dispersal) had significantly greater areas of suitable conditions compared to Didelphidae and xenarthrans [$p < 0.025$] in the earliest Paleocene Danian Age [66-61.6 Ma], Rupelian, and latest Oligocene Chattian Age [27.82-23.03 Ma]. There were no significant differences in suitable area during late Palaeocene or Eocene Ages. We therefore tentatively support a more complex biogeographical narrative of marsupial dispersal from South America to Australia, with the poor contiguity between projected areas of suitable climatic conditions in Palaeogene Antarctica suggesting that oceanic dispersal may have supplemented terrestrial routes. We further compare our niche projections to the spatial distribution of Palaeogene fossil occurrences to assess whether this approach, which assumes abiotic niche conservatism, is accurately representing the deep evolutionary history of extant mammalian clades. Finally, we resolve the ecological characteristics of the individual clades whose projections show a distinctive 'corridor' pattern of suitable climatic conditions in Palaeogene Antarctica to elucidate those traits that may have conferred the ability to undertake a trans-Antarctic dispersal.

INTRODUCTION

The mammalian clade Theria consists of two crown groups – marsupials and placentals. Marsupials are generally divided into Eomarsupialia and an American marsupial grade. Eomarsupialia is a group consisting of all marsupial taxa endemic to Australia, New Guinea, and Indonesia, including kangaroos, koalas, and Tasmanian devils (Wilson and Reeder 2005) (***Figure 2.1***). The grade leading to Eomarsupialia presently consists of Didelphidae (opossums), Caenolestidae (shrew opossums), and Microbiotheriidae (*monito del monte*); these families are today found in South America (barring some intrusions into North America), with Didelphidae and Caenolestidae sometimes paraphyletically grouped as 'Ameridelphia' (***Figure 2.1***) (Nilsson, Churakov et al. 2010, Gallus, Janke et al. 2015, Duchêne, Bragg et al. 2018). Many extant placental groups are also associated with the South American continent, including Xenarthra, which consists of the families Bradypodidae and Choloepodidae (sloths), Chlamyphoridae and

Dasypodidae (armadillos), and Cyclopedidae and Myrmecophagidae (anteaters) (Gaudin and Croft 2015) (***Figure 2.1***). Endemic 'ungulate' clades also inhabited South America through much of the Cenozoic (the South American Native Ungulates, or SANUs) (Croft, Gelfo et al. 2020), but these placentals are now extinct and thus are not further considered here.

Both Marsupialia and Xenarthra are thought to have first evolved and proliferated in South America, during the Late Cretaceous [100.5-66 Ma] or Palaeogene Periods [66-23.03 Ma] (Gaudin and Croft 2015, Beck 2017, Eldridge, Beck et al. 2019, Beck, Voss et al. 2022, Foley, Mason et al. 2023). Throughout much of this interval, South America was connected to Australia via Antarctica, as the last of the Gondwanan continents to separate. Previous hypotheses have suggested that present-day marsupial biogeographical patterns originated from basal members of Eomarsupialia undergoing a single 'dispersal' event from South America to Australia through Antarctica, prior to the final break-up of the Gondwanan supercontinent at some point in the Palaeogene (Nilsson, Churakov et al. 2010, Goin, Woodburne et al. 2016, Beck 2017, Reguero and Goin 2021). The latest this hypothetical event could have occurred is constrained by the full opening and deepening of the Tasmanian Seaway and possibly the Drake Passage, which may have occurred around the Priabonian-Rupelian boundary ~33.9 Ma (Sijp and England 2004, Scher, Whittaker et al. 2015, Beck 2017, Hodel, Grespan et al. 2021, Lauretano, Kennedy-Asser et al. 2021, Huang, Steel et al. 2022). Reguero et al. (2014, 2021) have proposed that a hypothetical shallow seaway dividing South America and Antarctica may have even restricted trans-Antarctic dispersal as early as the late Palaeocene [~55 Ma].

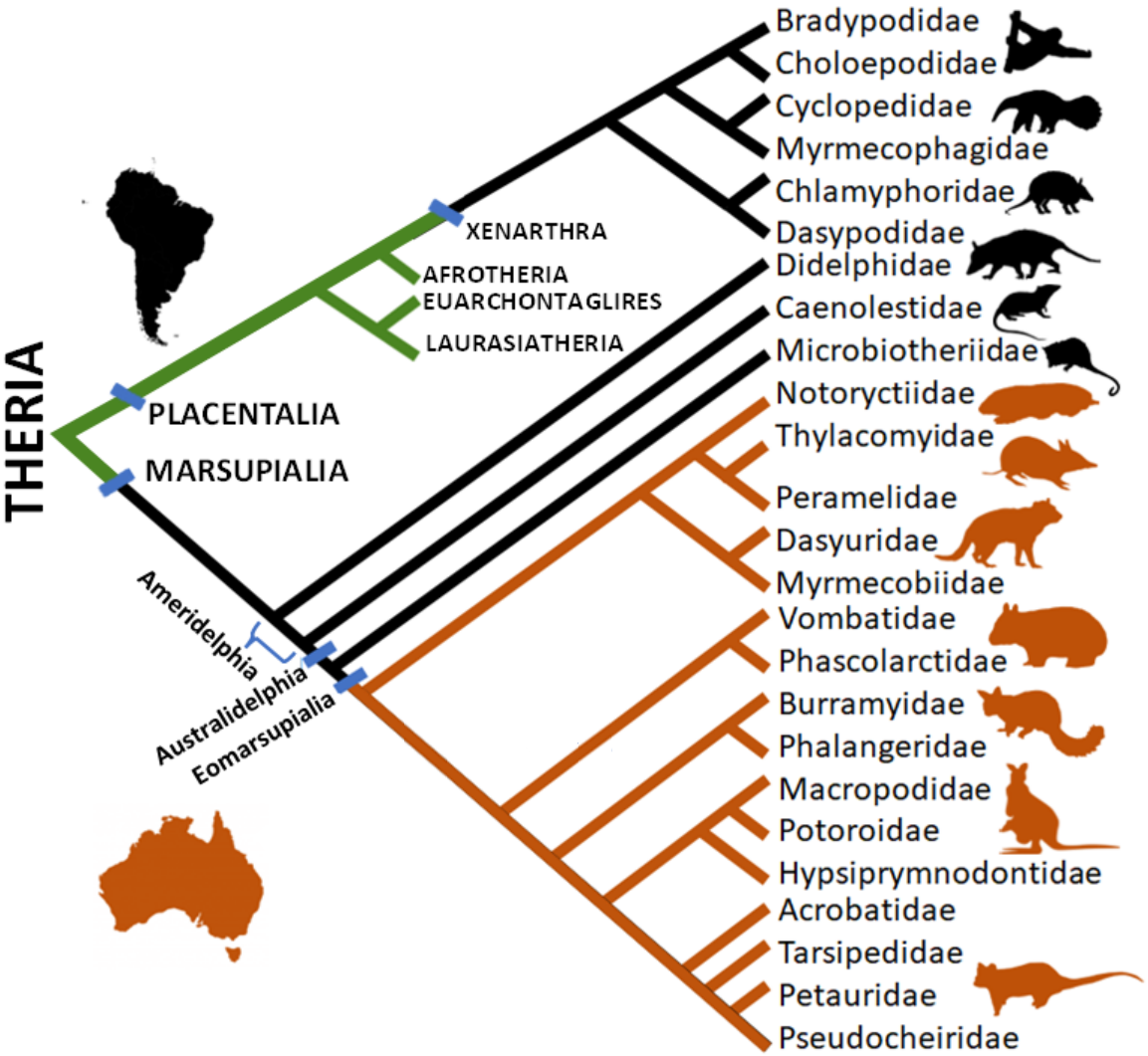

Figure 2.1. The relationships among Theria, emphasising the extant taxonomic families of Xenarthra and Marsupialia (Gaudin and Croft 2015, Duchêne, Bragg et al. 2018, Eldridge, Beck et al. 2019, Foley, Mason et al. 2023). Australian taxa are coloured in orange, South American taxa are in black, and those from elsewhere are in green. Caenolestidae, Microbiotheriidae and Notoryctiidae silhouettes by Sarah Werning on Phylopic (CC 3.0 Unported).

Despite this enticingly simple 'single dispersal' narrative, fossil evidence suggests modern marsupial biogeography emerged from a more complex series of trans-Antarctic dispersal events. However, the spatio-temporal patchiness, uneven sampling, and taxonomic uncertainty of the mammal fossil record across former Gondwanan continents limits the extent to which biogeographical hypotheses can be assessed robustly (Szalay 1994, Nilsson, Churakov et al. 2010,

Gaudin and Croft 2015, Goin, Woodburne et al. 2016, Bennett, Upchurch et al. 2018, Beck, Voss et al. 2022). Moreover, it is not clear if these palaeontological observations are the result of trans-Antarctic dispersal at all, or rather one pan-Gondwanan assemblage of therian taxa found across South America, Antarctica, and Australia (Beck 2017), although the Palaeogene restriction of Xenarthra and SANUs to South America (along with the very north of the Antarctic Peninsula), in spite of the clades' diversity and adaptability, is considered strong evidence for the former scenario (Gaudin and Croft 2015). Thus far, *Chulpasia* is the only example of a therian genus with attributed Palaeogene fossils from both South America and Australia (Crochet and Sigé 1993, Sigé, Archer et al. 2009). However, being only known from isolated molars, its position within Marsupialia, let alone the validity of its apparent pan-Gondwanan distribution, may be dubious (Goin, Woodburne et al. 2016, Sansom, Wills et al. 2017, Beck, Voss et al. 2022).

Dispersal from South America to Australia would have presumably required the presence of suitable environmental conditions in Antarctica during the Palaeogene. Therefore, we hypothesize that groups thought to have dispersed between continents during this time would have had more suitable abiotic conditions in Antarctica than groups considered to be non-dispersers. Here, we use ecological niche modelling to test two hypotheses of therian dispersal across Gondwana during the Palaeogene.

(1) The 'eomarsupial' hypothesis. Eomarsupialia, which includes all extant marsupial clades from Australia, was the only group to disperse from South America to Australia during the Palaeogene (Nilsson, Churakov et al. 2010, Reguero and Goin 2021). Under this framework, larger areas of abiotic suitability may be found for eomarsupial taxa in Palaeogene Antarctica compared to taxa outside Eomarsupialia, including Xenarthra and the three marsupial families currently restricted to South and North America. Areas of suitable abiotic conditions for taxa within Eomarsupialia should be more spatially contiguous than for taxa within other groups, to facilitate easier trans-Antarctic dispersal. This 'eomarsupial' hypothesis is the most parsimonious explanation for

modern biogeographical patterns and is additionally supported by fossil evidence of Eomarsupialia in both Australia and South America dating to the Palaeogene (Lorente, Chornogubsky et al. 2016, Zimicz and Goin 2020).

(2) The 'Australidelphian+' hypothesis. We also test the hypothesis that, in addition to Eomarsupialia, taxa from the total clades of Microbiotheriidae and Caenolestidae (Microbiotheria and Paucituberculata) (***Figures 1.2 and 2.1***) dispersed from South America to Australia during the Palaeogene. Under this 'Australidelphian+' hypothesis, we expect taxa within Eomarsupialia, Microbiotheriidae, and Caenolestidae to have larger areas of abiotic suitability within Palaeogene Antarctica than taxa outside these groups, specifically Xenarthra and Didelphidae. Areas of suitable abiotic conditions for taxa within Eomarsupialia, Microbiotheriidae, and Caenolestidae should also be more spatially contiguous than those for taxa within other groups, to facilitate easier trans-Antarctic dispersal. This hypothesis is based on possible Palaeogene fossil evidence of microbiotheres and paucituberculates in Australia (Archer, Arena et al. 1999, Beck 2012, Eldridge, Beck et al. 2019). Furthermore, the extinct Ypresian [56-47.8 Ma] Australian marsupial *Djarthia murgonensis* has been phylogenetically diagnosed as a basal-most member of the clade Australidelphia, which includes Eomarsupialia and Microbiotheria (***Figure 1.2 and 2.1***), leading in the hypothesis that Australidelphia evolved in Australia and the microbiotheres would have had to undertake a 'back-migration' from Australia to South America (Godthelp, Wroe et al. 1999, Beck, Godthelp et al. 2008). That said, based on these diagnoses, it is also possible that paucituberculates, microbiotheres and basal australidelphians like *Djarthia* all evolved in South America before independently dispersing to Australia. The only American marsupial clade to presently have no evidence of reaching Australia is the didelphid total clade Didelphimorphia (Castro, Dahur et al. 2021, Voss and Jansa 2021), suggesting all other extant marsupial groups could have dispersed across Antarctica from South America.

To test these hypotheses, we model suitable abiotic conditions across Palaeogene Gondwana for 34 marsupial and xenarthran family-level clades. Estimates of present-day abiotic tolerances were constructed for each clade using two calibration regions (a biogeographically informed continental region, and a 200 km radius around clade occurrences). These models were then projected onto palaeoclimate reconstructions for the Palaeogene (the Danian [66-61.6Ma] through Chattian [27.82-23.03 Ma] Ages). We quantified the extent and contiguity of projected suitable conditions available for these groups at six past time intervals in Palaeogene Antarctica and statistically compared suitable area among the monophyletic clades based on our two hypotheses.

It is important to note that this approach assumes that the abiotic niches across these groups have been conserved over the last 66 million years (Cooper, Jetz et al. 2010). Abiotic niche conservatism has been observed in many clades across long time scales (DeSantis, Beavins Tracy et al. 2012, Rodrigues, Villalobos et al. 2019, Saupe, Farnsworth et al. 2019, da Silva, Aires et al. 2020) and is supported in tropical specialist mammals (Cooper, Freckleton et al. 2011), a description matching many marsupial and xenarthran taxa. Ontogenetic constraints on the morphological evolution of marsupials may lead to slower rates of change in climatic tolerance and niche evolution (Sears 2004, Fabre, Dowling et al. 2021), while many ancestral marsupial nodes show a conserved habitat of closed wet environments (Mitchell, Pratt et al. 2014). Conversely, other work has proposed that family-level groups rarely maintain consistent abiotic tolerances over such a great timeframe (Peterson, Soberón et al. 1999), and in primates and carnivorans, reasonable estimates of clade geographical distribution cannot be derived from extant taxa alone (in the case of the former, especially before the Priabonian-Rupelian boundary) (Wisniewski, Lloyd et al. 2022, Faurby, Silvestro et al. 2024). The divergence of abiotic niches, at least between family-level groups, has also been identified as a driving force of mammalian evolution (Castro-Insua, Gómez-Rodríguez et al. 2018). Although we do not directly assess niche conservatism in this study, we additionally test whether geographical positions of fossil

occurrences for the modelled clades are predicted as suitable by the niche models projected onto Palaeogene palaeoclimate reconstructions (Saupe, Farnsworth et al. 2019).

In summary, our analyses provide the first indication of whether the modern distribution of Gondwanan mammal clades can be explained by differential dispersal opportunities early in the Cenozoic Era.

METHODS

Occurrence data

We chose to here focus on Marsupialia and Xenarthra, as these two clades make for ideal comparison – despite the fact that both have diversified in South America from the early Palaeogene to the present day, only the former seems to have reached Australia. Present-day marsupial and xenarthran occurrence data were derived from the Global Biodiversity Information Facility (GBIF) [www.gbif.org; see Supplementary Information X]. Most American marsupial records were downloaded on 27 June 2021, while those for *Hyladelphys*, *Cryptonanus*, and *Tlacuatzin* were downloaded on 11 May 2022, those for *Caenolestes*, *Chironectes*, and *Lutreolina* on 8 July 2022 and those for *Gracilinanus* on 10 July 2022. Most Australian marsupial records (sourced from Australia, New Guinea, and Indonesia) were downloaded on 17 and 18 September 2021, while those for *Macropus, Notamacropus*, and *Osphranter* were downloaded on 1 July 2022. Xenarthran records were downloaded on the 5 December 2022. The opossum *Chacodelphys* and the bandicoot *Rhynchomeles* did not have GBIF occurrence coordinates and were therefore excluded from analysis.

Downloaded occurrence data were cleaned using the CoordinateCleaner v.3.5 R package (Zizka, Silvestro et al. 2019), which removed potentially erroneous records outside species-level IUCN range polygons [https://www.iucnredlist.org/resources/spatial-data-download]. GBIF taxonomy was checked manually to assess congruence with IUCN taxonomy. After cleaning, we aggregated remaining occurrences into extant datasets for marsupial and xenarthran families. We used

families as our taxonomic unit, following previous work (Saupe, Farnsworth et al. 2019), because this rank allows for comparison with deep time fossil taxa; many mammals at the species rank survive for less than 5 million years (Prothero 2014), while the pygmy possum *Burramys* is the only mammalian genus considered here to have persisted from the Palaeogene to the present day (Archer, Bates et al. 2019). Taxonomic families, however, can vary considerably in the number of taxa they contain (Ereshefsky 1997, Bertrand, Pleijel et al. 2006, Laurin 2010), potentially confounding comparisons of ecological niches. For instance, one family may be estimated to have a broader climatic tolerance than another family simply due to the number of taxa included, which could impact our inferences of ecological niche differences among groups. We therefore subdivided larger families into 'family-level groups', to maintain similar clade sizes across our analyses. These exceptionally large families were identified as those exceeding the upper quartile fence in generic count, and consisted of Dasyuridae (most Australian marsupial carnivores), Didelphidae, and Macropodidae (kangaroos and wallabies). Family size was quantified using genera rather than species (Beck, Voss et al. 2022), because genera are more taxonomically consistent across the literature (Supplementary Information 2.3). These three large families were split into smaller monophyletic groups using published phylogenies (Phillips, Haouchar et al. 2013, Amador and Giannini 2016, Gibb, Condamine et al. 2016, Kealy and Beck 2017, Celik, Cascini et al. 2019) (Supplementary Information 2.4, Table A1). This subdivision separated the opossum genus *Hyladelphys* and the hare-wallaby genus *Lagostrophus* into their own family-level groups; we ultimately excluded these clades, because they were represented by only four occurrences each. We additionally removed the nine-banded armadillo *Dasypus novemcinctus* and the Virginia opossum *Didelphis virginiana* from the family-level grouping for Dasypodidae (long-nosed armadillos) and Didelphini (large American opossums), respectively. These taxa have shown recent range expansions, and their distributions are likely impacted by human presence (McBee and Baker 1982, Taulman and Robbins 1996, Feng and Papeş 2015, Walsh and Tucker 2018, Wait and Ahlers 2020). Their exclusion thus reduces the effect of recent

human activity on our results, and is an approach seen in previous work concerning Gondwanan mammal biogeography (Martin, Brand et al. 2022).

To further interrogate the impact of family size on our modelled results, we quantified the number of genera in each marsupial and xenarthran family-level group to assess whether generic number correlated with the extent of projected suitable conditions in Antarctica for these groups in the Palaeogene. Models with a biogeographically informed calibration region (see 'Background data' below) saw no linear correlation (adjusted R squared = -0.035 – 0.084, $p>0.05$) between the number of genera in a family-level group and the Antarctic area of suitable conditions in any Palaeogene time interval studied, suggesting success in controlling for this potential confounding factor. Models with a 200 km calibration region (see 'Background data' below), however, did show a correlation in all Palaeogene time intervals (adjusted R squared = 0.30 - 0.49, $p<0.05$), except for the Rupelian (adjusted R squared = -0.04 – 0.08, $p>0.05$). We therefore primarily focus on the models built using the biogeographically informed calibration region.

We modelled marsupial and xenarthran climatic tolerances using 34 family-level groups (Supplementary Information 2.4). For each of the family-level datasets, we filtered occurrence data to include only one unique occurrence at 5-minute resolution, which matched the resolution of our modern climate data (see below). Spatial filtering has been shown to improve ecological niche model performance and combat spatial sampling biases (Boria, Olson et al. 2014). We also filtered each dataset climatically, such that only climatically unique occurrences were retained, which can improve model performance (Varela, Anderson et al. 2014, Castellanos, Huntley et al. 2019). The families Microbiotheriidae and Myrmecobiidae (numbats) were only filtered climatically, as these datasets had limited occurrence data sourced over extremely small spatial areas (Varela, Anderson et al. 2014).

Using the filtered occurrence data, we derived 'training' and 'testing' datasets for each taxon using the 'split-sample validation' method, which randomly splits the occurrence data by a ratio

of 4:1. Split-sample validation is a common approach and performs well when using limited climatic variables (Santini, Benítez-López et al. 2021).

Background data

We used MaxEnt (Phillips, Anderson et al. 2006) to estimate species' climatic tolerances, which performs well compared to other algorithms under a range of modelling scenarios (Merow, Smith et al. 2013, Qiao, Soberón et al. 2015). Maxent uses background environmental information from which to compare the environmental conditions at occurrence localities (Guillera-Arroita, Lahoz-Monfort et al. 2014, Sillero and Barbosa 2021). The null hypothesis is that occurrences should be equally probable across the background or 'calibration region', regardless of abiotic environmental conditions (Merow, Smith et al. 2013). Thus, the calibration region should reflect the physical range over which a taxon could disperse and establish populations, were it not for the limitations of its climatic tolerance (Barve, Barve et al. 2011, Saupe, Barve et al. 2012, Merow, Smith et al. 2013).

Estimating the appropriate extent of the calibration region is difficult (Barve, Barve et al. 2011). A small calibration region can increase the extent of model extrapolation when projecting the modelled niche onto different geographies or different time intervals (Saupe, Barve et al. 2012), while a large calibration region can lead to less informative models or artificially inflated evaluation metrics (Giovanelli, de Siqueira et al. 2010). We therefore tested two calibration regions for every study taxon. In the first approach, we used biogeographically informed continental regions. These continental regions were chosen based on physical barriers for dispersal, such as deep seaways and mountainous regions. For clades found only in South America, we used the South American continent (-85° to -30° longitude, -60° to 15° latitude); for clades found in both North and South America, we used the Americas (-170° to -30° longitude, -60° to 70° latitude); for Eomarsupialia, we used the region from Australia to Southeast Asia (70° to 165° longitude, -45° to 35° latitude) (Supplementary Information 2.1, figures A, B and C). For

the second approach, we buffered every filtered occurrence by a 200 km radius and used the union of these buffers as the calibration region, to reflect the possibility that extant taxon ranges strongly reflect the maximum physical range over which a taxon could disperse. We focus on results using the biogeographically informed approach, as the second approach may be an overly conservative and unrealistic estimate. Furthermore, fewer models met our quality criteria when using the 200 km buffers (Supplementary Information 2.6, Tables C1 to C4) - from this reduced selection of models, the disparity between the number of hypothetical dispersers *versus* non-dispersers also risks devalidating statistical comparison (see Results).

Climatic variables

We used four climatic parameters to characterise the tolerances of our therian clades: maximum temperature of the warmest month, minimum temperature of the coldest month, precipitation of the wettest month, and precipitation of the driest month. We chose these variables because the life histories and geographical ranges of many marsupial and xenarthran species are sensitive to temperature and rainfall extremes (Geiser and Broome 1993, Woinarski, Oakwood et al. 2008, Martin 2010, Davies, Gramotnev et al. 2013, Lada, Thomson et al. 2013, Hing, Narayan et al. 2014, Seitz, Carrara et al. 2017, Wagner, Baker et al. 2020). Present-day data were downloaded from WorldClim 2 (Fick and Hijmans 2017) at 5 minute spatial resolution. This resolution was chosen to reflect the compromise between including precise environmental data associated with occurrences, and said occurrences' inherent spatial error (Sillero and Barbosa 2021).

Palaeoclimate data for the six Palaeogene time intervals were derived from the newly-generated HadCM3L generalised circulation models (Kennedy, Farnsworth et al. 2015, Lunt, Farnsworth et al. 2016). We included time intervals pre- and post-dating the predicted timing of Gondwanan break-up, and therefore bracketing any potential trans-Antarctic dispersal events. The six intervals examined are: Danian (the early Palaeocene) [66-61.6 Ma], Selandian (the mid Palaeocene) [61.6-59.2 Ma], Ypresian (the early Eocene) [56-47.8 Ma], Priabonian (the late

Eocene) [37.71-33.9 Ma], Rupelian (the early Oligocene) [33.9-27.82 Ma], and Chattian (the late Oligocene) [27.82-23.03 Ma]. The Oligocene probably post-dates final Gondwana break-up (Sijp and England 2004, Scher, Whittaker et al. 2015, Beck 2017, Hodel, Grespan et al. 2021, Lauretano, Kennedy-Asser et al. 2021, Huang, Steel et al. 2022), but was included in our analyses because the fossil records for many extant marsupial family-level groups considered here begin during this epoch. The new palaeoclimate simulations are similar to the previous HadCM3L iterations used in palaeo-ecological niche modelling by Saupe, Farnsworth et al. (2019), but integrate updated CO_2 information, more accurate ocean circulation, a fully-equilibrated deep ocean system, and warmer, more realistic high latitude temperatures, among other changes (see Supplementary Information 2.2).

Collinearity of the climatic variables can lead to model over-fitting (Sillero and Barbosa 2021), which is especially problematic when projecting to different time periods or regions (Dormann, Elith et al. 2013, Feng, Park et al. 2019). To reduce collinearity, we calculated variance inflation factors (VIFs) for climate data in the calibration region for each clade using the *vifstep* function in the R package *usdm* (Naimi, Hamm et al. 2014). We eliminated predictors with a VIF > 10 (O'brien 2007, Montgomery, Peck et al. 2021), which removed maximum temperature of the warmest month and precipitation of the wettest month from two family-level groups: (*Dorcopsis, Dorcopsulus*; forest-wallabies) and (*Dasycercus*, *Dasykaluta*, *Dasyuroides*, *Myoictis*, *Parantechinus*; dibblers, kalutas, kowaris, mulgaras and striped dasyures) when using the 200 km radius calibration region.

Niche model calibration

We used the *kuenm* v.1.1.9 R package (Cobos, Peterson et al. 2019) to calibrate ecological niche models, which called MaxEnt v.3.4.4 (Phillips, Anderson et al. 2006). The *kuenm* package can be used to automate the process of niche model construction, analysis, and projection, including testing combinations of regularisation parameter and feature classes (Cobos, Peterson et al.

2019). Regularisation parameters control the strength of the overfitting penalty applied to the 'gain function', which is a maximum likelihood function that serves to differentiate occurrences from background locations (Dudik, Phillips et al. 2004, Merow, Smith et al. 2013). Feature classes are types of mathematical transformations used to represent the relationship between the values of climatic variables and predicted abiotic suitability (Merow, Smith et al. 2013). We used the *kuenm_cal* function to test every combination of 17 regularisation parameters (ranging from 0.1 to 10) and 5 feature classes (linear, quadratic, power, hinge, threshold) for both versions of our calibration region (Cobos, Peterson et al. 2019). Thus, we generated 1,054 ecological niche models for every clade using their 'training' occurrence datasets (527 for each of the two calibration regions), equating to 35,836 across all groups.

Model selection and quality assessment

We used the *kuenm_ceval* function with the 'testing' occurrence datasets to evaluate model performance (Cobos, Peterson et al. 2019). Model parameterisations were initially selected based on statistical significance (the proportion of a 1000 bootstrap replicates, built from a 50% sample of testing data, with an AUC ratio ≤1) and an omission rate equal to or below 5% (Anderson, Lew et al. 2003). From these initial models, we estimated model quality via AICc (Akaike information criteria corrected), which accounts for small sample sizes and overfitting (Hurvich and Tsai 1989, Cavanaugh 1997), and selected only those models with a delta AICc value ≤ 2 for further analysis (Cobos, Peterson et al. 2019). The only exception to this protocol were for models constructed for Acrobatidae (feather-tailed possums and gliders), Microbiotheriidae, and Peramelidae (bandicoots) using the 200 km calibration region; for these models, the 'power' feature class caused a reproducible but seemingly unresolvable error in MaxEnt. Consequently, the next best model was selected based on omission rate and AICc (Supplementary Information 2.4, Table A1). Furthermore, in seven groups (Supplementary Information 2.5), statistical evaluation of the niche models built from 200 km radius calibration regions failed: very low suitability at occurrence localities was rounded down to zero by RStudio, which interfered with niche calculations. In these

situations, the localities were identified, recorded, and removed from the dataset, with the 'training' and 'testing' datasets and calibration region being adjusted accordingly.

After initial model evaluation by *kuenm*, we further assessed the quality of the best model(s) identified for each clade using the true skill statistic (TSS) (Allouche, Tsoar et al. 2006), continuous Boyce index (CBI) (Hirzel, Le Lay et al. 2006), and Area Under Curve (AUC). Models with a TSS or CBI below 0.5 or an AUC below 0.7 were removed from analysis – these values are based on those used by previous literature (Pearce and Ferrier 2000, Coetzee, Robertson et al. 2009, Farrell, Wang et al. 2019), and represent a compromise between excluding models of poor quality and retaining an adequate number to reflect Gondwanan therian diversity (Supplementary Information 2.6, Tables C1 to C4).

Projecting niche models onto past climates

The final niche models were projected to the six Palaeogene time intervals using the *kuenm_mod* function (Cobos, Peterson et al. 2019). We allowed for extrapolation when encountering novel climatic conditions, but not 'clamping' (treating any novel climatic conditions as if they are the minimum or maximum limits of known climatic conditions) as this can lead to biologically improbable scenarios – such an approach also follows Saupe, Farnsworth et al. (2019). Since MaxEnt is a machine-learning algorithm (Phillips, Anderson et al. 2006), results can vary across model runs (Sillero and Barbosa 2021), and thus the median of 10 bootstrap replicates was used as the best estimate of suitable conditions for each of the final models in each time interval.

Novel climatic conditions may be encountered when projecting models to new regions or time periods, which can affect predictive power (Owens, Campbell et al. 2013, Qiao, Feng et al. 2019). We assessed the extent of extrapolation for each niche projection using the *ecospat* v.3.4 R package (Di Cola, Broennimann et al. 2017). Multivariate environmental suitability surfaces (MESS) were generated to indicate how climatically similar each grid cell in the palaeoclimate projection region is compared to the climatic conditions of the present-day calibration region.

Higher MESS values indicate greater climatic similarity, and negative values indicate a novel environment for which the model projection extrapolated (Elith, Kearney et al. 2010).

Thresholding niche models

The median model projections were converted from a continuous suitability scale of 0 to 1, to a binary suitability (predicted to be abiotically suitable or unsuitable). We derived abiotic suitability thresholds using two methods: 95% least training presence (LTP), which identifies the lowest abiotic suitability that accounts for 95% of the occurrence dataset, and maxSSS, the threshold that maximises the sum of model sensitivity (1 – omission rate) and specificity (1 – commission rate) (Allouche, Tsoar et al. 2006, Liu, White et al. 2013) – though MaxEnt, which only includes taxon presence data and thus cannot directly calculate specificity, uses the 'fractional area of suitability' as a proxy. The MESS values were superimposed over the thresholded suitability maps to help identify geographical areas with non-extrapolative suitable abiotic conditions (MESS values greater than 0).

To test the hypothesis that Palaeogene Antarctica had more suitable areas for clades that may have dispersed using this route, we calculated the extent of thresholded suitable area in Palaeogene Antarctica for each family-level group using the Lambert azimuthal equal-area projection with the *raster* v3.11 package (Hijmans, Van Etten et al. 2015). This projection is often employed for accurate measurements of spatial area in polar or near-polar regions. Using the spatial area of suitable conditions, we tested whether clades belonging to Eomarsupialia (the 'eomarsupial' hypothesis) or to Eomarsupialia + Microbiotheriidae + Caenolestidae (the 'Australidelphian+' hypothesis) had more suitable abiotic area in Palaeogene Antarctica than clades which do not belong to these groups. Non-parametric Mann Whitney U tests were used, as the data were not normally distributed. We focus on non-extrapolated areas of suitable conditions (Supplementary Information 2.8, Tables E1 and E2) but also tested if the inclusion of extrapolated areas affected our results (Supplementary Information 2.8, Tables E3 and E4).

We additionally assessed whether the clades hypothesised to have dispersed via Antarctica had more contiguous (*versus* fragmented) areas of suitability in Palaeogene Antarctica based on the two hypotheses. Thresholded areas were used to examine the continuity of suitable conditions with the *landscapemetrics* v.2.0 package (Hesselbarth, Sciaini et al. 2019) using the *lsm_l_contig_cv* function. This metric produces a contiguity index value, which increases with larger and more numerous connections between groups of suitable raster cells. Using these metrics, we ran Mann Whitney U analyses to test whether clades belonging to Eomarsupialia (the 'eomarsupial' hypothesis) or to Eomarsupialia + Microbiotheriidae + Caenolestidae (the 'Australidelphian+' hypothesis) had higher contiguity index values in Palaeogene Antarctica than clades which do not belong to these groups. We also tested the effect of including *versus* excluding extrapolated areas of suitable conditions (Supplementary Information 2.9, Tables F1, F2, F3 and F4).

Fossil record comparisons

To determine whether suitability patterns estimated for each clade and past time interval coincide with the known fossil record of these groups, we compared fossil distributional data to projected model outputs, for all Palaeogene time intervals excluding the poorly fossiliferous Selandian [61.6-59.2 Ma]. This analysis follows Saupe, Farnsworth et al. (2019) and provides an indirect indication of whether broad-scale, clade-level tolerances are conserved over millions of years.

Fossil datasets were derived from the Palaeobiology Database (PBDB) [https://paleobiodb.org/]. South American marsupial data were downloaded on 26th January 2022, fossil data for Antarctic and Australian marsupial clades were downloaded on 31st January 2022, and fossil data for xenarthran data were downloaded on 26th March 2023. These fossil occurrence data were augmented by other published records, largely marsupial faunal lists (Long 2002, Megirian, Murray et al. 2004, Archer, Arena et al. 2006, Metzger and Retallack 2010, Travouillon, Escarguel

et al. 2011, Bennett, Upchurch et al. 2018, Eldridge, Beck et al. 2019, Abello, Toledo et al. 2020) (Supplementary Information 2.3). We assigned fossil occurrences to the same family-level groups as those used for our present-day occurrences; stem group fossils were included with their corresponding crown groups to ensure an adequately sized dataset. Datasets were spatially filtered at a resolution of one occurrence every 15 minutes, matching the resolution of our Palaeogene climate data.

We rotated fossil occurrence data to their paleo-plate location using GPlates 2.3.0 (Müller, Cannon et al. 2018) with PaleoAtlas v.3 (Scotese 2016), which reflected the mid-point of the time interval. Localities with a PBDB temporal range greater than 20 million years, or with a PBDB temporal range that intersected two Palaeogene time bins, were excluded from further study; the ambiguity in dating these occurrences may invalidate analyses at the temporal resolution of geological age. There is considerable uncertainty in converting fossil occurrence localities into palaeo-coordinates (Buffan, Jones et al. 2023), and thus each occurrence was given a spatial buffer of 150 km following Saupe, Farnsworth et al. (2019).

We assessed whether, in the time intervals of their deposition, fossil localities spatially corresponded with their respective clades' projected abiotically suitable areas globally. We used one-tailed binomial tests to determine whether fossils corresponded to said areas at a frequency higher than expected based on random chance alone. Only the projected areas of abiotic suitability corroborated by all a clade's best-supported niche models were used in our comparisons. We tested the effect of including *versus* excluding extrapolated areas of suitable conditions on results (Supplementary Information 2.9, Tables F1 to F4).

One effect of us comparing the global extent of suitability with fossil localities is that we have analytically integrated suitable areas that are almost certainly geographically inaccessible to Gondwanan marsupials and xenarthrans during the Palaeogene. However, selecting specific 'accessible' regions to analyse would require a diagnosis of therian dispersal dynamics, which

itself is the desired outcome of this study. Our assessments of corroboration between clades' present-day abiotic tolerances and fossil distribution are also likely to be conservative on a global scale, in that non-Gondwanan areas can never be corroborated by fossil localities of Gondwanan taxa - any significant results found are thus especially notable.

All analyses were conducted in the R programming language v. 4.2.2.

RESULTS

Niche modelling

Of the 34 family-level groups, 30 from across Marsupialia and Xenarthra met our quality criteria using a biogeographically informed calibration region, whereas only 14 met the criteria when using a 200 km radius as the calibration region (Supplementary Information 2.6, Tables C1, C2, C3 and C4). For models constructed using a biogeographically informed calibration region, the 'eomarsupial' hypothesis involved comparing 19 hypothesised 'disperser' family-level groups and 11 hypothesised 'non-disperser' groups, while the 'Australidelphian+' hypothesis involved comparing 21 'disperser' groups and 9 'non-disperser' groups. For models constructed using a 200 km radius calibration region, the 'eomarsupial' hypothesis involved comparing 11 hypothesised 'disperser' groups and 2 hypothesised 'non-disperser' groups, and the 'Australidelphian+' hypothesis involved comparing 12 'disperser' groups and 1 'non-disperser' group. The number of occurrences per group, after filtering, ranged from 15 for Myrmecobiidae to 3,722 for Petauridae (petaurid possums) (Supplementary Information 2.4, Tables A1 and A2). We applied a Bonferroni correction to our statistical comparisons, halving the standard alpha level of 0.05 to 0.025 given the two hypotheses being tested.

For models with a biogeographically informed calibration region, we found support for the 'eomarsupial' hypothesis only in the Rupelian, regardless of threshold method [$p<0.025$] (***Table 2.1***) (Supplementary Information 2.7). Support for the 'Australidelphian+' hypothesis is found for the Danian, Rupelian and Chattian [$p<0.025$] (***Table 2.1***), but only when using the maxSSS

threshold (Supplementary Information 2.7). When suitable, extrapolated area is included, support for the 'Australidelphian+' hypothesis is also found in the Rupelian regardless of threshold method, with the 'eomarsupial' hypothesis supported in the Rupelian if niche projections are thresholded using the 95% LTP [$p<0.025$] (Supplementary Information 2.7). The family-level group Acrobatidae had consistently higher Antarctic areas of suitable and non-extrapolative conditions than all other groups (maxSSS-thresholded average across all time intervals 1704901 ± 1533468 km^2 vs 115601 ± 228407 km^2) (***Figures 2.2 and 2.3***) – given that Mann Whitney U tests are rank-based, the magnitude of difference does not inherently devalidate our results (Nachar 2008). Under the same criteria, five more groups have an average area above 200000 km^2 across all time intervals – Burramyidae (pygmy possums), Phascogalini (marsupial mice), Pseudocheiridae (pseudocheirid possums), Vombatidae (wombats) and (*Dendrolagus, Petrogale, Thylogale)* (pademelons, rock-wallabies and tree kangaroos).

No significant results exist for models with a 200 km radius calibration region (Supplementary Information 2.7).

Projected time interval	*'Eomarsupial' hypothesis*				*'Australidelphian+' hypothesis*			
	Hypothesised disperser suitable extent (km^2)	**Hypothesised non-dispersers suitable extent (km^2)**	**W value**	**Statistical significance**	**Hypothesised disperser suitable extent (km^2)**	**Hypothesised non-dispersers suitable extent (km^2)**	**W value**	**Statistical significance**
Danian [66-61.6 Ma]	78111 ± 159044	31878 ± 61244	129.5	0.14	83180 ± 153428	9778 ± 19254	137.5	**0.023**
Selandian [61.6-59.2 Ma]	132208 ± 203074	52483 ± 78473	124	0.20	134982 ± 195143	28294 ± 43068	127	0.067
Ypresian [56-47.8 Ma]	277413 ± 272887	139082 ± 180863	129	0.14	281801 ± 262343	98106 ± 162703	128.5	0.063
Priabonian [37.71-33.9 Ma]	230066 ± 277037	79233 ±118191	130	0.14	221457 ± 266530	65801 ± 115255	126	0.076
Rupelian [33.9-27.82 Ma]	338486 ± 775826	8121 ± 18971	146.5	**0.013**	307760 ± 742400	6400 ± 19199	136	**0.012**
Chattian [27.82-23.03 Ma]	358711 ± 982122	3662 ± 10737	147	0.027	326294 ± 937347	401 ± 1075	144	**0.0089**

Table 2.1. The mean ± SD of Antarctic area of suitable and non-extrapolative conditions (km^2) for predicted dispersers vs. non-dispersers, for models built using a biogeographically informed calibration region and thresholded with maxSSS. The W value and statistical significance, as calculated via a Mann Whitney U test with Bonferroni correction, are also given. Significant results are in bold. Results for models built from a 200 km radius calibration region and/or with a 95% LTP threshold, as well as those which include extrapolated areas of suitable conditions, can be found in Supplementary Information 2.7.

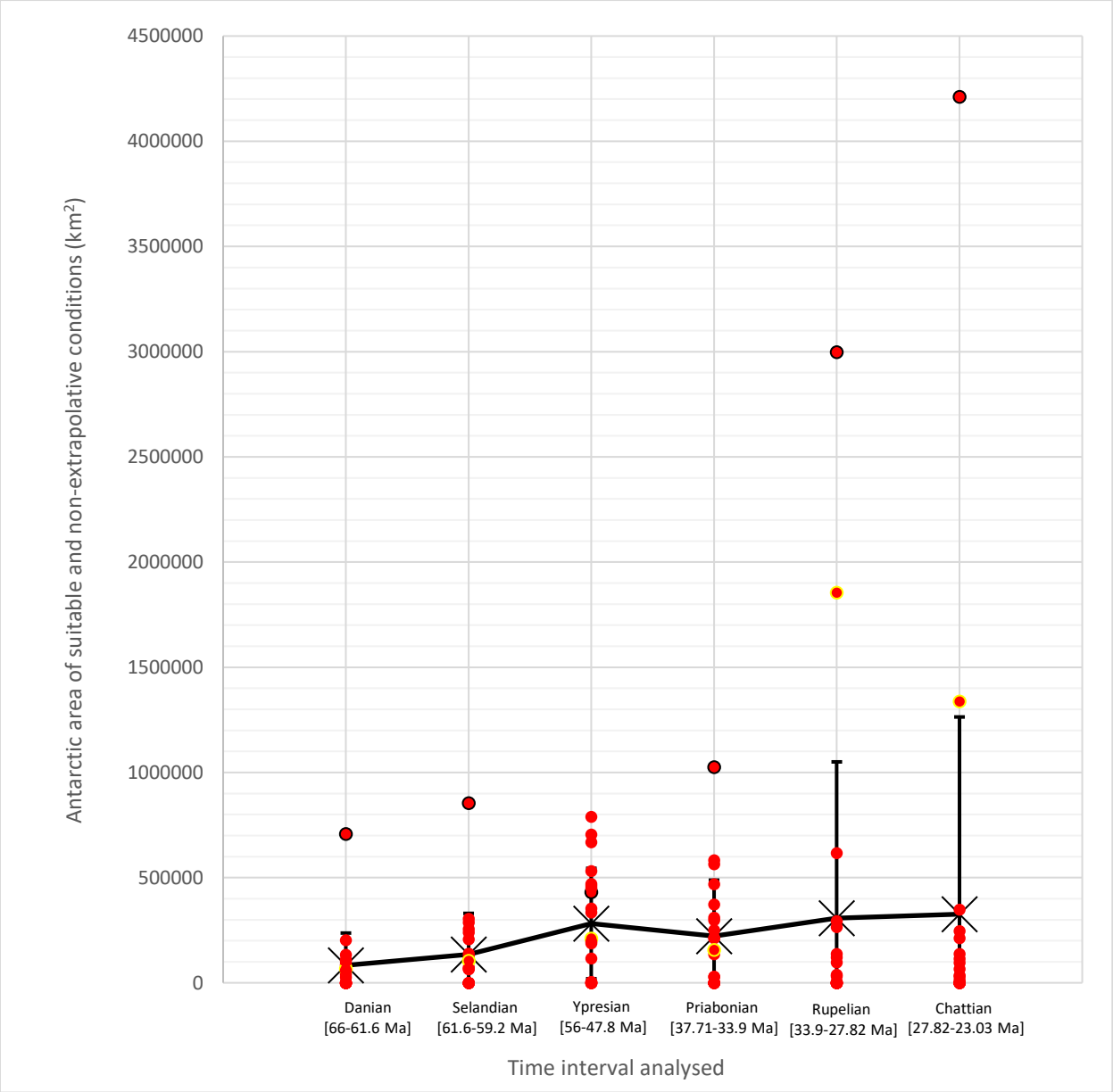

Figure 2.2. Antarctic areas of suitable and non-extrapolative conditions (km^2) for predicted dispersers as predicted by the 'Australidelphian+' hypothesis, for models built using a biogeographically informed calibration region and thresholded with maxSSS. The mean and SD are shown by a X with error bars. The family-level groups Acrobatidae and (*Dendrolagus, Petrogale, Thylogale)* (pademelons, rock-wallabies and tree kangaroos) have notably high areas and are thus highlighted in black and yellow respectively.

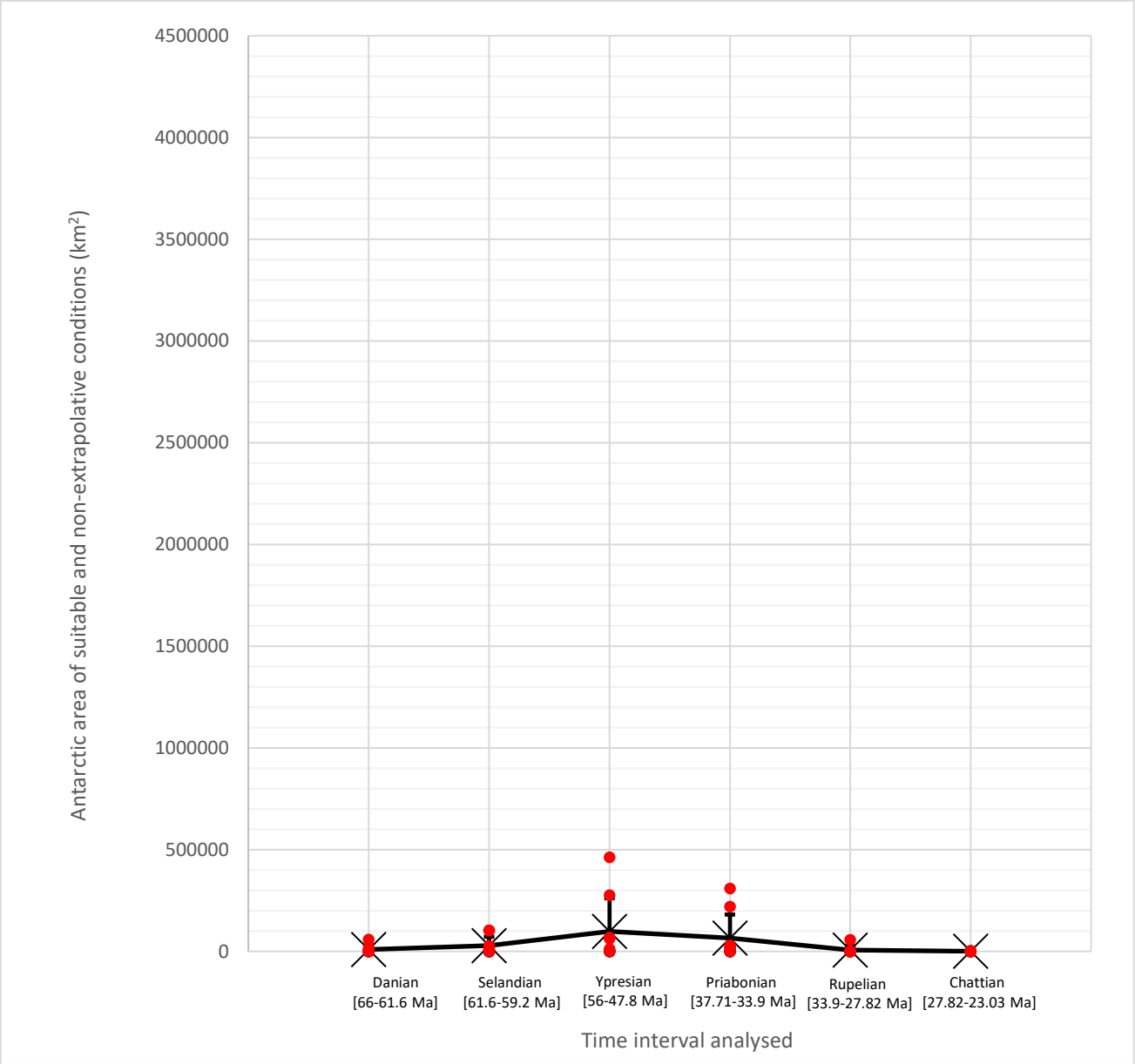

Figure 2.3. Antarctic areas of suitable and non-extrapolative conditions (km^2) for predicted non-dispersers as predicted by the 'Australidelphian+' hypothesis, for models built using a biogeographically informed calibration region and thresholded with maxSSS. The mean and SD are shown by a X with error bars.

No significant differences were found when comparing the contiguity index value of Antarctic areas of suitable climatic conditions, regardless of calibration region and whether extrapolated areas were included (Supplementary Information 2.8).

Fossil comparisons

Models with a biogeographically informed calibration region

Marsupial family-level groups with both statistically adequate models built from a biogeographically informed calibration region, and associated Palaeogene fossils, include Burramyidae (pygmy possums), Caenolestidae, Hypsiprymnodontidae (musky rat-kangaroos), Microbiotheriidae, Peramelidae, Petauridae, Phascolarctidae (koalas), Potoroidae (bettongs and potoroos), and Pseudocheiridae (***Table 2.2****)*. The xenarthran family-level groups with the same qualities are Chlamyphoridae (most armadillos) and Dasypodidae (long-nosed armadillos) (***Table 2.2****)*. For the Ypresian, model projections for Chlamyphoridae, Dasypodidae, and Microbiotheriidae (three of the four family-level groups with Ypresian fossil records) predict fossil occurrence data better than random chance (***Table 2.2***). For the Rupelian, only the Chlamyphoridae model (one out of four models) predicts fossil distribution better than random chance (***Table 2.2***). For the Chattian, model projections for Caenolestidae, Chlamyphoridae, Petauridae, Phascolarctidae, Potoroidae, and Pseudocheiridae (six out of eleven groups) predict fossil distributions better than random chance (***Table 2.2***). Results are consistent regardless of threshold method, except with Petauridae in the Chattian; the projection thresholded with maxSSS predicts fossil occurrence data better than random chance, while the projection thresholded with 95% LTP cannot (Supplementary Information 2.9, Table F1). Including extrapolative areas of suitable conditions also produces similar results to excluding these regions (Supplementary Information 2.9, Table F3). No Danian or Priabonian model projections from a biogeographically informed calibration region can predict the respective fossil records for clades better than random chance (***Table 2.2***).

Model projection:	**Danian** [66-61.6 Ma]	**Ypresian** [56-47.8 Ma]	**Priabonian** [37.71-33.9 Ma]	**Rupelian** [33.9-27.82 Ma]	**Chattian** [27.82-23.03 Ma
Burramyidae (pygmy possums)	n/a	n/a	n/a	n/a	1 out of 2, p>0.025
Caenolestidae (shrew opossums)	n/a	1 out of 3, p>0.025	n/a	1 out of 4, p>0.025	**4 out of 9, p<0.025**
Chlamyphoridae (most armadillos)	n/a	**4 out of 4, p<0.025**	2 out of 2, p>0.025	**8 out of 9, p<0.025**	**12 out of 19, p<0.025**
Dasypodidae (long-nosed armadillos)	n/a	**2 out of 3, p<0.025**	1 out of 3, p>0.025	1 out of 3, p>0.025	0 out of 2, p>0.025
Hypsiprymnodontidae (musky rat-kangaroos)	n/a	n/a	n/a	n/a	0 out of 4, p>0.025
Microbiotheriidae (*monito del monte*)	0 out of 1, p>0.025	**2 out of 4, p<0.025**	0 out of 1, p>0.025	1 out of 2, p>0.025	0 out of 1, p>0.025
Peramelidae (bandicoots)	n/a	n/a	n/a	n/a	1 out of 1, p>0.025
Petauridae (petaurid possums)	n/a	n/a	n/a	n/a	**2 out of 2, p<0.025**
Phascolarctidae (koalas)	n/a	n/a	n/a	n/a	**6 out of 6, p<0.025**
Potoroidae (bettongs and potoroos)	n/a	n/a	n/a	n/a	**5 out of 7, p<0.025**
Pseudocheiridae (pseudocheirid possums)	n/a	n/a	n/a	n/a	**5 out of 6, p<0.025**

Table 2.2. The proportion of family-level groups' fossil sites corresponding with suitable conditions projected onto Palaeogene palaeoclimate reconstructions. The p-value represents the probability fossil sites would correspond to being within 150 km of suitable regions, using a one-tailed binomial test (the one-tail halving the standard p-value of 0.05 to 0.025). Cells denoting significant results are coloured green, those denoting non-significant results are coloured orange and time intervals with no fossils attributable to extant groups are coloured white. Models described here were built from a biogeographically informed calibration region using a maxSSS

threshold; results for models built from a 200 km radius calibration region and/or with a 95% LTP threshold, as well as those that include extrapolated area of suitable conditions, are found in Supplementary Information 2.9.

Models with a 200 km radius calibration region

The marsupial family-level groups with both statistically adequate models built from a 200 km radius calibration region, and associated Palaeogene fossils, are Burramyidae, Caenolestidae, Hypsiprymnodontidae, Microbiotheriidae, Peramelidae, Potoroidae and Pseudocheiridae (Supplementary Information 2.9, Table F2*)*. The only xenarthran family-level group with the same qualities is Choloepodidae (two-toed sloths). Regardless of threshold, non-extrapolative model projections significantly predict the distribution of fossil occurrences for Caenolestidae and Potoroidae in the Chattian. The Ypresian projection thresholded with 95% LTP also predicts the Caenolestidae fossil record, though the projection thresholded with maxSSS cannot (Supplementary Information 2.9, Table F2*)*. Including extrapolative areas of suitable conditions also produces similar results to excluding these regions (Supplementary Information 2.9, Table F4).

DISCUSSION

Why marsupials were able to disperse from South America to Australia in the early Palaeogene, while co-existing placentals did not, is a persistent mystery in mammal evolution. Here, we took a novel approach to assess whether dispersing and non-dispersing clades differ in terms of abiotic niches by projecting suitable area into the early Cenozoic. Specifically, we tested whether Eomarsupialia (the 'eomarsupial' hypothesis) or Eomarsupialia + Microbiotheriidae + Caenolestidae (the 'Australidelphian+' hypothesis) had a larger and more contiguous area of suitable climatic conditions available within Palaeogene Antarctica compared to those clades hypothesised not to have dispersed from South America to Australia via Antarctica during this time period. Groups hypothesised to have not dispersed may still have had areas of suitable

climatic conditions in Palaeogene Antarctica, but the extent and contiguity of it is key, especially when considering the probabilistic nature of biogeographical dispersal.

Although six time intervals across the Palaeogene were considered here, the published fossil record suggests that results concerning the lower half of the Palaeogene - the Danian, Selandian and Ypresian - are likely most pertinent in elucidating trans-Antarctic dispersal (Archer, Arena et al. 1999, Beck, Godthelp et al. 2008, Sigé, Archer et al. 2009, Beck 2012, Lorente, Chornogubsky et al. 2016, Zimicz and Goin 2020). Appropriately, in the Danian, we found support for the 'Australidelphian+' hypothesis in niche model projections using a biogeographically informed calibration region thresholded by maxSSS, which are arguably the most scientifically sound modelling parameterisations (Liu, White et al. 2013). A Danian timing for dispersal would also correspond with the seaway predictions of Reguero et al. (2014, 2021).

Our Chattian analyses also support the 'Australidelphian+' hypothesis, while Rupelian analyses support both the 'eomarsupial' and 'Australidelphian+' hypotheses. A dispersal event in the Rupelian or Chattian, regardless of the taxonomic identity of the dispersers in question, is unlikely, as it would either coincide with or post-date the final break-up of Gondwana (Sijp and England 2004, Scher, Whittaker et al. 2015, Beck 2017, Hodel, Grespan et al. 2021, Lauretano, Kennedy-Asser et al. 2021, Huang, Steel et al. 2022), contradicting the aforementioned fossil evidence to a considerable degree. While suitability is a necessary prerequisite for dispersal, an area being climatically suitable for a taxon is not necessarily equivalent to the presence of a taxon in the region (Peterson and Soberón 2012). Our observations here may even correspond to a residual ecosystem, including marsupials, sustained in Antarctica after the final Gondwanan break-up – relating somewhat to the previously discussed concept of a pan-Gondwanan biota (Beck 2017). The fact that both the hypotheses we tested are supported in the Rupelian is not inherently an issue, given that said hypotheses are nested, but should be noted nonetheless.

Beyond our two hypotheses, considering the niche projections for individual family-level groups also provides notable insight. In many groups (though none within Xenarthra) and for many time intervals, we observe a substantial, non-extrapolative and somewhat continuous 'corridor' of suitable abiotic conditions connecting South America and Australia, along the length of the Pacific-facing Antarctic coast (***Figure 2.4***). The family-level groups Burramyidae, Microbiotheriidae, Peramelidae, Phascogalini, Pseudocheiridae, Vombatidae, and (*Dendrolagus, Petrogale, Thylogale*) (pademelons, rock-wallabies and tree kangaroos), all show such a pattern in the Ypresian - albeit only when their niche models used a biogeographically informed continental region as a calibration region. Under the same criterion, Peramelidae and Phascogalini also have such a corridor in the Priabonian; Phascogalini, Vombatidae and (*Dendrolagus, Petrogale, Thylogale*) in the Rupelian; and Peramelidae and (*Dendrolagus, Petrogale, Thylogale*) in the Chattian. Acrobatidae and Petauridae showed the pattern throughout all Palaeogene time intervals considered (Supplementary Information 2.10).

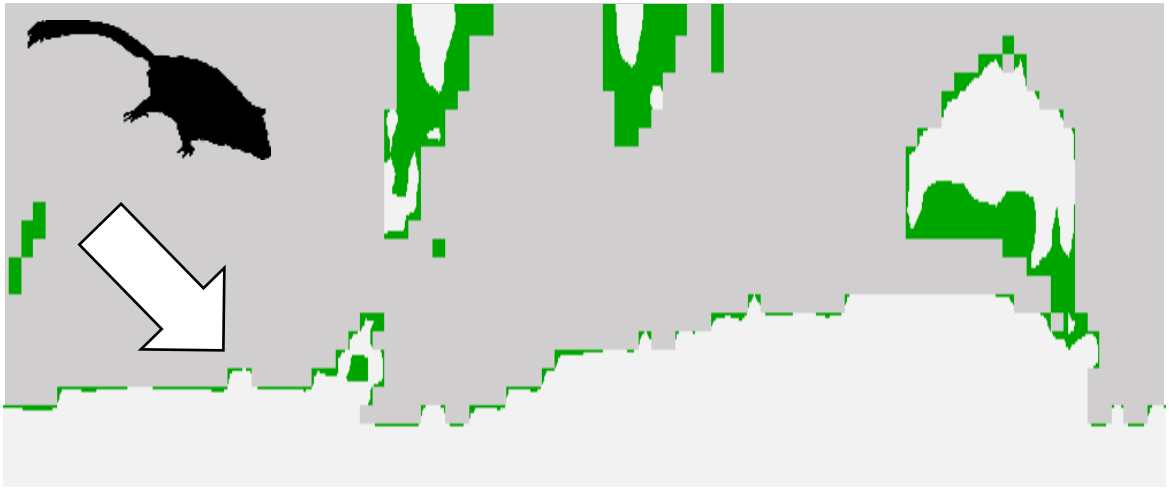

Figure 2.4. Regions of suitable conditions for Acrobatidae projected onto the Ypresian time interval from a niche model built using present-day occurrences. Only the Southern Hemisphere (with Antarctica at the bottom and Australia on the right) is shown for clarity. Model results were calibrated using a biogeographically informed continental region and thresholded via maxSSS (Liu, White et al. 2013). Areas of suitable, non-extrapolative climatic conditions are shown in

green. An arrow on the projection indicates the position of the hypothesised 'dispersal corridor' of suitable climatic conditions, along Antarctica's Pacific coast. Acrobatidae silhouette by Sarah Werning on Phylopic (CC 3.0 Unported).

While the consistent Ypresian presence of an abiotically suitable Antarctic 'corridor' still corresponds somewhat to the aforementioned dispersal timings suggested by the fossil record (Archer, Arena et al. 1999, Beck, Godthelp et al. 2008, Sigé, Archer et al. 2009, Beck 2012, Lorente, Chornogubsky et al. 2016, Zimicz and Goin 2020), it does not match the specific Danian timing suggested by our overarching analyses and Reguero et al. (2014, 2021) (***Table 2.1***). That said, the position of the corridor along the Pacific-facing coast of Antarctica avoids the potential dispersal barrier of the mountainous regions that cross the Antarctic continent (Elliot 2013, Beck 2017) and aligns hypothetical trans-Antarctic travel alongside the Ross Sea clockwise oceanic gyre (***Figure 2.4***). It has been proposed that one effect of South America and Australia being connected (or at least proximal) to Antarctica during much of the Palaeogene could be the strengthening of this gyre (Kennedy, Farnsworth et al. 2015, Zhang, Huck et al. 2020), which would have resulted in a strong east-west current running along the Antarctic coast. This may have facilitated some oceanic dispersal, which could have supplemented travel over land, especially at points where the dispersal corridor may be less spatially contiguous – reconciling the low contiguity index values seen in our projections (Supplementary Information 2.8). The current would also allow for trans-Antarctic dispersal in spite of the presence of Reguero et al.'s (2014, 2021) proposed seaway, and may have stopped xenarthrans and SANUs from reaching Australia - members of these clades may have been incapable of oceanic dispersal. It is worth acknowledging though that, while oceanic dispersal has long existed as an explanation for Gondwanan mammal biogeography (Simpson 1940), both marsupials and xenarthrans show little recorded propensity for it in the present day (Harrison, Harvey et al. 2017). The directionality of the Ross Sea coastal current would also restrict dispersal back from Australia to South America, meaning that the eomarsupials known from the Palaeogene fossil record of South America

(Lorente, Chornogubsky et al. 2016, Zimicz and Goin 2020) must have been part of the same stock which dispersed to Australia. A proposed 'back-migration' of microbiotheres is also unlikely in light of this (Beck, Godthelp et al. 2008) – i.e. the paucituberculate and microbiothere clades more likely evolved in South America, from which some taxa would have dispersed to Australia, leaving no modern descendants.

The groups that show a potential 'dispersal corridor' listed above is phylogenetically disparate, found across Marsupialia (Supplementary Information 2.10, Figures D1-D18) – in many cases, they may not have even evolved by the time of trans-Antarctic dispersal. However, many of the groups do share one or many of the following ecological characteristics: small body masses, generalised diets, arborealism, nocturnality, hibernation and tolerances to cooler or more seasonal conditions (Superina and Boily 2007, Wilman, Belmaker et al. 2014, Shiffman, Soo et al. 2017, Varriale, Russo et al. 2019, Stawski and Geiser 2020, Maclagan, Coates et al. 2021, Zufiaurre, Abba et al. 2021, Perea, Toriño et al. 2022, Geiser and Cooper 2023, Gracanin and Mikac 2023). These traits align with previous predictions of the mammalian attributes required to disperse across Palaeogene Gondwana (Beck 2017), and especially with Acrobatidae, the family-level group with the greatest area of suitable climatic conditions in many of our projections (Harris 2015) (***Figures 2.2 and 2.4***). Our results may, therefore, shed light on the ecological characteristics of the dispersing clades. Future work could use these polar-adapted characteristics to identify the fossil taxa that potentially dispersed through Palaeogene Antarctica, and further reveal the shifts in historical biogeography that resulted in the unique modern distribution of Gondwanan mammals. Perhaps members of Xenarthra, Didelphimorphia and other groups could not disperse from South America to Australia because, during the Palaeogene, they specifically lacked such characteristics. Alternatively, these groups may have just been geographically distant from Antarctica – didelphimorphs, for instance, are an adaptable group but their evolutionary history appears to have been based in Amazonia throughout the Palaeogene (Castro, Dahur et al. 2021).

The fact that our niche models calibrated with present-day data could not consistently predict Palaeogene fossil occurrences suggests that broad-scale abiotic niche conservatism is lacking in Gondwanan mammals, in contrast to what is seemingly observed in non-mammalian groups (Rodrigues, Villalobos et al. 2019, Saupe, Farnsworth et al. 2019). This potentially complicates our assumption that the abiotic tolerances of extant groups can be used as proxies for those of extinct taxa (see Chapters 3 and 4). Isolated time intervals where the niche models corresponded with fossil occurrences may not represent niche conservatism, but the convergent evolution of abiotic tolerances at different points in deep time. That said, our assessment of abiotic niche conservatism (or lack thereof) in Marsupialia and Xenarthra is indirect, and itself based on assumptions. For instance, our niche models can only estimate climatic tolerances, based on the available occurrence and environmental data – groups' actual abiotic niches may differ to a considerable degree. Our fossil occurrence localities may include inaccurate coordinate information, while the parameters used to construct our palaeoclimate reconstructions are based on their own set of presumptions (see Supplementary Information 2.2). Results derived from evaluating the extent of niche conservatism with family-level groups may also not apply to different taxonomic levels.

Further biogeographical and palaeontological conclusions may be drawn from the specific instances in which our niche models and their projections could not predict fossil occurrences. For example, the only niche models that could predict Rupelian fossil distribution were those for Chlamyphoridae (***Table 2.2***, Supplementary Information 2.9). The Priabonian-Rupelian boundary did see a significant faunal turnover among Gondwanan marsupials and placentals (Goin, Gelfo et al. 2012, Gaudin and Croft 2015, Goin, Woodburne et al. 2016, Eldridge, Beck et al. 2019, Abello, Toledo et al. 2020), so the particular lack of correspondence between present-day niches and Rupelian fossil distribution could reflect a time of evolutionary turmoil, during which mammals may have been conceivably driven to adapt to new environmental conditions.

Appositely to the 'Australidelphian+' hypothesis, caenolestid niche models most consistently predict the spatial distribution of its respective fossils in the Chattian (albeit with some success in the Ypresian) (***Table 2.2***, Supplementary Information 2.9). The diversity of extant caenolestids is small - only three South American genera - when compared to that of Paucituberculata during the Palaeogene, which saw radiations in now extinct groups like the Pichipilidae, Palaeothentidae and Abderitidae (Abello 2013, Abello, Toledo et al. 2020). Those groups are thought to have had a variety of life histories, habitats and diets (ranging from frugivory to carnivory) (see Chapter 3), while all modern representatives of the clade are restricted to montane Andean habitat and subsist primarily on invertebrates (Goin, Sánchez-Villagra et al. 2007, Abello 2013, Abello, Toledo et al. 2020, Abello, Martin et al. 2021). Indeed, modern caenolestids only seem to have evolved and diversified at the start of the Neogene [23.03-2.58 Ma] (Abello, Toledo et al. 2020, Abello, Martin et al. 2021), well after South America became isolated from Antarctica and Australia. Thus, during much of the Palaeogene, the abiotic niche of Paucituberculata probably occupied a broader or different region of environmental space to today, and maybe only began to transition or become restricted to its modern iteration in the latest Oligocene (just before the beginning of the Neogene), reflected in the ability for our niche models to predict fossil distribution at this time. Ultimately though, the clade is notably understudied, and more work is required to resolve the past and present ecology of this elusive group (Eldridge, Beck et al. 2019).

Our results also suggest that Ypresian microbiotheres show more similarities to their extant relatives than to those from other Palaeogene time intervals (***Table 2.2***, Supplementary Information 2.9), which could correspond to a more similar abiotic niche. Ypresian taxa like *Mirandatherium* and *Marambiotherium* were small-bodied invertivores or invertivore-frugivores (see Chapter 3) (Goin, Case et al. 1999, Case 2006, Zimicz 2012, Carneiro and Oliveira 2023), much like the sole modern microbiothere genus *Dromiciops*, found today in Chile and Argentina (Marshall 1978, Amico and Aizen 2000). Moreover, the palaeoflora sometimes associated with Ypresian microbiothere fossils – *Nothofagus, Araucaria* (monkey puzzle) and bamboo – is very

similar to the temperate rainforest plants found in the 'Valdivian' habitat of *Dromiciops* (see Chapter 4) (Hershkovitz 1999, Francis, Ashworth et al. 2008, Reguero, Goin et al. 2013). In this way, the presence of *Nothofagus* rainforest across Gondwana throughout much of the Palaeogene (Cook and Crisp 2005, Greenwood and Christophel 2005, Hinojosa, Gaxiola et al. 2016, Romero, Rodriguez Amenabar et al. 2019, Vento, Agrain et al. 2022) implies in itself that microbiotheres had the capacity to disperse between South America and Australia at this time. The Ypresian 'dispersal corridor' seen in Microbiotheriidae niche projections may yet be shown to reflect the range of said forests, though further analysis is required to this end (see Chapter 4).

The disparity between the extant microbiotheriid ecological niche and the fossil distribution of the only potential Danian microbiothere, *Khasia* (***Table 2.2***, Supplementary Information 2.9), may reflect the unlikelihood of a family having a conserved niche over a time interval of over 60 million years - *Khasia*'s classification as a microbiothere, and thus the validity of comparing it to modern microbiotheres, is also questionable (Szalay 1994, Beck, Voss et al. 2022, Beck 2023). The lack of post-Ypresian predictive success may be due to adaptive radiations in microbiothere clades which are ecologically dissimilar to *Dromiciops*. The family Woodburnodontidae, for example, had uniquely plesiomorphic dentition and body masses of over a kilogram (Goin, Zimicz et al. 2007, Beck 2023), while genera like *Pachybiotherium* and *Oligobiotherium* diversified in a morphologically distinct group to Microbiotheriidae (Goin, Abello et al. 2007). Marine transgressions after the conclusion of the Palaeogene are thought to have instigated modern microbiothere biogeographical patterns, pushing the *Nothofagus* forests into its present-day Andean range and, conceivably, driving microbiotheres to evolve ecological niches rarely seen in the group since the Ypresian (Quintero-Galvis, Saenz-Agudelo et al. 2021).

CONCLUSIONS

The analyses presented here offer some support for the 'Australidelphian+' hypothesis, that this group of marsupials had significantly more opportunity (i.e. more suitable habitat) for dispersal

between South America and Australia in the Palaeogene. While this support comes with caveats, it indicates that differences in abiotic niches in the early Cenozoic underlie the current, stark biogeographical patterns of mammals and suggests promising directions for future palaeoecological study. From resolving dispersal routes via niche projections and other palaeoclimatic inferences, to comparing niche conservatism (or lack thereof) to trends in the fossil record, we anticipate that multidisciplinary approaches especially will continue to inform the scientific consensus on the evolution of two of the most charismatic mammalian clades - Marsupialia and Xenarthra - and their biogeographical narratives across Palaeogene Gondwana.

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Statement of Authorship for joint/multi-authored papers for PGR thesis

To appear at the end of each thesis chapter submitted as an article/paper

The statement shall describe the candidate's and co-authors' independent research contributions in the thesis publications. For each publication there should exist a complete statement that is to be filled out and signed by the candidate and supervisor **(only required where there isn't already a statement of contribution within the paper itself).**

Title of Paper	On the absence of armadillos in Australia: Ecological niche modelling of mammalian dispersal across Palaeogene Gondwana
Publication Status	□Published □ Accepted for Publication □Submitted for Publication **X** Unpublished and unsubmitted work written in a manuscript style
Publication Details	Chapter 2 of DPhil – 'How has the biogeography of Gondwanan mammal clades changed over time?'

Student Confirmation

Student Name:	Jack McMinn		
Contribution to the Paper	Performed all analyses and data interpretations, and wrote the vast majority of the manuscript. Professors Erin Saupe and Anjali Goswami advised on draft revisions and research trajectories, while Dr Alex Farnsworth produced palaeoclimate reconstructions used in analyses and wrote Supplementary Information 2.2 (adapted from Fenton et al (2023)).		
Signature		Date	25th August 2024

Supervisor Confirmation

By signing the Statement of Authorship, you are certifying that the candidate made a substantial contribution to the publication, and that the description described above is accurate.

Supervisor name and title: Professor Erin E Saupe		
Supervisor comments I confirm that the candidate has written and performed the analyses within this chapter, and the work is his own.		
Signature 	Date	Aug 26 2024

This completed form should be included in the thesis, at the end of the relevant chapter.

Chapter 3 – Assessing ecological change in Gondwanan therians from the Palaeogene to the present day

Jack McMinn, Anjali Goswami and Erin Saupe

ABSTRACT

Today, South America and Australia are home to taxonomically distinct therian mammal groups, a biogeographical pattern which probably originated in part from differential dispersal events in the Palaeogene Period [66-23.03 Ma]. Because direct evidence to explain this pattern is obscured by an under-sampled and patchy mammal fossil record, we analyse biotic niche change in Gondwanan therians across deep time, under the assumption that the ecological roles of organisms have a significant influence on their biogeography. We hypothesise that the biotic niches of therians were stable through deep time, a concept known as niche conservatism – the presence of biotic niche conservatism could facilitate analyses comparing or otherwise involving extinct and extant therians. We compiled a dataset including every terrestrial therian genus in South America, Antarctica, and Australia in the Palaeogene and the present day and assign each a dietary category and weight class, traits which together can represent the total diversity of biotic niches occupied by mammals in those regions. Focusing in on five time bins (Palaeocene, Ypresian, Late Eocene, Oligocene and the present day), we then compared the biotic niches of therian genera in each continent using two dissimilarity metrics – Jaccard distances and Bray-Curtis dissimilarity matrices. We find little evidence for niche conservatism in former Gondwanan continents. The ecological roles of therians in South America and Australia appear to have changed substantially across deep time, often in line with global trends of mammalian evolution. Our dataset of therian biotic niches may prove a valuable resource for future research, while our overviews of biotic niche change within Gondwanan taxonomic groups over the Palaeogene

provide new insight into the origination of, and ecological changes associated with modern mammal biota in South America and Australia.

INTRODUCTION

During the Cretaceous [145-66 Ma] and Palaeogene [66-23.03 Ma], South America, Antarctica, and Australia were connected as the last remnants of the supercontinent Gondwana. This connection is uncontroversially identified as the reason for the ecological similarities between South America and Australia observed in both extinct and extant taxa (Veblen, Hill et al. 1996, Sanmartín and Ronquist 2004, Archer, Arena et al. 2006, Beck 2012, Lorente, Chornogubsky et al. 2016, Noben, Kessler et al. 2017, Truong, Sánchez-Ramírez et al. 2017, Brown and Moll 2019, Eldridge, Beck et al. 2019, Zimicz and Goin 2020, Flannery, Rich et al. 2022). Despite this connection, however, each continent has maintained unique groups of therians (metatherian/marsupial and eutherian/placental mammals). South America has early-diverging marsupial groups (the paraphyletic group 'Ameridelphia' and Microbiotheria) and Xenarthra (anteaters, armadillos and sloths) (Gaudin and Croft 2015, Beck 2017, Eldridge, Beck et al. 2019, Beck, Voss et al. 2022, Foley, Mason et al. 2023) along with the taxonomically obscure and recently extinct South American Native Ungulates (SANUs) (Buckley 2015, Westbury, Baleka et al. 2017, Avilla and Mothé 2021, Kramarz and Macphee 2023). Caviomorphs and anthropoids (New World native rodents and monkeys respectively) are also found in South America, arriving via oceanic dispersal from Africa in the late Eocene [47.8-33.9 Ma] or Oligocene [33.9-23.03 Ma] (Antoine, Marivaux et al. 2012, Croft 2016, Löwenberg-Neto 2024) – many other eutherian groups, including camelids and carnivorans, originated from geologically recent dispersal events from North America, such as the 'Great American Biotic Interchange' beginning ~10 Ma (Webb and Stehli 1985, Woodburne 2010, Croft 2016). Australia's therian fauna, on the other hand, is dominated by a single group within Metatheria, Eomarsupialia (Wilson and Reeder 2005), which seemingly replaced an assemblage of non-eomarsupial metatherians and the possible 'condylarth-like' eutherian *Tingamarra* during the Palaeogene (Godthelp, Archer et al. 1992, Beck

2013). Australian rodents likely dispersed from Asia in relative geological recency (Breed and Ford 2007, Rowe, Reno et al. 2008).

The biogeographical dynamics that led to this taxonomic specificity by continent are debated, in part due to the under-sampling and patchiness of the Gondwanan mammal fossil record (see Chapter 2) (Szalay 1994, Nilsson, Churakov et al. 2010, Gaudin and Croft 2015, Goin, Woodburne et al. 2016, Bennett, Upchurch et al. 2018, Beck, Voss et al. 2022). Understanding the ecological roles of therian taxa is likely a key consideration in understanding biogeographical trends both in the present day and across deep time (Barve, Barve et al. 2011, Thuiller, Calderón-Sanou et al. 2024). Reconciling ecology and biogeography is often a complex process - for instance, ecological interactions (including those which may mediate long-term colonisation of continents) can operate differently at different spatio-temporal resolutions, which is difficult to integrate into biogeographical modelling without making significant assumptions (Cassini 2011, Heads 2015). Nonetheless, a record of Gondwanan therian ecology across deep time could help to elucidate the biogeographical history of these under-sampled continents and act as a valuable resource for future research.

Here we document the biotic, or alpha, niches (i.e., collections of traits which correspond to an organism's ecological role) of Gondwanan mammals in the Palaeogene and present day, to quantitatively assess niche similarity in South America, Australia, and Antarctica over time. We hypothesize that Palaeogene therians were ecologically similar to their modern relatives, a concept called niche conservatism, meaning that equivalent ecological roles are maintained in taxonomic groups over intervals of geological time (Losos 2008, Wiens, Ackerly et al. 2010, Crisp and Cook 2012). Niche conservatism appears to be an important factor in explaining the spatial diversity gradients of many groups of organisms (Wiens and Donoghue 2004, Romdal, Araújo et al. 2013, Chiu, Yasuhara et al. 2020, Wang, Li et al. 2021, Egan, Bloom et al. 2022, Fernández, Seppey et al. 2022), and has previously facilitated analysis of the global historical biogeography of

both tropical birds and turtles (Rodrigues, Villalobos et al. 2019, Saupe, Farnsworth et al. 2019). We focus specifically on biotic niche conservatism, as alpha niche traits are thought to be more conserved over time than abiotic (or beta) niche traits (traits that correspond to an organism's role in a physical environment, like tolerances for temperature and precipitation) (Saban, Qu et al. 2023), though the extent of both abiotic and biotic niche conservatism is not consistent between different therian clades (Hadly, Spaeth et al. 2009, Buckley, Davies et al. 2010, Olalla-Tárraga, McInnes et al. 2011, DeSantis, Beavins Tracy et al. 2012, Ramos Pereira and Palmeirim 2013, DeSantis, Tseng et al. 2017, Olalla-Tárraga, González-Suárez et al. 2017).

Assessing the magnitude of niche conservatism for mammals in South America, Antarctica, and Australia may help to elucidate therian evolutionary narratives within these regions. While diagnosing biotic niche similarity across deep time is valuable in itself, acknowledging the extent of comparability between extinct and extant therians could inform future analyses, which may use living taxa as an ecological proxy for extinct equivalents (see Chapters 2 and 4). The Palaeogene is of particular relevance here, as this period is hypothesised to have been a time of significant therian dispersal between South America and Australia, which may have been a causal factor in establishing the distinct biogeographical patterns of Gondwanan therian groups (see Chapter 2) (Nilsson, Churakov et al. 2010, Goin, Woodburne et al. 2016, Beck 2017, Reguero and Goin 2021).

METHODS

To test for collective ecological similarity in therians across deep time, we follow the approach of Cribb et al. (2023), who examined global ecospace dynamics across the end-Triassic extinction by categorising fossil occurrence data within ecological groups. Their method, which involves collating ecological information from study taxa and comparing niche frequency across different time bins using dissimilarity metrics, was chosen because it is streamlined and can be easily

adapted to accommodate different study remits (in our case, Gondwanan therians in the Palaeogene and present day).

Our analyses use presence-only taxon information at generic taxonomic rank (Archer, Arena et al. 2006, Travouillon, Escarguel et al. 2011) across five time bins: four from the Palaeogene and one representing the present day. Using genera as our taxonomic rank is a compromise between maintaining adequate precision of biotic niche diagnosis, and allowing for an adequate sample size by not excluding fossil evidence unidentified at the species level (Mannion, Benson et al. 2015, Bennett, Upchurch et al. 2018). We quantified the generic count within each time bin, as well as each genus' biotic niche as represented by diet and body mass, and subsequently diagnosed biotic niche change (or stasis) in South American, Antarctic, and Australian therians over millions of years.

Time bins

Each fossil genus was placed into at least one of four Palaeogene time bins, representing the Palaeocene, Eocene, and Oligocene Epochs: Palaeocene [66-56 Ma], Ypresian (Early Eocene) [56-47.8 Ma], Late Eocene [47.8-33.9 Ma] and Oligocene [33.9-23.03 Ma]. Each time bin is characterised by a somewhat consistent duration of ~10 million years, though the Early Eocene is slightly shorter, and the Late Eocene slightly longer. Consistently sized time bins control for fossil sampling, as more genera may be included within longer time bins, which could artificially inflate the apparent ecological richness for that interval (Raup 1979, Alroy 2008, Dean, Chiarenza et al. 2020), although the relationship between time bin length and ecological richness is not always consistent (Butler, Benson et al. 2011, Mannion, Upchurch et al. 2011, Bennett, Upchurch et al. 2018). Our selected four time bins match the resolution of fossil dating generally found in the Palaeobiology Database (Alroy 2008) and are temporally bracketed by significant geological boundaries, corresponding with notable environmental events (including the Cretaceous-Palaeogene extinction event, the Palaeocene-Eocene Thermal Maximum, the Early Eocene

Climatic Optimum, and the predicted timing of final Gondwanan break-up) and subsequent faunal turnover (Woodburne, Goin et al. 2014, Korasidis, Wallace et al. 2019, Abello, Toledo et al. 2020, Huang, Steel et al. 2022, Thompson, Salzmann et al. 2022). Some genera were temporally associated with the Itaboraian, a South American Land Mammal Age (SALMA) that may overlap the Palaeocene-Eocene boundary (Oliveira and Goin 2011); we classified these taxa as Ypresian, based on the assessment of Woodburne, Goin et al. (2014). Time bins from the Neogene [23.03-2.58 Ma] or Quaternary [2.58-0 Ma] (excluding the present-day time bin) were beyond the remit of this study – by focussing on the Palaeogene and the present day, we can more easily compare our results here to those derived from analyses in Chapters 2 and 4.

To represent our 'modern' time bin, we assembled a list of every terrestrial therian genus that was extant at the beginning of the 20th century, an approach matching Wilson and Reeder (2005). We therefore included the thylacine *Thylacinus* (Rovinsky, Evans et al. 2020) and pig-footed bandicoot *Chaeropus* (Travouillon 2016) - two taxa which occupied unique biotic roles (Supplementary Information 3.4, Table C) but went extinct after 1900, presumably resulting in their exclusion from therian datasets like EltonTraits (from which our biotic niche information was derived) [https://mol.org/downloads/] (Wilman, Belmaker et al. 2014). Although our present-day time bin has a similar generic count to the Palaeogene time bins (***Table 3.1***), the interval of time it encompasses is significantly less than 10 million years, and thus our comparisons of Palaeogene and present-day therian ecospace should be considered with caution.

Dataset assembly

Our Palaeogene analyses used a total of 416 unique South American genera, 38 unique Australian genera, and 13 unique Antarctic genera across the four time bins. Our Palaeogene generic-level dataset (Supplementary Information 3.1, Tables A1, A2 and A3) was based initially on the Palaeobiology Database (PBDB) [https://paleobiodb.org/]. South American therian data were downloaded on 12th December 2023, while Antarctic and Australian therian data were

downloaded on 22nd December 2023. These data were supplemented from the same published faunal lists as discussed in Chapter 2 (Long 2002, Megirian, Murray et al. 2004, Archer, Arena et al. 2006, Metzger and Retallack 2010, Travouillon, Escarguel et al. 2011, Bennett, Upchurch et al. 2018, Eldridge, Beck et al. 2019, Abello, Toledo et al. 2020) (Supplementary Information 2.3), along with some additional resources (Hoffstetter 1954, Goin and Candela 1998, Reguero and Castro 2004, Ciancio and Carlini 2008, López, Ribeiro et al. 2010, Miño-Boilini 2012, Kramarz and Bond 2013, Defler 2019, Abello, Toledo et al. 2020, Mcgrath, Anaya et al. 2020, Martínez, Dozo et al. 2021, Crichton, Beck et al. 2023, Crichton, Worthy et al. 2023). Volant and marine mammals were removed, as were dubious genera and genera with limited available description, including *Dasypodon* (Castellanos 1925)*, Eutrochodon* (Roth 1904)*, Fiandraia* (Mones and Ubilla 1978)*, Florentinoameghinia* (Simpson 1932), and Oligocene presences of *Macrauchenia, Scelidodon* and *Vassallia* (Tournouër 1903, Mones and Ubilla 1978). One Oligocene ichnotaxon, '*Tacheria'*, was retained, as the detail to which it has been described was adequate for our analyses. This taxon represents the footprints of a caviomorph rodent which was related to, but twice as large as, the extant pacarana *Dinomys* (Krapovickas and Nasif 2011), and was similar to the extinct Quaternary [2.58-0 Ma] rodent *Josephoartigasia* (Millien 2008). No other extinct genus in our Palaeogene time bins appears to be morphologically similar to '*Tacheria',* so its inclusion is important for accurately representing the range of ecological roles used by Gondwanan therians.

Our modern dataset included a total of 214 unique South American genera and 69 unique Australian genera. The present-day generic dataset (Supplementary Information 3.2, Table B) was based on EltonTraits, which we checked against the ASM Mammal Diversity Database [https://www.mammaldiversity.org/]. The EltonTraits data consist of a list of mammalian species and their associated ecological characteristics. From this database, we extracted all terrestrial therian genera that live in South America and Australia. Antarctica has no extant endemic non-marine mammals, so was not included in any analyses involving the present day.

Diagnosis of biotic niches

To represent biotic niches, we classified every Palaeogene Gondwanan therian genus by diet and body mass. These two traits, considered together, were used to represent biotic niches. Previously published diagnoses of diet and body mass were prioritised in our classification of these traits for each genus, followed by attributes of closely related or anatomically comparable taxa, followed by our own assessments and calculations of diet and body mass based on anatomical traits and measurements. Full information as to every Palaeogene genus' diet and body mass, along with how they were derived, can be found in Supplementary Information 3.1.

We chose diet and body mass to collectively represent our biotic niches, as they can both be assessed from molars, the most consistently preserved hard tissue structures in the therian fossil record (Gingerich 1974, Gingerich 1977). A mammal's diet can be extrapolated from molar characters or wear (Zimicz 2012, Croft 2016, DeSantis 2016), while body mass predictions can be calculated from logarithmic regression equations integrating molar area (Legendre 1986, Damuth 1990, Janis 1990, Bloch, Rose et al. 1998, Myers 2001, Gordon 2003, Millien and Bovy 2010, Scarano, Carlini et al. 2011). Many extinct Palaeogene mammals in Gondwana are only known from molar fossils (Zimicz 2012, Croft 2016), precluding any interpretation of other ecological characteristics that may additionally inform the representation of a biotic niche, like locomotion or activity patterns.

We chose eight overarching categories to fully represent the scope and diversity of therian diets, and to highlight any significant ecological transitions evident across deep time. For example, distinguishing the 'folivore' and 'grazer' categories is significant in identifying overarching transitions in therians from forested to open habitats (Linder 2017, Bellosi, Genise et al. 2021, Palazzesi, Hidalgo et al. 2022, Jaramillo 2023). Our categories were used in both the Palaeogene and present-day time bins. Genera were classified in a dietary category if that category comprised ≥50% of their annual diet (Pineda-Munoz and Alroy 2014). This simplistic approach

follows that used in EltonTraits, which represents species' diet by the percentage contribution of dietary categories, and allows for qualitative assessments of diet of extinct taxa, where precision is more limited and only a majority dietary preference may be obvious.

The dietary categories we used in this study were:

- Carnivore – vertebrate flesh or carrion. Carnivorous therians tend to have prominent caniniform teeth and reduced talonid regions on their molars (Zimicz 2012).
- Invertivore – invertebrates. The molars of invertivorous therians also tend to have reduced talonid regions but have more prominent lingual ridges than those of specialised carnivores (Zimicz 2012). Invertivore dentition can also be reduced or absent, as is the case with armadillos and anteaters (Gaudin and Croft 2015).
- Folivore – leaves and other forms of browse. Folivorous therians tend to have low-crowned (brachydont) molars and can thus be readily identified in the mammal fossil record (Janis 2008, Saarinen 2019). Fungivory (the consumption of fungus) is included within this category, as it is an obscure and understudied dietary trait primarily associated with folivorous species (McIlwee and Johnson 1998, Luoma, Trappe et al. 2003, Elliott, Truong et al. 2022). Evolutionary transitions between folivory and grazing in therian clades, and their relation to concurrent environmental changes, are well described in previous literature (Janis 2008, Saarinen 2019) – to test for similar trends within our analytical framework, we focussed on these two broader categories, at the expense of their more specific aspects. Identification of fungivory is also near-absent in fossil taxa, despite the fact that the trait almost certainly existed in deep time. Including fungivory as a distinct dietary category for present-day genera could thus inaccurately skew statistical comparisons of diet between Palaeogene and present-day time bins.
- Frugivore – fruits. Frugivorous therians tend to have enlarged talonid regions on their molars to aid with mastication (Zimicz 2012).

- Granivore – seeds, nuts, and grain. The molars of granivorous therians also tend to have enlarged talonid regions, but have longer and more angular ridges than those of frugivores (Zimicz 2012).
- Grazer – grasses, sedges, and other low-lying plants. Grazing therians tend to have high-crowned (hypsodont) molars and can thus be readily identified in the mammal fossil record (Williams and Kay 2001, Damuth and Janis 2011, Saarinen 2019), though this association has been questioned in some South American mammal herbivores, with a high presence of environmental particles being proposed as an alternative cause for hypsodonty evolution (Janis 2008, Strömberg, Dunn et al. 2013).
- Herbivore – a category used if a genus consumes two or more of the above plant-based categories without a ≥50% preference for any one, or if it consumes plant matter not covered by the above plant-based categories (e.g. nectar or plant exudates), or if it is unclear what manner of plant matter it consumes.
- Omnivore – a category used if a genus appears to consume both animals and plants/fungi without a ≥50% preference for either. An omnivorous genus with a notable preference for another dietary category is given an appropriate suffix as part of its categorisation. For instance, according to EltonTraits, the diet of the Oligocene and present-day mountain pygmy possum *Burramys* consists of 40% invertebrates, 30% fruit, and 30% seed. No single category reaches ≥50% dietary composition, yet 60% of its diet is comprised of the two plant-based categories, so *Burramys* is classified as an 'omnivore-herbivore'.

Most modern diet classifications were taken directly from EltonTraits, though the diet classification system used within the EltonTraits dataset does not differentiate between what we refer to as the 'folivore', 'grazer', and 'herbivore' categories, instead including all three options under a generic 'herbivore' category. Additional sources was required for all modern taxa in the EltonTraits 'herbivore' category, both in South America (Jackson and Giulietti 1988, Taber, Doncaster et al. 1994, Puig, Videla et al. 1996, Baker, Bradley et al. 2003, Daigle, Crête et al. 2004, Samuels 2009, Vila, Galende et al. 2009, Borgnia, Vilá et al. 2010, Prado 2013, Upham, Ojala-

Barbour et al. 2013, Kissling, Dalby et al. 2014, Pavez-Fox, Pino et al. 2015, Gainsbury, Tallowin et al. 2018, Marin, Fernández et al. 2020) and Australia [https://animaldiversity.org/] (Begg and Dunlop 1985, Hollis, Robertshaw et al. 1986, Carron, Happold et al. 1990, McIlwee and Johnson 1998, Murray, Dickman et al. 1999, Hayward 2005, Arman and Prideaux 2015, Westerman, Loke et al. 2022). Full information as to every present-day genus' diet and body mass can be found in Supplementary Information 3.2.

Body mass was binned into weight classes, each representing an order of magnitude range: 1-10g, 10-100g, 100g-1 kg, 1-10kg, 10-100kg, 100kg-1 tonne and 1-10 tonnes (Dickman, Lunney et al. 2001, Lunney and Matthews 2004, Guibourd de Luzinais, Du Pontavice et al. 2023) (the bins are upper limit inclusive but lower limit exclusive). Binning compensates for the uncertainty in calculating the body masses of extinct taxa and follows previous work (Yapuncich 2018, Faurby, Morlo et al. 2021, Solorzano and Nunez-Flores 2021). The Ypresian and Late Eocene genus *Thomashuxleya*, for instance, has a large range of predicted masses derived from differing methodologies (Supplementary Information 3.1, Table A1) (Elissamburu 2012, Croft 2016, Carrillo and Asher 2017, Lorente 2019). If a genus has multiple species with body masses in different weight classes, the weight class of the mean body mass for that genus was used to represent the whole genus. Where molar teeth were not available to apply to molar-based regression equations for body mass (Legendre 1986, Damuth 1990, Janis 1990, Bloch, Rose et al. 1998, Myers 2001, Gordon 2003, Millien and Bovy 2010, Scarano, Carlini et al. 2011), other similar teeth were used as a proxy, as was the case with the South American ungulate *Palaeocladosictis* (de Paula Couto 1961) and Australian vombatimorph *Ayekaye* (Megirian, Murray et al. 2004) (Supplementary Information 3.1, Tables A1 and A2). For the South American litoptern *Notodiaphorus,* which is only known from skeletal remains (de Paula Couto 1961), we calculated body mass from femoral length and circumference (Campione and Evans 2012). The Palaeogene armadillo fossil record is lacking in both teeth and bones, with many genera known only from isolated, and sometimes fragmentary, osteoderms (Gaudin and Croft 2015). We thus calculated

the body masses of *Amblytatus, Archaeutatus, Mazzoniphractus, Pseudeutatus*, and *Pseudostegotherium* by volumetrically comparing their isolated osteoderms to those of *Utaetus*, an Eocene armadillo genus with known skeletal remains and, subsequently, a well-constrained body mass (Gaudin and Croft 2015, Croft 2016).

Analysis of biotic niches

We used two dissimilarity metrics to quantify collective biotic niche change in Gondwanan therians from the Palaeogene to the present day. These metrics were used to compare the combined dietary and body mass classifications of genera in each time bin for each continent. To account for differing numbers of genera in each time bin, we used a bootstrapping procedure based on Bennett, Upchurch et al. (2018). For each continent, we subsampled down the time bins with higher generic counts to the sample size of the time bin with the smallest generic count (***Table 3.1***). This approach allowed us to keep the generic sample size the same across time bins. Our bootstrap subsampling was repeated 100 times for each time bin. Using these bootstrap subsamples, we then quantified ecological dissimilarity using the dissimilarity metrics, calculating the mean, standard deviation, and confidence intervals across subsamples. We primarily focus our analyses on South America, since this was the only continent of the three with a fossil record across all time bins and with sufficient (>50) generic counts in each time bin (***Table 3.1***).

We used *vegan 2.6-4* (Oksanen, Kindt et al. 2007) and *labdsv 2.1-0* (Roberts and Roberts 2016) in R to compare collective therian biotic niches represented in a continent's time bins, using Jaccard distances and Bray-Curtis dissimilarity indices. The Jaccard distance (1 – Jaccard similarity index) (Jaccard 1901) is widely used in ecological studies to quantify dissimilarity in biotic composition between two sites (Birks 1987). The metric here calculates the number of biotic niches not shared between two time bins, divided by the total number of biotic niches represented within the two time bins. The Bray-Curtis dissimilarity index (Bray and Curtis 1957) is also well established in previous literature, widely used for comparing two sites' species abundances (the number of

individuals representing different species) (Ricotta and Podani 2017, Ricotta and Pavoine 2022, Cribb et al. 2023). Here we apply the metric to the number of genera representing different biotic niches in two time bins. Thus, the Bray-Curtis index accounts for the abundance of genera in each biotic niche, as opposed to just niche presence information (as seen in Jaccard distances). Despite our bootstrap subsampling procedure, the number of genera known from each time bin, and thus from each biotic niche, is almost certainly affected by the biases of the Gondwanan mammal fossil record (Szalay 1994, Nilsson, Churakov et al. 2010, Gaudin and Croft 2015, Goin, Woodburne et al. 2016, Bennett, Upchurch et al. 2018, Beck, Voss et al. 2022), arguably more so than simple assessments of niche presence or absence. Bray-Curtis index results should thus be viewed with greater caution than Jaccard distance results.

We calculated Jaccard distances and Bray-Curtis dissimilarity indices within three frameworks of comparison:

- Using the earliest time bin of a continent as a baseline and comparing it to all subsequent time bins of that same continent – an approach also used by Cribb et al. (2023). In South America, the earliest time bin was the Palaeocene, while in Australia and Antarctica, the earliest time bin was the Ypresian. This framework allows for the analysis of the extent to which therian biotic niches have changed since the early Cenozoic Era.
- Using the present-day time bin of a continent as a baseline and comparing it to Palaeogene time bins of that same continent. As mentioned previously, Antarctica is precluded from this framework. This framework allows for the analysis of biotic niche differences between the Palaeogene and the present day.
- Comparing each of a continent's time bins to the one that temporally precedes it (i.e., a stepwise approach of assessing a continent's biotic niche change) – an approach also used by Cribb et al. (2023). This framework allows for the analysis of biotic niche change across deep time.

We did not calculate Jaccard distances and Bray-Curtis dissimilarity indices comparing time bins of different continents. The varying spatial area of each continent can impact the extent of their respective fossil records and generic counts, which can thus strongly affect ecological comparability between continents (Guo 1999, Barnosky, Carrasco et al. 2005, Close, Benson et al. 2017).

We ran comparisons for all therian genera together, for only metatherian genera and individually for only eutherian genera - we subsampled the data separately in each case, to account for varying sample sizes between time bins. The Ypresian time bin for Australia included just five genera (***Table 3.1***), and thus a concerningly small subsample size. We performed additional Australian analyses that only included the Oligocene and present-day time bins, which were bootstrapped around the new smallest generic count (***Table 3.1***).

All analyses were conducted in the R programming language v. 4.3.3.

Continent	Palaeocene [66-56 Ma]	Ypresian [56-47.8 Ma]	Late Eocene [47.8-33.9 Ma]	Oligocene [33.9-23.03 Ma]	Present day [0 Ma]
South America	55 (20 metatherian genera, 35 eutherian genera)	104 (42 metatherian genera, 62 eutherian genera)	162 (38 metatherian genera, 124 eutherian genera)	223 (43 metatherian genera, 180 eutherian genera)	214 (20 metatherian genera, 194 eutherian genera)
Australia	*No therian genera known*	5 (4 metatherian genera, 1 eutherian genus)	*No therian genera known*	59 (59 metatherian genera, 0 eutherian genera)	69 (55 metatherian genera, 14 eutherian genera)
Antarctica	*No therian genera known*	11 (9 metatherian genera, 2 eutherian genera)	11 (7 metatherian genera, 4 eutherian genera)	*No therian genera known*	*No (terrestrial) therian genera known*

Table 3.1. Therian generic counts for each continent and time bin considered.

Qualitative overview of therian niche trends

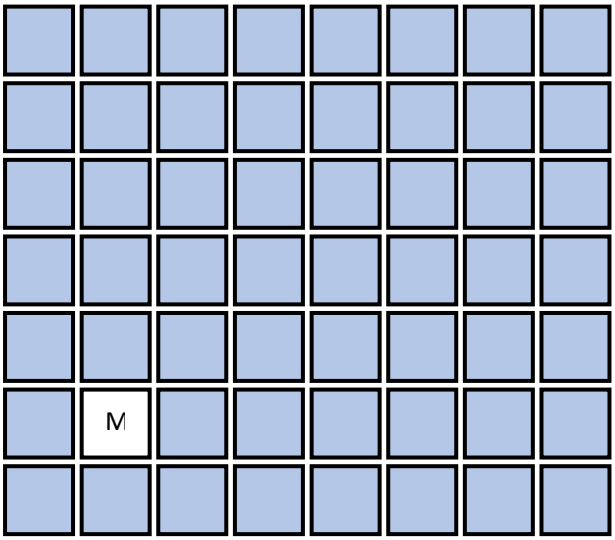
A qualitative overview of biotic niche trends shows that some Gondwanan therian ecologies have persisted from the Palaeogene to the present day (***Figure 3.1***). For example, the same biotic niche – that of a 10-100g invertivore – is evident in the marsupial clades Microbiotheria (*monito del monte*) and Paucituberculata (shrew opossums) from the Palaeogene to the present day, albeit with additional respective radiations into frugivory during the Ypresian and Oligocene. The armadillo clade Cingulata follows a similar pattern, with a familiar array of smaller (~1kg) invertivorous/omnivore-invertivorous niches persisting from the Ypresian to the present day, with large-bodied (100kg-1 tonne) herbivores and grazers exclusive to the late Eocene and

Oligocene (at least within the remit of this study). Folivorans (sloths) show little biotic niche similarity between the Palaeogene and the present day, reflecting the prevalence of large ground-dwelling sloths in South America in the late Eocene and Oligocene [47.8-23.03 Ma] – 'ground sloths' became extinct only a few thousand years ago (Lima-Ribeiro, Varela et al. 2012).

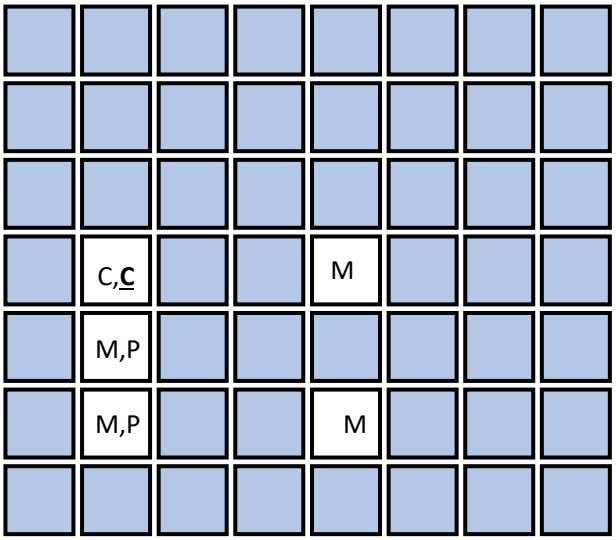
Although caviomorphs and anthropoids both arrived in South America at a similar time (Antoine, Marivaux et al. 2012, Croft 2016, Löwenberg-Neto 2024), these groups differ in how their biotic niches have changed since (***Figure 3.1***). Caviomorph niche change is almost accumulative, with each successive time bin including new biotic niches, while maintaining almost all the niches from the previous time bin. Anthropoid niche change shows less directionality, with somewhat different biotic niches in the Oligocene *versus* the present day (albeit with a continuous presence of 100g-1kg omnivores, 100g-1kg frugivores, and 1-10kg frugivores) (Marivaux, Negri et al. 2023).

The four major modern clades within Eomarsupialia (Australian marsupials) all originated within the Oligocene (Mitchell, Pratt et al. 2014, Eldridge, Beck et al. 2019), with arguably the most prominent change being the distribution of carnivory between taxonomic groups (Supplementary Information 3.4, Table C). Dasyuromorphs (Australian carnivorous marsupials), Peramelemorphia (bandicoots and bilbies), Macropodiformes (kangaroos and kin), and Vombatiformes (wombats, koalas and kin) included carnivorous or partially carnivorous genera in the Palaeogene, with minimal overlap in weight class suggesting little niche competition; today, almost all carnivorous marsupial roles in Australia are filled by dasyuromorphs. Vombatiformes, in particular, have seen a major reduction from their Oligocene niche diversity, with the extinction of not only the flesh-eating 'marsupial lions' but the herbivorous 'marsupial tapirs' and 'giant wombats' (Beck, Louys et al. 2020, Beck, Voss et al. 2022). In present-day Australia, most large-bodied herbivorous marsupial niches are now occupied by Macropodiformes, while the two main possum clades (Petauroidea and Phalangeroidea) have remained small-bodied and largely herbivorous from the Oligocene to the present day

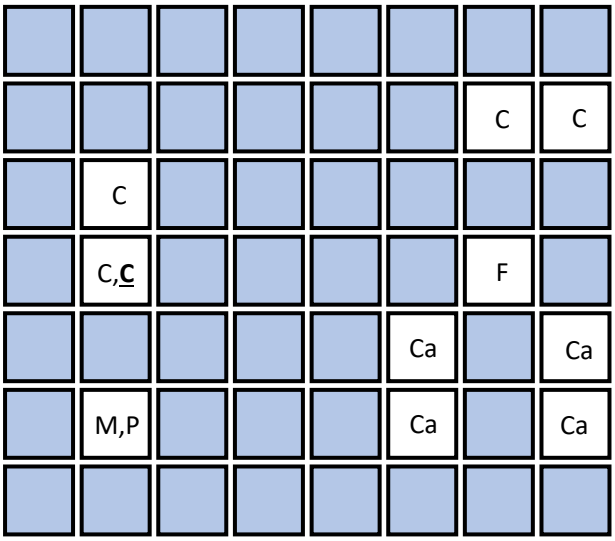
Palaeocene [66-56 Ma]



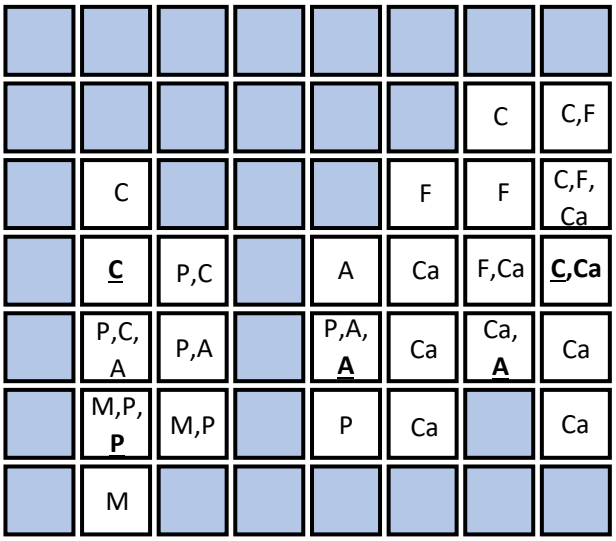
Ypresian [56-47.8 Ma]



Late Eocene [47.8-33.9 Ma]



Oligocene [33.9-23.03 Ma]



Present day [0 Ma]

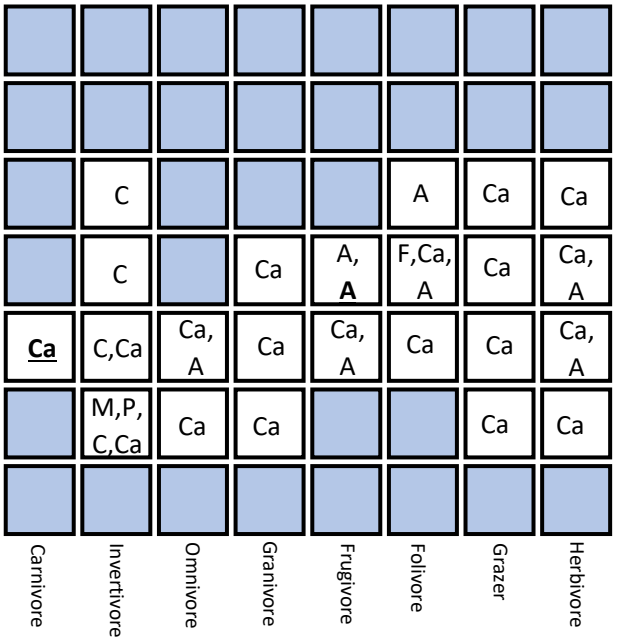


Figure 3.1 – South American therian clades found in both the Palaeogene and the present day, and their diets and body masses – M (Microbiotheria), P (Paucituberculata), C (Cingulata), F (Folivora), Ca (Caviomorpha) and A (Anthropoidea). Bold and underlined initials represent groups that are omnivorous but with a notable preference for a dietary category (omnivore-invertivore, omnivore-herbivore etc.). Didelphidae/Didelphimorphia (opossums) and Myrmecophagidae (anteaters) are not included as their fossil records begin in the Miocene (Dunn, Madden et al. 2013, Goin and Abello 2013, Gaudin and Croft 2015). This figure is based on Figure 1 in Cribb et al. (2023). A different version of this figure with named genera can be found in Supplementary Information 3.4, Table C.

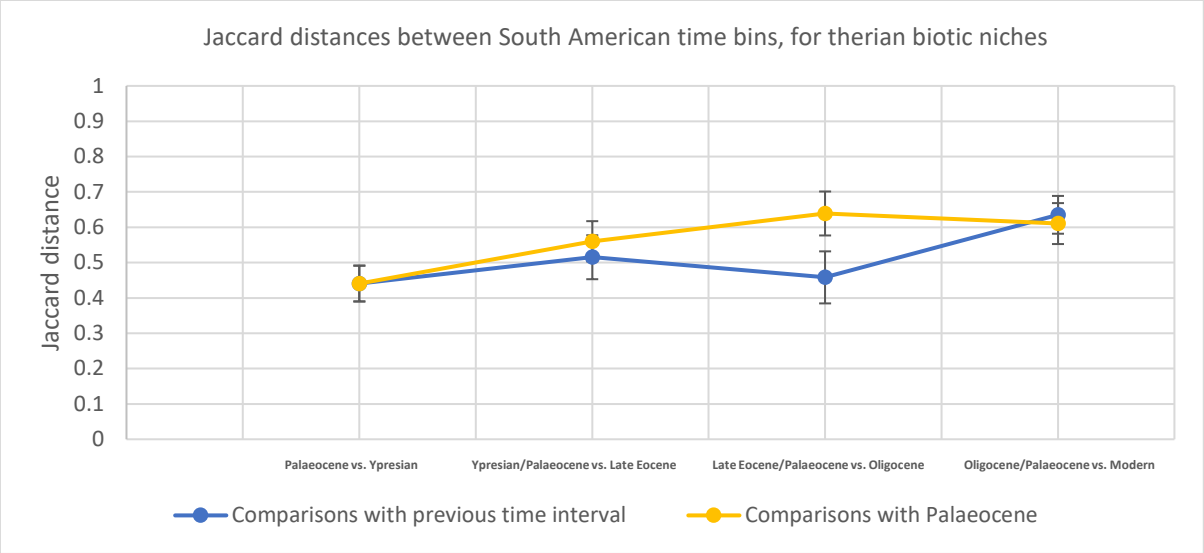
Jaccard distances and Bray-Curtis dissimilarity indices

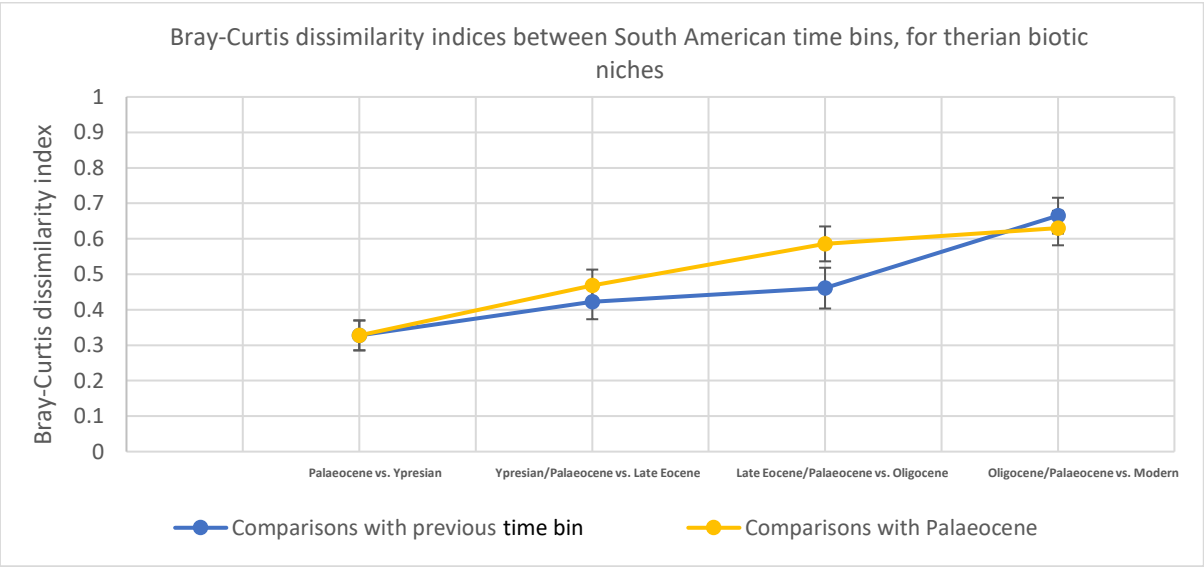
South America

Considering all South American therian genera together, Jaccard distances (and thus niche turnover) remained broadly consistent across the Palaeogene, as derived from stepwise comparisons (***Figure 3.2***) - the 95% confidence intervals for the Palaeocene *vs.* Ypresian (0.441 ± 0.051 SD) and Late Eocene *vs.* Oligocene (0.458 ± 0.074 SD) overlap, while the Ypresian *vs.* Late Eocene distances (0.515 ± 0.062 SD) are significantly, but only slightly, greater. Unsurprisingly, the Jaccard distances between the Oligocene and present day were the largest out of the stepwise comparisons (0.635 ± 0.053 SD), given the ~23-million-year gap between those two time bins. The increase in mean Jaccard distance between the Palaeocene and progressively later time bins (Palaeocene *vs.* Late Eocene, 0.560 ± 0.057 SD; and the Palaeocene and the Oligocene, 0.639 ± 0.062 SD) may reflect an overall directionality of Palaeogene niche change in therians.

Bray-Curtis dissimilarity indices also increased over the Palaeogene for therians (***Figure 3.3***), regardless of whether the comparisons were stepwise (Palaeocene *vs.* Ypresian 0.328 ± 0.042 SD; Ypresian *vs.* Late Eocene 0.422 ± 0.049 SD; Late Eocene *vs.* Oligocene 0.461 ± 0.057 SD) or using the Palaeocene as a fixed baseline (Palaeocene *vs.* Ypresian 0.328 ± 0.042 SD; Palaeocene *vs.* Late

Eocene 0.468 ± 0.045 SD; Palaeocene *vs.* Oligocene 0.586 ± 0.049 SD). All comparisons involving the present-day time bin produced consistently high Jaccard distances and Bray-Curtis dissimilarities for therians (Jaccard distances – 0.570 to 0.635; Bray-Curtis dissimilarity indices – 0.630 to 0.665) (Supplementary Information 3.3, Figures B1 and B2).





Figures 3.2 and 3.3. The mean (±SD) Jaccard distances and Bray-Curtis dissimilarity indices for comparison between time bins, for South American therian biotic niches, using a stepwise approach (blue) and comparisons with the Palaeocene baseline (yellow). Means and SD are calculated from 100 bootstrap replicates. This figure is based on Figures 2 and 6 in Cribb et al. (2023).

The individual metatherian and eutherian datasets produced generally similar trends to the collective therian dataset in terms of stepwise comparisons, except that only eutherians showed increased dissimilarity in Bray-Curtis indices across the Palaeogene (Supplementary Information 3.3, Figures C2). While eutherians showed increased Bray-Curtis dissimilarity over time in comparisons using the Palaeocene as a baseline (Palaeocene *vs.* Ypresian 0.329 ± 0.047 SD; Palaeocene *vs.* Late Eocene 0.451 ± 0.063 SD; Palaeocene *vs.* Oligocene 0.589 ± 0.055 SD; Palaeocene *vs.* Present day 0.747 ± 0.061 SD), metatherians did not (***Figure 3.4***). Indeed, the comparison between Palaeocene and present-day metatherians resulted in a relatively small Bray-Curtis dissimilarity index (0.45 [*no SD, as both time bins had the same generic count – this sample size was also the smallest metatherian generic count, so no subsampling*]) (***Figures 3.4 and 3.5*****;** Supplementary Information 3.3, Figures D2 and E2). Metatherian comparisons between the more recent Palaeogene time bins and the present-day time bin actually produced higher Bray-Curtis indices (***Figure 3.5***) (Palaeocene *vs.* Present day 0.45, Ypresian *vs.* Present day 0.580 ± 0.071 SD; Late Eocene *vs.* Present day 0.640 ± 0.065 SD; Oligocene *vs.* Present day 0.747 ± 0.061 SD). This suggests that present-day metatherian occupation of biotic niches is more similar to that of older Palaeogene time bins. This trend is not seen in analyses based on the eutherian dataset (***Figure 3.5***), nor with Jaccard distances.

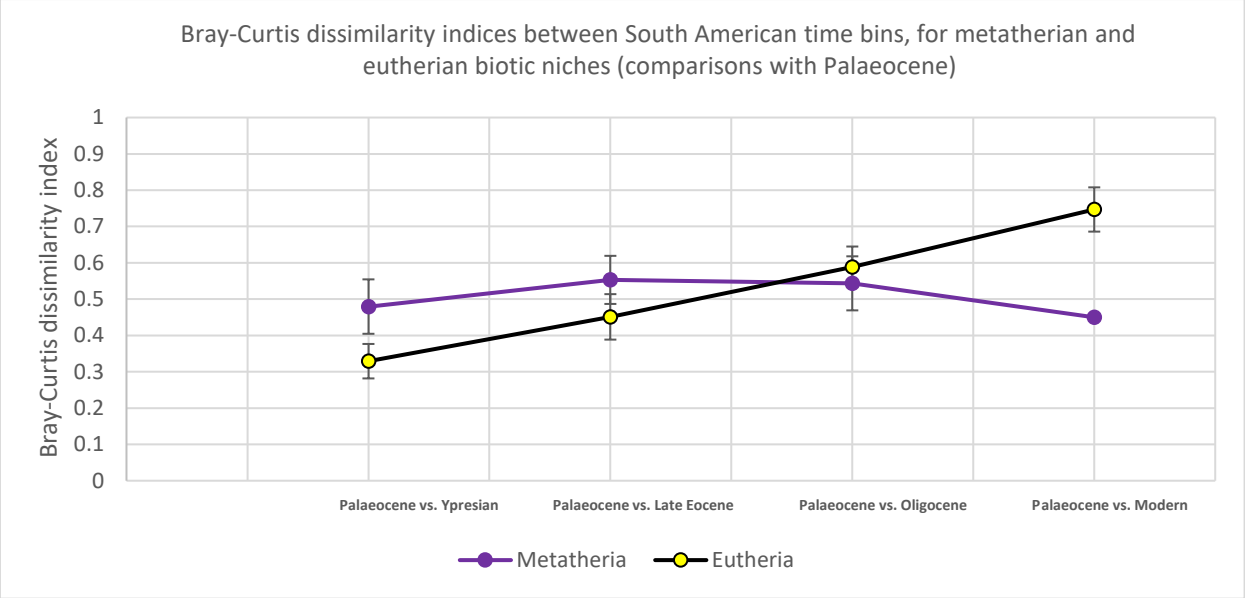


Figure 3.4. The mean (±SD) Bray-Curtis dissimilarity indices for comparison between the Palaeocene time bin and other time bins, for South American metatherian and eutherian biotic niches. Means and SD are calculated from 100 bootstrap subsamples. This figure is based on Figures 2 and 6 in Cribb et al. (2023).

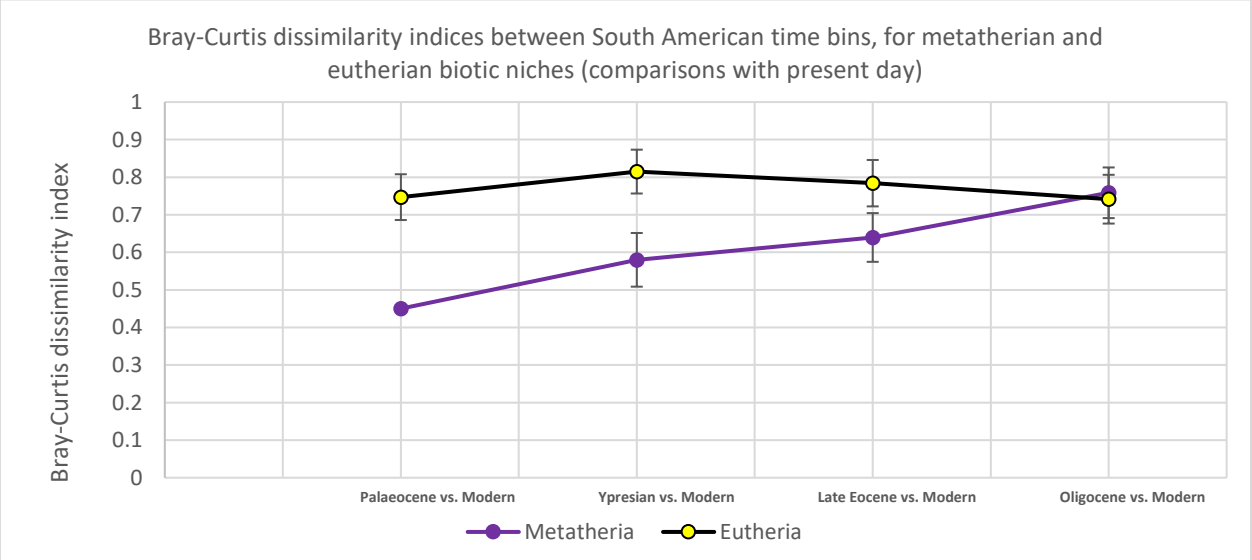


Figure 3.5. The mean (±SD) Bray-Curtis dissimilarity indices for comparison between the present-day time bin and other time bins, for South American metatherian and eutherian biotic niches. Means and SD are calculated from 100 bootstrap subsamples. This figure is based on Figures 2 and 6 in Cribb et al. (2023).

Antarctica and Australia

Comparisons between the older time intervals and the present day in Australia yielded very high Jaccard distances (Ypresian *vs.* Oligocene 0.939 ± 0.081 SD; Oligocene *vs.* Present day 0.846 ± 0.113 SD; Ypresian *vs.* Present day 0.895 ± 0.101 SD) and Bray-Curtis dissimilarity indices (Ypresian *vs.* Oligocene 0.9 ± 0.135 SD; Oligocene *vs.* Present day 0.762 ± 0.167 SD; Ypresian *vs.* Present day 0.83 ± 0.164 SD), which was almost certainly a result of the aforementioned small size of subsamples in Australia. When considering only the Oligocene and present-day time bins in Australia, and adjusting our bootstrapping procedure accordingly, both metrics are considerably reduced (Oligocene *vs.* Present day – Jaccard distance 0.589 ± 0.029 SD, Bray-Curtis dissimilarity index 0.489 ± 0.020 SD). Comparisons between Antarctic therian genera in the Ypresian and Late Eocene yielded low Jaccard distances (0.182) and Bray-Curtis dissimilarity indices (0.333), suggesting little ecological turnover between the two time bins in this region. However, the sample size of Antarctic fossil therian genera is very small (***Table 3.1***) and localised to a single locality (Seymour/Marambio Island) (Gelfo, Goin et al. 2019), so results should be treated with caution.

DISCUSSION

We constructed a large dataset of Palaeogene and present-day terrestrial therian genera from South America, Australia, and Antarctica, along with their respective biotic niches as represented by dietary category and weight class. We adapted two metrics commonly used for assemblage comparisons, to test the hypothesis that the ecological roles occupied by Gondwanan therians have been maintained across the Cenozoic in South American, Australia, and Antarctica.

Our findings suggest that Gondwanan mammals have undergone significant ecological change over the past 66 million years. Invertivory, for instance, is a component in the dietary categories of 11% of the 18 biotic niches present in South American Palaeocene therians, which increases to 25% (of 24) in the Ypresian, then decreases to 20% (of 30) in the Late Eocene, 17.5% (of 40) in the

Oligocene, and 11.8% (of 34) in the present day. Grazing, on the other hand, increases from 5.6% of niches in the Palaeocene, to 8.3% in the Ypresian, and 13.3% in the Late Eocene (down slightly to 12.5% in the Oligocene and 11.8% in the present day).

The distribution of weight classes has also changed over time in South America, most notably in the proportional increase of large-bodied genera. The 100 kg-1 tonne weight class represents 5.6% of South American Palaeocene biotic niches, 8.3% in the Ypresian, and 10% in the Late Eocene and Oligocene (down to 8.82% in the present day, possibly due to Quaternary megafaunal extinctions). The 1 tonne-10 tonnes weight class is not present at all until the Late Eocene. Although small body sizes can be undersampled in the fossil record (Cooper, Maxwell et al. 2006, Brocklehurst, Upchurch et al. 2012, Dean, Mannion et al. 2016), our observed patterns of South American mammalian size and diet evolution reflect those seen in other continents (Raia, Carotenuto et al. 2012, Lovegrove and Mowoe 2013, Saarinen 2019, Huang, Saarinen et al. 2022), which are generally related to a global transition from forested to more open environments (Linder 2017, Bellosi, Genise et al. 2021, Palazzesi, Hidalgo et al. 2022, Jaramillo 2023). Intriguingly, the 'medium-sized' weight classes (1-10kg and 10-100kg) remained present even with the apparent advent of more open environments in the latter half of the Palaeogene, an observation that contradicts previous literature (Pineda-Munoz, Evans et al. 2016).

It is worth noting that the evolution of SANUs, which make up a large proportion of our Palaeogene datasets (Supplementary Information 3.1, Table A1), is not thought to be strongly correlated with environmental shifts (Gomes Rodrigues, Cornette et al. 2018, Croft, Gelfo et al. 2020, Croft and Lorente 2021). Nonetheless, SANUs in South America generally show a high rate of morphological evolution (Goswami, Noirault et al. 2022) and, subsequently, a large variety of body plans (Croft 2016, Houssaye, Fernandez et al. 2016, Croft, Gelfo et al. 2020). This could explain why our stepwise analyses involving South American therian and eutherian datasets show somewhat consistent Jaccard distances over the Palaeogene, yet increasing Bray-Curtis

dissimilarity indices (***Figure 3.2;*** Supplementary Information 3.3, Figure C2). As previously discussed, the biotic niches that were present in each successive time bin in South America appear to have steadily changed over the Palaeogene (as described by Jaccard distances), likely in line with global trends of Cenozoic mammalian evolution – meanwhile, SANU diversification within these existing niches may have driven the increasingly rapid change in the number of genera actually representing each niche (as described by Bray-Curtis dissimilarity indices).

The biotic niches seen in Antarctic therians, by contrast, seem to have remained more or less static across the Eocene. Although Antarctica underwent substantial environmental change in the Eocene, including temperature fluctuations and the appearance of ephemeral ice sheets (Pandey, Pant et al. 2021, McKay, Escutia et al. 2022), temperate rainforest populated by the southern beech *Nothofagus* remained widespread (see Chapter 4) (Reguero, Marenssi et al. 2002, Macphail, Carpenter et al. 2022, Thompson, Salzmann et al. 2022), which may have reduced evolutionary pressures acting on animal life. This may also explain why some Antarctic taxa, including the SANU *Notiolofos*, show marked stasis in their morphological evolution across the Eocene (Gelfo 2016). The lack of change in both biotic niches and generic turnover (9 out of 11 Late Eocene genera in Antarctica are also present in the Ypresian) suggests that little to no mammalian dispersal into Antarctica occurred in the Eocene, in turn implying the presence of dispersal barriers (see Chapter 2).

Only five therian genera are known from Ypresian Australia, but their biotic niches are similar to many Ypresian taxa from South America - the omnivore-frugivore genus *Chulpasia* may have even been present on both continents in the same time bin (Crochet and Sigé 1993, Sigé, Archer et al. 2009). Australia transitioned from tropical forests in the Ypresian to a more open mosaic forest environment in the Oligocene (Guerin and Hill 2006, Martin 2006, Travouillon, Legendre et al. 2009, Metzger and Retallack 2010) - reflected by an increase in Australian therian body size across the Palaeogene, as well as a mixed Oligocene composition of both arboreal and grazing

metatherians (Supplementary Information 3.4, Table C). The more familiar arid biomes seen in present-day Australia originated more recently (Martin 2006, Fujioka and Chappell 2010, Byrne and Murphy 2020, Pepper and Keogh 2021).

Our hypothesis of overall biotic niche conservatism in Theria sees little support in our South American datasets (Supplementary Information 3.3), with Jaccard distances and Bray-Curtis dissimilarity indices remaining generally high throughout. However, individual groups (like Microbiotheria and Paucituberculata) seem to have retained the same ecological roles from their origination to the present day, while also temporarily invading other areas of niche space. Furthermore, although Bray-Curtis dissimilarity indices may be plagued by more biases than Jaccard distances, it is interesting to note that this metric indicates that, collectively, older South American metatherians are more ecologically similar to those of the present day (***Figure 3.4***). This pattern may reflect a true signal from the fossil record, as most present-day metatherian genera from South America are members of Didelphidae (opossums), the earliest-diverging extant metatherian clade and the crown group of Didelphimorphia (Mitchell, Pratt et al. 2014, Eldridge, Beck et al. 2019). Many metatherian groups that were prominent at the beginning of the Palaeogene have also been historically classified within Didelphimorphia on account of apparent anatomical similarities, but such assessments appear to be the result of purely plesiomorphic characters (Ladevèze, Selva et al. 2020, Beck, Voss et al. 2022). This evident physical resemblance suggests that many modern didelphids occupy a similar biotic niche to said Palaeogene stock, and to ancestral therians in general: being comparatively small-bodied, climbing, and often invertivorous (Supplementary Information 3.2, Table B) (Szalay 1994, O'Leary, Bloch et al. 2013, Mitchell, Pratt et al. 2014, Amador and Giannini 2021). This may explain why South America's modern metatherian biota seems to have ecologically approached its previous Palaeocene state. Parallels can be drawn, perhaps, between the dispersal abilities of modern didelphids, especially *Didelphis* (Walsh and Tucker 2018, Wait and Ahlers 2020), and the hypothesised South-America-to-Australia dispersal of metatherians during the Palaeogene (see Chapter 2) (Nilsson, Churakov

et al. 2010, Goin, Woodburne et al. 2016, Beck 2017, Reguero and Goin 2021). However, there is little in the way of explanation as to why Jaccard distances do not also show this pattern, so further research is necessary to elucidate the validity of ecologically comparing early Palaeogene and modern metatherians in South America.

CONCLUSIONS

Gondwanan therians have collectively seen distinct patterns of ecological change across the Cenozoic, often in line with global environmental shifts. Overall, our results show little evidence for biotic niche conservatism in South America – while our Australian and Antarctic results are strongly affected by sample size, overall niche conservatism in Antarctica across the Eocene is perhaps supported. Some of our findings suggest biotic niche similarities between South American metatherians from the early Palaeogene and the present day. If this signal holds, it is likely not an example of niche conservatism, but of present-day South American marsupials reverting to an ancestral biotic niche state, which would subvert the intuitive expectation that more recent taxa ecologically resemble the present day to a greater degree. This further complicates our understanding of Gondwanan ecology and therian evolution across the past 66 million years.

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Statement of Authorship for joint/multi-authored papers for PGR thesis

To appear at the end of each thesis chapter submitted as an article/paper

The statement shall describe the candidate's and co-authors' independent research contributions in the thesis publications. For each publication there should exist a complete statement that is to be filled out and signed by the candidate and supervisor **(only required where there isn't already a statement of contribution within the paper itself).**

Title of Paper	Assessing ecological change in Gondwanan therians from the Palaeogene to the present day
Publication Status	□Published □ Accepted for Publication □Submitted for Publication **X** Unpublished and unsubmitted work written in a manuscript style
Publication Details	Chapter 3 of DPhil – 'How has the biogeography of Gondwanan mammal clades changed over time?'

Student Confirmation

Student Name:	Jack McMinn		
Contribution to the Paper	Performed all analyses and data interpretations, and wrote the vast majority of the manuscript. Professors Erin Saupe and Anjali Goswami advised on draft revisions and research trajectories.		
Signature		Date	25th August 2024

Supervisor Confirmation

By signing the Statement of Authorship, you are certifying that the candidate made a substantial contribution to the publication, and that the description described above is accurate.

Supervisor name and title: Professor Erin E Saupe		
Supervisor comments I confirm that the candidate has written and performed the analyses within this chapter, and the work is his own.		
Signature 	Date	Aug 26 2024

This completed form should be included in the thesis, at the end of the relevant chapter.

Chapter 4 – Ecology of the microbiothere: *Dromiciops*, Valdivian vegetation and implications for Palaeogene Gondwanan marsupial dispersal

Jack McMinn, Anjali Goswami, Alexander Farnsworth and Erin Saupe

ABSTRACT

Microbiotheria is a marsupial clade represented today by the crown group Microbiotheriidae and its sole extant representative *Dromiciops gliroides,* the *monito del monte*. Microbiotheres probably originated in South America, where *D. gliroides* is also currently found – however, microbiothere fossils dating to the Palaeogene [66-23.03 Ma] have also been found in Antarctica and possibly Australia. *D. gliroides* today is found largely within the 'Valdivian' temperate rainforest in Chile and Argentina, which is dominated by the southern beech *Nothofagus*. In the Valdivian rainforest, *D. gliroides* uses the Chilean bamboo *Chusquea culeou* for nest construction and the fruit of the quintral mistletoe *Tristerix corymbosus* for food. Based on the apparent strength of these ecological relationships, it has been suggested that the Microbiotheria have maintained a significant association with Valdivian vegetation since the clade's origination, and that co-evolution between microbiotheres and Valdivian plants may have facilitated, or otherwise influenced, microbiothere dispersal between Gondwanan continents. In this case study, we quantify the present-day environmental space occupied by *D. gliroides, C. culeou, T. corymbosus*, and *Nothofagus dombeyi* (the *Nothofagus* species most associated with *D. gliroides*). We examine the niche overlap among these species in environmental space and project their abiotic tolerances of onto six Palaeogene time intervals to assess the extent of their potential geographical overlap in Antarctica across deep time. We find that, while the abiotic niches of the four species overlap significantly, the abiotically suitable areas for *D. gliroides* in Palaeogene

Antarctica make up only a small fraction of the areas for *C. culeou* and *N. dombeyi*, the latter of which show some geographical correspondence with the global distribution of *Nothofagus* fossils. There is also comparatively little spatial overlap between the Antarctic areas for *D. gliroides* and *T. corymbosus.* Our results suggest that microbiotheres may have been found in *Nothofagus* forests during the Palaeogene, but were only a localised aspect of a wider biome - the present-day relationship between *D. gliroides* and *T. corymbosus* may have also not be an example of co-evolution. *Dromiciops, Nothofagus*, and *Chusquea* niche projections in Palaeogene Antarctica all show a distinctive 'corridor' pattern of suitable climatic conditions, suggesting that microbiotheres could have dispersed between South America and Australia through an Antarctic Valdivian rainforest in the early Palaeogene.

INTRODUCTION

Dromiciops gliroides (Thomas 1894) (***Figure 4.1A***) is a species, or maybe three (see D'Elia, Hurtado et al. (2016)), of small arboreal and primarily invertivorous marsupial, commonly known as the *monito del monte* (Marshall 1978, Fontúrbel, Franco et al. 2022), found in southern Chile and Argentina (Hershkovitz 1999, Fontúrbel, Franco et al. 2022). The species is the sole extant taxon within Microbiotheria (crown group Microbiotheriidae), a clade with many extinct representatives possibly dating back to the Palaeocene Epoch [66-56 Ma] (Marshall 1982, Marshall and DeMuizon 1988, Archer, Arena et al. 1999, Eldridge, Beck et al. 2019, Gelfo, Goin et al. 2019).

Despite currently residing in South America (barring some fossils in the very north of the Antarctic Peninsula), Microbiotheria is considered the earliest diverging group in Australidelphia, a clade that otherwise contains all Australian marsupials (Szalay 1994, Meredith, Westerman et al. 2008, Gallus, Janke et al. 2015, Duchêne, Bragg et al. 2018, Beck, Voss et al. 2022). Given that South America and Australia were both connected to Antarctica throughout much of the Palaeogene Period [66-23.03 Ma] as part of Gondwana, it has been proposed that Australidelphia

originated in South America, with non-microbiothere australidelphians dispersing across Antarctica into Australia (Nilsson, Churakov et al. 2010, Goin, Woodburne et al. 2016, Beck 2017, Reguero and Goin 2021). However, the oldest definitive australidelphian fossils are from Palaeogene Australia (Godthelp, Wroe et al. 1999), as are undescribed fossils purportedly of microbiotheres (Archer, Arena et al. 1999, Eldridge, Beck et al. 2019). This suggests more complex models of trans-Antarctic dispersal, including the hypothesis that Australidelphia actually originated in Australia and microbiotheres underwent a 'back-migration' to South America (see Chapter 2) (Beck, Godthelp et al. 2008). Relevant to reconstructions of marsupial biogeographical and evolutionary history, both *D. gliroides* and many extinct microbiothere taxa show morphological and behavioural attributes predicted to have facilitated marsupial dispersal across Palaeogene Antarctica, including arborealism and small body masses (see Chapter 2) (Beck 2017, Fontúrbel, Franco et al. 2022).

Today, *Dromiciops gliroides* lives primarily in 'Valdivian' temperate rainforest dominated by southern beech *Nothofagus spp.* (most commonly *N. dombeyi* (Martin 2010) (***Figure 4.1C***)) and Chilean bamboo *Chusquea spp.* (Hershkovitz 1999). Within this habitat, *D. gliroides* maintains distinctive biotic interactions with many plant taxa. The leaves of the Chilean bamboo, *Chusquea culeou* (***Figure 4.1B***), for instance, are used to construct spherical nests 1.2 to 3 metres above the ground (Rageot 1979), while the green fruit of the quintral mistletoe, *Tristerix corymbosus* (***Figure 4.1D***), is an important food source in the austral summer (Amico and Aizen 2000, Cortés, Franco et al. 2011, Fontúrbel, Franco et al. 2022). The distribution and abundance of *D. gliroides* varies with *C. culeou* cover and the availability of *T. corymbosus* fruit (Rodriguez-Cabal and Branch 2011, Fontúrbel, Salazar et al. 2017). The microbiothere, in turn, controls the mistletoe's spatial distribution within the Valdivian rainforest, dispersing *T. corymbosus* seeds via its droppings (García, Rodríguez-Cabal et al. 2009).

Given these ecological relationships, it has been hypothesised that Microbiotheria has been intimately associated with *Nothofagus/Chusquea* habitats for over 60 million years (Hershkovitz 1999) and has been an important agent in Gondwanan mistletoe evolution. For example, microbiothere arborealism potentially instigated the transition from mistletoe root parasitism to stem parasitism in the Southern Hemisphere, by depositing their seeds on branches within their droppings (Watson 2020, Fontúrbel, Franco et al. 2022).

Valdivian-like biomes were widespread in the Southern Hemisphere during the late Cretaceous [100.5-66 Ma] and Palaeogene. *Nothofagus* is thought to have first appeared in Antarctica at this time (Vento, Agrain et al. 2024), forming large polar forests across Gondwana (Reguero, Marenssi et al. 2002, Francis, Ashworth et al. 2008, Bowman, Francis et al. 2014, Macphail, Carpenter et al. 2022, Thompson, Salzmann et al. 2022). Across the late Palaeogene and Neogene, these forests subsequently diminished in scale given tropical conditions in Australia (Greenwood and Christophel 2005), icehouse conditions in Antarctica (Hodel, Grespan et al. 2021, Lauretano, Kennedy-Asser et al. 2021, Huang, Steel et al. 2022) and marine transgressions in South America (Quintero-Galvis, Saenz-Agudelo et al. 2021). If microbiotheres did disperse across Gondwana (or ecologically represent the marsupials that did so), examining the biogeographical history of this group in relation to its apparent co-evolution with Valdivian plant taxa could shed light onto the origination of modern marsupial distributions.

Although a compelling narrative, there is some evidence that contradicts the strength and specificity of microbiothere–plant co-evolutionary associations. *Dromiciops gliroides* has been recorded in fragments of secondary non-*Nothofagus* woodland (Franco, Quijano et al. 2011) and can readily breed within pine plantations and logged areas (Celis-Diez, Hetz et al. 2012, Fontúrbel, Franco et al. 2012, Uribe, Chiappe et al. 2017). *Tristerix corymbosus* is also capable of growing outside the Valdivian rainforest, and, in areas of dry shrubland, its seeds are dispersed by birds in the absence of *D. gliroides* (Amico, Rodriguez-Cabal et al. 2011). This implies that the association

between *D. gliroides* and *T. corymbosus* may be an example of 'ecological fitting' (two taxa with coincidentally corresponding ecological roles encountering one another by chance and subsequently establishing an ecological relationship) (Janzen 1985), and that many ecological relationships between microbiotheres and Valdivian plant taxa emerged in geological recency.

In this case study, we examine the hypothesis that microbiotheres and Valdivian plant taxa have maintained a strong association since trans-Antarctic marsupial dispersal during the Palaeogene. Specifically, we ask whether conditions suitable for *Dromiciops gliroides,* and for the plants it relies on, overlap in geographical and environmental space more than would be expected by chance during both the Palaeogene and the present day. To do so, we quantify the degree of abiotic niche overlap for *D. gliroides, Chusquea culeou, Tristerix corymbosus*, and *Nothofagus dombeyi* in present-day environmental space, as well as the spatial overlap between these four species in abiotic niche projections representing six Palaeogene time intervals. Significant overlap of 'realised' abiotic niches in geographical and environmental space between microbiotheres and plant taxa over millions of years may suggest sustained, significant, and likely co-evolutionary ecological relationships.

Although the three Valdivian plant genera considered here are ecologically relevant to *D. gliroides* in the present day, it should be noted that our Palaeogene niche projections extend further back in time than the earliest fossil evidence for both *C. culeou* and *T. corymbosus* (Amico, Vidal-Russell et al. 2007, Wilf 2020). Molecular evidence points to a *Tristerix* origination in the Eocene Epoch [56-33.9 Ma] (Liu, Le et al. 2018), but *Chusquea* appears to have first diversified in the Neogene (Ruiz-Sanchez 2011), so its inclusion here is largely for the sake of comparison - a plant species with whom microbiotheres have established a perhaps geologically recent, yet undeniably strong, ecological relationship. Our *Chusquea* results may also be contextually considered to represent generic understory Valdivian plants, though it is unclear whether any fossil plant taxon ecologically corresponds to *Chusquea* specifically.

Our work builds upon previous niche analysis of *Dromiciops* by Martin (2010), which predicted the present-day South American distribution of the species using ecological niche modelling, along with the environmental factors that most influenced said distribution. Through our analyses, we hope to resolve the extent to which extant microbiothere ecological relationships may inform the reconstruction of the clade's biogeographical narratives across deep time.

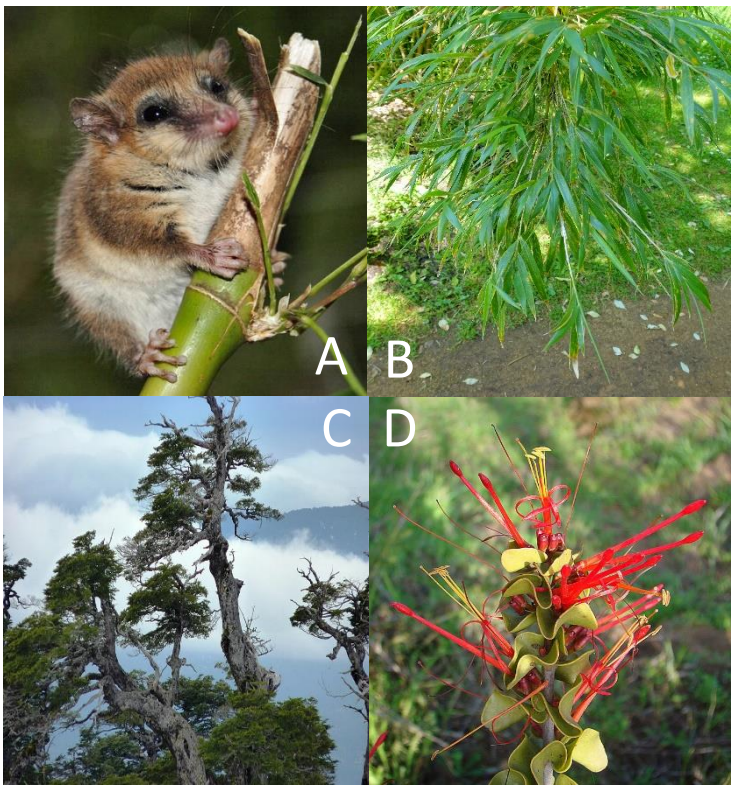

Figure 4.1. (A) *Dromiciops gliroides* (*monito del monte*), (B) *Chusquea culeou* (Chilean bamboo), (C) *Nothofagus dombeyi* (Dombey's beech), and (D) *Tristerix corymbosus* (quintral). *D. gliroides* lives in forest composed of *N. dombeyi*, builds nests from *C. culeou*, and eats the fruit of *T. corymbosus*. *Dromiciops, Nothofagus*, and *Tristerix* photography by Jose Luis Bartheld, Pato Novoa, and Dick Culbert under a CC Attribution 2.0 Generic license.

METHODS

Occurrence data

Present-day occurrence data were derived from the Global Biodiversity Information Facility (GBIF) [www.gbif.org; see Supplementary Information X]. *Dromiciops gliroides* occurrence data were downloaded on 27 June 2021 and used previously in Chapter 2 to represent the Microbiotheria/Microbiotheriidae clade, while *Chusquea culeou, Nothofagus dombeyi*, and *Tristerix corymbosus* occurrence data were downloaded on 20th May 2024. The new occurrence data were cleaned to remove occurrences beyond the known ranges of the plant species (as these records are likely to be sourced from botanical gardens or feral populations), and were then filtered climatically to improve model performance (Varela, Anderson et al. 2014, Castellanos, Huntley et al. 2019). As in Chapter 2, we constructed 'training' and 'testing' datasets for each species using the 'split-sample validation' method, which randomly splits the occurrence data by a ratio of 4:1 (Santini, Benítez-López et al. 2021).

Niche comparisons in present-day environmental space

To quantify differences in the abiotic tolerances of *Dromiciops gliroides* and the three Valdivian plant taxa in the present day, we replicated the framework of Silva et al. (2016), which is based on methods developed by Broennimann, Fitzpatrick et al. (2012) and Guisan, Petitpierre et al. (2014). This approach compares environmental information associated with occurrence data, to quantify differences in abiotic niches via selected similarity metrics.

In our analyses, we used the South American continent (-85° to -30° longitude, -60° to 15° latitude) as a calibration region (Merow, Smith et al. 2013), given the geographical distributions of the taxa. We extracted climatic data from the same four environmental variables as in Chapter 2 (maximum temperature of the warmest month, minimum temperature of the coldest month, precipitation of the wettest month, and precipitation of the driest month) (Fick and Hijmans 2017) across the entirety of our calibration region, and used the *dudi.pca* function of the *ade4*

1.7-22 R package (Dray and Dufour 2007) to generate eigenvectors representing available environmental space. We then extracted the climatic conditions associated with every occurrence for each species, which were converted into eigenvalues and plotted on our South American two-dimensional principal component (PC) grid using the *ecospat.grid.clim.dyn* function of the *ecospat* v.4.0 R package (Di Cola, Broennimann et al. 2017) (***Figure 4.2***). The species' eigenvalues collectively represented their 'realised' abiotic niches within available environmental space in present-day South America (Barve, Barve et al. 2011).

Using the representation of the species' niches in environmental space, we quantified niche overlap using three metrics. We first used the *ecospat.niche.overlap* function to calculate Schoener's D (Schoener 1970), which scores niche overlap between 0 (no overlap) and 1 (complete overlap). To derive a p-value for niche similarity, we used the *ecospat.niche.similarity* function to calculate the statistical impact of randomising one species' occurrence data within environmental space on niche overlap patterns, replicating the randomisation process 100 times (Silva, Vilela et al. 2016). We also used the *ecospat.niche.dyn.index* function to quantify 'niche expansion', which refers to the fractional proportion of a species' niche that extends beyond that of another species in environmental space.

Niche comparisons in Palaeogene geographical space

Our procedure for ecological niche modelling and projection was identical to that described in Chapter 2. We used functions within the *kuenm* v.1.1.9 R package (Cobos, Peterson et al. 2019), which calls MaxEnt v.3.4.4 (Phillips, Anderson et al. 2006), for automated niche model construction, analysis, and projection (testing 527 combinations of regularisation parameter and feature class per species). We used the South American continent as the only calibration region, and projected the best present-day niche model parameterisation for each plant species onto palaeoclimate data (Kennedy, Farnsworth et al. 2015, Lunt, Farnsworth et al. 2016), representing the same six Palaeogene time intervals as in Chapter 2: the Danian (the early Palaeocene) [66-

61.6 Ma], Selandian (the mid Palaeocene) [61.6-59.2 Ma], Ypresian (the early Eocene) [56-47.8 Ma], Priabonian (the late Eocene) [37.71-33.9 Ma], Rupelian (the early Oligocene) [33.9-27.82 Ma], and Chattian (the late Oligocene) [27.82-23.03 Ma] (see Supplementary Information 2.2).

Our methodology resulted in Palaeogene niche projections (the median of 10 bootstrap replicates) thresholded to binary presence vs. absence maps (i.e., suitable or unsuitable conditions) using the 95% LTP or maxSSS thresholds (Allouche, Tsoar et al. 2006, Liu, White et al. 2013), with overlaid MESS (multivariate environmental similarity surface) values indicating geographical areas where the model projection had been forced to extrapolate (see Chapter 2). For *Dromiciops gliroides*, we used the same Microbiotheriidae projections as in Chapter 2 (albeit only those that used South America as its calibration region). The complete niche projections can be found in Supplementary Information 2.10 (microbiotheres) and 4.4 (Valdivian plants).

Using the Lambert azimuthal equal-area projection with the *raster* v3.11 package (Hijmans, Van Etten et al. 2015), we diagnosed the extent of spatial overlap between the species' abiotically suitable areas within Antarctica over the six time intervals. We only measured area of overlap within Antarctica as, given that this continent connected South America and Australia during the Palaeogene, it is likely a key consideration in resolving Gondwanan therian dispersal patterns (see Chapter 2). Excluding or including extrapolated areas of suitable abiotic conditions did not affect the extent of overlapping areas (Supplementary Information 4.3, Table C1-C12).

Nothofagus fossil record comparisons

As in Chapter 2, we compared *Nothofagus* fossil occurrence data to projected model outputs for all Palaeogene time intervals, excluding the poorly fossiliferous Selandian [61.6-59.2 Ma], following the protocol of Saupe, Farnsworth et al. (2019). *Nothofagus* is the only Valdivian plant taxon analysed this way, as *Chusquea* and *Tristerix* have no Palaeogene fossil records (Amico, Vidal-Russell et al. 2007, Wilf 2020). We included fossil data from both *Nothofagus* and *Nothofagidites,* a genus thought to represent fossilised *Nothofagus* pollen (Pujana, Fernández et

al. 2021). It is worth noting that *Nothofagus* pollen can be transported over long distances via wind-mediated pollination (Macphail, Alley et al. 1994, McGlone, Mildenhall et al. 1996), although short-distance dispersal dominates (Marchelli, Smouse et al. 2012). While this long-distance dispersal may impact our perception of *Nothofagus* distributions across deep time, our fossil occurrence data did not extend beyond South America, Antarctica, and Australia, where *Nothofagus* are known to have primarily resided (excluding some potential North American evidence, which was not analysed here (Morrison 2023)).

Fossil data were downloaded from the Palaeobiology Database (PBDB) [https://paleobiodb.org/] on 22nd May 2024, spatially filtered at a resolution of one occurrence every 15 minutes (matching that of the palaeoclimate data), and rotated to their palaeo-plate location using GPlates 2.5.0 (Müller, Cannon et al. 2018) with PaleoAtlas v.3 (Scotese 2016), reflecting the mid-point of each time interval. Localities with a PBDB temporal range greater than 20 million years, or with a PBDB temporal range that intersected two Palaeogene time bins, were excluded from further study, with additional changes documented in Supplementary Information 4.5. Each occurrence was given a spatial buffer of 150 km following Saupe, Farnsworth et al. (2019), to account for palaeo-plate rotation uncertainty (Buffan, Jones et al. 2023).

We assessed whether, in the time intervals of their deposition, fossil localities spatially corresponded with their respective clades' projected abiotically suitable areas. We used one-tailed binomial tests to determine whether fossils corresponded to said areas at a frequency higher than expected based on random chance alone. We tested the effect of including *versus* excluding extrapolated areas of suitable conditions on results (Supplementary Information 4.6, Table D). As was the case with Chapter 2, the Palaeogene fossil records of *Nothofagus* are restricted to South America, Antarctica and Australia, while our niche projections are on a global scale.

Assumptions of niche conservatism

Our approach assumes that the abiotic niches of microbiotheres and Valdivian plant taxa were conserved since the Palaeogene. While he distribution of microbiothere fossil data from the Ypresian spatially aligns with *Dromiciops* niche projections for that same time interval, other time intervals do not show equivalent corroboration, suggesting limited niche conservatism (see Chapter 2) (***Table 4.2***). *Nothofagus* is often cited as an example of a genus with a highly conserved ecological niche (Crisp and Cook 2012), but some analyses concerning *Nothofagus* ancestral niche reconstruction and forest composition dispute this assumption (Hinojosa, Gaxiola et al. 2016, Tiede, Homeier et al. 2016). That being said, the fact that most *Nothofagus* fossil data spatially align with Palaeogene projections of suitable conditions derived from present-day models indirectly suggests at least some degree of broad-scale niche conservatism or, at least, consistency (see Results) (Saupe, Farnsworth et al. 2019). The lack of a Palaeogene fossil record for *Chusquea* and *Tristerix*, on the other hand (Amico, Vidal-Russell et al. 2007, Wilf 2020), complicates assessments of niche conservatism in these taxa. While *Chusquea* may not have even existed in the Palaeogene (Ruiz-Sanchez 2011) (and assigning an equivalent abiotic niche to generic understory plants can only be an assumption), niche conservatism has been suggested in passing as a potential causal factor of mistletoe macroecological patterns in present-day Australia (Kavanagh and Burns 2012), which, along with the Eocene timing for *Tristerix* origination (Liu, Le et al. 2018), would imply conserved abiotic preferences for Gondwanan mistletoes since the Palaeogene.

All analyses were conducted in the R programming language v. 4.3.3.

RESULTS

The total number of occurrences per species, after environmental filtering, was 115 for *Dromiciops gliroides*, 142 for *Chusquea culeou*, 326 for *Nothofagus dombeyi*, and 331 for *Tristerix corymbosus*.

Niche comparisons in present-day environmental space

The first principal component axis (PC1) generated in our analyses represents 59.26% of environmental variation across present-day South America, and the second axis (PC2) represents 27.34% of environmental variation (***Figure 4.2***). The most explanatory variable for PC1 was maximum temperature of the warmest month, while the most explanatory variable for PC2 was the minimum temperature of the coldest month (Supplementary Information 4.7, Table E).

All plant species had similar niches to that of *Dromiciops gliroides* (*p<0.05*), with high levels of niche overlap (***Table 4.1***) (Supplementary Information 4.8, Table F1 and F2). *Tristerix corymbosus* showed the lowest niche overlap with *Dromiciops gliroides*, as well as the greatest extent of 'niche expansion' beyond that of *D. gliroides*, potentially suggesting that it had the most dissimilar abiotic niche to microbiotheres out of the plants considered here (***Table 4.1***) (Supplementary Information 4.8, Table F3).

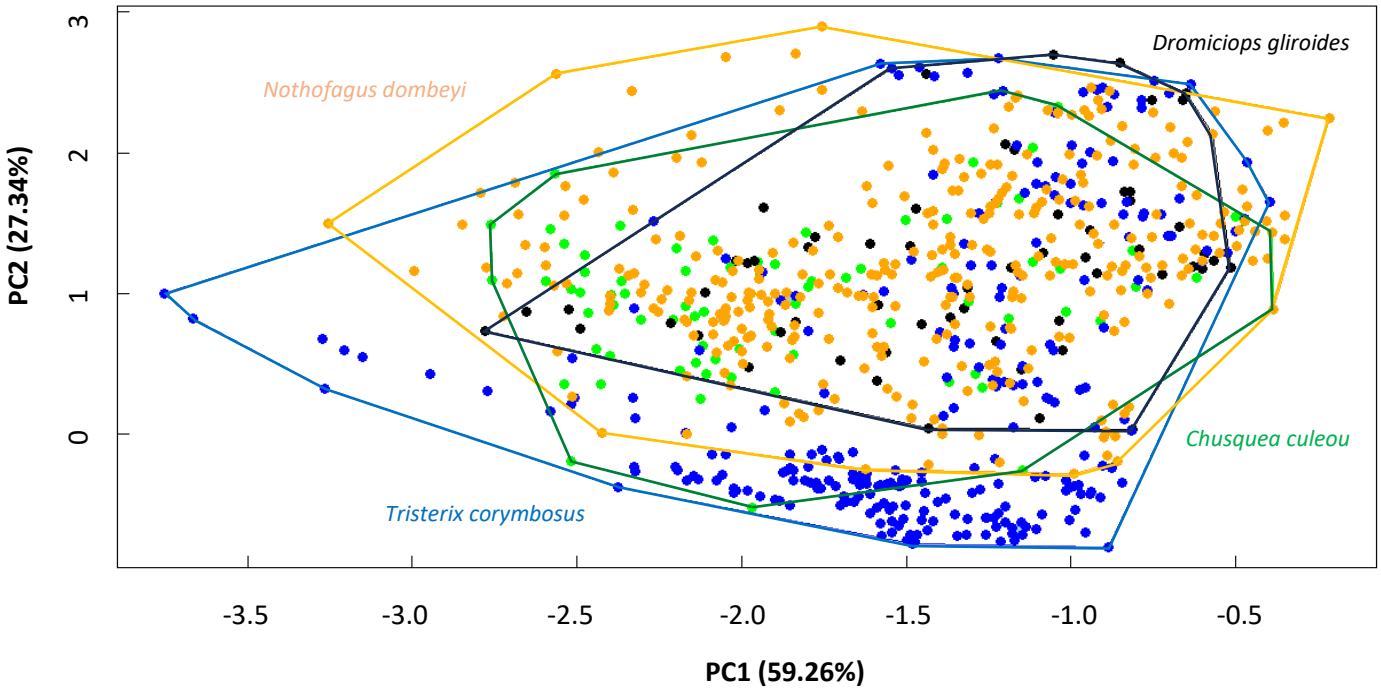

Figure 4.2. The four species' present-day abiotic tolerances as represented by convex hulls plotted in environmental space representing present-day South America. Each point represents a species' occurrence that has been converted into its respective eigenvalues. *Dromiciops gliroides*, *Chusquea culeou, Nothofagus dombeyi* and *Tristerix corymbosus* are represented by black, green, orange and blue points respectively.

Species	Niche overlap with *Dromiciops* (Schoener's D score)	Niche similarity with *Dromiciops* (p-value)	'Niche expansion' beyond *Dromiciops* (fraction of niche in environmental space beyond that of *Dromiciops*)
Chusquea culeou	0.724	*0.02*	0.087
Nothofagus dombeyi	0.781	*0.01*	0.122
Tristerix corymbosus	0.675	*0.01*	0.462

Table 4.1. Metrics used to assess differences between the ecological niches of *Dromiciops gliroides, Chusquea culeou, Nothofagus dombeyi*, and *Tristerix corymbosus*. Complete ecological niche comparisons can be found in Supplementary Information 4.8.

Niche comparisons in Palaeogene geographical space

Niche model selection resulted in one optimal model for each of the four species (Supplementary Information 4.1, Table A). Tests of model quality using the true skill statistic (TSS) (Allouche, Tsoar et al. 2006), continuous Boyce index (CBI) (Hirzel, Le Lay et al. 2006), and Area Under Curve (AUC) suggested that these models performed statistically well (TSS >0.9, CBI >0.7, AUC>0.95) (Supplementary Information 4.1, Table A).

All four species had areas of abiotic suitability in Antarctica during the Danian, Selandian, Ypresian and Priabonian time intervals (Supplementary Information 4.2, Table B1 and B2). *Nothofagus dombeyi* was the only species to have any suitable Antarctic area during the Rupelian time interval, albeit only when thresholded via maxSSS (Supplementary Information 4.2, Table B1 and B2). *N. dombeyi* is also the only species with any extrapolated suitable area in Antarctica (as defined by a negative MESS value). When extrapolated regions were included, they increased the Antarctic area predicted to be abiotically suitable for *Nothofagus* by up to 15 times (Supplementary Information 4.2, Table B1 and B2). *Tristerix corymbosus* had the smallest suitable area in Antarctica in almost every set of projections, aside from *Dromiciops gliroides* for Priabonian projections thresholded using 95% LTP (Supplementary Information 4.2, Table B1 and B2).

We found consistent spatial overlap among the species' predicted abiotic suitability in Palaeogene Antarctica. The smallest area of overlap was 777 km^2 between *Dromiciops* with *Chusquea*/*Nothofagus* in the Chattian, using projections thresholded via maxSSS (this area corresponds to 100% of *Dromiciops*'s total Antarctic area, 0.5% of *Chusquea*'s and 0.4% of *Nothofagus*'s (0.2% if extrapolated *Nothofagus* area is included)). The greatest area of overlap was 2,404,626 km^2, between *Chusquea* and *Nothofagus* in the Priabonian, with projections thresholded via maxSSS (this area corresponds to 92.2% of *Chusquea*'s total Antarctic suitable

area and 40.6% of *Nothofagus*'s suitable area (22.3% if extrapolated *Nothofagus* area is included)) (Supplementary Information 4.3, Tables C1-C12).

Area of overlap between *D. gliroides* and *T. corymbosus*, where it existed, comprised only 10–21.4% of *D. gliroides*'s total suitable Antarctic area across Palaeogene time intervals (Supplementary Information 4.2, Table B1 and B2; Supplementary Information 4.3, Tables C1-C12). In contrast, suitable Antarctic area for *D. gliroides* entirely overlapped with that of *C. culeou* and *N. dombeyi* in the Danian, Selandian, Priabonian, and Chattian time intervals, barring the Ypresian projections, with overlap of 98.3-98.7% for *D. gliroides* with that of *N. dombeyi* (Supplementary Information 4.2, Table B1 and B2; Supplementary Information 4.3, Tables C1-C12). However, the overlap with *D. gliroides* makes up only a small fraction of the total suitable areas for *C. culeou* (0.5-23.1%) and *N. dombeyi* (0.4-9.8% [0.2-7% if extrapolated area is included]) (Supplementary Information 4.2, Table B1 and B2; Supplementary Information 4.3, Tables C1-C12).

In many time intervals, model projections for *Nothofagus dombeyi* and *Chusquea culeou* showed a substantial, non-extrapolative and somewhat continuous 'corridor' of suitable abiotic conditions connecting South America and Australia, along the length of the Pacific-facing Antarctic coast (***Figure 4.3***) (Supplementary Information 4.4, Figures A1-A4). This pattern is also seen in *Dromiciops gliroides*/Microbiotheriidae and may support its potential Palaeogene dispersal route between continents (see Chapter 2). *Tristerix corymbosus* showed no such pattern (Supplementary Information 4.4, Figures A5 and A6).

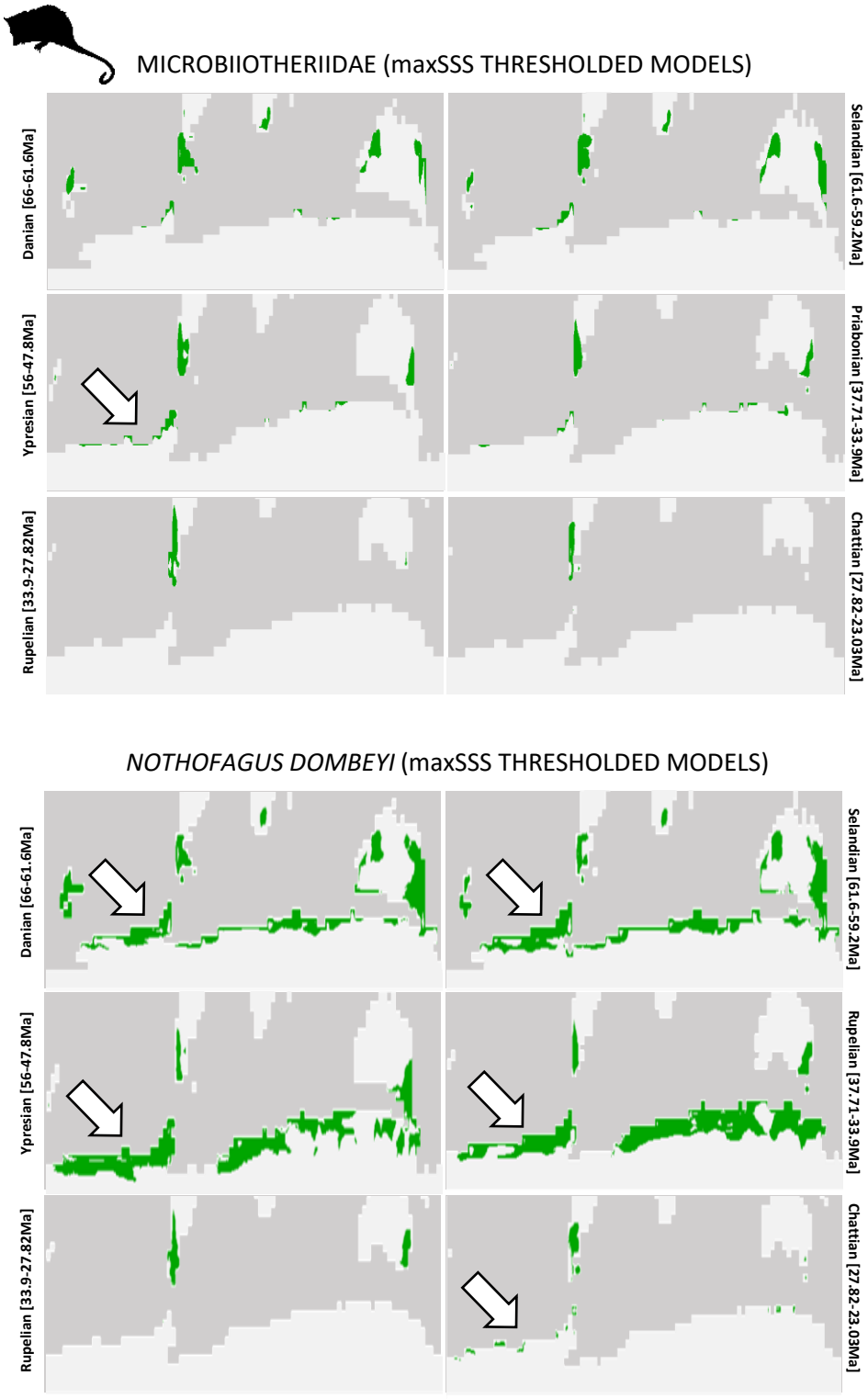

Figure 4.3. Regions of suitable conditions for Microbiotheriidae (as derived from *Dromiciops gliroides*) and *Nothofagus* (as derived from *N. dombeyi*) projected onto Palaeogene time intervals from a model built using present-day occurrences. Only the Southern Hemisphere (with Antarctica at the bottom and Australia on the right) is shown for clarity. Model results were

thresholded via maxSSS (Liu, White et al. 2013). Areas of suitable, non-extrapolative climatic conditions are shown in green. An arrow on the projections indicates the position of a hypothesised 'dispersal corridor' of suitable climatic conditions, along Antarctica's Pacific coast.

Nothofagus fossil record comparisons

Fossil occurrence data for *Nothofagus dombeyi* correspond with niche projections more so than expected by random chance during the Danian and Chattian, regardless of threshold metric or whether extrapolated area is considered (***Table 4.2***) (Supplementary Information 4.6, Table D). Niche projections in the Rupelian predict fossil evidence if only non-extrapolative area is included, and niche projections in the Ypresian only significantly predict fossil data when thresholded via maxSSS (Supplementary Information 4.6, Table D).

Model projection:	**Danian** [66-61.6 Ma]	**Ypresian** [56-47.8 Ma]	**Priabonian** [37.71-33.9 Ma]	**Rupelian** [33.9-27.82 Ma]	**Chattian** [27.82-23.03 Ma
Nothofagus*, represented by *Nothofagus dombeyi	**6 out of 6, p<0.025**	**3 out of 4, p<0.025**	3 out of 8, p>0.025	**1 out of 2, p<0.025**	**5 out of 8, p<0.025**
Microbiotheria/Microbiotheriidae, represented by *Dromiciops gliroides*	0 out of 1, p>0.025	**2 out of 4, p<0.025**	0 out of 1, p>0.025	1 out of 2, p>0.025	0 out of 1, p>0.025

Table 4.2. The proportion of *Dromiciops* and *Nothofagus* fossil sites corresponding with suitable conditions projected onto Palaeogene palaeoclimate reconstructions, excluding areas of extrapolated suitable conditions. The p-value represents the probability fossil sites would correspond to being within 150 km of suitable regions, using a one-tailed binomial test (the one-tail halving the standard p-value of 0.05 to 0.025). A significant p-value ($p < 0.025$) means that the fossil occurrence data correspond with predicted suitable conditions more so than expected by chance. Cells denoting significant results are coloured green, those denoting non-significant results are coloured orange. Models described here were built using a maxSSS threshold, with the

South American continent as a calibration region. Complete *Nothofagus* fossil comparisons can be found at Supplementary Information 4.6, Table D. Complete microbiothere fossil comparisons can be found in Supplementary Information 2.9, Table F1.

DISCUSSION

We examined the environmental preferences of three Valdivian rainforest plant species (*Chusquea culeou, Nothofagus dombeyi* and *Tristerix corymbosus*) and *Dromiciops gliroides*, a unique marsupial that is the sole extant microbiothere. To examine the strength of environmental association between microbiotheres and Valdivian plants in the present day and throughout deep time, we modelled the abiotic tolerances of the groups in the present day and projected these models onto estimates of past climate for six past time intervals: the Danian, Selandian, Ypresian, Priabonian, Rupelian and Chattian. We then examined the degree of abiotic niche overlap in present-day environmental space and in geographical space across the Palaeogene. Strong similarities in present-day abiotic tolerances and significant overlap of niche projections across deep time may provide support for the co-evolutionary hypothesis and help inform biogeographical reconstructions of the group.

Our metrics for environmental niche similarity suggest that the three plant taxa in the present day have somewhat similar abiotic niches to *Dromiciops gliroides*, which is also reflected in their similarly located areas of abiotic suitability in Palaeogene Antarctica. However, the predicted areas of suitability for *Chusquea culeou* and *Nothofagus dombeyi* are much larger than those of *D. gliroides* (Supplementary Information 4.2). Indeed, using present-day occurrences to quantify the abiotic niche of *Nothofagus* may actually underestimate the taxon's true total area of suitable conditions in Palaeogene Antarctica (Chevalier, Broennimann et al. 2024). In the present day, Valdivian rainforest is a relict habitat in South America, with its modern extent severely restricted in space by both the lasting impact of marine transgressions and by human activity (Myers, Mittermeier et al. 2000, Smith-Ramírez 2004, Quintero-Galvis, Saenz-Agudelo et al. 2021). A

major discrepancy may thus exist between the 'realised' abiotic niche we have derived from present-day occurrence data, and the 'fundamental' niche *Nothofagus* could hypothetically occupy. Niche projections which include extrapolation, and thus have greater areas of abiotic suitability, may well reflect true temperate rainforest cover in Palaeogene Antarctica to a greater degree.

Abiotic niche spatial overlap results suggest that, while microbiotheres were found in Antarctic forests during the Palaeogene, they were not a ubiquitous aspect of this biome. *Nothofagus* polar forests may have covered a large portion of Palaeogene Antarctica, of which microbiotheres were restricted to a small area. Although microbiotheres may have evolved to live in *Nothofagus* forests, their impact on forest evolution itself is unlikely to have been significant. It is worth acknowledging, however, that these assessments are based solely on abiotic tolerances, and that other influences (including biotic factors) may have affected the true spatial overlap between microbiothere and *Nothofagus* forest distribution beyond what is resolved here (Barve, Barve et al. 2011), which in turn may have influenced the actual strength of ecological relationships. Indeed, in some North American mammals, biotic factors (like food availability) have been shown to ameliorate or even counteract the impact of living near the 'cold limit' of abiotic niches (the niche limit probably most relevant to microbiotheres in Antarctic conditions) (Sirén, Sutherland et al. 2021). This consideration applies to all interpretations of spatial overlap between niche projections in this study.

Nearly half (46.2%) of the suitable conditions for *Tristerix corymbosus* in the present day extended beyond those of *D. gliroides* (***Table 4.1***) – the extent to which microbiotheres spatially overlapped with mistletoes in Palaeogene projections also appears to be minimal compared to that of overlap with *Nothofagus dombeyi* and *Chusquea culeou* (Supplementary Information 4.4, Figures A1-A6). This could suggest that, while a microbiothere–mistletoe ecological relationship may well have existed during the Palaeogene, with said relationship informing the distributions of

microbiotheres and mistletoes on a fine spatial scale (as is the case in the present day) (García, Rodríguez-Cabal et al. 2009, Rodriguez-Cabal and Branch 2011, Fontúrbel, Salazar et al. 2017), *Tristerix*-like mistletoes did not depend on microbiotheres (and vice-versa) and did not moderate or influence trans-Antarctic dispersal of marsupials to any considerable degree. Indeed, most Palaeogene microbiotheres do not appear to be any more specialised for frugivory than *D. gliroides,* so there is no evidence that any extinct representatives of the group were especially adapted to consuming mistletoe fruit (see Supplementary Information 3.4, Table C). The diet of the purportedly omnivorous Oligocene *Clenia* is somewhat ambiguous (Zimicz 2012), the seemingly frugivorous Ypresian *Monodelphopsis* may not be a microbiothere (De Muizon and Cifelli 2001, Oliveira and Goin 2011, Carneiro and Oliveira 2023), and the larger size of the likely frugivorous Ypresian *Woodburnodon* may preclude it from regular consumption of small (0.5-1 cm diameter) *Tristerix*-like fruit (Fontúrbel and Medel 2017). It is true that physical characters that strongly reflect a predominantly invertivorous diet (as are widely seen in many fossil microbiotheres) do not necessarily exclude mammal species from novel dietary opportunities - for instance, invertivorous mountain tree shrews, *Tupaia montana,* in present-day Borneo have been observed feeding on the exudates of the pitcher plant *Nepenthes*, to the extent that the plant has specifically evolved to attract the shrews and collect their nitrogen-rich droppings (Chin, Moran et al. 2010, Clarke, Moran et al. 2010). Nonetheless, we propose that the 'ecological fitting' hypothesis best explains our findings and the extant *Dromiciops*-*Tristerix* relationship (Amico, Rodriguez-Cabal et al. 2011), and that the transition from mistletoe root parasitism to stem parasitism occurred independently of microbiothere activity (Vidal-Russell and Nickrent 2008, Zhao, Li et al. 2023).

Marsupial trans-Antarctic dispersal is hypothesized to have occurred during the Palaeocene or Eocene (Archer, Arena et al. 1999, Beck, Godthelp et al. 2008, Sigé, Archer et al. 2009, Beck 2012, Lorente, Chornogubsky et al. 2016, Zimicz and Goin 2020). Consistent with this hypothesis, the Ypresian niche projections for *D. gliroides*, *C. culeou*, and *N. dombeyi* (especially when

thresholded by maxSSS (Liu, White et al. 2013)) all show a coastal 'dispersal corridor', supporting the idea that microbiotheres potentially dispersed between continents through a Valdivian rainforest habitat.

Martin (2010) found that austral winter precipitation was the most important abiotic variable for *Dromiciops gliroides*, proposing that this may be functionally due to the resulting winter soil moisture controlling the growth of ecologically important Valdivian plants. In contrast, our results emphasise the significance of the maximum temperature of the warmest month and minimum temperature of the coldest month, as these were the most important variables in both our present-day principal component analysis (Supplementary Information 4.7, Table E) and our niche models (Supplementary Information 4.1, Table A). Although our choice of calibration region may have caused this discrepancy (to calibrate his model, Martin (2010) used 10,000 background points seemingly sourced across all global land area), temperature controlling the niche limits of our four species corresponds well with present-day ecological observations. *Nothofagus dombeyi* models are most informed by the environmental variable corresponding to the maximum temperature of the warmest month (corresponding to a 37.4% model contribution; Supplementary Information 4.1, Table A) - this fits with expectations, since *N. dombeyi* is highly resistant to low temperatures compared to other members of its genus (Reyes-Díaz, Alberdi et al. 2005), yet its growth is severely impacted by higher temperatures (Suarez, Villalba et al. 2015). The importance of the same environmental variable in *D. gliroides* niche models fits with the fact that warmer temperatures risks disrupting its hibernation (Bozinovic, Ruiz et al. 2004, Fontúrbel, Nespolo et al. 2021). Conversely, *Tristerix corymbosus* flowers during the austral winter (Aizen 2003, Aizen 2005) and *Chusquea culeou* growth can be highly sensitive to snowfall (Veblen 1982), which fits with their models being most informed by the environmental variable corresponding to the minimum temperature of the coldest month. Considered collectively, it appears that while these species have quantifiably similar abiotic niches, their tolerances are defined by different environmental factors, which in turn suggests that the entire Valdivian rainforest habitat may be

the result of 'ecological fitting'. Even through this lens of comparison though, microbiotheres remain associated with the similarly cold-adapted *Nothofagus.*

CONCLUSIONS

Overall, our results suggest that the suitable abiotic conditions for *Dromiciops gliroides*, *Nothofagus dombeyi*, *Chusquea culeou*, and *Tristerix corymbosus* were similar to one another, albeit to different degrees, over millions of years. Microbiotheres may have adapted to live in Valdivian *Nothofagus* forests over the Palaeogene, an association which may have facilitated and moderated trans-Antarctic dispersal. However, our niche projections for *Nothofagus* and understory flora (represented by *Chusquea*) extend beyond that of microbiotheres, suggesting that the marsupial group was a localised presence within a much larger biome. Similarly, microbiotheres may not have had as strong of a relationship with mistletoes during the Palaeogene as they seem to in present-day Valdivian forests. As the palaeontological application of abiotic niche modelling expands (Myers, Stigall et al. 2015, Chiarenza, Mannion et al. 2019, Belfiore, Mondanaro et al. 2024, Mills, Schreve et al. 2024), interpretations of deep time biogeography and ecological relationships will likely become more commonplace in scientific literature, yet it remains important to account for all factors before directly relating abiotic tolerances to actual taxon distribution.

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Statement of Authorship for joint/multi-authored papers for PGR thesis

To appear at the end of each thesis chapter submitted as an article/paper

The statement shall describe the candidate's and co-authors' independent research contributions in the thesis publications. For each publication there should exist a complete statement that is to be filled out and signed by the candidate and supervisor **(only required where there isn't already a statement of contribution within the paper itself).**

Title of Paper	Ecology of the microbiothere: *Dromiciops*, Valdivian vegetation and implications for Palaeogene Gondwanan marsupial dispersal
Publication Status	□Published □ Accepted for Publication □Submitted for Publication **X** Unpublished and unsubmitted work written in a manuscript style
Publication Details	Chapter 4 of DPhil – 'How has the biogeography of Gondwanan mammal clades changed over time?'

Student Confirmation

Student Name:	Jack McMinn		
Contribution to the Paper	Performed all analyses and data interpretations, and wrote the vast majority of the manuscript. Professors Erin Saupe and Anjali Goswami advised on draft revisions and research trajectories, while Dr Alex Farnsworth produced palaeoclimate reconstructions used in analyses.		
Signature		Date	25th August 2024

Supervisor Confirmation

By signing the Statement of Authorship, you are certifying that the candidate made a substantial contribution to the publication, and that the description described above is accurate.

Supervisor name and title: Professor Erin E Saupe		
Supervisor comments I confirm that the candidate has written and performed the analyses within this chapter, and the work is his own.		
Signature 	Date	Aug 26 2024

This completed form should be included in the thesis, at the end of the relevant chapter.

Chapter 5 – Discussion

Jack McMinn

CHAPTER SUMMARIES

In Chapter 2, I visualised, measured and compared the extent of abiotically suitable area available for Gondwanan therians in Antarctica, by estimating abiotic tolerances of marsupial and xenarthran family-level groups and projecting them onto Palaeogene palaeoclimate reconstructions. I found, using Mann Whitney U tests, that eomarsupials (Australian marsupials), paucituberculates (shrew opossums), and microbiotheres (*monito del monte*) had greater regions of abiotic suitability in Antarctica during the Danian [66-61.6 Ma] than did didelphimorphs (opossums) or xenarthrans (sloths, armadillos and anteaters). This pattern supports the hypothesis that the former groups were better able to disperse between South America and Australia at this time (Archer, Arena et al. 1999, Beck 2012, Eldridge, Beck et al. 2019) to establish the biogeographical patterns observable in the present day, which opposes the hypothesis that only Eomarsupialia were able to undergo this dispersal across Antarctica (Nilsson, Churakov et al. 2010, Goin, Woodburne et al. 2016, Beck 2017, Reguero and Goin 2021). Antarctic niche projections for some marsupial family-level groups (most prominently Acrobatidae, the feather-tailed possums and gliders) showed a 'corridor' of suitable abiotic conditions during some Palaeogene time intervals, which would have potentially provided a dispersal route between South America and Australia. The position of the corridor along the Pacific coast avoids the potential dispersal barrier of Antarctica's mountainous regions (Elliot 2013, Beck 2017) and runs alongside the east-west coastal currents of the Ross Sea oceanic gyre, which may have facilitated some supplementary oceanic dispersal between continents (Kennedy, Farnsworth et al. 2015, Zhang, Huck et al. 2020). While it is unlikely that the specific groups with a suitable Antarctic corridor in Antarctica existed during the time intervals in question, they all collectively share anatomical and behavioural traits (including small body sizes, hibernation and a tolerance for seasonal conditions) that may have facilitated easier dispersal in Antarctic conditions; these types

of traits could therefore reflect the ecological characteristics of dispersing Palaeogene marsupials (Beck 2017).

To test the degree of biotic niche change in Gondwanan terrestrial therians through time, I estimated the diet and body mass of every Palaeogene and present-day genus from South America, Antarctica and Australia, before collating these traits to represent the biotic niche at generic level (see Chapter 3). I then contrasted the collective metatherian and eutherian biotic niches present on each continent at different time intervals, using Jaccard distances and Bray-Curtis dissimilarity indices. I found evidence for significant biotic change in both Metatheria and Eutheria across deep time. There was little support for overall biotic niche conservatism in these two groups, although the present-day ecological roles seen in some individual, smaller clades (such as Microbiotheria and Cingulata, or armadillos) have been retained since their origination. Results from Australia and Antarctica were almost certainly affected by small sample sizes, but Antarctica showed little change in its represented therian biotic niches between the Ypresian [56-47.8 Ma] and Late Eocene [47.8-33.9 Ma] time intervals, suggesting greater biotic niche stability. A comparatively low Bray-Curtis dissimilarity index between South American metatherians in the early Palaeogene and the present day was also notable, suggesting similar collective ecological roles. Given the ecological traits of some extant didelphids have allowed them to disperse across North America (Walsh and Tucker 2018, Wait and Ahlers 2020), it is possible similar traits were present in metatherians in the early Palaeogene, which could have facilitated their dispersal across Antarctica. However, Bray-Curtis dissimilarity indices are particularly affected by sample size biases, being based here around generic count, so results derived from this metric (especially when not replicated in Jaccard distances) should be treated with caution.

In Chapter 4, I tested the strength of ecological relationships between microbiotheres and temperate forest plants by modelling abiotic niches and measuring niche overlap in both present-day environmental space and geographical space within Palaeogene Antarctica. I found that

these groups share broadly similar climatic tolerances, with the abiotic niches of both microbiotheres and the southern beech *Nothofagus* being best 'explained' by the same environmental variable (the maximum temperature of the warmest month). However, the spatial overlap between their Palaeogene niche projections suggests that microbiotheres were only a localised presence within *Nothofagus*-dominated temperate rainforests across deep time, while the present-day relationship between microbiotheres and mistletoes (the former disperses the latter's seeds in its droppings (Amico, Rodriguez-Cabal et al. 2011)) may have originated in geological recency, as an example of 'ecological fitting' (Janzen 1985). These findings oppose previous hypotheses that Microbiotheria has been intimately associated with *Nothofagus* forests across the Palaeogene (Hershkovitz 1999) and shaped the evolution of Gondwanan mistletoes, including initiating the plants' transition from root to shoot parasitism (Watson 2020, Fontúrbel, Franco et al. 2022).

ASSUMPTIONS AND LIMITATIONS

Abiotic niche conservatism

Arguably the most significant assumption of my analyses was that therian clades have conserved their abiotic niches across millions of years, hence justifying the usage of present-day abiotic tolerances to represent tolerances throughout the Palaeogene (Saupe, Farnsworth et al. 2019). My comparisons in Chapter 2 between the palaeoclimatic projections of a clade's present-day niche, and the spatial distribution of its fossil record, may suggest an overall lack of broad-scale abiotic niche conservatism in Gondwanan therians across deep time. However, this methodology assumes that my estimates of climatic tolerances represent true abiotic niches, that my fossil occurrences are both spatially and taxonomically accurate, and that my palaeoclimate reconstructions accurately reflect environmental conditions. The temporal resolution used is also inconsistent - geological ages lasting up to 8.2 million years (as is the case of the Ypresian) are treated as functionally equivalent to the present day, in terms of being used as comparable 'snap-

shots' of a clade's abiotic tolerances (a similar issue exists in Chapter 3, which compares collectives of taxa representing ~10 million year time intervals with a collective representing ~100 years). Other methods of assessing niche conservatism tend to require extensive fossil records – for example, using the distribution of fossil occurrences as a direct proxy for taxa's geographical ranges, and hence niches, across deep time (Hadly et al (2009)). Circumventing the need to assume niche conservatism is another option. Modelling separate abiotic niches for each individual time interval, via the extraction of palaeoclimatic information from temporally appropriate fossil occurrence localities, avoids many of the previously discussed issues (Myers, Stigall et al. 2015, Chiarenza, Mannion et al. 2019) but, as noted in the Introduction, risks producing excessively extrapolative abiotic niches constructed from potentially inaccurate estimates of calibration regions.

It could be even argued that, given how a taxon's biotic traits inform their abiotic tolerances (Pörtner 2002, Chemisquy, Tarquini et al. 2021), Chapter 3's evidence for a lack of collective biotic niche conservatism in Metatheria and Eutheria implies that abiotic niche conservatism also does not exist in these groups. However, it is significant that my data chapters studied different taxonomic scopes. Chapter 2 concerned family-level groups within Marsupialia and Xenarthra, Chapter 3 compared the groups Metatheria and Eutheria (with some qualitative attention given to biotic niches evident in smaller clade divisions), and Chapter 4 examined the abiotic niches of the individual species *Dromiciops gliroides, Nothofagus dombeyi, Tristerix corymbosus* and *Chusquea culeou* (each standing in for larger phylogenetic groupings - respectively Microbiotheria, Palaeogene *Nothofagus* and *Tristerix* species, and understory rainforest plants). Taxonomic resolution can be a significant confounding factor in studies of present-day ecosystems (Nielsen, Shiel et al. 1998, Anderson, Connell et al. 2005, Jones 2008, Storch and Šizling 2008), with Ellis (1985) inventing the term 'taxonomic sufficiency' to refer to the analytical usage of different taxonomic levels for detecting different ecological patterns (Olsgard, Somerfield et al. 1997, Clarke and Warwick 1998). Crucially, the factors influencing the extent of

niche conservatism can also differ when considering different taxonomic levels (Hadly, Spaeth et al. 2009, Pearman, D'Amen et al. 2010); if both abiotic and biotic niche conservatism are indeed correlated (see Synthesis), a lack of biotic niche conservatism in Metatheria and Eutheria would not necessarily correspond to abiotic niche conservatism in family-level groups or individual species. It is likely, then, that the approaches detailed here for modelling abiotic niches across deep time all have differing and often situational advantages and drawbacks, largely based on the extent of available fossil data and taxonomic resolution, which future researchers should take care to note.

The Gondwanan fossil record

The fact that the Gondwanan mammal fossil record in South America, Antarctica, and Australia is limited is well recorded (Nilsson, Churakov et al. 2010, Bennett, Upchurch et al. 2018, Beck, Voss et al. 2022). Aside from the aforementioned impact on abiotic niche modelling in Chapters 2 and 4, the fragmentary nature of many Gondwanan therian fossils restricted the traits I could use to represent Chapter 3's biotic niches to estimates of weight class and dietary category - in this way excluding a multitude of biotic characters that can also inform mammal ecological roles to a significant degree, such as activity patterns or extent of scansoriality. Reproductive strategy is undetectable in most fossil taxa but may be a particularly relevant biotic trait within the remit of this thesis – the short gestation period and altricial young of marsupials are thought to be an adaptation for lowering the energetic cost and risk of reproduction in environmentally unstable conditions (Edwards and Deacon 2012), and so may have been a key (albeit coincidental) advantage for metatherians when dispersing across Antarctica's polar forests.

Future efforts to improve the quality of the record should involve not only the discovery of new specimens and taxa, but the description of new Gondwanan localities in previously unrepresented geographical regions, so as to reduce the spatio-temporal patchiness of the fossil record. A wider application of successful fossil excavation methods across already described sites

would also produce a more complete perspective of Gondwanan mammal fauna across deep time. For instance, Gelfo et al. (2019) propose that sieving techniques, which facilitated the discovery of many Ypresian mammal fossils on Antarctica's Seymour/Marambio Island, may prove similarly effective in less surveyed, but equivalently dated, deposits on the nearby Cockburn Island. Some fossil specimens with potentially sizeable implications for the study of Gondwanan mammal biogeography simply await proper scientific description, as is the case with the possible microbiotheres and 'condylarths' of the Tingamarra Local Fauna (Archer, Arena et al. 1999, Long 2002, Beck 2017). However, perhaps the most important step for improving the Gondwanan mammal fossil record would be for the political systems surrounding palaeontological study in South America and Australia to be supported to a much greater degree. Many specimens from these regions have been reposited (often illegally) to Western collections and are thus inaccessible to local workers (Percival 2014, Cisneros, Raja et al. 2022), a scientific practice that stems from colonialism and delayed the establishment of unique palaeontological perspectives in these continents by decades (McNamara and Dodds 1986, Lopes and Podgorny 2000).

SYNTHESIS

My three data chapters each concern a different factor relevant to biogeographical distributions: climatic tolerances, broad biotic traits, and specific ecological interactions, respectively. My results from Chapter 2 demonstrate that modelling and projecting abiotic niches can produce feasible potential dispersal routes for marsupials across Antarctica in the Danian Age (part of the Palaeocene Epoch), while Chapter 3's findings show some questionable evidence that biotic niches seen in South American metatherians may have facilitated trans-Antarctic dispersal in earlier time intervals in the Palaeogene, especially in the Palaeocene. It is tempting to hypothesise that the temporal corroboration seen here suggests an alignment between abiotic and biotic niches that uniquely 'equipped' South American metatherians to travel to and subsequently populate Australia at this time. Previous studies have emphasised how the interplay

between abiotic and biotic factors appears to control the distribution and geographical diversity of mammal clades to a greater extent than either niche individually (Cantalapiedra, Domingo et al. 2018), an observation made in ungulates (Lewis, Farnsworth et al. 2017, Speed, Skjelbred et al. 2019), lagomorphs (Leach, Montgomery et al. 2016), and carnivorans (González-Salazar, Stephens et al. 2013, King, Vynne et al. 2021). Sirén et al. (2021) noted that the great extent of intercorrelation between the abiotic and biotic niches of North American carnivorans can even obscure other ecological signals (Godsoe, Franklin et al. 2017). These studies demonstrate the complexity of abiotic and biotic niche interplay in the present day, which in turn suggests the presence of similarly complex, and as of yet unresolved, relationships acting on geological timescales. Indeed, the scope of my thesis concerns only the effect of abiotic and biotic niches on the capacity of mammals to disperse, yet the inverse relationship may also exist: although greater niche breadth can increase a taxon's capacity to disperse (Qiao, Saupe et al. 2016), a greater capacity to disperse is also thought to reduce the control of abiotic factors over the extent of mammal ranges (Faurby and Antonelli 2018, Magnus, Machado et al. 2018), thereby resulting in a broader abiotic niche. Biotic interactions and dispersal capacity affect the extent to which taxa fill their 'fundamental niches' (Barve, Barve et al. 2011) – indeed, the abiotic niche projections in Chapters 2 and 4 only represent groups' 'realised' present-day niches, informed and restricted by environmental factors which did not exist in the geological past (e.g. human activity). Uncertainty thus persists as to the extent to which these projections reflect actual taxon occupancy and dispersal across deep time. To better assess the degree to which patterns observable in projections (such as the coastal 'corridor' in Chapters 2 and 4) reflect the true distributions of extinct taxa, a methodology for modelling and predicting complete niche dynamics across deep time is required.

The results of Chapter 4 suggest that, while South American metatherians (including microbiotheres) may have dispersed through Antarctic 'Valdivian' temperate rainforest, any ecological relationships between metatherians and Valdivian plants were an emergent property

of coincidental abiotic niche similarity, as opposed to a co-evolutionary dynamic established across deep time. Mammals in particular are rarely specialised for interactions with specific plant species (Shipley, Forbey et al. 2009), and 'ecological fitting' does appear to be a common causal factor for animal-plant ecological relationships. For instance, several species of herbivorous insect, thought to have co-evolved alongside specific host plants, can instead establish equivalent relationships with newly available plant taxa (Agosta 2006, Cipollini and Peterson 2018), while African sunbirds will rapidly and effectively adopt pollinator roles for unfamiliar flower species within an experimental framework (Janeček et al. 2020). Indeed, the apparent lack of ecological specialisation in microbiotheres may even corroborate findings made in my other data chapters. In Chapter 2, I demonstrate how many of the marsupial family-level groups that show a 'corridor' of suitable abiotic conditions in Palaeogene Antarctica are also known for their generalised diets (Beck 2017), and I have already discussed here the possible ecological similarities resolved in Chapter 3 between Palaeocene metatherians and present-day didelphids, a clade known for their generalised morphology (Chemisquy, Tarquini et al. 2021). In this way, it is feasible that a lack of ecological specialisation may have been an important facilitator of metatherian dispersal from South America to Australia, allowing taxa to adapt to polar environments rapidly via 'ecological fitting'.

To summarise, we may use the collective findings of my thesis, alongside hypotheses proposed in pre-existing scientific literature, to produce the following hypothetical scenario for the origination of biogeographical trends in Gondwanan therians:

- In the early Palaeocene, both Metatheria and Eutheria were seemingly well established in South America - the marsupial clades Paucituberculata, Microbiotheria and Eomarsupialia may have already originated, along with placentals like SANUs and perhaps Xenarthra (Chapter 2 and 3).
- Some representatives of these three marsupial clades, likely situated in the south of the continent, were seemingly pre-adapted for surviving in and dispersing through Antarctic

Nothofagus forest, given their pre-existing abiotic tolerances, arborealism, ecological generalism, and their capacity to tolerate seasonal conditions - attributes seen readily in present-day members of the family Acrobatidae (Chapters 2, 4 and potentially 3).

- Microbiotheres may have shown particular adaptability in terms of establishing beneficial ecological relationships with plant species they encountered in their environment (via 'ecological fitting'), including mistletoes (Chapter 4).
- Populations of the three marsupial clades may have dispersed south into the Antarctic Peninsula, along with xenarthran and SANU taxa, before the formation of an epicontinental seaway ~55 Ma acted as an effective biogeographical barrier between South America and Antarctica (Reguero, Gelfo et al. 2014, Reguero and Goin 2021) (Chapter 2).
- Xenarthrans and SANUs appear to have been restricted to the Peninsula, possibly given their abiotic tolerances. The apparent insularity and consistent forest biome of the Peninsula may have resulted in low turnover of its mammal genera across the early Palaeogene, suggesting little therian dispersal into Antarctica after the Ypresian (Chapter 2 and 3).
- Given their previously mentioned attributes, eomarsupials, paucituberculates, and microbiotheres may have been able to disperse westwards from the Peninsula and along the Pacific coast of Antarctica. This dispersal may have been aided by some oceanic dispersal via the Ross Sea oceanic gyre. Alternatively, this gyre may have allowed for marsupial dispersal from South America after the formation of the epicontinental seaway, perhaps during the Ypresian (Chapter 2).
- Although *Nothofagus* forest may have covered a large area of Antarctica at this time, dispersing marsupials were possibly restricted to the coast by their limitations of their abiotic niches (Chapter 4).
- Eomarsupials, paucituberculates, and microbiotheres may have dispersed into Australia. Paucituberculata and Microbiotheria then became extinct in Australia. At some point, Eomarsupialia became extinct in South America (Chapter 2).

- The presence of the 'condylarth' genus *Tingamarra* in Australia suggests that some eutherian dispersal may have also occurred around this time, although no extant representatives of this event remain (Chapter 3).
- Antarctica may have retained *Nothofagus* forest (and an associated 'Gondwanan biota') throughout much of the Palaeogene, including after final Gondwanan break-up. The eventual disappearance of the forest was likely caused by a switch from 'greenhouse' to 'icehouse' conditions, and resulted in the extinction of all terrestrial therians in Antarctica (Chapter 2 and 4).
- By the time of the final break-up of the Gondwanan supercontinent, South America and Australia each had geographically unique therian clades. Substantial rates of biotic niche change across the Palaeogene and up to the present day reflect how South America and Australia have since seen both significant therian ecological evolution and the arrival of new therian clades via dispersal from other continents (Chapter 2 and 3).

In light of the findings within this thesis, future directions of study which may further elucidate therian biogeographical narratives include the following:

- Examining the impact of a greater variety of environmental factors on therian abiotic niches, including novel variables (e.g. terrain, altitude) as well as elaborations on those examined here (e.g. distinguishing rainfall and snowfall, as opposed to grouping both under 'precipitation').
- Resolving the interplay between abiotic and biotic factors to a more specific case-by-case extent, and how said interplay may affect the ranges and dispersal capacity of extant and extinct therian clades.
- Examining the ecological impact of biotic traits beyond body mass and dietary category, including reproductive strategy (see Assumptions and Limitations), ontogeny, extent of arboreality and seasonality.
- Exploring further statistical methods to compare the biotic niches of therians across deep time beyond Jaccard distances and Bray-Curtis dissimilarity indices – these could, for instance, be used

to test the validity of our surprising but inconsistent result that Palaeocene and present-day metatherians in South America may show notable biotic niche similarity.

- Examining ecological relationships beyond those involving microbiotheres, to test how they may have affected the broader biogeographical history of Gondwanan therian clades.
- Improving the Gondwanan fossil record, by expanding the spatial coverage of fossil surveying and diagnosing the taxonomic identities of presently ambiguous but potentially significant specimens (see Assumptions and Limitations).

It is now common consensus within the field of mammalogy (Clemens 1968, Schmidt-Nielsen, Bolis et al. 1980, Mark and Marotte 1992, Bewell 2004, Gaudin and Croft 2015, Ashby 2021) that the colonial background of Western science has resulted in the historical depiction of Gondwanan mammals as 'strange' or 'archaic'. For instance, Professor George Gaylord Simpson, arguably the most influential Western figure in Gondwanan mammal palaeontology, wrote in 1937 that while the mammal biotas of Eurasia and North America all 'modernized' during the Palaeogene, South America remained 'primitive' until the end of the Neogene [~2.6 Ma], and in Australia 'this change never took place (aside from the agency of man)' (Simpson 1937). In contrast to Simpson's appraisal, my thesis shows that Gondwanan mammal ecology has been complex and ever-changing since at least the Cretaceous-Palaeogene boundary. The endemic clades of South America and Australia are as 'modernized' as taxa more familiar to Western scientists, having evolved continuously across deep time to produce some of the most important global hotspots for mammal diversity (Burgin, Colella et al. 2018). The multidisciplinary methodologies used here have facilitated new perspectives on previously obscure biogeographical narratives, demonstrating pipelines of analysis that avoid or otherwise compensate for an especially lacking fossil record. Future analyses may improve, expand and elaborate upon these methodologies to provide further insight into one of the least known, yet potentially most significant, periods of mammalian evolution.

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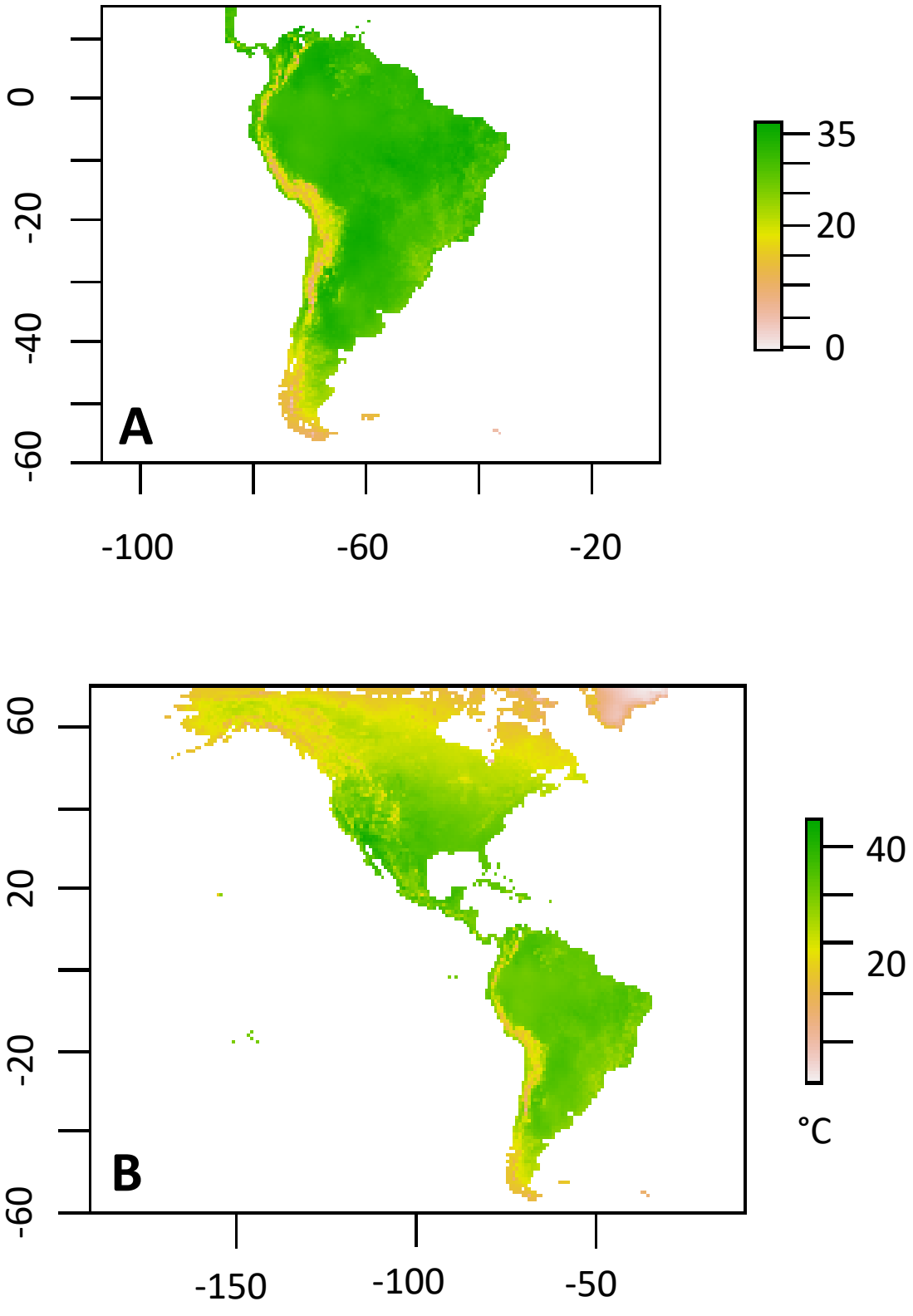
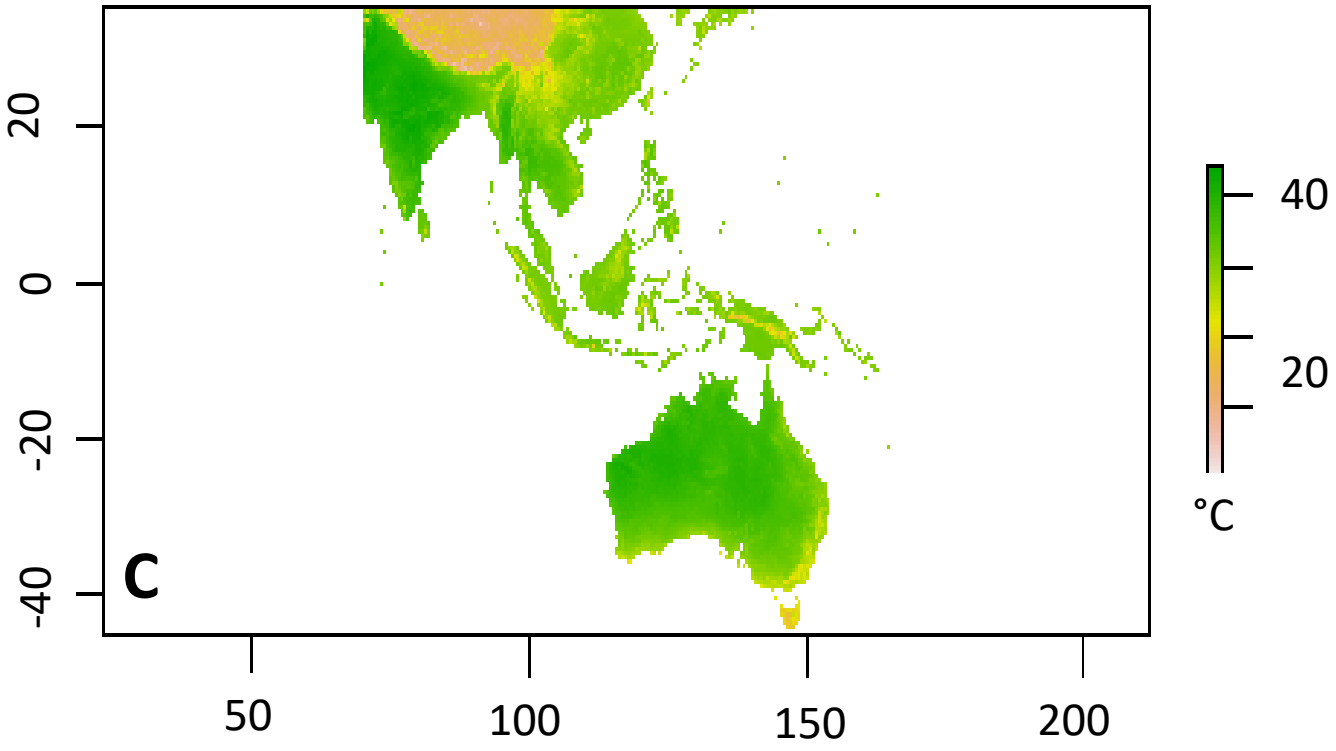
Supplementary Information

Jack McMinn, Anjali Goswami, Alexander Farnsworth and Erin Saupe

CONTENTS

2.1





Figures A, B and C – Biogeographically informed clipped calibration regions for clades only found in South America (-85° to -30° longitude, -60° to 15° latitude), clades found in both North and South America (-170° to -30° longitude, -60° to 70° latitude) and Eomarsupialia (70° to 165° longitude, -45° to 35° latitude). The variable being displayed is WorldClim 2's maximum temperature of the warmest month (Fick and Hijmans 2017). The bounds of the American calibration regions are defined by continental extent, while the bounds of the Eomarsupialia calibration region are defined by mountainous regions which surround South-East Asia and act as a substantial dispersal barrier in the present day.

2.2

(The following was written by Dr. Alexander Farnsworth [University of Bristol], who developed the palaeoclimate models used in this work. This extract was adapted and used in Fenton et al. (2023).)

Palaeoclimate model

Paleoclimate model simulations were carried out using a recent version of the UK MetOffice coupled Atmosphere-Ocean General Circulation Model (AOGCM), HadCM3 (specifically HadCM3L-M2.1D), following the nomenclature of Valdes, Armstrong et al. (2017). HadCM3L-M2.1D has a model resolution of 3.75° longitude × 2.5° latitude in the atmosphere and ocean (~250 km grid squares in the tropics), with 19 hybrid levels in the atmosphere and 20 vertical levels in the ocean with equations solved on the Arakawa B-grid. As is common in all climate models, sub-grid scale processes such as cloud, convection and oceanic eddies are parameterized as they cannot be resolved at the scales required (usually meters to several kilometres) of the model resolution. Due to a lack of geological spatiotemporal data recording land surface vegetation and soil characteristics in deep time climates we use modern day vegetation expressions for broadleaf trees, deciduous trees, shrubs, C3 and C4 grasses (five in total) and a globally uniform distribution of a medium loam soil characteristics in the model land surface scheme (MOSES 2.1) (Cox, Betts et al. 1999). The land surface scheme also includes evaporation from sub-grid scale lakes (which are prescribed as a lake fraction in each grid box, at the start of the simulation). We use a version of the model that includes the dynamical vegetation model TRIFFID (Top-Down Representation of Interactive Foliage and Flora Including Dynamics). TRIFFID predicts the distribution and properties of global vegetation based on plant functional types (PFTs), in the form of fractional coverage (and thus PFT co-existence) within a grid-cell and are in turn based on competition equations based on the climate tolerance of the five plant functional types.

The model has a further update that includes modification to cloud condensation nuclei density and cloud droplet effective radius following recent work (Kiehl and Shields 2013, Sagoo, Valdes et al. 2013). This raises higher latitude temperatures without significantly changing tropical temperatures reducing the pole-to-equator temperature gradient in line with proxy observations. This update is also found to work under both hot, cool and ice house conditions, as well under pre-industrial boundary conditions making it appropriate for use across modern and deep time.

The ocean model is based on the model of Cox, et al. (1984) and is a full primitive equation, three-dimensional model of the ocean. A second order numerical scheme is used along with centred advection to remove nonlinear instabilities. Flux adjustments (such as artificial heat and salinity adjustments in the ocean component model (Collins, Tett et al. 2001) to prevent it from drifting to unrealistic values) are not required in this model which is crucial for long paleoclimate simulations (Farnsworth, Lunt et al. 2019). Sea-ice is calculated on a zero layer model with partial sea ice coverage possible with a consistent salinity assumed for ice.

Each simulation was initialised from an equilibrated pre-industrial state in the atmosphere and ocean. Surface vegetation was uniformly set as shrub everywhere and would evolve via TRIFFID based on the evolution of the local climate.

The HadCM3 family of models has extensively contributed to the Coupled Model Intercomparison Project (CMIP 1-5) experiments, as well as the Paleoclimate Modelling Intercomparison Project (PMIP 1-4) demonstrating skill at reproducing the modern day climate (Valdes, Armstrong et al. 2017) and an array of paleoclimate experiments (Farnsworth, Lunt et al. 2019, Valdes, Scotese et al. 2021, Jones, Mannion et al. 2022). Paleoclimate experiments require in the order of hundreds of years to reach a near-surface equilibrium state but substantially longer (many thousands of years) for the deep ocean (Farnsworth, Lunt et al. 2019, Valdes, Scotese et al. 2021), and true climate equilibrium, due to the long period of adjustment of ocean circulation to applied forcings. Lower resolution models are less computationally expensive allowing fully equilibrated

simulations of deep time climate to be undertaken which would not be possible with higher-resolution, more complex models.

Snapshot simulations, specific boundary conditions and spin-up

We ran 'snapshot' simulations over the Cenozoic with each simulations having time specific boundary conditions. Paleogeographic digital elevation models (DEMs) were produced the EarthByte group as part of the PALEOMAP project (Scotese 2021). Each stage and time specific DEM are interpolated from a 1°x1° grid onto the HadCM3L 3.75°x2.5° grid. Similarly, land ice is also transformed onto the model grid assuming a simple parabolic shape to estimate the ice sheet height (m). 'Realistic' pCO_2 concentrations for each simulation are based on Foster, et al. (2017). Time specific solar luminosity for each simulation was based on Gough (1981). All other boundary conditions (such as orbital parameters, volcanic aerosol concentrations, etc.) are held constant at pre-industrial values. To ensure each simulation have fully adjusted to the boundary conditions we follow a 3-stage spin-up protocol so that each simulation is fully equilibrated:

- The globally and volume-integrated annual mean ocean temperature trend is less than 1°C per 1000 years
- trends in surface air temperature are less than 0.3°C per 1000 years
- net energy balance at the top of the atmosphere, averaged over a 100-year period at the end of the simulation, is less than 0.25/W m2.

In general, these simulations have been run for over 9,000 model years to ensure full Earth system equilibrium. Climate means (i.e. mean annual temperature [MAT], mean annual precipitation [MAP], seasonal variation in temperature, and seasonal variation in precipitation) were produced from the last 100 years of the simulation.

Spatiotemporal interpolation techniques

We then take each snapshot simulation and interpolate the model data and boundary conditions over the Cenozoic. First, the DEM (bathymetry & topography) is linearly interpolated between each pair of snapshot simulations at 0.5 million increments onto a 1°x1° longitude by latitude grid. Each increment is time weighted between the two interpolated snapshot simulations DEMs. The land sea mask is generated for each newly generated interpolated DEM where any grid above 0m is taken as a land point, whereas any grid point below 0m is an ocean point. Isolated ocean points are removed if 6 of the surrounding grid boxes are land with the corresponding topography set the mean of the surrounding grid boxes.

The snapshot model data (e.g. surface temperature, precipitation) is then interpolated using bicubic remapping for each variable onto the interpolated created land sea mask. Sea surface temperature and salinity fields are then extrapolated to fill in grid boxes that are newly created using Poisson's equation (elliptic partial differential equation) over the input domain.

Palaeo-ecological niche modelling requires global-scale datasets of key environmental variables, such as temperature and precipitation, through geological time. Global proxy databases with large spatiotemporal coverage are available for past time periods; however, proxy evidence becomes increasingly less constrained, and the amount of spatiotemporal data increasingly diminishes, further into the geologic past. This necessitates the use of paleoclimate models to provide these global datasets. Paleoclimate simulations of deep-time climates are challenging. In part, this is because there are many uncertainties that need to be considered when undertaking a model simulation which, depending on the time period, can be relatively unconstrained by observations. Uncertainties can in general be partitioned into two main sources, boundary condition uncertainty, and model uncertainty.

Boundary conditions

Boundary conditions are spatiotemporally varying parameters that are required by climate models but cannot be calculated internally by the model and instead need to be provided by the user. The most important boundary conditions for the model used here are (a) Paleogeographic reconstructions, (b) Ice sheet height and extent, (c) Solar luminosity, (e) Orbital configuration, and (e) Greenhouse gas concentrations.

a) A large source of uncertainty arises from paleogeographic reconstruction. DEMs, constrained by paleo-databases, provide topography, bathymetry, and land-sea concentration. These are crucial for determining local, regional, and global atmospheric and ocean circulation and as a result the underlying climate in the model. The further into the geologic record, the greater the reduction in the proxies, creating larger uncertainties in these reconstructions. However, our understanding of plate tectonics, spreading ridges, weathering rates and basinal deposition allows in general an accurate first order approximation of deep-time paleogeography. The largest uncertainties usually result from the height and depth of topographic and bathymetric surfaces and their spatial coverage because of proxy uncertainty (e.g. Farnsworth, Valdes et al. (2021)). Multi-stage paleogeographic reconstruction are currently only available from two datasets, the PALEOMAP project (used in this study) and Getech Plc.
b) Ice sheets (and associated sea-level height) can have a large impact not only on regional climate, but also global climate primarily due to changes in land surface area, planetary albedo and modification to ocean and atmospheric circulation. Currently the vast majority of paleoclimate models prescribe the height and extent of ice sheets based on proxy-evidence.
c) Solar luminosity, essentially the amount of energy received by a planetary body from its parent star is fairly well known. Gough (1981) approximated the amount of energy based on a simple model based on the age of the parent star. Apart from the first 0.2 Gyr this approximation is shown to agree well with observations (Bahcall, Pinsonneault et al. 2001).

d) Orbital configuration - the eccentricity, obliquity, and precession of the planet's orbit around its parent star and rotation on its own axis can have a substantial impact on the seasonal and latitudinal climate signal, which in turn, can lead to significant changes in climate state (glacial to interglacial). This is due to ice sheet formation and associated changes in global atmospheric and oceanic response. Often for deep-time simulations a modern orbital configuration is imposed. There are several reasons for this. Firstly, chronological uncertainty in proxies we wish to compare the model against often will cover many orbital cycles. This may result in the proxy being more representative of a mean orbital state (akin to the modern day). Secondly, it makes it easier to understand how different a deep-time climate is compared to our modern climate. Orbital variation will have its largest impact on climate where ice sheets are able to grow, in part this is reflective of the amount of pCO_2 in the atmosphere and associated global temperature.

e) Greenhouse gas concentrations, more specifically, pCO_2 concentrations, can be variable through the geologic past. Proxy type, age, techniques, and calibration uncertainty when converting to a pCO_2 estimate, as well as the number of records through the geologic past, can make constraining a deep time pCO_2 concentration problematic (Foster, Royer et al. 2017). Furthermore, although a combination of multiple proxy sources can improve the robustness of the estimated pCO_2 estimates, it may also hinder where the combination of errors is combined to produce a mean pCO_2 estimate. There is also the issue of time averaging. While for the most part paleogeography changes on geological timescales, pCO_2 concentrations can vary on hundreds to million-year timescales. Here we are only interested in the long-term background geological signal (millions of years), with scatter around the mean typically ~400ppm (Foster, Royer et al. 2017).

Model uncertainty

Although all globally available paleoclimate models use the same well-known sets of equations to simulate the large-scale behaviour of the atmosphere and ocean, results from different models

can vary, in particular at the local and regional scale. This is due to the complexity of each model, resolution dependencies, spin-up and the applied initial state, and parameterizations used to approximate processes such as cloud formation that cannot be explicitly resolved at the grid-scale of all current paleoclimate models. In an ideal world such paleoclimate simulations would be run by multiple paleoclimate modelling groups as is done in the Climate Model Intercomparison Project (CMIP) for near future climate change studies.

Unfortunately, it is not in the scope of this manuscript to fully address this question (for instance, these simulations took over two years to complete on a high-performance supercomputer) and few paleoclimate modelling groups have the capability to such sets of deep time simulations. However, confidence in the robustness of our results can be obtained by the following facts:

a) The HadCM3 family of models, although 20 years older than many of its contemporaries, still compares reasonably well with models form the previous IPCC Coupled CMIP fifth assessment models (Valdes, Armstrong et al. 2017).
b) HadCM3L-M2.1D has seen continued development (Valdes, Armstrong et al. 2017). Here we use an updated version of the model which solves a persistent problem with the majority of paleoclimate model known as the 'cold pole paradox' where the simulated higher latitudes were previously much cooler than suggested by proxy-observations.
c) These simulations have been run out for over 9000 model years. Often paleoclimate simulations are run for only a couple of thousands of years due to the computational costs. However, it can take upward of 5,000 years to truly allow a model simulation to equilibrate to all the applied model forcings, in particular for the deep ocean, and as such, the global ocean circulation to be fully representative of the deep-time period.
d) Although model uncertainty is important to constrain it has been shown that scenario uncertainty, in other words the applied boundary conditions, is a larger source of error, at least for future climate simulations (Hawkins and Sutton 2009).

2.3

Changes to GBIF extant marsupial genus records, in order to corroborate them with the IUCN classification system, were as follows:

- *Notamacropus* and *Osphranter* presences were changed to *Macropus* (Celik, Cascini et al. 2019).
- *Micromurexia*, *Murexechinus*, *Paramurexia* and *Phascomurexia* presences were changed to *Murexia* (Van Dyck 1999, Van Dyck 2002).
- Presences for *Antechinus puteus*, *Antechinus yammal*, *Antechinus yuna*, *Bettongia anhydra, Bettongia pusilla, Burramys triradiatus, Dasyurus dunmalli*, *Didelphis solimoensis, Hypsiprymnodon bartholomaii, Lagorchestes asomatus, Lagorchestes leporides, Lutreolina materdei, Macropus atlas, Macropus goliah, Macropus greyi, Macropus mundjabus, Macropus pan, Macropus rama, Macropus thor, Macropus woodsi, Macrotis leuceri, Marmosa contrerasi, Onychogalea lunata, Pachysiagon ferragus, Perameles allinghamensis, Perameles bowensis, Perameles eremiana, Phascolarctos maris, Phascolarctos stirtoni, Potorous platyops, Pseudochirops winteri*, *Pseudocheirus stirtoni, Sarcophilus moornaensis, Sminthopsis floravillensis, Strigocuscus notialis, Strigocuscus reidi*, *Thylamys minutus, Trichosurus dicksoni, Trichosurus hamiltonensis, Wallabia kitcheneri, Wyulda asherjoeli* and *Zygolestes entrerianus* were listed as part of an extant genus, but were excluded given their extinction (Owen 1873, Turnbull and Lundelius 1970, Mones 1980, Archer 1982, Crabb and Archer 1982, Van Dyck 1982, Dawson and Flannery 1985, Flannery and Archer 1987, Flannery and Archer 1987, Flannery, Turnbull et al. 1987, Turnbull, Rich et al. 1987, Flannery 1989, Goin 1997, Wales 1997, Wroe and Mackness 1998, Crosby, Nagy et al. 2001, Mackness and Archer 2001, Prideaux 2004, Piper 2005, Cozzuol, Goin et al. 2006, Crosby 2007, Turvey 2009, Cramb and Hocknull 2010, Goin and Reyes 2011, Goin 2013, McDowell, Haouchar et al. 2015).
- *Antechinus argentus* presences were excluded, in order to ensure that an identical filtering procedure was followed for all considered taxa - no IUCN polygon existed for *A. argentus* at the

time of analysis, and it was not considered part of an already described species (Baker, Mutton et al. 2013).

- *Antechinus arktos* presences were changed to *Antechinus swainsonii* (Baker, Mutton et al. 2014).
- *Antechinus mysticus* presences were excluded – no IUCN polygon existed for this taxon at the time of analysis, and being spatially sympatric with other described *Antechinus* species, it is difficult to say what species *A. mysticus* occurrences would have been previously attributed to, prior to its own description (Baker, Mutton et al. 2012).
- *Caenolestes obscurus* presences were excluded, as it was difficult to tell if they were equivalent to *Caenolestes convelatus* or *Caenolestes fuliginosus* (Gardner 2019).
- *Dactylopsila palpator* presences were changed to *Dactylonax palpator* (Haltenorth 1958).
- *Dromiciops bozinovici* presences were changed to *Dromiciops gliroides* (D'Elía, Hurtado et al. 2016).
- *Gracilinanus agricolai* presences were changed to *Cryptonanus agricolai* (Voss, Lunde et al. 2005).
- *Isoodon fusciventer* and *Isoodon peninsulae* presences were changed to *Isoodon obesulus* (Driessen and Rose 2015).
- *Kangurus veterum* presences were changed to *Dorcopsis muelleri* (Meredith, Westerman et al. 2009).
- *Marmosa isthmica* presences were changed to *Marmosa robinsoni* (O'Connell 1983).
- *Marmosa waterhousei* presences were changed to *Marmosa murina* (Gutiérrez, Soriano et al. 2011).
- *Marmosops dorothea* presences were changed to *Marmosops noctivagus* (Voss, Tarifa et al. 2004).
- *Marmosops marina* and *Marmosops woodalli* presences were changed to *Marmosops pinheiroi* (Guimarães, Rocha et al. 2021).
- *Monodelphis sorex* presences were changed to *Monodelphis dimidiata* (Pavan, Jansa et al. 2014).

- *Monodelphis theresa* and *Monodelphis gardneri* presences were changed to *Monodelphis scalops* (Solari, Pacheco et al. 2012, Pavan, Jansa et al. 2014).
- *Monodelphis touan* presences were changed to *Monodelphis brevicaudata* (Pavan, Rossi et al. 2012).
- *Perameles pallescens* presences were changed to *Perameles nasuta* (Travouillon 2016).
- *Perameles papillon* presences were changed to *Perameles bourgainville* (Travouillon and Phillips 2018).
- *Phascogale hillieri* presences were changed to *Dasycercus cristicauda* (Woolley 2005).
- *Sarcophilus laniarius* presences were excluded - the species name is used interchangeably in previous literature to refer to both a fossil taxon and the extant *Sarcophilus harrisii,* and we wanted to reduce the risk of accidentally including occurrences from extinct species (Rose, Pemberton et al. 2017).
- *Sminthopsis fuliginosus* presences were excluded - no IUCN polygon existed for this 'data deficient' taxon at the time of analysis (Hohnen, P. Murphy et al. 2019).
- *Tarsipes spenserae* presences were changed to *Tarsipes rostratus* (Mahoney 1981).
- *Thylamys sponsorius* presences were changed to *Thylamys cinderella* (Braun, Van Den Bussche et al. 2005).
- *Tlacuatzin balsasensis* presences were changed to *Tlacuatzin canescens* (Arcangeli, Light et al. 2018).
- *Trichosurus arnhemensis* and *Trichosurus johnstonii* presences were changed to *Trichosurus vulpecula* (Kerle, McKay et al. 1991).

Other changes to xenarthran records elicited by the IUCN classification system were as follows:

- *Dasypus neogaeus, Nunezia caroloameghinoi* and *Tatu bellus* presences were listed as part of an extant genus, but were excluded given their extinction (Simpson and Whitaker 1949, Scillato 2013, Gaudin, Hicks et al. 2018).

- *Chaetophractus nationi* presences were changed to *Chaetophractus vellerosus (Abba, Cassini et al. 2015).*
- *Cyclopes catellus*, *Cyclopes dorsalis, Cyclopes ida, Cyclopes rufus,* and *Cyclopes thomasi* presences were changed to *Cyclopes didactylus* (Miranda, Casali et al. 2018).
- *Dasypus mazzai* presences were changed to *Dasypus yepesi* (Feijo and Cordeiro-Estrela 2014).
- *Dasypus minutus* presences were changed to *Zaedyus pichiy* (Superina and Abba 2014).

Changes to PBDB records of fossil marsupials taxonomically diagnosed to the family level are as follows (changes nullified by automated aspects of our filtering have not been mentioned):

- Caroloameghiniids, derorhynchids, herpetotheriids, peradectids, protodidelphids, pucadelphyids and other similar extinct groups are removed from Didelphidae/Didelphimorphia (Beck, Voss et al. 2022). Modern didelphid groups likely originated and developed in relative geological recency (Jansa, Barker et al. 2014, Beck and Taglioretti 2020, Castro, Dahur et al. 2021) yet the clade retains many plesiomorphic traits from ancestral marsupial stock (Voss and Jansa 2009, Williamson, Brusatte et al. 2014, Voss and Jansa 2021) – thus, extinct taxa from the stem or crown base of Marsupialia have often been classified as didelphimorphs. The earliest Australian marsupials is also thought to have resembled the same extinct taxa, and hence didelphimorphs by extension (Szalay 1994).
- Given the aforementioned ambiguous atavisms of morphology between groups, all fragmentary remains assigned to 'Didelphimorphia' are excluded from further study.
- The Santa Rosa local fauna and the Contamana sites CTA-27/CTA-29 in South America are re-assigned to the Rupelian, along with their associated paucituberculates (members of the caenolestid total clade) (*Sasawatsu, Perulestes*), and microbiotheres (members of the microbiotheriid total clade) (*Kirutherium*) (Antoine, Abello et al. 2016, Campbell Jr, O'Sullivan et al. 2021, Arnal, Pérez et al. 2022) – in contrast, see (Campbell Jr, Frailey et al. 2004, Arnal, Kramarz et al. 2020).

- The Leaf locality at Lake Ngapakaldi in Australia is re-assigned to the early Miocene – it and its associated taxa are excluded from further study (Chamberlain, Travouillon et al. 2016, Janis, Damuth et al. 2016).
- Faunal Zone B of the Riversleigh World Heritage Area in Australia is reassigned to the Miocene, along with the associated phalangerid *Wyuldia* – this taxon is thus excluded from further study (Schwartz 2006, Travouillon, Escarguel et al. 2011).
- An isolated calcaneus from Ypresian Australia (*QM F30060*) is considered a paucituberculate (as it clusters with the group in Bayesian phylogenetic analysis) (Beck 2012). Possible microbiothere fossils have been found in the same fossil locality (the Tingamarra local fauna), but given their lack of any formal description, these are not considered here (Archer, Arena et al. 1999, Eldridge, Beck et al. 2019).
- *Balbaroo, Nambaroo* and *Ganawamaya* are considered hypsiprymnodonts (as a stem group) (Cooke 1992, Butler, Travouillon et al. 2021). While some species of *Nambaroo* have been reclassified as *Ganawamaya* (Butler, Travouillon et al. 2018), the records of both genera were not changed, as the taxonomic resolution of this study made such measures irrelevant.
- *Cookeroo, Ngamaroo, Purtia* and *Wakiewakie* are considered macropodids (Eldridge, Beck et al. 2019, Travouillon, Butler et al. 2022).
- *Fieratherium* is considered a paucituberculate (as a stem group) (Forasiepi, Goin et al. 2014).
- *Marambiotherium* is considered a microbiothere (Goin, Case et al. 1999, Defler 2019).
- *Marlu, Nambaroo* and *Wakiewakie*, as well as indeterminate peramelid remains, are recorded as present at the Chattian Australian Kangaroo Well Local Fauna (Megirian, Murray et al. 2004).
- *Balbaroo,* the macropodid *Bulungamaya* (Travouillon, Butler et al. 2022)*, Burramys,* the hypsiprymnodont *Ekaltadita* (Wroe, Brammall et al. 1998), *Ganawamaya*, the macropodid *Gumardee* (Travouillon, Butler et al. 2022)*, Nambaroo, Pildra,* the macropodid *Wabularoo* (Travouillon, Archer et al. 2015) and the macropodid *Wururoo* (Archer, Arena et al. 2006)*,* as well as indeterminate pseudocheirid remains, are recorded as present at the Chattian Australian

'White Hunter Site', Riversleigh (Long 2002, Pledge 2005, Archer, Arena et al. 2006, Travouillon, Escarguel et al. 2011, Travouillon, Cooke et al. 2014, Travouillon, Archer et al. 2015).

- *Balbaroo, Bulungamaga,* the hypsiprymnodont *Galanarla* (Cooke 1992, Butler, Travouillon et al. 2018), *Gumardee* and *Wabularoo* are recorded as present at the Chattian Australian 'D Site', Riversleigh (Long 2002, Archer, Arena et al. 2006, Travouillon, Escarguel et al. 2011).
- *Bulungamaya* and *Ganawamaya*, as well as indeterminate phalangerid remains, are recorded as present at the Chattian Australian 'Quantum Leap Site', Riversleigh (Long 2002, Archer, Arena et al. 2006, Travouillon, Escarguel et al. 2011, Butler, Travouillon et al. 2018).
- *Burramys, Marlu, Nambaroo, Pildra* and *Purtia*, as well as indeterminate macropodid, petaurid and vombatid remains, are recorded as present at the Chattian Australian Ngama Local Fauna near Lake Palankarinna (Brammall and Archer 1997, Metzger and Retallack 2010).
- *Purtia* is recorded as present at the Chattian Australian Tedford Locality near Lake Palankarinna (Bennett, Upchurch et al. 2018).
- *Ekaltadita* is recorded as present at the Chattian Australian 'Hiatus Site', Riversleigh (Long 2002, Archer, Arena et al. 2006, Travouillon, Escarguel et al. 2011).
- The phalangerid *Eocuscus* (Case, Meredith et al. 2008) is recorded as present at the Chattian Australian 'SAM Quarry' near Lake Palankarinna (Case, Meredith et al. 2008).
- The potoroid *Kyeema* (Janis, Damuth et al. 2016) is recorded as present at Lake Palankarinna (Meredith, Westerman et al. 2008, Janis, Damuth et al. 2016).
- The phascolarctid *Nimiokoala* (Black and Archer 1997) is recorded as present at the Chattian Australian 'South Prospect B Site' near Lake Palankarinna (Bennett, Upchurch et al. 2018).
- The paucituberculate *Pilchenia* (Abello, Toledo et al. 2020) is recorded as present at the Chattian South American sites of Branisa V-2 and Tapial Pampa (Abello 2007, Bennett, Upchurch et al. 2018).
- *Pildra* is recorded as present at Chattian Australian Lake Pinpa Sites B and C (Bennett, Upchurch et al. 2018).

Changes to PBDB xenarthran records are as follows (redundant changes nullified by the filtering system mentioned below have not been mentioned):

- While the family Dasypodidae presently describes the long-nosed armadillos (*Dasypus*) and their kin, it has been previously used to distinguish armadillos from the giant glyptodont superfamily Glyptodontoidea within the order Cingulata (McKenna and Bell 1997, Delsuc, Stanhope et al. 2003, Carlini, Ciancio et al. 2009). However, recent molecular evidence indicates that at least some glyptodonts are phylogenetically nested among the armadillos (Delsuc, Gibb et al. 2016, Mitchell, Scanferla et al. 2016), nullifying the previous classification system. As the taxonomic assessments of many Palaeogene cingulates were made before these new publications, all fossils classified as dasypodids by PBDB are here carefully reassessed.
- PBDB records for '*Scelidodon*' and '*Vassallia*' in South America refers to ambiguous remains in the Fray Bentos Formation (Mones and Ubilla 1978) – they are reassigned to being indeterminate choloepodids and chlamyphorids respectively.
- The Bajo Palangana site in South America is reassigned to the Ypresian, along with its associated indeterminate chlamyphorid (*Utaetus*-like) remains (Simpson 1935, Vera and Krause 2020).
- *Archaeutatus, Barrancatatus, Clypeotherium, Coelutaetus, Doellotatus, Glyptatelus, Kuntinaru, Meteutatus, Neoglyptatelus, Palaeopeltis, Parutaetus, Proeuphractus, Prozaedyus, Pseudeutatus, Pseudoplohophorus, Urotherium* and *Utaetus* are considered chlamyphorids (Simpson 1948, McKenna and Bell 1997, Carlini, Ciancio et al. 2009, Ciancio, Krmpotic et al. 2019, Ciancio, Vieytes et al. 2021, Herrera, Esteban et al. 2021, Pujos, Ciancio et al. 2021).
- *Astegotherium, Dasypodon, Parastegosimpsonia, Prostegotherium, Riostegotherium* and *Stegosimpsonia* are considered dasypodids (Vizcaino 1994, McKenna and Bell 1997, Carlini, Ciancio et al. 2009, Ciancio, Carlini et al. 2013, Ciancio, Krmpotic et al. 2019, Ciancio, Vieytes et al. 2021, Barasoain, González-Ruiz et al. 2022).
- *Deseadognathus* is considered a bradypodid (as a stem group) (Carlini and Scillato-Vane 2004, Presslee, Slater et al. 2019).

- The PBDB entry marked as *Meteutatus* n. sp. *attonsus/*Dasypodidae is reassigned to Chlamyphoridae (Simpson 1948).
- *Octodontotherium, Paroctodontotherium* and *Proplatyarthrus* are considered choloepodids (as a stem group) (McKenna and Bell 1997, Shockey and Anaya 2011, Kalthoff and Green 2018, Presslee, Slater et al. 2019).
- The chlamyphorid *Amblytatus,* as well as indeterminate chlamyphorid (palaeopeltid) remains, is recorded as present at the Chattian South American Lacayani Fauna site (*Isutaetus* is also present but is synonymised with *Pseudeutatus*) (Pujos, Pérez et al. 2021).
- Indeterminate bradypodid (as part of a stem group) remains are recorded as present at the Chattian Puerta Rican Yauco site (MacPhee and Iturralde-Vinent 1995, Schweitzer, Iturralde-Vinent et al. 2006).
- *Octodontotherium* is recorded as present at the Chattian South American Quebrada Fiera site (Pujos, Ciancio et al. 2021).
- The choloepodid (as part of a stem group) *Orophodon* is recorded as present at the Chattian South American Las Cascadas site (Boscaini, Pujos et al. 2019).

2.4

MARSUPIAL FAMILY-LEVEL GROUP	GENERA INCLUDED	OPTIMAL MODEL COMBINATIONS FOR BIOGEOGRAPHICALLY INFORMED CALIBRATION REGION (regularisation parameter - feature classes)	OPTIMAL MODEL COMBINATIONS FOR 200 KM BUFFER CALIBRATION REGION (regularisation parameter and feature classes)	NUMBER OF 'TRAINING' OCCURRENCES	NUMBER OF 'TESTING' OCCURRENCES
Acrobatidae	*Acrobates, Distoechurus*	0.1-l, 0.2-l	0.1-qp [originally 4p]	946	237
Burramyidae	*Burramys, Cercatetus*	0.2-lqph	0.5-lpt, 0.5-pt, 0.6-lt, 0.6-t	1114	278
Caenolestidae	*Caenolestes, Lestoros, Rhyncholestes*	0.4-lp	0.1-qp, 0.2-qp, 0.3-qp, 0.4-qp	54	14
Hypsiprymnodontidae	*Hypsiprymnodon*	0.3-lq	0.2-lp, 0.3-l, 0.4-l, 0.4-lp, 0.5-l, 0.6-l, 0.7-l, 0.8-l, 0.8-lq, 0.9-l, 0.9-lq, 1-l	33	8
Microbiotheriidae	*Dromiciops*	5-qh	10-h [originally 8p, 10p]	92	23
Myrmecobiidae	*Myrmecobius*	0.1-lq	1-lpt, 1-pt, 1-t	12	3
Notoryctidae	*Notoryctes*	0.8-t, 1-t	0.6-qp, 0.8-lqp, 0.8-qp, 0.9-qp, 1-qp	76	19
Peramelidae	*Echymipera, Isoodon, Microperoryctes, Perameles, Peroryctes*	4-lqh, 4-qh	0.5-qp [originally 0.1p]	2196	549
Petauridae	*Dactylonax, Dactylopsila, Gymnobelideus, Petaurus*	3-lqph, 3-qph	4-t	2978	744
Phalangeridae	*Ailurops, Phalanger, Spilocuscus, Strigocuscus, Trichosurus*	4-lqph, 4-qph	5-t, 6-lph	5645	1411
Phascolarctidae	*Phascolarctos*	0.1-lph, 0.1-ph	0.3-lpt, 0.3-lpth, 0.3-lqpt, 0.3-lqpth,	2234	558

			0.3-lqt, 0.3-lqth, 0.3-lt, 0.3-lth, 0.3-pt, 0.3-pth, 0.3-qpt, 0.3-qpth, 0.3-qt, 0.3-qth, 0.3-t, 0.3-th, 0.4-lpt, 0.4-lpth, 0.4-lqpt, 0.4-lqpth, 0.4-lqt, 0.4-lqth, 0.4-lt, 0.4-lth, 0.4-pt, 0.4-pth, 0.4-qpt, 0.4-qpth, 0.4-qt, 0.4-qth, 0.4-t, 0.4-th		
Potoroidea	*Aepyprymnus, Bettongia, Potorous*	10-qpt	0.1-lqp	914	229
Pseudocheiridae	*Hemibelideus, Petauroides, Petropseudes, Pseudocheirus, Pseudochirops, Pseudochirulus*	0.1-qph	1-lqpth, 1-qpth	2807	702
Tarsipedidae	*Tarsipes*	0.9-lqpt, 1-lqpt, 1-qpt	0.1-qp, 0.2-qp	194	49
Thylacomyidae	*Macrotis*	0.7-pt, 0.7-t	0.8-t, 0.9-t	334	83
Vombatidae	*Lasiorhinus, Vombatus*	0.1-lph	0.3-lqph	2042	511
Dibblers, kalutas, kowaris, mulgaras and striped dasyures	*Dasycercus, Dasykaluta, Dasyuroides, Myoictis, Parantechinus*	1-lpth, 1-lth, 1-pth, 1-th	3-lqth, 3-lth	389	97
Marsupial shrews, quolls, speckled dasyures and Tasmanian devils	*Dasyurus, Neophascogale, Phascolosorex, Sarcophilus*	8-pt, 8-t	4-t	2442	610
Phascogalini	*Antechinus, Murexia, Phascogale*	0.4-lqph, 0.4-qph	0.6-lp	2891	723
Pseudantechinus	*Pseudantechinus*	2-lqpt, 2-lqt, 2-qpt, 2-qt	2-lpt, 2-pt	281	70
Sminthopsinae	*Antechinomys, Ningaui, Planigale, Sminthopsis*	0.4-qph	0.8-lqt, 0.8-lt, 0.8-qt, 0.8-t	4518	1129
Caluromyinae	*Caluromys, Caluromysiops, Glironia*	0.1-lqp	0.2-lqp	302	75
Didelphini	*Chironectes, Didelphis, Lutreolina,*	0.7-lqpth, 0.7-qpth	0.8-lt, 0.8-t	1837	459

	Metachirus, Philander				
Marmosini	*Marmosa, Monodelphis, Tlacuatzin*	1-lpt, 1-pt	3-lqpth	651	163
Thylamyini	*Cryptonanus, Gracilinanus, Lestodelphys, Marmosops, Thylamys*	0.6-lqp	0.3-lqp, 2-qh	389	98
Forest-wallabies	*Dorcopsis, Dorcopsulus*	1-pt, 2-lqt, 2-lt	2-h, 2-lh, 2-lph, 2-lpth, 2-lqph, 2-lqpth, 2-lth, 2-ph, 2-pth, 2-qph, 2-qpth, 2-th	21	5
Kangaroos and wallabies	*Lagorchestes, Macropus, Onychogalea, Setonix, Wallabia*	0.1-lqp	0.2-lpth, 0.2-qpt, 0.2-qt	11724	2931
Pademelons, rock-wallabies and tree kangaroos	*Dendrolagus, Petrogale, Thylogale*	0.4-lph	2-t	1411	353

Table A1 – The 'family-level' groups within Marsupialia, the genera included within them, their most suitable niche models as selected by kuenm (Cobos, Peterson et al. 2019) and the number of 'training' and 'testing' occurrences. 'True' taxonomic families are in bold, while monophyletic groups derived from the families Dasyuridae, Didelphidae and Macropodidae are below (Phillips, Haouchar et al. 2013, Amador and Giannini 2016, Kealy and Beck 2017, Celik, Cascini et al. 2019). Terminology from previous literature has been used as much as possible. Underlined combinations indicate where a reproducible error in R/RStudio forced us to select the next best niche model for analysis, with the original most 'suitable' model given in []. Key to feature classes – l = linear, q = quadratic, p = power, t = threshold, h = hinge.

XENARTHRAN FAMILY-LEVEL GROUP	GENERA INCLUDED	OPTIMAL MODEL COMBINATIONS FOR BIOGEOGRAPHICALLY INFORMED CALIBRATION REGION (regularisation parameter and feature classes)	OPTIMAL MODEL COMBINATIONS FOR 200 KM BUFFER CALIBRATION REGION (regularisation parameter and feature classes)	NUMBER OF 'TRAINING' OCCURRENCES	NUMBER OF 'TESTING' OCCURRENCES
Chlamyphoridae	*Cabassous, Calyptophractus, Chaetophractus, Chlamyphorus, Euphractus, Priodontes, Tolypeutes, Zaedyus*	0.8-lqpth, 0.8-qpth	0.8-t, 0.8-lt, 0.8-qt, 0.8-lqt, 0.6-t, 0.6-lt, 0.6-qt, 0.6-lqt, 0.6-pt, 0.6-lpt	855	214
Dasypodidae	*Dasypus*	1-lqpt	3-lpth	115	29
Bradypodidae	*Bradypus*	0.1-lqp	3-pt	746	187
Choloepodidae	*Choloepus*	0.2-lqp	1-lpt	442	111
Cyclopedidae	*Cyclopes*	0.1-lqp	0.2-lq, 0.3-lq, 0.9-lqp, 1-lqp, 0.1-lq	154	38
Myrmecophagidae	*Myrmecophaga, Tamandua*	10-t	8-h	1477	369

Table A2 – The 'family-level' groups within Xenarthra, the genera included within them, and their most suitable niche models as selected by kuenm (Cobos, Peterson et al. 2019). Key to feature classes – l = linear, q = quadratic, p = power, t = threshold, h = hinge.

2.5

FAMILY-LEVEL GROUP	EXCLUDED COORDINATES DUE TO R/RSTUDIO ROUNDING [LON, LAT]
Acrobatidae	[143.416667, -12.6], [152.927951, -31.462264], [150.01487, -36.637479]
Petauridae	[132.080734, -0.5]
Phalangeridae	[141, -5]
Dibblers, kalutas, kowaris, mulgaras and striped dasyures	[141, -5], [153.00004, -30.74869]
Didelphini	[-76.55, 5.5], [70.5833, -13.25]
Kangaroos and wallabies	[134.08267, -32.92033]
Marsupial shrews, quolls, speckled dasyures and Tasmanian devils	[145.67076, -38.66883]

Table B – The 'family-level' groups and the coordinates that were removed from their occurrence datasets, due to R/RStudio rounding the abiotic suitability at these localities down to 0 (which caused the ecological niche modelling process to crash). 'True' taxonomic families are in bold, while monophyletic groups derived from the families Dasyuridae, Didelphidae and Macropodidae are below (Phillips, Haouchar et al. 2013, Amador and Giannini 2016, Kealy and Beck 2017, Celik, Cascini et al. 2019).

2.6

MARSUPIAL FAMILY-LEVEL GROUP	OPTIMAL MODEL COMBINATIONS	TSS	CBI	AUC	Included in final analyses?
Acrobatidae	0.1-l	0.504	0.963	0.79945	Yes
	0.2-l	0.49505	0.96	0.79745	No
Burramyidae	0.2-lqph	0.7746	0.991	0.9179	Yes
Caenolestidae	0.4-lp	0.9192	0.864	0.9775	Yes
Hypsiprymnodontidae	0.3-lq	0.96345	0.647	0.99375	Yes
Microbiotheriidae	5-qh	0.96575	0.862	0.98925	Yes
Myrmecobiidae	0.1-lq	0.96105	0.605	0.9839	Yes
Notoryctidae	0.8-t	0.80735	0.779	0.95515	Yes
	1-t	0.7887	0.893	0.9509	Yes
Peramelidae	4-lqh	0.5809	0.999	0.84715	Yes
	4-qh	0.5841	0.999	0.84725	Yes
Petauridae	3-lqph	0.58035	0.992	0.8296	Yes
	3-qph	0.5746	0.989	0.82795	Yes
Phalangeridae	4-lqph	0.46505	0.99	0.7604	No
	4-qph	0.4645	0.994	0.76025	No
Phascolarctidae	0.1-lph	0.7097	0.98	0.87645	Yes
	0.1-ph	0.7048	0.991	0.8743	Yes
Potoroidea	10-qpt	0.7761	0.994	0.92685	Yes
Pseudocheiridae	0.1-qph	0.66125	0.868	0.8537	Yes
Tarsipedidae	0.9-lqpt	0.9179	0.817	0.97925	Yes
	1-lqpt	0.9234	0.941	0.9804	Yes
	1-qpt	0.91945	0.847	0.98045	Yes
Thylacomyidae	0.7-pt	0.8385	0.967	0.9613	Yes
	0.7-t	0.8429	0.904	0.9615	Yes
Vombatidae	0.1-lph	0.7544	0.931	0.8923	Yes
Dibblers, kalutas, kowaris, mulgaras and striped dasyures	1-lpth	0.7985	0.911	0.9467	Yes
	1-lth	0.80505	0.941	0.94505	Yes
	1-pth	0.8046	0.906	0.9473	Yes
	1-th	0.80225	0.931	0.94545	Yes
Marsupial shrews, quolls, speckled dasyures and Tasmanian devils	8-pt	0.6011	0.857	0.84165	Yes
	8-t	0.59385	0.839	0.8406	Yes
Phascogalini	0.4-lqph	0.63315	0.933	0.8472	Yes
	0.4-qph	0.63835	0.923	0.84615	Yes
Pseudantechinus	2-lqpt	0.7223	0.929	0.92325	Yes
	2-lqt	0.72295	0.953	0.923	Yes
	2-qpt	0.73245	0.938	0.92425	Yes
	2-qt	0.7246	0.859	0.9227	Yes

Sminthopsinae	0.4-qph	0.39225	0.997	0.7259	No
Caluromyinae	0.1-lqp	0.7353	0.894	0.91845	Yes
Didelphini	0.7-lqpth	0.57085	0.992	0.83855	Yes
	0.7-qpth	0.5702	0.986	0.8381	Yes
Marmosini	1-lpt	0.6426	0.986	0.8816	Yes
	1-pt	0.64655	0.985	0.8816	Yes
Thylamyini	0.6-lqp	0.5999	0.887	0.8623	Yes
Forest-wallabies	1-pt	0.84835	0.84	0.96255	Yes
	2-lqt	0.8591	0.129	0.9474	No
	2-lt	0.85765	-0.007	0.9401	No
Kangaroos and wallabies	0.1-lqp	0.2384	0.989	0.64995	No
Pademelons, rock-wallabies and tree kangaroos	0.4-lph	0.5469	0.999	0.84625	Yes

Table C1 – The 'family-level' groups within Marsupialia, their most suitable niche models built around a biogeographically informed calibration region as selected by kuenm (Cobos, Peterson et al. 2019), and their associated model quality metrics. 'True' taxonomic families are in bold, while monophyletic groups derived from the families Dasyuridae, Didelphidae and Macropodidae are in standard text format (Phillips, Haouchar et al. 2013, Amador and Giannini 2016, Kealy and Beck 2017, Celik, Cascini et al. 2019). Models with a TSS and CBI over 0.5, and an AUC over 0.7, were included in further analysis, following previous literature (Pearce and Ferrier 2000, Coetzee, Robertson et al. 2009, Farrell, Wang et al. 2019) – these are highlighted in green. Those that were excluded are highlighted in red. Niche models are labelled with their associated regularisation parameter and the feature classes included. Key to feature classes – l = linear, q = quadratic, p = power, t = threshold, h = hinge.

MARSUPIAL FAMILY-LEVEL GROUP	OPTIMAL MODEL COMBINATIONS	TSS	CBI	AUC	Included in final analyses?
Acrobatidae	0.1-qp	0.5953	0.981	0.85115	Yes
Burramyidae	0.5-lpt	0.551	0.992	0.837	Yes
	0.5-pt	0.54885	0.99	0.8397	Yes
	0.6-lt	0.5315	0.993	0.83275	Yes
	0.6-t	0.53725	0.994	0.83245	Yes
Caenolestidae	0.1-qp	0.6702	0.189	0.8779	No
	0.2-qp	0.6754	0.398	0.87245	No
	0.3-qp	0.6596	0.673	0.8739	Yes
	0.4-qp	0.6707	0.469	0.87615	No
Hypsiprymnodontidae	0.2-lp	0.91525	0.668	0.96665	Yes
	0.3-l	0.87605	0.831	0.95605	Yes
	0.4-l	0.8596	0.707	0.9583	Yes
	0.4-lp	0.8829	0.671	0.9644	Yes
	0.5-l	0.8666	0.792	0.95835	Yes
	0.6-l	0.87085	0.753	0.96165	Yes
	0.7-l	0.86325	0.811	0.95975	Yes
	0.8-l	0.87145	0.805	0.95745	Yes
	0.8-lq	0.86785	0.756	0.96205	Yes
	0.9-l	0.86835	0.824	0.9612	Yes
	0.9-lq	0.8854	0.704	0.96525	Yes
	1-l	0.8674	0.746	0.9591	Yes
Microbiotheriidae	10-h	0.5631	0.393	0.83275	No
Myrmecobiidae	1-lpt	0.74965	0.605	0.91385	Yes
	1-pt	0.82295	0.383	0.93255	No
	1-t	0.69285	-0.375	0.8898	No
Notoryctidae	0.6-qp	0.3947	0.674	0.72975	No
	0.8-lqp	0.4044	0.683	0.73695	No
	0.8-qp	0.35035	0.644	0.7163	No
	0.9-qp	0.33005	0.707	0.7317	No
	1-qp	0.4108	0.733	0.7293	No
Peramelidae	0.5-qp	0.51005	0.997	0.8053	Yes
Petauridae	4-t	0.47855	0.992	0.78085	No
Phalangeridae	5-t	0.39995	0.993	0.73475	No
	6-lph	0.39725	0.998	0.73325	No
Phascolarctidae	0.3-lpt	0.4748	0.994	0.7916	No
	0.3-lpth	0.47245	0.998	0.7924	No
	0.3-lqpt	0.471	0.997	0.7904	No
	0.3-lqpth	0.4716	0.998	0.7925	No
	0.3-lqt	0.47285	0.998	0.7914	No
	0.3-lqth	0.47425	0.998	0.79115	No
	0.3-lt	0.47585	0.998	0.79075	No
	0.3-lth	0.47035	0.999	0.7924	No

	0.3-pt	0.47035	0.998	0.79095	No
	0.3-pth	0.4789	0.998	0.79335	No
	0.3-qpt	0.4761	0.999	0.7919	No
	0.3-qpth	0.46985	0.997	0.78685	No
	0.3-qt	0.47575	0.997	0.7925	No
	0.3-qth	0.46185	0.997	0.7906	No
	0.3-t	0.4751	0.999	0.79155	No
	0.3-th	0.4724	0.998	0.7963	No
	0.4-lpt	0.4623	0.998	0.7876	No
	0.4-lpth	0.46935	0.999	0.78965	No
	0.4-lqpt	0.46595	0.996	0.7902	No
	0.4-lqpth	0.47205	0.993	0.7907	No
	0.4-lqt	0.4642	0.998	0.788	No
	0.4-lqth	0.46535	0.995	0.79015	No
	0.4-lt	0.46635	0.998	0.7883	No
	0.4-lth	0.46705	0.996	0.78885	No
	0.4-pt	0.4713	0.998	0.7916	No
	0.4-pth	0.4696	0.995	0.7903	No
	0.4-qpt	0.47	0.998	0.7895	No
	0.4-qpth	0.4652	0.998	0.7926	No
	0.4-qt	0.4712	0.998	0.7889	No
	0.4-qth	0.4669	0.998	0.7876	No
	0.4-t	0.46775	0.998	0.78865	No
	0.4-th	0.4746	0.995	0.78855	No
Potoroidea	0.1-lqp	0.54195	0.962	0.8395	Yes
Pseudocheiridae	1-lqpth	0.5406	0.993	0.81205	Yes
	1-qpth	0.54185	0.982	0.811	Yes
Tarsipedidae	0.1-qp	0.58605	0.825	0.86005	Yes
	0.2-qp	0.59345	0.862	0.86	Yes
Thylacomyidae	0.8-t	0.6943	0.972	0.89055	Yes
	0.9-t	0.66035	0.967	0.8865	Yes
Vombatidae	0.3-lqph	0.56545	0.993	0.8316	Yes
Dibblers, kalutas, kowaris, mulgaras and striped dasyures	3-lqth	0.3738	0.92	0.74855	No
	3-lth	0.37375	0.958	0.74255	No
Marsupial shrews, quolls, speckled dasyures and Tasmanian devils	4-t	0.5078	0.957	0.80575	Yes
Phascogalini	0.6-lp	0.4895	0.99	0.77195	No
Pseudantechinus	2-lpt	0.41345	0.936	0.7645	No
	2-pt	0.3964	0.934	0.74825	No
Sminthopsinae	0.8-lqt	0.1708	0.956	0.616	No
	0.8-lt	0.168	0.961	0.61475	No
	0.8-qt	0.17585	0.967	0.61745	No

	0.8-t	0.1825	0.953	0.61465	No
Caluromyinae	0.2-lqp	0.2766	0.84	0.66525	No
Didelphini	0.8-lt	0.29415	0.993	0.69625	No
	0.8-t	0.2943	0.982	0.69335	No
Marmosini	3-lqpth	0.30045	0.983	0.68105	No
Thylamyini	0.3-lqp	0.2806	0.907	0.67395	No
	2-qh	0.32985	0.934	0.70905	No
Forest-wallabies	2-h	0.35235	0.858	0.6568	No
	2-lh	0.3507	-0.306	0.61135	No
	2-lph	0.3685	0.782	0.6726	No
	2-lpth	0.33845	0.663	0.64925	No
	2-lqph	0.37285	0.535	0.6862	No
	2-lqpth	0.42765	0.357	0.70725	No
	2-lth	0.4021	0.58	0.69845	No
	2-ph	0.42065	0.655	0.6648	No
	2-pth	0.4229	0.803	0.71595	No
	2-qph	0.39635	0.703	0.68185	No
	2-qpth	0.39515	0.752	0.70505	No
	2-th	0.48815	0.565	0.7005	No
Kangaroos and wallabies	0.2-lpth	0.153	0.998	0.6034	No
	0.2-qpt	0.14215	0.995	0.60045	No
	0.2-qt	0.1471	0.99	0.6005	No
Pademelons, rock-wallabies and tree kangaroos	2-t	0.4995	0.938	0.808	No

Table C2 – The 'family-level' groups within Marsupialia, their most suitable niche models built around a 200 km buffer calibration region as selected by kuenm (Cobos, Peterson et al. 2019), and their associated model quality metrics. 'True' taxonomic families are in bold, while monophyletic groups derived from the families Dasyuridae, Didelphidae and Macropodidae are in standard text (Phillips, Haouchar et al. 2013, Amador and Giannini 2016, Kealy and Beck 2017, Celik, Cascini et al. 2019). Models with a TSS and CBI over 0.5, and an AUC over 0.7, were included in further analysis, following previous literature (Pearce and Ferrier 2000, Coetzee, Robertson et al. 2009, Farrell, Wang et al. 2019). Niche models are labelled with their associated regularisation parameter and the feature classes included. Key to feature classes – l = linear, q = quadratic, p = power, t = threshold, h = hinge.

XENARTHRAN FAMILY-LEVEL GROUP	OPTIMAL MODEL COMBINATIONS	TSS	CBI	AUC	Included in final analyses?
Chlamyphoridae	0.8-lqpth	0.60315	0.989	0.8655	Yes
	0.8-qpth	0.60195	0.995	0.86385	Yes
Dasypodidae	1-lqpt	0.77905	0.898	0.95	Yes
Bradypodidae	0.1-lqp	0.73095	0.969	0.9029	Yes
Choloepodidae	0.2-lqp	0.80835	0.983	0.9477	Yes
Cyclopedidae	0.1-lqp	0.81895	0.827	0.94525	Yes
Myrmecophagidae	10-t	0.5945	0.354	0.8252	No

Table C3 – The 'family-level' groups within Xenarthra, their most suitable niche models built around a biogeographically informed calibration region as selected by kuenm (Cobos, Peterson et al. 2019), and their associated model quality metrics. Models with a TSS and CBI over 0.5, and an AUC over 0.7, were included in further analysis, following previous literature (Pearce and Ferrier 2000, Coetzee, Robertson et al. 2009, Farrell, Wang et al. 2019). Niche models are labelled with their associated regularisation parameter and the feature classes included. Key to feature classes – l = linear, q = quadratic, p = power, t = threshold, h = hinge.

XENARTHRAN FAMILY-LEVEL GROUP	OPTIMAL MODEL COMBINATIONS	TSS	CBI	AUC	Included in final analyses?
Chlamyphoridae	0.6-lpt	0.3866	0.985	0.75155	No
	0.6-lqt	0.3954	0.994	0.75295	No
	0.6-lt	0.3702	0.971	0.74	No
	0.6-pt	0.37545	0.988	0.74935	No
	0.6-qt	0.37155	0.988	0.74425	No
	0.6-t	0.3664	0.978	0.74705	No
	0.8-lqt	0.35315	0.972	0.73135	No
	0.8-lt	0.37395	0.987	0.7397	No
	0.8-qt	0.36145	0.992	0.7347	No
	0.8-t	0.36385	0.969	0.7388	No
Dasypodidae	3-lpth	0.27045	0.278	0.67995	No
Bradypodidae	3-pt	0.357	0.965	0.72425	No
Choloepodidae	1-lpt	0.51755	0.949	0.8164	Yes
Cyclopedidae	0.1-lq	0.29585	0.723	0.6664	No
	0.2-lq	0.2393	0.742	0.6576	No
	0.3-lq	0.2476	0.767	0.65805	No
	0.9-lqp	0.30095	0.847	0.6738	No
	1-lqp	0.3106	0.715	0.6753	No
Myrmecophagidae	8-h	0.1948	0.871	0.636	No

Table C4 – The 'family-level' groups within Xenarthra, their most suitable niche models built around a 200 km buffer calibration region as selected by kuenm (Cobos, Peterson et al. 2019), and their associated model quality metrics. Models with a TSS and CBI over 0.5, and an AUC over 0.7, were included in further analysis, following previous literature (Pearce and Ferrier 2000, Coetzee, Robertson et al. 2009, Farrell, Wang et al. 2019). Niche models are labelled with their associated regularisation parameter and the feature classes included. Key to feature classes – l = linear, q = quadratic, p = power, t = threshold, h = hinge.

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NICHE MODELS WITH BIOGEOGRAPHICALLY INFORMED CALIBRATION REGIONS	*'Eomarsupial' hypothesis [extrapolative area excluded]*	*'Australidelphian+' hypothesis [extrapolative area excluded]*
Danian [66-61.6 Ma] projections thresholded by 95% LTP	191227 ± 402168 vs 17766 ± 25175 [W=140.5, p>0.025]	178088 ± 383830 vs 9879 ± 17672 [W=139.5, p>0.025]
Danian [66-61.6 Ma] projections thresholded by maxSSS	78111 ± 159044 vs 31878 ± 61244 [W=129.5, p>0.025]	83180 ± 153428 vs 9778 ± 19254 [W=137.5, **p<0.025**]
Selandian [61.6-59.2 Ma] projections thresholded by 95% LTP	285676 ± 533774 vs 37549 ± 49519 [W=133, p>0.025]	263739 ± 511122 vs 33597 ± 53969 [W=126, p>0.025]
Selandian [61.6-59.2 Ma] projections thresholded by maxSSS	132208 ± 203074 vs 52483 ± 78473 [W=124, p>0.025]	134982 ± 195143 vs 28294 ± 43068 [W=127, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by 95% LTP	600512 ± 1147869 vs 124911 ± 190265 [W=134, p>0.025]	557187 ± 1097643 vs 120312 ± 210920 [W=126, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by maxSSS	277413 ± 272887 vs 139082 ± 180863 [W=129.5, p>0.025]	281801 ± 262343 vs 98106 ± 162703 [W=128.5, p>0.025]
Priabonian [37.71-33.9 Ma] projections thresholded by 95% LTP	566705 ± 1157406 vs 69933 ± 138425 [W=131, p>0.025]	514998 ± 1110094 vs 80188 ± 152561 [W=120, p>0.025]
Priabonian [37.71-33.9 Ma] projections thresholded by maxSSS	230066 ± 277037 vs 79233 ± 118191 [W=130, p>0.025]	221457 ± 266530 vs 65801 ± 115255 [W=126, p>0.025]
Rupelian [33.9-27.82 Ma] projections thresholded by 95% LTP	453582 ± 856872 vs 31878 ± 61244 [W=146.5, **p<0.025**]	411309 ± 823797 vs 9113 ± 27338 [W=136, **p<0.025**]
Rupelian [33.9-27.82 Ma] projections thresholded by maxSSS	338486 ± 775826 vs 8121 ± 18971 [W=152, **p<0.025**]	307760 ± 742400 vs 6400 ± 19199 [W=140, **p<0.025**]

Chattian [27.82-23.03 Ma] projections thresholded by 95% LTP	530149 ± 1152119 vs 2583 ± 6937 [W=140.5, p>0.025]	480768 ± 1104073 vs 568 ± 1032 [W=129, p>0.025]
Chattian [27.82-23.03 Ma] projections thresholded by maxSSS	358711 ± 982122 vs 3662 ± 10737 [W=147, p>0.025]	326294 ± 937347 vs 401 ± 1075 [W=144, **p<0.025**]

Table D1 – The mean ± SD of the area of suitable non-extrapolative Antarctic area (km^2) for predicted dispersers vs. non-dispersers, for models built using a biogeographically informed calibration region. The W value and statistical significance, as calculated via a Mann Whitney U test with Bonferroni correction, are given in [].

NICHE MODELS WITH 200 KM RADIUS CALIBRATION REGIONS	*'Eomarsupial' hypothesis [extrapolative area excluded]*	*'Australidelphian+' hypothesis [extrapolative area excluded]*
Danian [66-61.6 Ma] projections thresholded by 95% LTP	93738 ± 80802 vs 22870 ± 32344 [W=16, p>0.025]	89738 ± 78278 vs 0 [W=10, p>0.025]
Danian [66-61.6 Ma] projections thresholded by maxSSS	85685 ± 79775 vs 19908 ± 28154 [W=16, p>0.025]	81862 ± 77207 vs 0 [W=10, p>0.025]
Selandian [61.6-59.2 Ma] projections thresholded by 95% LTP	161529 ± 142540 vs 33288 ± 47076 [W=16, p>0.025]	153616 ± 138643 vs 0 [W=10, p>0.025]
Selandian [61.6-59.2 Ma] projections thresholded by maxSSS	147302 ± 141237 vs 29175 ± 41260 [W=15, p>0.025]	139890 ± 137091 vs 0 [W=10, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by 95% LTP	487919 ± 464110 vs 58042 ± 78105 [W=14, p>0.025]	456699 ± 455536 vs 2814 [W=8, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by maxSSS	399963 ± 422908 vs 47438 ± 67087 [W=15, p>0.025]	374539 ± 412733 vs 0 [W=10, p>0.025]
Priabonian [37.71-33.9 Ma] projections thresholded by 95% LTP	364870 ± 337576 vs 40643 ± 57478 [W=17.5, p>0.025]	341238 ± 332113 vs 0 [W=11.5, p>0.025]
Priabonian [37.71-33.9 Ma] projections thresholded by maxSSS	303899 ± 312264 vs 31875 ± 45078 [W=16, p>0.025]	283887 ± 305696 vs 0 [W=11, p>0.025]
Rupelian [33.9-27.82 Ma] projections thresholded by 95% LTP	0 ± 0 vs 80480 ± 44782 [W=0, p>0.025]	4068 ± 14091 vs 112146 [W=0, p>0.025]
Rupelian [33.9-27.82 Ma] projections thresholded by maxSSS	0 ± 0 vs 63379 ± 25764 [W=0, p>0.025]	3763 ± 13037 vs 81596 [W=0, p>0.025]

Chattian [27.82-23.03 Ma] projections thresholded by 95% LTP	48238 ± 57425 vs 57659 ± 19491 [W=9, p>0.025]	47875 ± 54767 vs 71441 [W=4, p>0.025]
Chattian [27.82-23.03 Ma] projections thresholded by maxSSS	39394 ± 52105 vs 29494 ± 11214 [W=9, p>0.025]	39230 ± 49684 vs 21564 [W=6, p>0.025]

Table D2 – The mean ± SD of the area of suitable non-extrapolative Antarctic area (km^2) for predicted dispersers vs. non-dispersers, for models built using a 200 km radius calibration region. The W value and statistical significance, as calculated via a Mann Whitney U test with Bonferroni correction, are given in [].

NICHE MODELS WITH BIOGEOGRAPHICALLY INFORMED CALIBRATION REGIONS	*'Eomarsupial' hypothesis [extrapolative area included]*	*'Australidelphian+' hypothesis [extrapolative area included]*
Danian [66-61.6 Ma] projections thresholded by 95% LTP	196160 ± 406018 vs 25605 ± 31027 [W=137, p>0.025]	182751 ± 387543 vs 18992 ± 29277 [W=132, p>0.025]
Danian [66-61.6 Ma] projections thresholded by maxSSS	79519 ± 163663 vs 37714 ± 60979 [W=124, p>0.025]	84767 ± 157650 vs 16178 ± 24465 [W=134, p>0.025]
Selandian [61.6-59.2 Ma] projections thresholded by 95% LTP	286501 ± 535055 vs 37550 ± 49519 [W=133, p>0.025]	264485 ± 512360 vs 33598 ± 53969 [W=126, p>0.025]
Selandian [61.6-59.2 Ma] projections thresholded by maxSSS	132583 ± 204477 vs 52526 ± 78482 [W=126, p>0.025]	135344 ± 196444 vs 28295 ± 43069 [W=129, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by 95% LTP	600512 ± 1147870 vs 125079 ± 190238 [W=134, p>0.025]	557275 ± 1097605 vs 120313 ± 210921 [W=126, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by maxSSS	277414 ± 272888 vs 139362 ± 180963 [W=129.5, p>0.025]	281947 ± 262294 vs 98106 ± 162703 [W=128.5, p>0.025]
Priabonian [37.71-33.9 Ma] projections thresholded by 95% LTP	566749 ± 1157457 vs 69933 ± 138425 [W=131, p>0.025]	515039 ± 1110144 vs 80188 ± 152562 [W=120, p>0.025]
Priabonian [37.71-33.9 Ma] projections thresholded by maxSSS	230111 ± 277172 vs 79234 ± 118191 [W=130, p>0.025]	221498 ± 266658 vs 65802 ± 115256 [W=126, p>0.025]
Rupelian [33.9-27.82 Ma] projections thresholded by 95% LTP	1254119 ± 3359919 vs 1767 ± 5861 [W=154, **p<0.025**]	1135605 ± 3209402 vs 0 ± 0 [W=144, **p<0.025**]
Rupelian [33.9-27.82 Ma] projections thresholded by maxSSS	1035499 ± 3289868 vs 2885 ± 9569 [W=159, p>0.025]	938391 ± 3136080 vs 0 ± 0 [W=148.5, p<0.025]

Chattian [27.82-23.03 Ma] projections thresholded by 95% LTP	1163985 ± 3243455 vs 1253698 ± 4148627 [W=128, p>0.025]	1054239 ± 3096474 vs 1529708 ± 4587208 [W=114, p>0.025]
Chattian [27.82-23.03 Ma] projections thresholded by maxSSS	196160 ± 406018 vs 25605 ± 31028 [W=133, p>0.025]	182751 ± 387543 vs 18992 ± 29278 [W=128, p>0.025]

Table D3 – The mean ± SD of the area of suitable Antarctic area (km^2), including extrapolative area, for predicted dispersers vs. non-dispersers, for models built using a biogeographically informed calibration region. The W value and statistical significance, as calculated via a Mann Whitney U test with Bonferroni correction, are given in [].

NICHE MODELS WITH 200 KM RADIUS CALIBRATION REGIONS	*'Eomarsupial' hypothesis [extrapolative area included]*	*'Australidelphian+' hypothesis [extrapolative area included]*
Danian [66-61.6 Ma] projections thresholded by 95% LTP	6686645 ± 5764359 vs 23379 ± 31626 [W=21, p>0.025]	6133236 ± 5820847 vs 1016 [W=12, p>0.025]
Danian [66-61.6 Ma] projections thresholded by maxSSS	5741558 ± 5398543 vs 19908 ± 28155 [W=21, p>0.025]	5266413 ± 5404067 vs 0 [W=12, p>0.025]
Selandian [61.6-59.2 Ma] projections thresholded by 95% LTP	7051911 ± 5945430 vs 33335 ± 47010 [W=21, p>0.025]	6469799 ± 6016719 vs 95 [W=12, p>0.025]
Selandian [61.6-59.2 Ma] projections thresholded by maxSSS	6063025 ± 5644799 vs 29176 ± 41261 [W=20, p>0.025]	5562636 ± 5654355 vs 0 [W=12, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by 95% LTP	6425439 ± 5659684 vs 58043 ± 78105 [W=21, p>0.025]	5899425 ± 5695639 vs 2815 [W=12, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by maxSSS	5132254 ± 5305095 vs 47438 ± 67088 [W=20, p>0.025]	4712472 ± 5263087 vs 0 [W=12, p>0.025]
Priabonian [37.71-33.9 Ma] projections thresholded by 95% LTP	7596839 ± 6268553 vs 70426 ± 15361 [W=20, p>0.025]	6970543 ± 6358417 vs 59564 [W=11, p>0.025]
Priabonian [37.71-33.9 Ma] projections thresholded by maxSSS	6539801 ± 5953348 vs 31876 ± 45079 [W=20, p>0.025]	6000130 ± 5976225 vs 0 [W=12, p>0.025]
Rupelian [33.9-27.82 Ma] projections thresholded by 95% LTP	5732143 ± 5286187 vs 6662686 ± 9330017 [W=10, p>0.025]	5259912 ± 5299005 vs 13260003 [W=2, p>0.025]
Rupelian [33.9-27.82 Ma] projections thresholded by maxSSS	4256064 ± 4526191 vs 5182540 ± 7259136 [W=9, p>0.025]	3905522 ± 4483142 vs 10315524 [W=1, p>0.025]

Chattian [27.82-23.03 Ma] projections thresholded by 95% LTP	5976072 ± 5497340 vs 5126762 ± 7188284 [W=12, p>0.025]	5481723 ± 5514162 vs 10209645 [W=2, p>0.025]
Chattian [27.82-23.03 Ma] projections thresholded by maxSSS	4669377 ± 4842988 vs 3933569 ± 5509982 [W=12, p>0.025]	4283381 ± 4807309 vs 7829714 [W=3, p>0.025]

Table D4 – The mean ± SD of the area of suitable Antarctic area (km^2), including extrapolative area, for predicted dispersers vs. non-dispersers, for models built using a 200 km radius calibration region. The W value and statistical significance, as calculated via a Mann Whitney U test with Bonferroni correction, are given in [].

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NICHE MODELS WITH BIOGEOGRAPHICALLY INFORMED CALIBRATION REGIONS	*'Eomarsupial' hypothesis [extrapolative area excluded]*	*'Australidelphian+' hypothesis [extrapolative area excluded]*
Danian [66-61.6 Ma] projections thresholded by 95% LTP	57 ± 20 vs 60 ± 14 [W=37, p>0.025]	57 ± 19 vs 63 ± 16 [W=27, p>0.025]
Danian [66-61.6 Ma] projections thresholded by maxSSS	68 ± 44 vs 68 ± 14 [W=26, p>0.025]	68 ± 41 vs 65 ± 15 [W=27, p>0.025]
Selandian [61.6-59.2 Ma] projections thresholded by 95% LTP	70 ± 40 vs 58 ± 15 [W=52, p>0.025]	67 ± 38 vs 62 ± 15 [W=37, p>0.025]
Selandian [61.6-59.2 Ma] projections thresholded by maxSSS	66 ± 22 vs 66 ± 19 [W=40, p>0.025]	64 ± 22 vs 72 ± 18 [W=24, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by 95% LTP	47 ± 20 vs 82 ± 35 [W=17, p>0.025]	49 ± 20 vs 90 ± 37 [W=14, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by maxSSS	48 ± 17 vs 76 ± 34 [W=20, p>0.025]	49 ± 17 vs 83 ± 36 [W=13, p>0.025]
Priabonian [37.71-33.9 Ma] projections thresholded by 95% LTP	52 ± 15 vs 86 ± 35 [W=14, p>0.025]	55 ± 16 vs 91 ± 41 [W=15, p>0.025]
Priabonian [37.71-33.9 Ma] projections thresholded by maxSSS	46 ± 15 vs 69 ± 34 [W=26, p>0.025]	48 ± 17 vs 73 ± 38 [W=22, p>0.025]
Rupelian [33.9-27.82 Ma] projections thresholded by 95% LTP	66 ± 45 vs 121 [W=2, p>0.025]	71 ± 46 vs n/a
Rupelian [33.9-27.82 Ma] projections thresholded by maxSSS	65 ± 51 vs 97 [W=2, p>0.025]	67 ± 49 vs n/a

Chattian [27.82-23.03 Ma] projections thresholded by 95% LTP	50 ± 22 vs 142 ± 32 [W=0, p>0.025]	56 ± 27 vs 152 ± 30 [W=0, p>0.025]
Chattian [27.82-23.03 Ma] projections thresholded by maxSSS	61 ± 23 vs 133 ± 41 [W=2, p>0.025]	67 ± 26 vs 165 ± 33 [W=0, p>0.025]

Table E1 – The mean ± SD of the contiguity index value (which increases with less fragmentation (Hesselbarth, Sciaini et al. 2019)) of suitable non-extrapolative Antarctic area (km^2) for predicted dispersers vs. non-dispersers, for models built using a biogeographically informed calibration region. The W value and statistical significance, as calculated via a Mann Whitney U test with Bonferroni correction, are given in [].

NICHE MODELS WITH 200 KM RADIUS CALIBRATION REGIONS	*'Eomarsupial' hypothesis [extrapolative area excluded]*	*'Australidelphian+' hypothesis [extrapolative area excluded]*
Danian [66-61.6 Ma] projections thresholded by 95% LTP	62 ± 10 vs 105 [W=0, p>0.025]	67 ± 18 vs n/a
Danian [66-61.6 Ma] projections thresholded by maxSSS	69 ± 5 vs 96 [W=0, p>0.025]	73 ± 11 vs n/a
Selandian [61.6-59.2 Ma] projections thresholded by 95% LTP	65 ± 14 vs 103 [W=0, p>0.025]	69 ± 19 vs n/a
Selandian [61.6-59.2 Ma] projections thresholded by maxSSS	69 ± 14 vs 72 [W=3, p>0.025]	69 ± 13 vs n/a
Ypresian [56-47.8 Ma] projections thresholded by 95% LTP	44 ± 8 vs 55 ± 2 [W=2, p>0.025]	45 ± 8 vs 56 [W=1, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by maxSSS	48 ± 10 vs 65 [W=0, p>0.025]	50 ± 11 vs n/a
Priabonian [37.71-33.9 Ma] projections thresholded by 95% LTP	56 ± 23 vs 56 [W=2, p>0.025]	56 ± 22 vs n/a
Priabonian [37.71-33.9 Ma] projections thresholded by maxSSS	70 ± 34 vs 64 [W=4, p>0.025]	70 ± 32 vs n/a
Rupelian [33.9-27.82 Ma] projections thresholded by 95% LTP	n/a vs n/a	n/a vs n/a
Rupelian [33.9-27.82 Ma] projections thresholded by maxSSS	n/a vs n/a	n/a vs n/a

Chattian [27.82-23.03 Ma] projections thresholded by 95% LTP	68 ± 3 vs 90 ± 50 [W=5, p>0.025]	77 ± 24 vs 54 [W=6, p>0.025]
Chattian [27.82-23.03 Ma] projections thresholded by maxSSS	74 ± 7 vs 97 ± 8 [W=0, p>0.025]	79 ± 13 vs 92 [W=1, p>0.025]

Table E2 – The mean ± SD of the contiguity index value (which increases with less fragmentation (Hesselbarth, Sciaini et al. 2019)) of suitable non-extrapolative Antarctic area (km^2) for predicted dispersers vs. non-dispersers, for models built using a 200 km radius calibration region. The W value and statistical significance, as calculated via a Mann Whitney U test with Bonferroni correction, are given in [].

NICHE MODELS WITH BIOGEOGRAPHICALLY INFORMED CALIBRATION REGIONS	*'Eomarsupial' hypothesis [extrapolative area included]*	*'Australidelphian+' hypothesis [extrapolative area included]*
Danian [66-61.6 Ma] projections thresholded by 95% LTP	55 ± 22 vs 59 ± 15 [W=39, p>0.025]	55 ± 21 vs 63 ± 16 [W=28, p>0.025]
Danian [66-61.6 Ma] projections thresholded by maxSSS	67 ± 49 vs 68 ± 15 [W=28, p>0.025]	68 ± 46 vs 65 ± 15 [W=30, p>0.025]
Selandian [61.6-59.2 Ma] projections thresholded by 95% LTP	62 ± 26 vs 58 ± 15 [W=47, p>0.025]	60 ± 24 vs 62 ± 15 [W=34, p>0.025]
Selandian [61.6-59.2 Ma] projections thresholded by maxSSS	76 ± 38 vs 67 ± 18 [W=48, p>0.025]	73 ± 36 vs 72 ± 18 [W=30, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by 95% LTP	49 ± 19 vs 82 ± 35 [W=19, p>0.025]	50 ± 19 vs 90 ± 37 [W=15, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by maxSSS	49 ± 17 vs 76 ± 34 [W=23, p>0.025]	49 ± 16 vs 83 ± 36 [W=15, p>0.025]
Priabonian [37.71-33.9 Ma] projections thresholded by 95% LTP	51 ± 16 vs 86 ± 35 [W=14, p>0.025]	54 ± 17 vs 91 ± 41 [W=15, p>0.025]
Priabonian [37.71-33.9 Ma] projections thresholded by maxSSS	47 ± 14 vs 69 ± 34 [W=27, p>0.025]	49 ± 16 vs 73 ± 38 [W=22, p>0.025]
Rupelian [33.9-27.82 Ma] projections thresholded by 95% LTP	64 ± 36 vs 121 [W=1, p>0.025]	70 ± 38 vs n/a
Rupelian [33.9-27.82 Ma] projections thresholded by maxSSS	68 ± 45 vs 97 [W=1, p>0.025]	71 ± 44 vs n/a

Chattian [27.82-23.03 Ma] projections thresholded by 95% LTP	48 ± 23 vs 142 ± 32 [W=0, p>0.025]	54 ± 29 vs 152 ± 30 [W=0, p>0.025]
Chattian [27.82-23.03 Ma] projections thresholded by maxSSS	62 ± 25 vs 133 ± 41 [W=2, p>0.025]	68 ± 27 vs 165 ± 33 [W=0, p>0.025]

Table E3 – The mean ± SD of the contiguity index value (which increases with less fragmentation (Hesselbarth, Sciaini et al. 2019)) of suitable Antarctic area (km^2), including extrapolative area, for predicted dispersers vs. non-dispersers, for models built using a biogeographically informed calibration region. The W value and statistical significance, as calculated via a Mann Whitney U test with Bonferroni correction, are given in [].

NICHE MODELS WITH 200 KM RADIUS CALIBRATION REGIONS	*'Eomarsupial' hypothesis [extrapolative area included]*	*'Australidelphian+' hypothesis [extrapolative area included]*
Danian [66-61.6 Ma] projections thresholded by 95% LTP	60 ± 25 vs 71 ± 48 [W=10, p>0.025]	63 ± 27 vs 36 [W=10, p>0.025]
Danian [66-61.6 Ma] projections thresholded by maxSSS	66 ± 31 vs 96 [W=2, p>0.025]	68 ± 31 vs n/a
Selandian [61.6-59.2 Ma] projections thresholded by 95% LTP	62 ± 33 vs 75 ± 40 [W=9, p>0.025]	66 ± 33 vs 46 [W=9, p>0.025]
Selandian [61.6-59.2 Ma] projections thresholded by maxSSS	69 ± 35 vs 72 [W=5, p>0.025]	69 ± 33 vs n/a
Ypresian [56-47.8 Ma] projections thresholded by 95% LTP	62 ± 20 vs 55 ± 2 [W=13, p>0.025]	62 ± 19 vs 56 [W=6, p>0.025]
Ypresian [56-47.8 Ma] projections thresholded by maxSSS	63 ± 33 vs 65 [W=3, p>0.025]	63 ± 31 vs n/a
Priabonian [37.71-33.9 Ma] projections thresholded by 95% LTP	52 ± 16 vs 42 ± 20 [W=15, p>0.025]	53 ± 15 vs 28 [W=12, p>0.025]
Priabonian [37.71-33.9 Ma] projections thresholded by maxSSS	72 ± 26 vs 64 [W=6, p>0.025]	71 ± 25 vs n/a
Rupelian [33.9-27.82 Ma] projections thresholded by 95% LTP	51 ± 42 vs 59 ± 40 [W=8, p>0.025]	55 ± 41 vs 31 [W=7, p>0.025]
Rupelian [33.9-27.82 Ma] projections thresholded by maxSSS	56 ± 35 vs 77 ± 19 [W=3, p>0.025]	60 ± 35 vs 64 [W=3, p>0.025]

Chattian [27.82-23.03 Ma] projections thresholded by 95% LTP	43 ± 15 vs 79 ± 66 [W=7, p>0.025]	52 ± 30 vs 33 [W=8, p>0.025]
Chattian [27.82-23.03 Ma] projections thresholded by maxSSS	48 ± 18 vs 75 ± 39 [W=4, p>0.025]	53 ± 24 vs 48 [W=5, p>0.025]

Table E4 – The mean ± SD of the contiguity index value (which increases with less fragmentation (Hesselbarth, Sciaini et al. 2019)) of suitable Antarctic area (km^2), including extrapolative area, for predicted dispersers vs. non-dispersers, for models built using a 200 km radius calibration region. The W value and statistical significance, as calculated via a Mann Whitney U test with Bonferroni correction, are given in [].

NICHE MODELS WITH BIOGEOGRAPHICALLY INFORMED CALIBRATION REGIONS	Danian with maxSSS threshold	Danian with 95% LTP threshold	Ypresian with maxSSS threshold	Ypresian with 95% LTP threshold	Priabonian with maxSSS threshold	Priabonian with 95% LTP threshold	Rupelian with maxSSS threshold	Rupelian with 95% LTP threshold	Chattian with maxSSS threshold	Chattian with 95% LTP threshold
Burramyidae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	1/2, p>0.025 **[1/2, p>0.025]**	1/2, p>0.025 **[1/2, p>0.025]**
Caenolestidae	n/a	n/a	1/3, p>0.025 **[1/3, p>0.025]**	1/3, p>0.025 **[1/3, p>0.025]**	n/a	n/a	0/4, p>0.025 **[1/4, p>0.025]**	0/4, p>0.025 **[1/4, p>0.025]**	3/9, p>0.025 **[4/9, p<0.025]**	2/9, p>0.025 **[4/9, p<0.025]**
Chlamyphoridae	n/a	n/a	3/4, p<0.025 **[4/4, p<0.025]**	3/4, p>0.025 **[4/4, p<0.025]**	2/2, p>0.025 **[2/2, p>0.025]**	2/2, p>0.025 **[2/2, p>0.025]**	7/9, p<0.025 **[8/9, p<0.025]**	7/9, p<0.025 **[8/9, p<0.025]**	9/19, p<0.025 **[12/19, p<0.025]**	10/19, p>0.025 **[15/19, p<0.025]**
Dasypodidae	n/a	n/a	0/3, p>0.025 **[2/3, p<0.025]**	1/3, p>0.025 **[3/3, p<0.025]**	0/3, p>0.025 **[1/3, p>0.025]**	0/3, p>0.025 **[1/3, p>0.025]**	0/3, p>0.025 **[1/3, p>0.025]**	0/3, p>0.025 **[1/3, p>0.025]**	0/2, p>0.025 **[0/2, p>0.025]**	0/2, p>0.025 **[0/2, p>0.025]**
Hypsiprymnodontidae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0/4, p>0.025 **[0/4, p>0.025]**	0/4, p>0.025 **[0/4, p>0.025]**
Microbiotheriidae	0/1, p>0.025 **[0/1, p>0.025]**	0/1, p>0.025 **[0/1, p>0.025]**	2/4, p<0.025 **[2/4, p<0.025]**	2/4, p<0.025 **[2/4, p<0.025]**	0/1, p>0.025 **[0/1, p>0.025]**	0/1, p>0.025 **[0/1, p>0.025]**	0/2, p>0.025 **[1/2, p>0.025]**	0/2, p>0.025 **[1/2, p>0.025]**	0/1, p>0.025 **[0/1, p>0.025]**	0/1, p>0.025 **[0/1, p>0.025]**
Peramelidae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	1/1, p>0.025 **[1/1, p>0.025]**	1/1, p>0.025 **[1/1, p>0.025]**
Petauridae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	2/2, p<0.025 **[2/2, p<0.025]**	2/2, p>0.025 **[2/2, p>0.025]**
Phascolarctidae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	6/6, p<0.025 **[6/6, p<0.025]**	6/6, p<0.025 **[6/6, p<0.025]**
Potoroidae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	5/7, p<0.025 **[5/7, p<0.025]**	5/7, p<0.025 **[5/7, p<0.025]**
Pseudocheiridae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	4/6, p<0.025 **[5/6, p<0.025]**	5/6, p<0.025 **[5/6, p<0.025]**

Table F1– The proportion of a family-level group's fossil sites predicted by its niche models projected onto Palaeogene palaeoclimate rasters, and the statistical significance of this capacity as calculated via one-tailed binomial test [p<0.025] - excluding areas of extrapolated suitable conditions. Models described here were built from a biogeographically informed calibration

region. Square brackets show equivalent information if fossils within 150 km of suitable areas are considered to be 'predicted' (results outside of the square brackets reflect fossil sites precisely within suitable areas). The results shown here are based on fossil locality coordinates rotated to reflect the mid-point of the geological age considered.

NICHE MODELS WITH 200 KM RADIUS CALIBRATION REGIONS	Ypresian with maxSSS threshold	Ypresian with 95% LTP threshold	Priabonian with maxSSS threshold	Priabonian with 95% LTP threshold	Rupelian with maxSSS threshold	Rupelian with 95% LTP threshold	Chattian with maxSSS threshold	Chattian with 95% LTP threshold
Burramyidae	n/a	n/a	n/a	n/a	n/a	n/a	0/2, p>0.025 **[0/2, p>0.025]**	0/2, p>0.025 **[0/2, p>0.025]**
Caenolestidae	0/3, p>0.025 [**1/3, p>0.025]**	0/3, p>0.025 [**2/3, p<0.025]**	n/a	n/a	1/4, p>0.025 **[1/4, p>0.025**]	1/4, p>0.025 **[1/4, p>0.025**]	3/9, p<0.025 **[4/9, p<0.025**]	3/9, p<0.025 **[4/9, p<0.025**]
Choloepodidae	n/a	n/a	n/a	n/a	0/2, p>0.025 **[0/2, p>0.025]**	0/2, p>0.025 **[0/2, p>0.025]**	0/8, p>0.025 **[0/8, p>0.025]**	0/8, p>0.025 **[1/8, p>0.025]**
Hypsiprymnodontidae	n/a	n/a	n/a	n/a	n/a	n/a	0/4, p>0.025 **[0/4, p>0.025]**	0/4, p>0.025 **[0/4, p>0.025]**
Peramelidae	n/a	n/a	n/a	n/a	n/a	n/a	0/1, p>0.025 **[0/1, p>0.025]**	0/1, p>0.025 **[0/1, p>0.025]**
Potoroidae	n/a	n/a	n/a	n/a	n/a	n/a	7/7, p<0.025 **[7/7, p<0.025]**	7/7, p<0.025 **[7/7, p<0.025]**
Pseudocheiridae	n/a	n/a	n/a	n/a	n/a	n/a	3/6, p>0.025 **[3/6, p>0.025]**	3/6, p>0.025 **[3/6, p>0.025]**

Table F2– The proportion of a family-level group's fossil sites predicted by its niche models projected onto Palaeogene palaeoclimate rasters, and the statistical significance of this capacity as calculated via one-tailed binomial test [p<0.025] - excluding areas of extrapolated suitable conditions. Models described here were built from a 200 km radius calibration region. Square brackets show equivalent information if fossils within 150 km of suitable areas are considered to be 'predicted' (results outside of the square brackets reflect fossil sites precisely within suitable areas). The results shown here are based on fossil locality coordinates rotated to reflect the mid-point of the geological age considered.

NICHE MODELS WITH BIOGEOGRAPHICALLY INFORMED CALIBRATION REGIONS	Danian with maxSSS threshold	Danian with 95% LTP threshold	Ypresian with maxSSS threshold	Ypresian with 95% LTP threshold	Priabonian with maxSSS threshold	Priabonian with 95% LTP threshold	Rupelian with maxSSS threshold	Rupelian with 95% LTP threshold	Chattian with maxSSS threshold	Chattian with 95% LTP threshold
Burramyidae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	1/2, p>0.025 **[1/2, p>0.025]**	1/2, p>0.025 **[1/2, p>0.025]**
Caenolestidae	n/a	n/a	1/3, p>0.025 **[2/3, p<0.025]**	1/3, p>0.025 **[2/3, p<0.025]**	n/a	n/a	1/4, p>0.025 **[1/4, p>0.025]**	1/4, p>0.025 **[1/4, p>0.025]**	3/9, p>0.025 **[4/9, p<0.025]**	3/9, p>0.025 **[4/9, p<0.025]**
Chlamyphoridae	n/a	n/a	3/4, p>0.025 **[4/4, p<0.025]**	3/4, p>0.025 **[4/4, p<0.025]**	2/2, p>0.025 **[2/2, p>0.025]**	2/2, p>0.025 **[2/2, p>0.025]**	7/9, p<0.025 **[8/9, p<0.025]**	7/9, p<0.025 **[8/9, p<0.025]**	9/19, p<0.025 **[12/19, p<0.025]**	10/19, p>0.025 **[15/19, p<0.025]**
Dasypodidae	n/a	n/a	1/3, p>0.025 **[3/3, p<0.025]**	1/3, p>0.025 **[3/3, p<0.025]**	2/3, p>0.025 **[3/3, p<0.025]**	2/3, p>0.025 **[3/3, p>0.025]**	1/3, p>0.025 **[1/3, p>0.025]**	1/3, p>0.025 **[1/3, p>0.025]**	0/2, p>0.025 **[1/2, p>0.025]**	1/2, p>0.025 **[2/2, p>0.025]**
Hypsiprymnodontidae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	1/4, p>0.025 **[1/4, p>0.025]**	2/4, p>0.025 **[2/4, p>0.025]**
Microbiotheriidae	0/1, p>0.025 **[0/1, p>0.025]**	0/1, p>0.025 **[0/1, p>0.025]**	2/4, p<0.025 **[3/4, p<0.025]**	2/4, p<0.025 **[3/4, p<0.025]**	0/1, p>0.025 **[0/1, p>0.025]**	0/1, p>0.025 **[0/1, p>0.025]**	1/2, p>0.025 **[1/2, p>0.025]**	1/2, p>0.025 **[1/2, p>0.025]**	0/1, p>0.025 **[0/1, p>0.025]**	0/1, p>0.025 **[0/1, p>0.025]**
Peramelidae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	1/1, p>0.025 **[1/1, p>0.025]**	1/1, p>0.025 **[1/1, p>0.025]**
Petauridae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	2/2, p<0.025 **[2/2, p<0.025]**	2/2, p>0.025 **[2/2, p>0.025]**
Phascolarctidae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	6/6, p<0.025 **[6/6, p<0.025]**	6/6, p<0.025 **[6/6, p<0.025]**
Potoroidae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	7/7, p<0.025 **[7/7, p<0.025]**	7/7, p<0.025 **[7/7, p<0.025]**
Pseudocheiridae	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	6/6, p<0.025 **[6/6, p<0.025]**	6/6, p<0.025 **[6/6, p<0.025]**

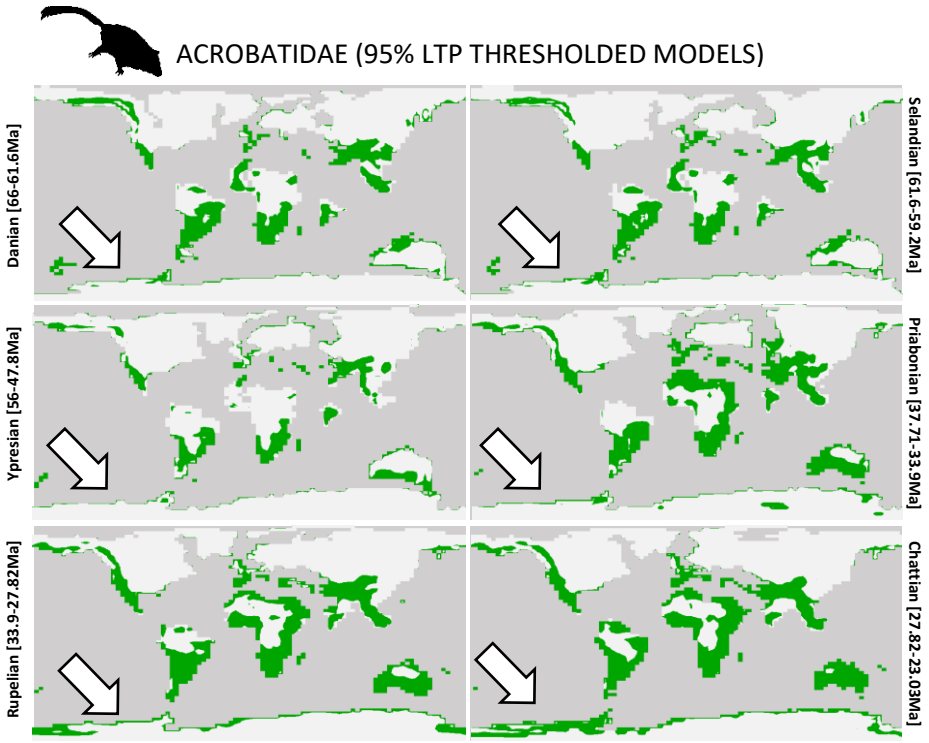
Table F3– The proportion of a family-level group's fossil sites predicted by its niche models projected onto Palaeogene palaeoclimate rasters, and the statistical significance of this capacity as calculated via one-tailed binomial test [p<0.025] - including areas of extrapolated suitable conditions. Models described here were built from a biogeographically informed calibration region. Square brackets show equivalent information if fossils within 150 km of suitable areas are considered to be 'predicted' (results outside of the square brackets reflect

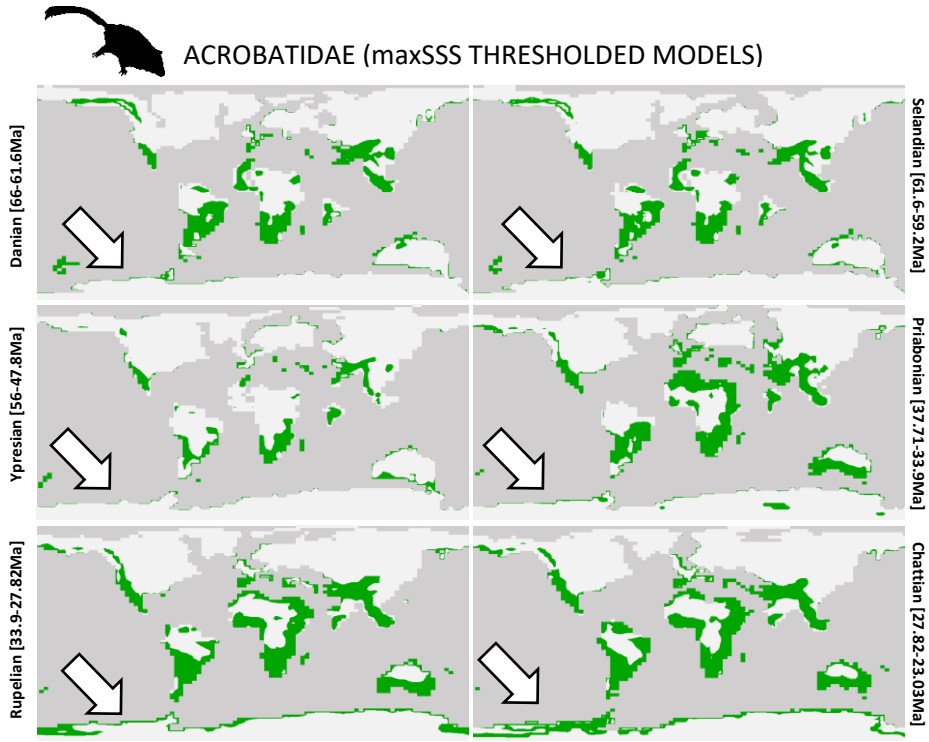
fossil sites precisely within suitable areas). The results shown here are based on fossil locality coordinates rotated to reflect the mid-point of the geological age considered.

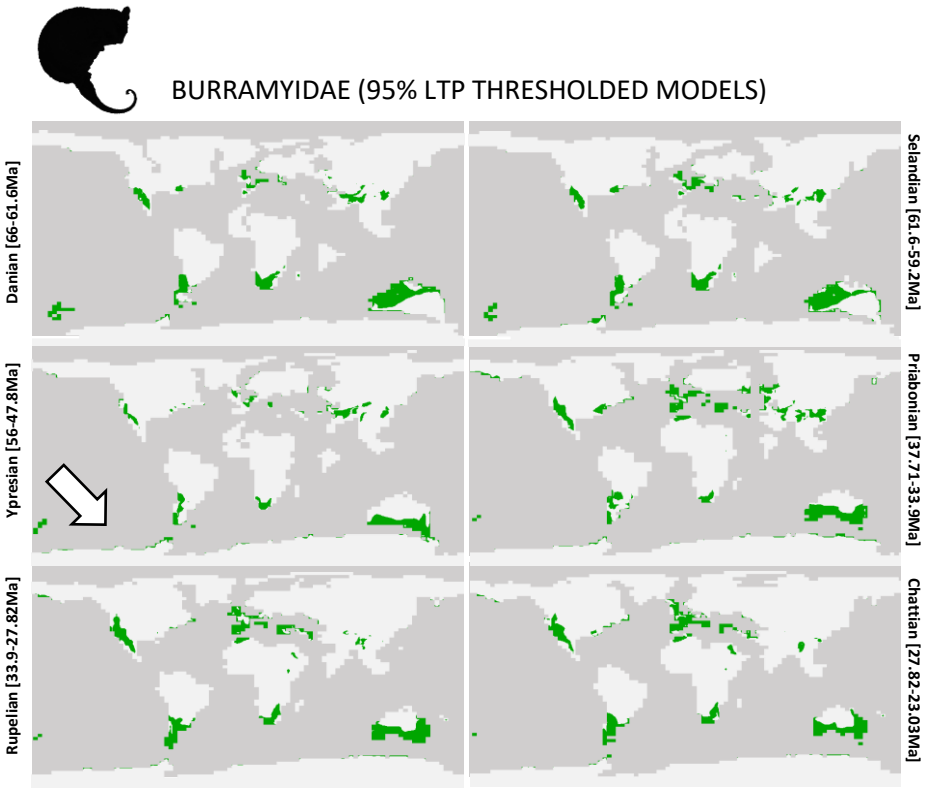
NICHE MODELS WITH 200 KM RADIUS CALIBRATION REGIONS	Ypresian with maxSSS threshold	Ypresian with 95% LTP threshold	Priabonian with maxSSS threshold	Priabonian with 95% LTP threshold	Rupelian with maxSSS threshold	Rupelian with 95% LTP threshold	Chattian with maxSSS threshold	Chattian with 95% LTP threshold
Burramyidae	n/a	n/a	n/a	n/a	n/a	n/a	0/2, p>0.025 **[0/2, p>0.025]**	0/2, p>0.025 **[0/2, p>0.025]**
Caenolestidae	1/3, p>0.025 [**2/3, p<0.025]**	1/3, p>0.025 [**2/3, p<0.025]**	n/a	n/a	1/4, p>0.025 **[1/4, p>0.025**]	1/4, p>0.025 **[1/4, p>0.025**]	3/9, p<0.025 **[4/9, p<0.025**]	3/9, p<0.025 **[4/9, p<0.025**]
Choloepodidae	n/a	n/a	n/a	n/a	1/2, p>0.025 **[1/2, p>0.025]**	1/2, p>0.025 **[1/2, p>0.025]**	3/8, p<0.025 **[4/8, p<0.025]**	3/8, p<0.025 **[4/8, p<0.025]**
Hypsiprymnodontidae	n/a	n/a	n/a	n/a	n/a	n/a	0/4, p>0.025 **[0/4, p>0.025]**	0/4, p>0.025 **[0/4, p>0.025]**
Peramelidae	n/a	n/a	n/a	n/a	n/a	n/a	0/1, p>0.025 **[0/1, p>0.025]**	0/1, p>0.025 **[0/1, p>0.025]**
Potoroidae	n/a	n/a	n/a	n/a	n/a	n/a	1/7, p>0.025 **[1/7, p>0.025]**	1/7, p>0.025 **[1/7, p>0.025]**
Pseudocheiridae	n/a	n/a	n/a	n/a	n/a	n/a	3/6, p>0.025 **[3/6, p>0.025]**	3/6, p>0.025 **[3/6, p>0.025]**

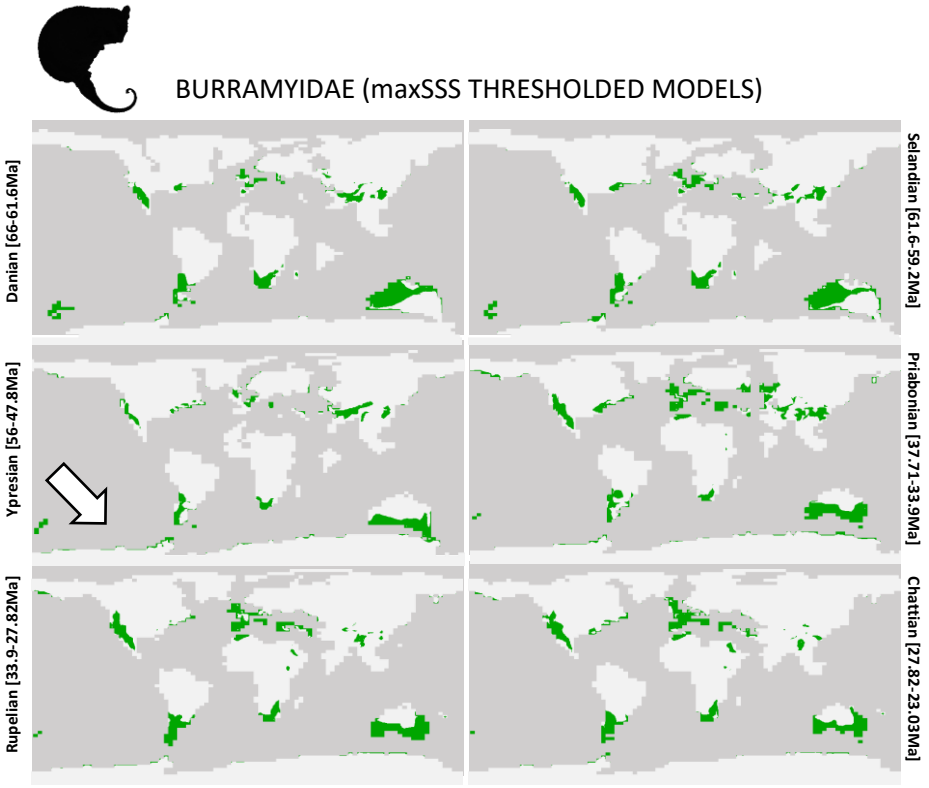
Table F4– The proportion of a family-level group's fossil sites predicted by its niche models projected onto Palaeogene palaeoclimate rasters, and the statistical significance of this capacity as calculated via one-tailed binomial test [p<0.025] - including areas of extrapolated suitable conditions. Models described here were built from a 200 km radius calibration region. Square brackets show equivalent information if fossils within 150 km of suitable areas are considered to be 'predicted' (results outside of the square brackets reflect fossil sites precisely within suitable areas). The results shown here are based on fossil locality coordinates rotated to reflect the mid-point of the geological age considered.

2.10

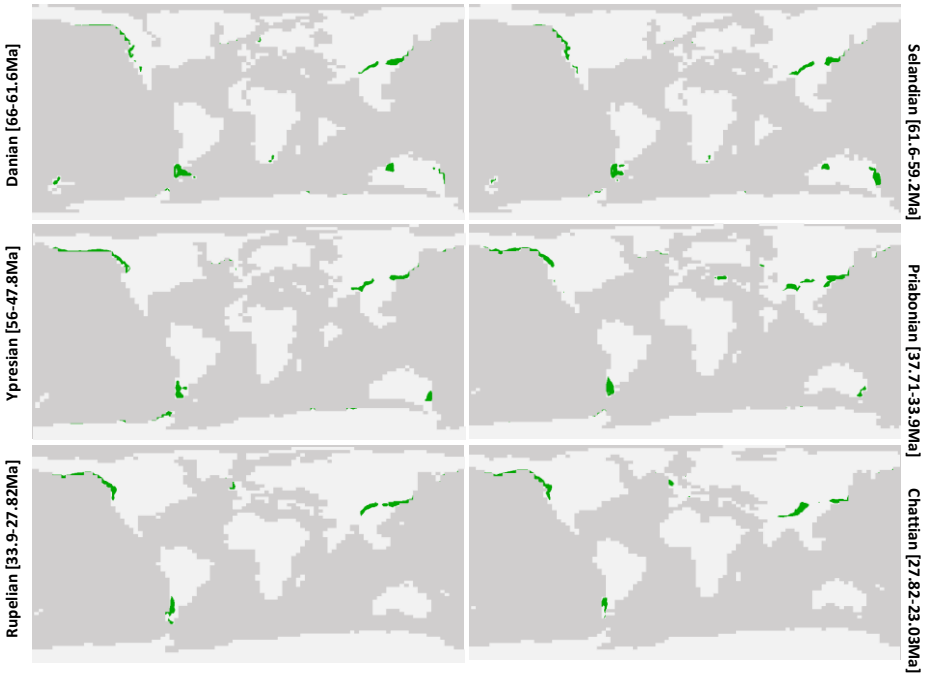

ACROBATIDAE (95% LTP THRESHOLDED MODELS)
Danian [66-61.6Ma]
Selandian [61.6-59.2Ma]
Ypresian [56-47.8Ma]
Priabonian [37.71-33.9Ma]
Rupelian [33.9-27.82Ma]
Chattian [27.82-23.03Ma]


ACROBATIDAE (maxSSS THRESHOLDED MODELS)
Danian [66-61.6Ma]
Selandian [61.6-59.2Ma]
Ypresian [56-47.8Ma]
Priabonian [37.71-33.9Ma]
Rupelian [33.9-27.82Ma]
Chattian [27.82-23.03Ma]

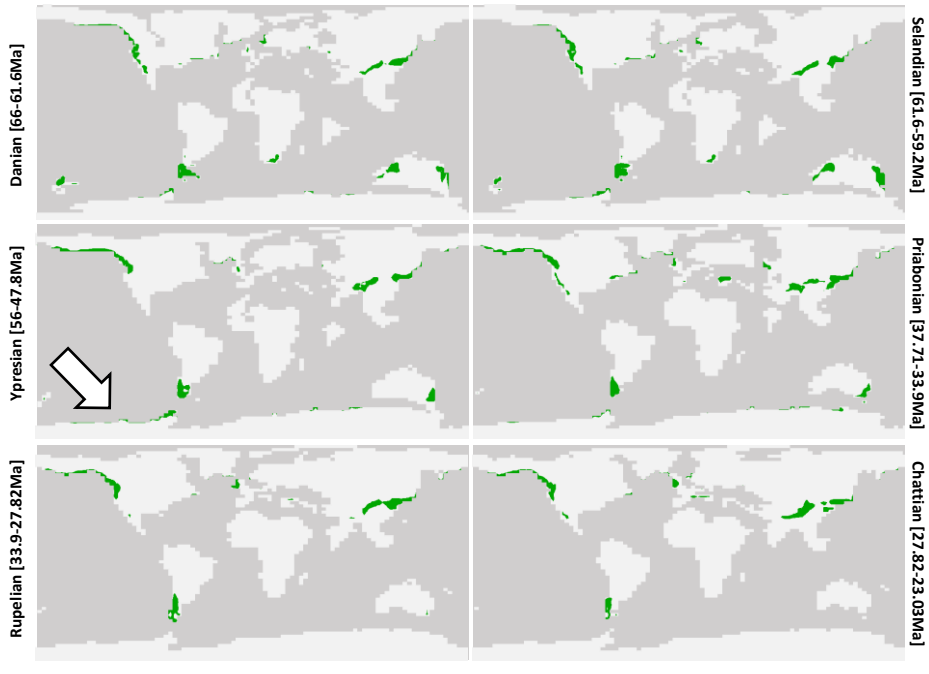

BURRAMYIDAE (95% LTP THRESHOLDED MODELS)
Danian [66-61.6Ma]
Selandian [61.6-59.2Ma]
Ypresian [56-47.8Ma]
Priabonian [37.71-33.9Ma]
Rupelian [33.9-27.82Ma]
Chattian [27.82-23.03Ma]


BURRAMYIDAE (maxSSS THRESHOLDED MODELS)
Danian [66-61.6Ma]
Selandian [61.6-59.2Ma]
Ypresian [56-47.8Ma]
Priabonian [37.71-33.9Ma]
Rupelian [33.9-27.82Ma]
Chattian [27.82-23.03Ma]

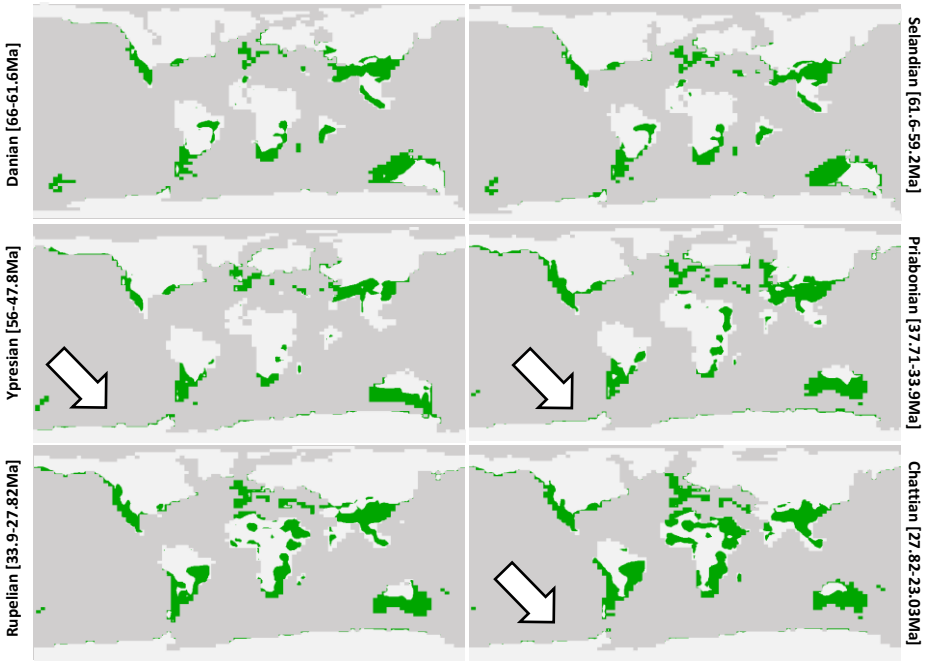
MICROBIIOTHERIIDAE (95% LTP THRESHOLDED MODELS)



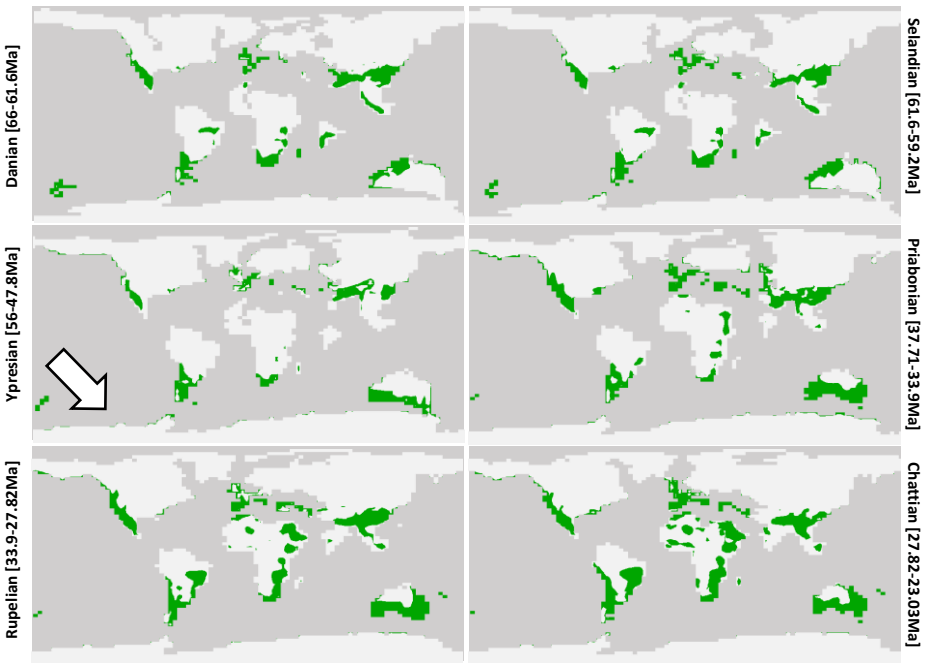
MICROBIIOTHERIIDAE (maxSSS THRESHOLDED MODELS)



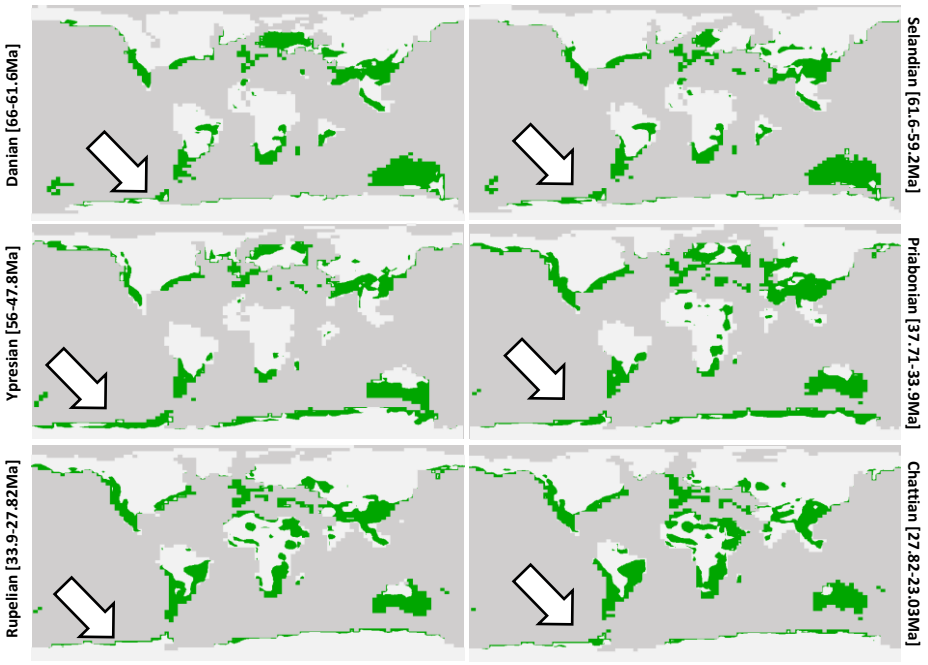
PERAMELIDAE (95% LTP THRESHOLDED MODELS)



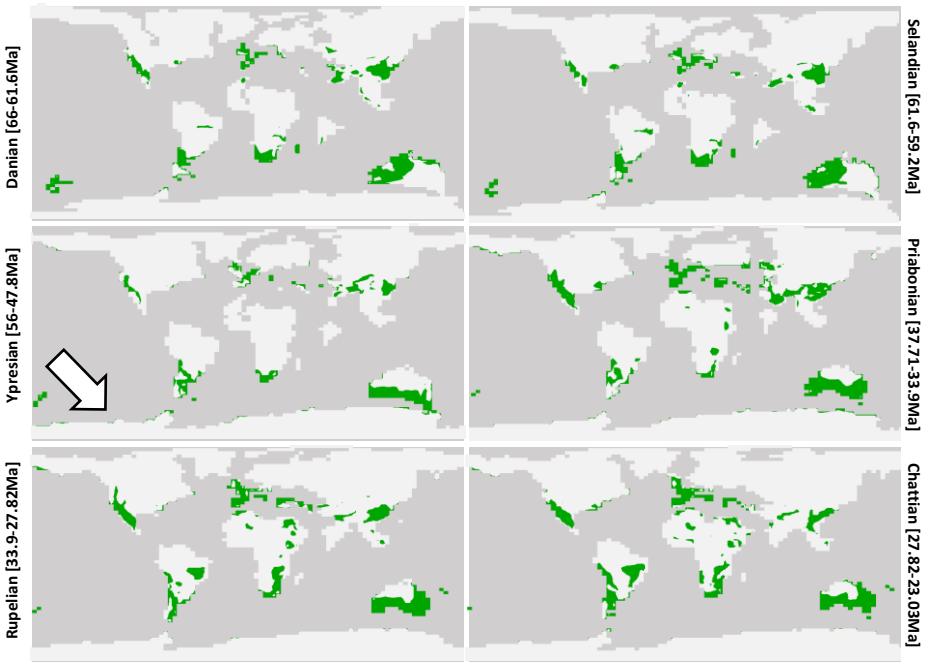
PERAMELIDAE (maxSSS THRESHOLDED MODELS)



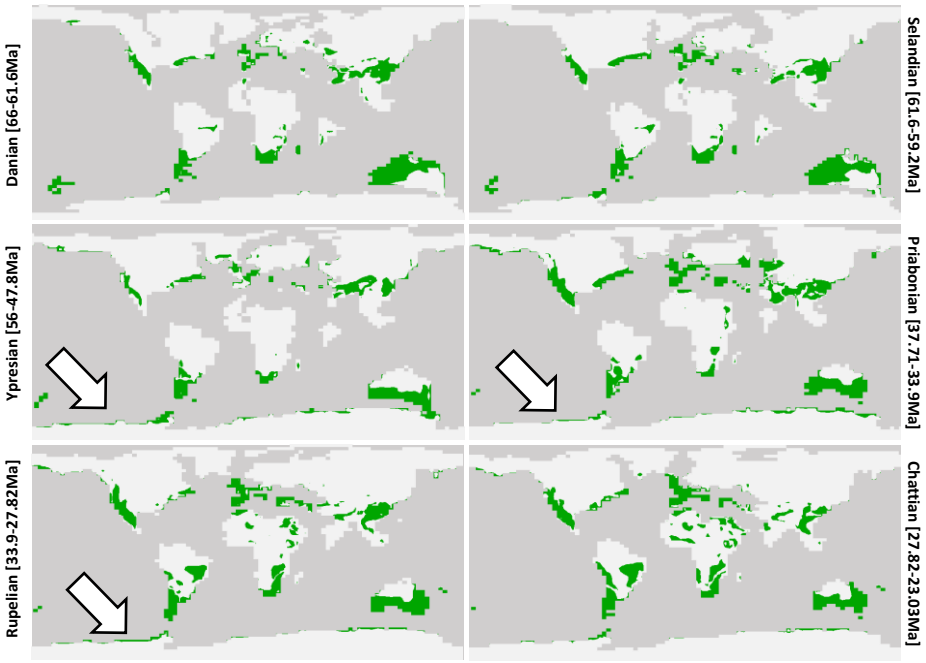
PETAURIDAE (95% LTP THRESHOLDED MODELS)



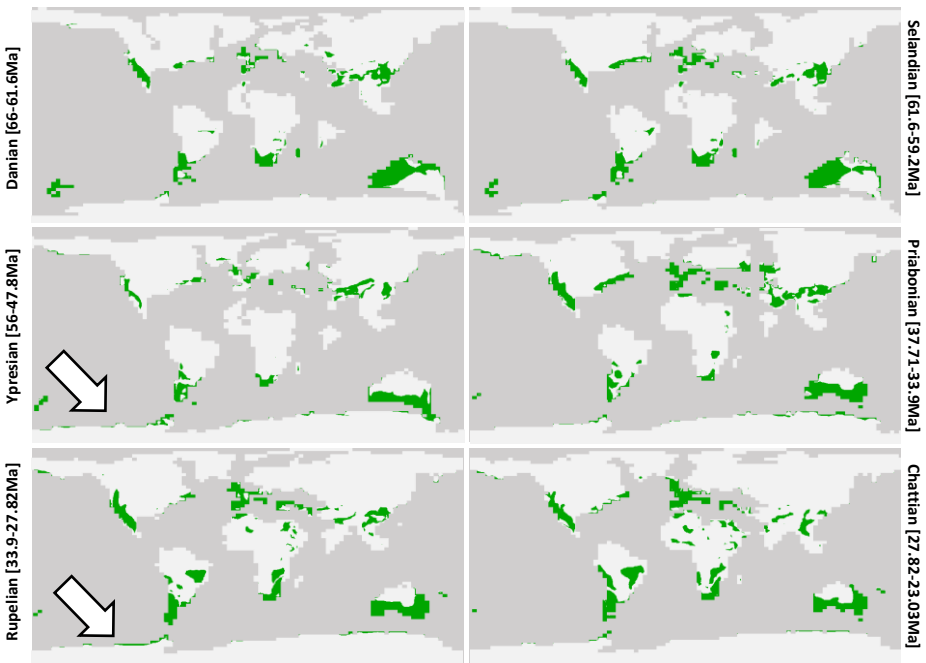
PETAURIDAE (maxSSS THRESHOLDED MODELS)



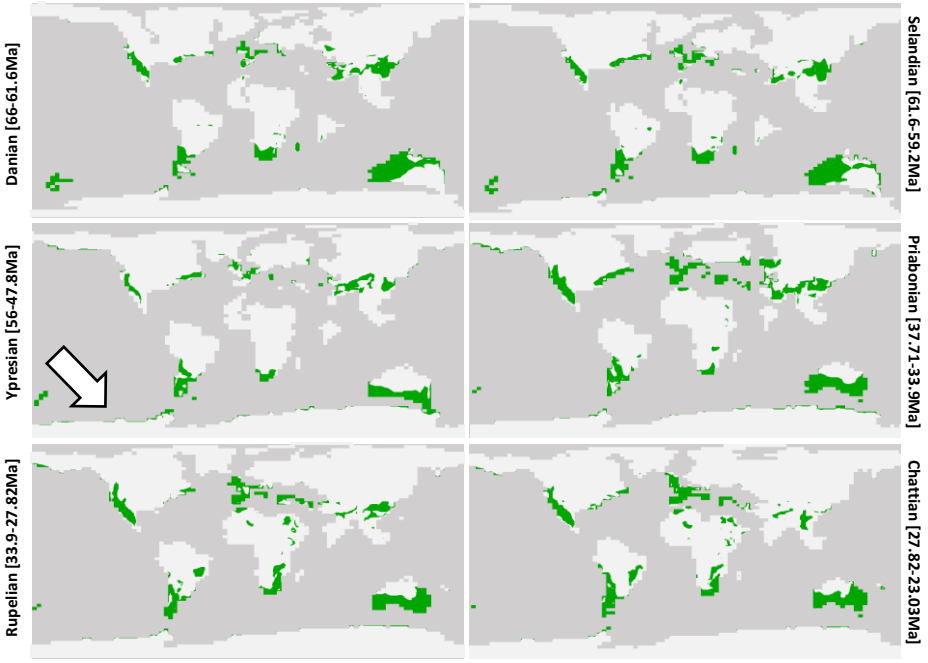
PHASCOGALINI (95% LTP THRESHOLDED MODELS)



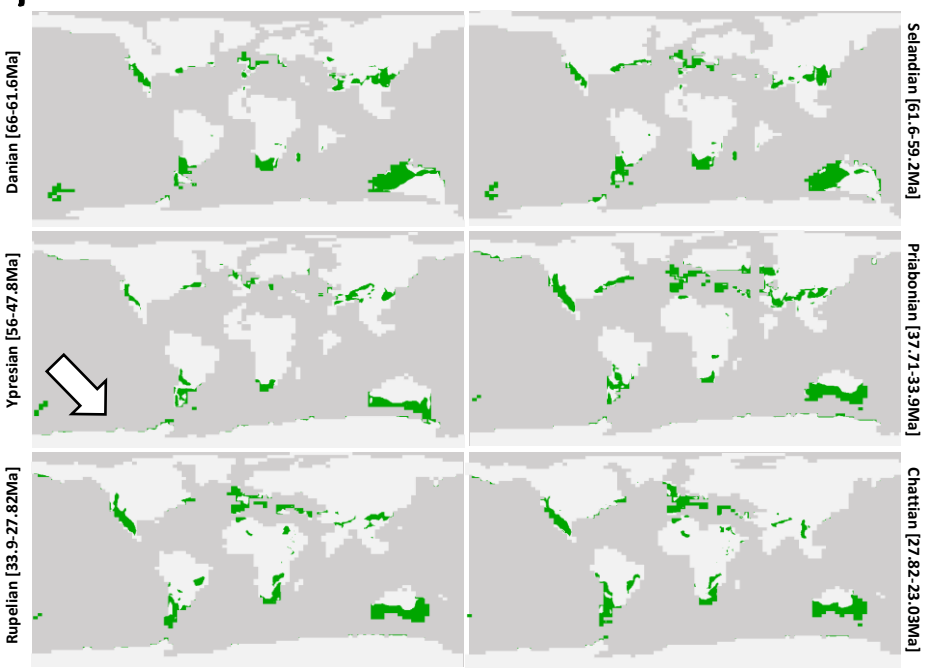
PHASCOGALINI (maxSSS THRESHOLDED MODELS)



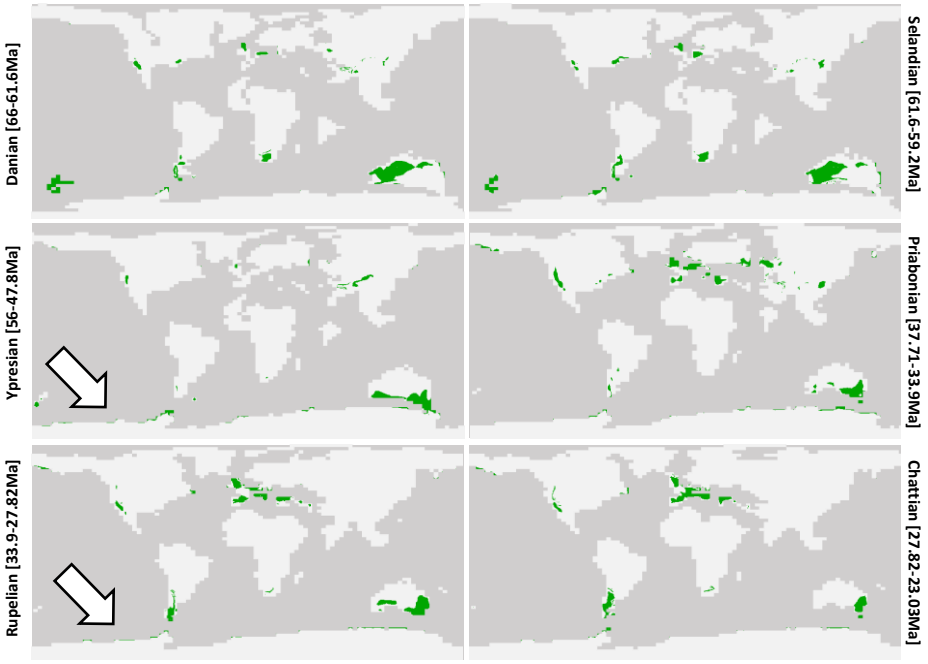
PSEUDOCHEIRIDAE (95% LTP THRESHOLDED MODELS)



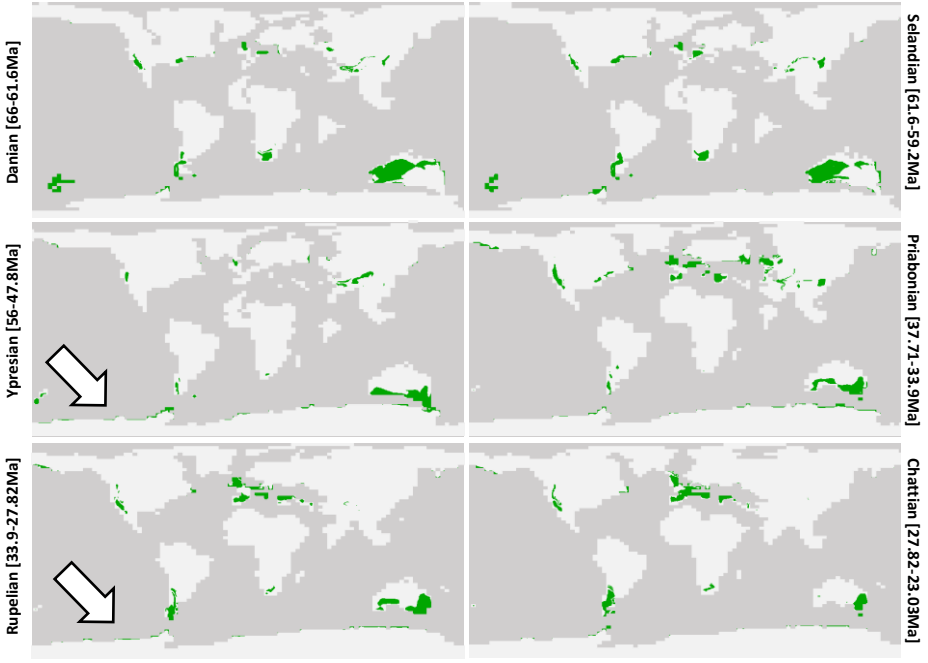
PSEUDOCHEIRIDAE (maxSSS THRESHOLDED MODELS)

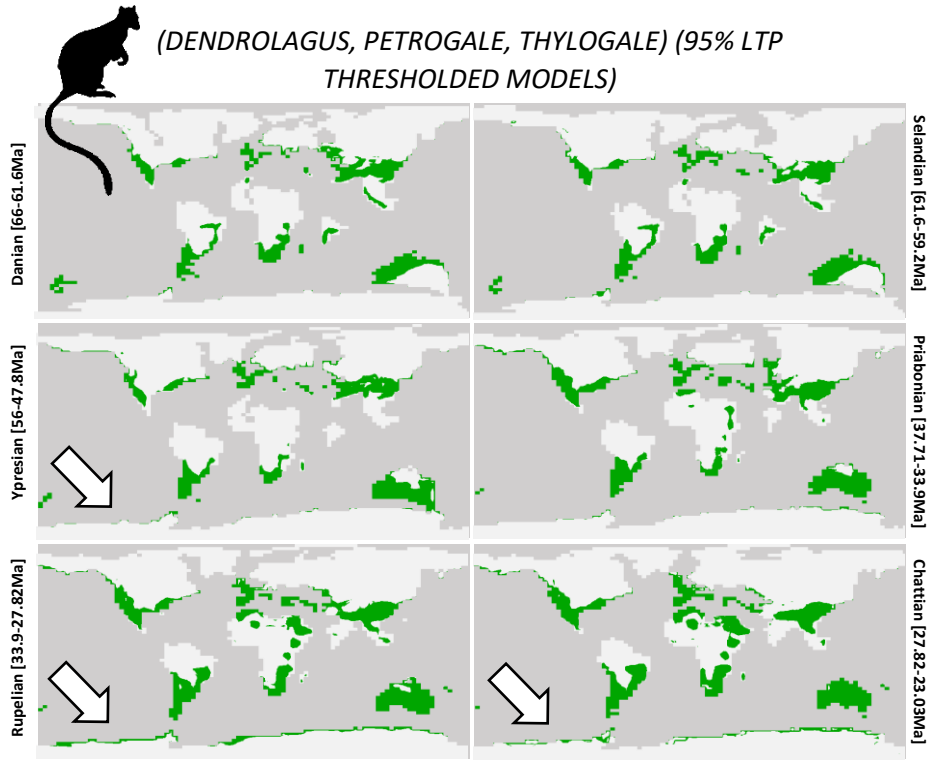


VOMBATIDAE (95% LTP THRESHOLDED MODELS)



VOMBATIDAE (maxSSS THRESHOLDED MODELS)




(DENDROLAGUS, PETROGALE, THYLOGALE) (95% LTP THRESHOLDED MODELS)
Danian [66-61.6Ma]
Selandian [61.6-59.2Ma]
Ypresian [56-47.8Ma]
Priabonian [37.71-33.9Ma]
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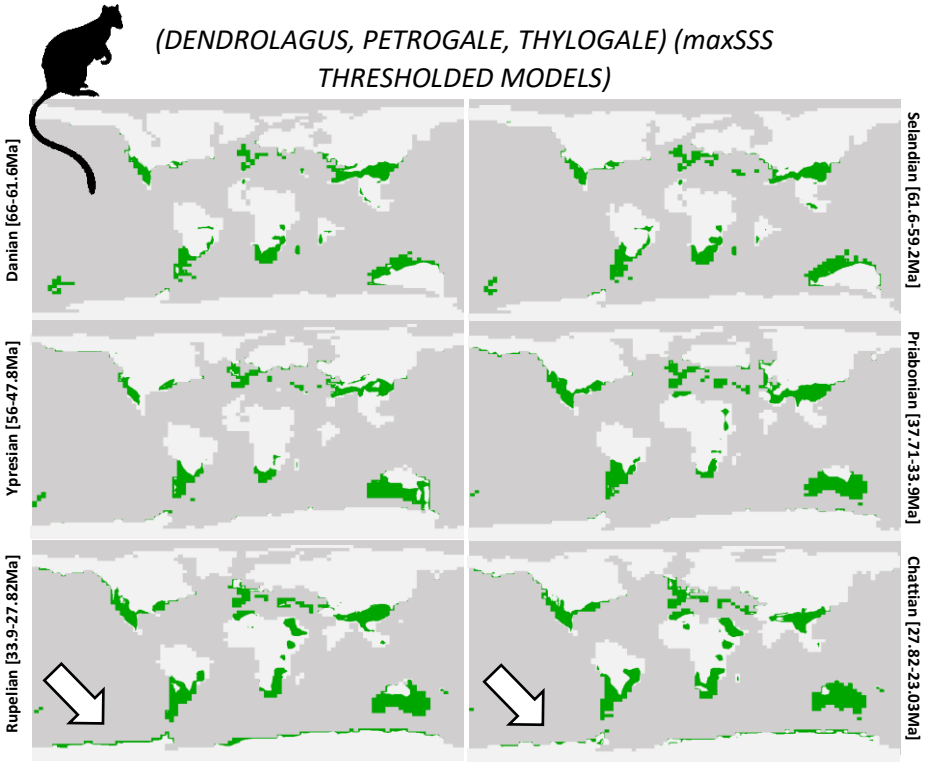
(DENDROLAGUS, PETROGALE, THYLOGALE) (maxSSS THRESHOLDED MODELS)
Danian [66-61.6Ma]
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Figures D1-D18 – Regions of suitable conditions projected onto Palaeogene time intervals for a niche model built using present-day occurrences of select marsupial family-level groups. Models were here calibrated using a biogeographically informed continental region. Areas of suitable, non-extrapolative abiotic area are in green. An arrow on the Ypresian projection indicates the position of the hypothesised 'dispersal corridor' of suitable abiotic area – the presence of which unites these groups - along Antarctica's Pacific coast. Acrobatidae and Microbiotheriidae silhouette by Sarah Werning on Phylopic (CC 3.0 Unported).

3.1

Genus	Diet classification	Fine diet classification	Body mass	Diet source	Body mass source	Metatherian or eutherian	Time bin
Alcidedorbignya	omnivore	omnivore-herbivore	100 g-1 kg	(De Muizon, Billet et al. 2015)	(De Muizon, Billet et al. 2015, Gelfo, Alonso et al. 2019)	eutherian	Palaeocene
Allqokirus	carnivore	carnivore	100 g-1 kg	(Zimicz 2012, De Muizon, Ladevèze et al. 2018, Engelman, Anaya et al. 2020)	(Zimicz 2012)	metatherian	Palaeocene
Amphidolops	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Palaeocene
Andinodelphys	carnivore	carnivore	1 kg-10 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Palaeocene
Andinodus	herbivore	herbivore	1 kg-10 kg	(Halliday, Upchurch et al. 2017, Defler 2019)	Calculated from molar dimensions of De Muizon and Cifelli (2000) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Anisolambda	herbivore	folivore	10 kg-100 kg	(Reguero, Marenssi et al. 2002, Croft 2024)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Archaeogaia	herbivore	folivore	10 kg-100 kg	(Zimicz, Fernández et al. 2020, Croft 2024)	(Vizcaíno, Cassini et al. 2012, Zimicz, Fernández et al. 2020)	eutherian	Palaeocene
Archaeopithecus	herbivore	herbivore	1 kg-10 kg	(Croft 2016, Croft 2024)	Calculated from molar dimensions of López, Gelfo et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Brandmayria	herbivore	herbivore	10 kg-100 kg	(Simpson 1967, Lorente, Gelfo et al. 2019)	(Simpson 1967, Elissamburu 2012, Vizcaíno, Cassini et al. 2012, Lorente, Gelfo et al. 2019)	eutherian	Palaeocene
Camargomendesia	herbivore	folivore	1 kg-10 kg	(Line and Bergqvist 2005, Croft 2016, Croft 2024)	Calculated from molar dimensions of Billet and De Muizon (2013) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Carodnia	herbivore	herbivore	100 kg-1 tonne	(Croft 2016)	(Croft 2016, Defler 2019, Gelfo, García-López et al. 2020)	eutherian	Palaeocene
Cimolestes	carnivore	invertivore	10 g-100 g	(Defler 2019)	Estimated from molar dimensions of similar invertivore (Marshall and De Muizon 1988) and the averaged processes of Legendre (1986) and Bloch, Rose et al. (1998)	eutherian	Palaeocene
Cocatherium	omnivore	omnivore	100 g-1 kg	Based on the closely related *Sillustania* and, in turn, *Roberthoffstetteria* (Chornogubsky and Goin 2015, Goin 2022)	Calculated from molar dimensions of Goin, Pascual et al. (2006) and the process of Gordon (2003) [pooled marsupials, *Caluromys* excluded]	metatherian	Palaeocene

Derorhynchus	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Palaeocene
Didelphopsis	herbivore	frugivore	100 g-1 kg	(Zimicz 2012, Carneiro and Oliveira 2017)	(Zimicz 2012)	metatherian	Palaeocene
Eoastrapostylops	omnivore	omnivore-herbivore	10 kg-100 kg	(De Muizon, Billet et al. 2015, Kramarz, Bond et al. 2017, Defler 2019)	(Gelfo, García-López et al. 2020)	eutherian	Palaeocene
Eohyrax	herbivore	grazer	10 kg-100 kg	(Billet, Patterson et al. 2007, Croft 2024)	(Elissamburu 2012)	eutherian	Palaeocene
Ernestokokenia	herbivore	frugivore	1 kg-10 kg	(Croft, Gelfo et al. 2020)	Calculated from molar dimensions of De Muizon and Cifelli (2000) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Escribania	omnivore	omnivore-herbivore	1 kg-10 kg	(Defler 2019)	Calculated from molar dimensions of De Muizon and Cifelli (2000) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Etayoa	herbivore	herbivore	1 kg-10 kg	(Antoine, Billet et al. 2015)	(Gelfo, García-López et al. 2020)	eutherian	Palaeocene
Gashternia	herbivore	folivore	1 kg-10 kg	(Zimicz 2012, Zimicz 2014)	(Zimicz 2012, Zimicz 2014)	metatherian	Palaeocene
Henricosbornia	herbivore	folivore	1 kg-10 kg	(Croft 2024)	Calculated from molar dimensions of Zheng, Nanxiong et al. (1979) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Incadelphys	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Palaeocene
Indalecia	herbivore	folivore	1 kg-10 kg	(Cifelli and Soria 1983, Croft 2024)	Calculated from molar dimensions of Saade, García-López et al. (2023) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Isotemnus	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Lorente 2019)	eutherian	Palaeocene
Jaskhadelphys	carnivore	invertivore	1 g-10 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Palaeocene
Khasia	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Palaeocene
Kibenikhoria	herbivore	folivore	1 kg-10 kg	(Croft 2016, Croft 2024)	Calculated from molar dimensions of Vera and Krause (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Mayulestes	carnivore	carnivore	100 g-1 kg	(De Muizon, Ladevèze et al. 2018, Engelman, Anaya et al. 2020)	Calculated from molar dimensions of De Muizon (1998) and the process of Gordon (2003) [pooled marsupials, *Caluromys* excluded]	metatherian	Palaeocene
Mizquedelphys	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Palaeocene
Molinodus	herbivore	frugivore	1 kg-10 kg	(Croft 2016)	Calculated from molar dimensions of De Muizon and	eutherian	Palaeocene

					Cifelli (2000) and De Muizon, Billet et al. (2019) and the process of Scarano, Carlini et al. (2011)		
Nemolestes	carnivore	carnivore	1 kg-10 kg	(Prevosti and Forasiepi 2018, Rangel, Carneiro et al. 2019)	(Prevosti and Forasiepi 2018)	metatherian	Palaeocene
Notoetayoa	herbivore	herbivore	10 kg-100 kg	(Antoine, Billet et al. 2015)	(Gelfo, García-López et al. 2020)	eutherian	Palaeocene
Notonychops	herbivore	folivore	1 kg-10 kg	(Soria 1988, Croft 2024)	(Gelfo, García-López et al. 2020)	eutherian	Palaeocene
Othnielmarshia	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Palaeocene
Palangania	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Palaeocene
Peradectes	omnivore	omnivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Palaeocene
Pleurostylodon	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Elissamburu 2012)	eutherian	Palaeocene
Polydolops	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Palaeocene
Pucadelphys	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Palaeocene
Pucanodus	herbivore	herbivore	100 g-1 kg	(Halliday, Upchurch et al. 2017, Defler 2019)	Calculated from molar dimensions of De Muizon and Cifelli (2000) and De Muizon, Billet et al. (2019) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Raulvaccia	omnivore	omnivore-herbivore	1 kg-10 kg	(Gelfo 2007, Defler 2019)	Based on the closely related *Escribania* and *Asmithwoodwardia* (De Muizon and Cifelli 2000, Gelfo 2007, Scarano, Carlini et al. 2011)	eutherian	Palaeocene
Requisia	herbivore	folivore	1 kg-10 kg	Based on the closely related *Notonychops* (Soria 1988, Bonaparte and Morales 1997)	Calculated from molar dimensions of Bonaparte and Morales (1997) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Ricardolydekkeria	herbivore	folivore	1 kg-10 kg	(Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Roberthoffstetteria	omnivore	omnivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Palaeocene
Rodcania	herbivore	herbivore	100 kg-1 tonne	(Gelfo, García-López et al. 2020)	(Gelfo, García-López et al. 2020)	eutherian	Palaeocene
Satshatemnus	herbivore	folivore	1 kg-10 kg	(Soria 1989, Croft 2024)	(Gelfo, García-López et al. 2020)	eutherian	Palaeocene
Simoclaenus	herbivore	herbivore	1 kg-10 kg	(Halliday, Upchurch et al. 2017, Defler 2019)	Calculated from molar dimensions of De Muizon and Cifelli (2000) and De Muizon, Billet et al. (2019) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Simpsonotus	herbivore	folivore	1 kg-10 kg	(Croft 2024)	(Croft, Gelfo et al. 2020)	eutherian	Palaeocene
Szalinia	carnivore	invertivore	10 g-100 g	(De Muizon and Cifelli 2001)	Calculated from molar dimensions of De Muizon and	metatherian	Palaeocene

					Cifelli (2001) and the process of Gordon (2003) [pooled didelphids, *Caluromys* excluded]		
Tiuclaenus	herbivore	herbivore	100 g-1 kg	(Halliday, Upchurch et al. 2017, Defler 2019)	Calculated from molar dimensions of De Muizon and Cifelli (2000) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Tiulordia	carnivore	invertivore	10 g-100 g	(De Muizon and Cifelli 2001)	Calculated from molar dimensions of Marshall and De Muizon (1988) and the process of Gordon (2003) [pooled didelphids, *Caluromys* excluded]	metatherian	Palaeocene
Trigonostylops	herbivore	herbivore	10 kg-100 kg	(Croft 2016)	(Croft 2016)	eutherian	Palaeocene
Victorlemoineia	herbivore	herbivore	100 kg-1 tonne	(Cassini, Cerdeño et al. 2012)	(Vizcaíno, Cassini et al. 2012)	eutherian	Palaeocene
Wainka	herbivore	folivore	1 kg-10 kg	(Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Simpson (1935) and the process of Scarano, Carlini et al. (2011)	eutherian	Palaeocene
Acoelodus	herbivore	herbivore	1 kg-10 kg	(Vera 2013, Croft 2024)	Calculated from molar dimensions of Vera (2013) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Acoelohyrax	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Ypresian
Albertogaudrya	herbivore	herbivore	10 kg-100 kg	(Cassini, Cerdeño et al. 2012)	(Vizcaíno, Cassini et al. 2012)	eutherian	Ypresian
Amphidolops	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Anisolambda	herbivore	folivore	10 kg-100 kg	(Reguero, Marenssi et al. 2002, Croft 2024)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Antepithecus	herbivore	herbivore	1 kg-10 kg	(Croft 2016, Croft 2024)	(Scarano, Carlini et al. 2011)	eutherian	Ypresian
Archaeopithecus	herbivore	herbivore	1 kg-10 kg	(Croft 2016, Croft 2024)	Calculated from molar dimensions of López, Gelfo et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Argyrolestes	carnivore	carnivore	1 kg-10 kg	(Prevosti and Forasiepi 2018)	(Prevosti and Forasiepi 2018)	metatherian	Ypresian
Asmithwoodwardia	omnivore	omnivore-herbivore	1 kg-10 kg	(Gelfo, Alonso et al. 2019)	Calculated from molar dimensions of De Muizon and Cifelli (2000) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Astegotherium	carnivore	invertivore	1 kg-10 kg	(Ciancio, Vieytes et al. 2014, Defler 2019)	Based on *Dasypus novemcinctus* (Farina and Vizcaino 1997, Ciancio, Vieytes et al. 2014)	eutherian	Ypresian

Austropediomys	omnivore	omnivore	10 g-100 g	(Carneiro and Oliveira 2023)	Calculated from molar dimensions of Carneiro, Oliveira et al. (2018) and the process of Gordon (2003) [pooled marsupials, *Caluromys* excluded]	metatherian	Ypresian
Bardalestes	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012, Abello, Toledo et al. 2020)	metatherian	Ypresian
Bergqvistherium	herbivore	frugivore	10 g-100 g	(Goin, Oliveira et al. 1998, Carneiro 2018)	Calculated from molar dimensions of Carneiro (2018) and the process of Gordon (2003) [pooled didelphids, *Caluromys* excluded]	metatherian	Ypresian
Bobbschaefferia	omnivore	omnivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Bonapartherium	herbivore	herbivore	100 g-1 kg	(Zimicz 2012, Zimicz 2014, Babot, Rougier et al. 2020)	(Zimicz 2012, Zimicz 2014)	metatherian	Ypresian
Camargomendesia	herbivore	folivore	1 kg-10 kg	(Line and Bergqvist 2005, Croft 2016, Croft 2024)	Calculated from molar dimensions of Billet and De Muizon (2013) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Campanorco	herbivore	herbivore	1 kg-10 kg	(Reguero, Candela et al. 2010)	(Reguero, Candela et al. 2010)	eutherian	Ypresian
Carodnia	herbivore	herbivore	100 kg-1 tonne	(Croft 2016)	(Croft 2016, Defler 2019, Gelfo, García-López et al. 2020)	eutherian	Ypresian
Caroloameghinia	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Carolocoutoia	herbivore	frugivore	1 kg-10 kg	(Goin, Oliveira et al. 1998, Oliveira and Goin 2011, Zimicz 2012, Carneiro 2018)	(Zimicz 2012)	metatherian	Ypresian
Carolopaulacoutoia	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Chulpasia	omnivore	omnivore-frugivore	100 g-1 kg	(Beck 2013)	(Beck 2013)	metatherian	Ypresian
Coelutaetus	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on possibly closely related *Utaetus* (Simpson 1948, Croft 2016)	eutherian	Ypresian
Colbertia	herbivore	folivore	1 kg-10 kg	(Croft 2016)	(Elissamburu 2012, Croft 2016)	eutherian	Ypresian
Coona	omnivore	omnivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Derorhynchus	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Didelphopsis	herbivore	frugivore	100 g-1 kg	(Zimicz 2012, Carneiro and Oliveira 2017)	(Zimicz 2012)	metatherian	Ypresian
Didolodus	omnivore	omnivore-herbivore	1 kg-10 kg	(Croft, Gelfo et al. 2020)	(Croft, Gelfo et al. 2020)	eutherian	Ypresian
Diogenesia	carnivore	invertivore	10 g-100 g	(Oliveira, Carneiro et al. 2021)	(Oliveira, Carneiro et al. 2021)	metatherian	Ypresian
Edvardotrouessartia	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Ypresian
Eobrasilia	carnivore	carnivore	1 kg-10 kg	(Carneiro and Oliveira 2017, Rangel, Carneiro et al. 2019)	Calculated from molar dimensions of Simpson, Price et al. (1947) and Marshall	metatherian	Ypresian

					(1984) and the process of Gordon (2003) [pooled didelphids, *Caluromys* excluded]		
Eolicaphrium	herbivore	folivore	1 kg-10 kg	(Croft 2024)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Eomicrobiotherium	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Epidolops	herbivore	herbivore	100 g-1 kg	(Zimicz 2012, Zimicz 2014)	(Zimicz 2012, Zimicz 2014)	metatherian	Ypresian
Ernestohaeckelia	herbivore	herbivore	1 kg-10 kg	(Cassini, Cerdeño et al. 2012)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Ernestokokenia	herbivore	frugivore	1 kg-10 kg	(Croft, Gelfo et al. 2020)	Calculated from molar dimensions of De Muizon and Cifelli (2000) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Eudolops	herbivore	herbivore	1 kg-10 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Gashternia	herbivore	folivore	1 kg-10 kg	(Zimicz 2012, Zimicz 2014)	(Zimicz 2012, Zimicz 2014)	metatherian	Ypresian
Gaylordia	carnivore	invertivore	10 g-100 g	(Carneiro and Oliveira 2017)	(Oliveira and Goin 2015)	metatherian	Ypresian
Griphotherion	herbivore	herbivore	1 kg-10 kg	(Sosa and Garcia Lopez 2018)	Calculated from molar dimensions of García López and Powell (2011) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Guggenheimia	carnivore	invertivore	100 g-1 kg	(Goin, Oliveira et al. 1998, Zimicz 2012, Carneiro and Oliveira 2017, Carneiro 2018)	(Zimicz 2012)	metatherian	Ypresian
Henricosbornia	herbivore	folivore	1 kg-10 kg	(Croft 2024)	Calculated from molar dimensions of Zheng, Nanxiong et al. (1979) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Ignigena	herbivore	herbivore	100 g-1 kg	(Hitz, Flynn et al. 2006)	Calculated from molar dimensions of Hitz, Flynn et al. (2006) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Isolophodon	herbivore	grazer	100 kg-1 tonne	(Billet, Patterson et al. 2007, Croft 2024)	(Vizcaíno, Cassini et al. 2012, Kramarz and Bond 2013, Defler 2019)	eutherian	Ypresian
Isotemnus	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Lorente 2019)	eutherian	Ypresian
Itaboraidelphys	carnivore	invertivore	100 g-1 kg	(Zimicz 2012, Rangel, Carneiro et al. 2019)	(Zimicz 2012)	metatherian	Ypresian
Itaboraitherium	herbivore	folivore	1 kg-10 kg	(Line and Bergqvist 2005, Croft 2016, Croft 2024)	Calculated from molar dimensions of Billet and De Muizon (2013) and the	eutherian	Ypresian

					process of Scarano, Carlini et al. (2011)		
Kibenikhoria	herbivore	folivore	1 kg-10 kg	(Croft 2016, Croft 2024)	Calculated from molar dimensions of Vera and Krause (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Kramadolops	herbivore	herbivore	1 kg-10 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Lambdaconus	herbivore	folivore	10 kg-100 kg	(Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Lamegoia	herbivore	frugivore	10 kg-100 kg	(Couto 1952, Croft, Gelfo et al. 2020)	Calculated from molar dimensions of Couto (1952) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Marmosopsis	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Maxschlosseria	herbivore	folivore	1 kg-10 kg	(Croft 2016, Croft 2024)	(Elissamburu 2012)	eutherian	Ypresian
Miguelsoria	omnivore	omnivore-herbivore	1 kg-10 kg	(Defler 2019)	Calculated from molar dimensions of De Muizon and Cifelli (2000) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Minusculodelphis	carnivore	invertivore	1 g-10 g	(Oliveira, Zimicz et al. 2016, Carneiro and Oliveira 2017)	(Oliveira, Zimicz et al. 2016, Babot, Rougier et al. 2020)	metatherian	Ypresian
Mirandatherium	carnivore	invertivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Monodelphopsis	herbivore	frugivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Nanolophodon	herbivore	folivore	1 kg-10 kg	(Castro, García-López et al. 2021, Croft 2024)	Calculated from molar dimensions of Castro, García-López et al. (2021) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Nemolestes	carnivore	carnivore	1 kg-10 kg	(Prevosti and Forasiepi 2018, Rangel, Carneiro et al. 2019)	(Prevosti and Forasiepi 2018)	metatherian	Ypresian
Noatherium	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on assessment as a 'medium-sized' armadillo (Farina and Vizcaino 1997, Fernicola, Zimicz et al. 2021)	eutherian	Ypresian
Notopithecus	herbivore	herbivore	1 kg-10 kg	(Croft 2016)	(Elissamburu 2012, Croft 2016)	eutherian	Ypresian
Notostylops	herbivore	herbivore	10 kg-100 kg	(Lorente, Gelfo et al. 2019)	(Elissamburu 2012, Vizcaíno, Cassini et al. 2012)	eutherian	Ypresian
Oldfieldthomasia	herbivore	folivore	1 kg-10 kg	(Croft 2016, Croft 2024)	(Elissamburu 2012, Vizcaíno, Cassini et al. 2012)	eutherian	Ypresian
Orome	herbivore	folivore	1 kg-10 kg	(Croft 2024)	Calculated from molar dimensions of Bauzá, Gelfo et al. (2019) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian

Paginula	herbivore	folivore	10 kg-100 kg	(Croft 2016, Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Ypresian
Palaeocladosictis	omnivore	omnivore-herbivore	1 kg-10 kg	(Marshall 1978, Defler 2019)	Calculated from dimensions of de Paula Couto (1961) and the process of Scarano, Carlini et al. (2011) [used upper premolar as proxy for molar]	eutherian	Ypresian
Pampahippus	herbivore	folivore	10 kg-100 kg	(Reguero, Candela et al. 2010, Croft 2016)	(Vizcaíno, Cassini et al. 2012)	eutherian	Ypresian
Paranisolambda	herbivore	folivore	1 kg-10 kg	(Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Pascualodus	herbivore	herbivore	1 kg-10 kg	(Halliday, Upchurch et al. 2017, Defler 2019)	Calculated from molar dimensions of Gelfo (2004) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Patene	carnivore	carnivore	1 kg-10 kg	(Zimicz 2012, Prevosti and Forasiepi 2018, Rangel, Carneiro et al. 2019)	(Zimicz 2012, Prevosti and Forasiepi 2018)	metatherian	Ypresian
Peradectes	omnivore	omnivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Peripantostylops	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Ypresian
Periprotodidelphis	herbivore	frugivore	100 g-1 kg	(Goin, Oliveira et al. 1998, Carneiro 2018)	Calculated from molar dimensions of Oliveira and Goin (2011) and the process of Gordon (2003) [pooled didelphids, *Caluromys* excluded]	metatherian	Ypresian
Perutherium	omnivore	omnivore-herbivore	100 g-1 kg	(Marshall, de Muizon et al. 1983)	Calculated from molar dimensions of Marshall, de Muizon et al. (1983) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Pleurostylodon	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Elissamburu 2012)	eutherian	Ypresian
Polydolops	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Prepidolops	omnivore	omnivore	10 g-100 g	(Zimicz 2012, Zimicz 2014, Babot, Rougier et al. 2020)	(Zimicz 2012, Zimicz 2014)	metatherian	Ypresian
Proargyrohyrax	herbivore	grazer	1 kg-10 kg	(Hitz, Reguero et al. 2000)	(Scarano, Carlini et al. 2011)	eutherian	Ypresian
Procaroloameghinia	herbivore	frugivore	100 g-1 kg	(Oliveira and Goin 2011, Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Proectocion	omnivore	omnivore-herbivore	1 kg-10 kg	(Defler 2019)	Calculated from molar dimensions of Ameghino (1904) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Prostegotherium	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Dasypus novemcinctus* and *hybridus* (Farina and Vizcaino 1997, Babot, López et al. 2012)	eutherian	Ypresian

Proticia	herbivore	herbivore	100 kg-1 tonne	(Sánchez-Villagra, Burnham et al. 2000)	Calculated from molar dimensions of Patterson (1977) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Ypresian
Protodidelphis	herbivore	frugivore	1 kg-10 kg	(Goin, Oliveira et al. 1998, Zimicz 2012, Carneiro and Oliveira 2017, Carneiro 2018)	(Zimicz 2012)	metatherian	Ypresian
Protolipterna	herbivore	folivore	1 kg-10 kg	(Croft 2016, Croft 2024)	Calculated from molar dimensions of De Muizon and Cifelli (2000) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Pseudhyrax	herbivore	grazer	1 kg-10 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003)	eutherian	Ypresian
Pucatherium	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Dasypus novemcinctus* (Farina and Vizcaino 1997, Herrera, Esteban et al. 2019)	eutherian	Ypresian
Ricardocifellia	omnivore	omnivore-herbivore	1 kg-10 kg	(Defler 2019)	Calculated from molar dimensions of De Muizon and Cifelli (2000) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Ricardolydekkeria	herbivore	folivore	1 kg-10 kg	(Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Riolestes	carnivore	invertivore	100 g-1 kg	(Carneiro 2017)	Calculated from molar dimensions of Goin, Candela et al. (2009) and the process of Gordon (2003) [pooled marsupials, *Caluromys* excluded]	metatherian	Ypresian
Riostegotherium	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Dasypus hybridus* (Farina and Vizcaino 1997, Oliveira and Bergqvist 1998)	eutherian	Ypresian
Rosendolops	omnivore	omnivore-invertivore	10 g-100 g	(Zimicz 2012, Zimicz 2014)	(Zimicz 2012, Zimicz 2014)	metatherian	Ypresian
Saltaodus	omnivore	omnivore-herbivore	100 g-1 kg	(Gelfo, Alonso et al. 2019)	(Gelfo, Alonso et al. 2019)	eutherian	Ypresian
Scaglia	herbivore	herbivore	100 kg-1 tonne	(Cassini, Cerdeño et al. 2012)	(Vizcaíno, Cassini et al. 2012, Kramarz and Bond 2013)	eutherian	Ypresian
Sillustania	omnivore	omnivore	10 g-100 g	Based on the closely related *Roberthoffstetteria* (Chornogubsky and Goin 2015)	Calculated from molar dimensions of Chornogubsky and Goin (2015) and the process of Gordon (2003)	metatherian	Ypresian
Teratopithecus	herbivore	herbivore	1 kg-10 kg	(Croft 2016, Croft 2024)	Calculated from molar dimensions of López, Gelfo et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian

Tetragonostylops	herbivore	herbivore	100 kg-1 tonne	(Cassini, Cerdeño et al. 2012)	(Vizcaíno, Cassini et al. 2012)	eutherian	Ypresian
Thomashuxleya	herbivore	folivore	10 kg-100 kg	(Croft 2016)	(Elissamburu 2012, Croft 2016, Carrillo and Asher 2017, Lorente 2019) [large variety of mass estimates – 100kg estimated here as compromise]	eutherian	Ypresian
Transpithecus	herbivore	herbivore	1 kg-10 kg	(Hitz, Reguero et al. 2000)	Calculated from molar dimensions of Vera (2012) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Trigonostylops	herbivore	herbivore	10 kg-100 kg	(Croft 2016)	(Croft 2016)	eutherian	Ypresian
Umayodus	omnivore	omnivore-herbivore	1 kg-10 kg	(Gelfo and Sigé 2011, Defler 2019)	Calculated from molar dimensions of Gelfo and Sigé (2011) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Utaetus	carnivore	invertivore	1 kg-10 kg	(Ciancio, Vieytes et al. 2014, Croft 2016)	(Croft 2016)	eutherian	Ypresian
Victorlemoineia	herbivore	herbivore	100 kg-1 tonne	(Cassini, Cerdeño et al. 2012)	(Vizcaíno, Cassini et al. 2012)	eutherian	Ypresian
Woodburnodon	herbivore	frugivore	1 kg-10 kg	(Zimicz 2012, Gelfo, Goin et al. 2019)	(Zimicz 2012, Gelfo, Goin et al. 2019)	metatherian	Ypresian
Zeusdelphys	herbivore	frugivore	1 kg-10 kg	(Zimicz 2012, Carneiro and Oliveira 2017)	(Zimicz 2012)	metatherian	Ypresian
Acamana	herbivore	folivore	100 kg-1 tonne	(Croft 2024)	Calculated from molar dimensions of Simpson, Minoprio et al. (1962) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Late Eocene
Acoelodus	herbivore	herbivore	1 kg-10 kg	(Vera 2013, Croft 2024)	Calculated from molar dimensions of Vera (2013) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Acoelohyrax	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Adiantoides	herbivore	folivore	1 kg-10 kg	(Cifelli and Soria 1983, Croft 2024)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Albertogaudrya	herbivore	herbivore	10 kg-100 kg	(Cassini, Cerdeño et al. 2012)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Allalmeia	herbivore	folivore	1 kg-10 kg	(Lorente, Gelfo et al. 2014, Croft 2016)	(Lorente, Gelfo et al. 2014)	eutherian	Late Eocene
Amilnedwardsia	herbivore	herbivore	1 kg-10 kg	(Cassini, Cerdeño et al. 2012)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Amphidolops	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene

Angelocabrerus	carnivore	carnivore	10 kg-100 kg	(Zimicz 2012, Prevosti and Forasiepi 2018)	(Zimicz 2012, Prevosti and Forasiepi 2018)	metatherian	Late Eocene
Anisolambda	herbivore	folivore	10 kg-100 kg	(Reguero, Marenssi et al. 2002, Croft 2024)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Anisotemnus	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Antepithecus	herbivore	herbivore	1 kg-10 kg	(Croft 2016, Croft 2024)	(Scarano, Carlini et al. 2011)	eutherian	Late Eocene
Antofagastia	herbivore	folivore	1 kg-10 kg	(García-López 2015, Croft 2024)	Calculated from molar dimensions of García-López (2015) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Apeirodon	herbivore	herbivore	10 g-100 g	(Babot, Rougier et al. 2020)	Calculated from molar dimensions of Goin, Candela et al. (2009) and Babot, Rougier et al. (2020) and the process of Gordon (2003) [pooled marsupials, *Caluromys* excluded]	metatherian	Late Eocene
Archaeohyracotherium	omnivore	omnivore-herbivore	1 kg-10 kg	(Defler 2019)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Archaeohyrax	herbivore	grazer	10 kg-100 kg	(Croft and Weinstein 2008)	(Croft and Weinstein 2008, Elissamburu 2012)	eutherian	Late Eocene
Archaeopithecus	herbivore	herbivore	1 kg-10 kg	(Croft 2016, Croft 2024)	Calculated from molar dimensions of López, Gelfo et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Arminiheringia	carnivore	carnivore	10 kg-100 kg	(Zimicz 2012, Prevosti and Forasiepi 2018)	(Zimicz 2012, Prevosti and Forasiepi 2018)	metatherian	Late Eocene
Asmithwoodwardia	omnivore	omnivore-herbivore	1 kg-10 kg	(Gelfo, Alonso et al. 2019)	Calculated from molar dimensions of De Muizon and Cifelli (2000) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Astegotherium	carnivore	invertivore	1 kg-10 kg	(Ciancio, Vieytes et al. 2014, Defler 2019)	Based on *Dasypus novemcinctus* (Farina and Vizcaino 1997, Ciancio, Vieytes et al. 2014)	eutherian	Late Eocene
Astraponotus	herbivore	herbivore	100 kg-1 tonne	(Cassini, Cerdeño et al. 2012)	Calculated from molar dimensions of Kramarz, Bond et al. (2011) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Late Eocene
Balsayacuy	herbivore	folivore	10 g-100 g	(Boivin, Marivaux et al. 2022)	Calculated from molar dimensions of Boivin, Marivaux et al. (2022) and the	eutherian	Late Eocene

					process of Millien and Bovy (2010)		
Bardalestes	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012, Abello, Toledo et al. 2020)	metatherian	Late Eocene
Barrancatatus	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Zaedyus* and *Euphractus* (Robinson and Redford 1986, Farina and Vizcaino 1997, Carlini, Ciancio et al. 2010)	eutherian	Late Eocene
Bonapartherium	herbivore	herbivore	100 g-1 kg	(Zimicz 2012, Zimicz 2014, Babot, Rougier et al. 2020)	(Zimicz 2012, Zimicz 2014)	metatherian	Late Eocene
Boreastylops	herbivore	herbivore	10 kg-100 kg	(Sosa and Garcia Lopez 2018)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Brachystephanus	herbivore	folivore	1 kg-10 kg	(Croft 2016, Croft 2024)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Bryanpattersonia	herbivore	grazer	1 kg-10 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003)	eutherian	Late Eocene
Cachiyacuy	herbivore	herbivore	10 g-100 g	(Defler 2019)	(Antoine, Marivaux et al. 2012)	eutherian	Late Eocene
Callistoe	carnivore	carnivore	10 kg-100 kg	(Zimicz 2012, Prevosti and Forasiepi 2018, Babot, Rougier et al. 2020)	(Zimicz 2012, Prevosti and Forasiepi 2018, Babot, Rougier et al. 2020)	metatherian	Late Eocene
Campanorco	herbivore	herbivore	1 kg-10 kg	(Reguero, Candela et al. 2010)	(Reguero, Candela et al. 2010)	eutherian	Late Eocene
Canaanimys	herbivore	herbivore	10 g-100 g	(Defler 2019)	(Antoine, Marivaux et al. 2012)	eutherian	Late Eocene
Caroloameghinia	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Carolozittelia	herbivore	folivore	100 kg-1 tonne	(Hooker 2000, Vizcaíno, Cassini et al. 2012)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Chachapoyamys	herbivore	folivore	100 g-1 kg	(Boivin, Marivaux et al. 2022)	Calculated from molar dimensions of Boivin, Marivaux et al. (2022) and the process of Millien and Bovy (2010)	eutherian	Late Eocene
Chlorocyon	carnivore	carnivore	1 kg-10 kg	(Engelman, Flynn et al. 2018)	(Engelman, Flynn et al. 2018)	metatherian	Late Eocene
Coelostylodon	herbivore	folivore	10 kg-100 kg	(Croft 2024)	Calculated from molar dimensions of Simpson (1970) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Colbertia	herbivore	folivore	1 kg-10 kg	(Croft 2016)	(Elissamburu 2012, Croft 2016)	eutherian	Late Eocene
Colombitherium	herbivore	folivore	100 kg-1 tonne	(Hooker 2000)	Calculated from molar dimensions of Billet, Orliac et al. (2010) and the averaged	eutherian	Late Eocene

					processes of Damuth (1990) and Janis (1990)		
Coloradolops	omnivore	omnivore	10 g-100 g	Based on the closely related *Prepidolops* (Zimicz 2012, Zimicz 2014, Chornogubsky, Zimicz et al. 2019, Babot, Rougier et al. 2020)	Calculated from molar dimensions of Chornogubsky, Zimicz et al. (2019) and the process of Gordon (2003) [pooled marsupials, *Caluromys* excluded]	metatherian	Late Eocene
Coona	omnivore	omnivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Coquenia	herbivore	folivore	100 kg-1 tonne	(Shockey, Flynn et al. 2012)	Calculated from molar dimensions of Deraco, Powell et al. (2008) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Late Eocene
Derorhynchus	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Didolodus	omnivore	omnivore-herbivore	1 kg-10 kg	(Croft, Gelfo et al. 2020)	(Croft, Gelfo et al. 2020)	eutherian	Late Eocene
Distylophorus	herbivore	folivore	100 kg-1 tonne	(Croft 2024)	Calculated from molar dimensions of Simpson (1967) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Late Eocene
Dolichostylodon	herbivore	folivore	1 kg-10 kg	(Croft 2016, Croft 2024)	Calculated from molar dimensions of García López and Powell (2009) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Edvardotrouessartia	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Eobranisamys	herbivore	herbivore	100 g-1 kg	(Frailey and Campbell Jr 2004)	Calculated from molar dimensions of Frailey and Campbell Jr (2004) and the process of Millien and Bovy (2010)	eutherian	Late Eocene
Eoespina	herbivore	herbivore	10 g-100 g	(Frailey and Campbell Jr 2004)	Calculated from molar dimensions of Frailey and Campbell Jr (2004) and the process of Millien and Bovy (2010)	eutherian	Late Eocene
Eohegetotherium	herbivore	grazer	1 kg-10 kg	(Simpson 1967)	Calculated from molar dimensions of Simpson (1967) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Eohyrax	herbivore	grazer	10 kg-100 kg	(Billet, Patterson et al. 2007, Croft 2024)	(Elissamburu 2012)	eutherian	Late Eocene
Eoincamys	herbivore	herbivore	100 g-1 kg	(Álvarez, Ercoli et al. 2020, Rasia, Candela et al. 2021)	Calculated from molar dimensions of Frailey and Campbell Jr (2004) and Boivin, Marivaux et al. (2018) and the	eutherian	Late Eocene

					process of Millien and Bovy (2010)		
Eomicrobiotherium	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Eomorphippus	herbivore	herbivore	10 kg-100 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003, Elissamburu 2012)	eutherian	Late Eocene
Eopachyrucos	herbivore	grazer	1 kg-10 kg	(Reguero, Ubilla et al. 2003)	(Reguero, Ubilla et al. 2003)	eutherian	Late Eocene
Ernestohaeckelia	herbivore	herbivore	1 kg-10 kg	(Cassini, Cerdeño et al. 2012)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Ernestokokenia	herbivore	frugivore	1 kg-10 kg	(Croft, Gelfo et al. 2020)	Calculated from molar dimensions of De Muizon and Cifelli (2000) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Eudolops	herbivore	herbivore	1 kg-10 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Gashternia	herbivore	folivore	1 kg-10 kg	(Zimicz 2012, Zimicz 2014)	(Zimicz 2012, Zimicz 2014)	metatherian	Late Eocene
Glyptatelus	carnivore	invertivore	10 kg-100 kg	Based on *Neoglyptatelus* (Vizcaíno, Rinderknecht et al. 2003, Croft 2016)	Based on *Eocoleophorus* and thus *Propaopus* (Farina and Vizcaino 1997, Oliveira, Ribeiro et al. 1997)	eutherian	Late Eocene
Griphodon	herbivore	folivore	100 kg-1 tonne	Based on *Pyrotherium* (Shockey and Daza 2004, Croft 2016)	Calculated from molar dimensions of Kramarz and Bond (2014) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Late Eocene
Groeberia	herbivore	herbivore	100 g-1 kg	(Zimicz 2012, Zimicz and Goin 2020)	(Zimicz 2012, Zimicz and Goin 2020)	metatherian	Late Eocene
Grypolophodon	herbivore	herbivore	100 kg-1 tonne	(Cassini, Cerdeño et al. 2012)	(Bostelmann, Le Roux et al. 2013)	eutherian	Late Eocene
Guilielmofloweria	herbivore	folivore	10 kg-100 kg	(Simpson 1948, Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Guilielmoscottia	herbivore	folivore	10 kg-100 kg	(Simpson 1948, Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of (Simpson 1948) and the process of (Scarano, Carlini et al. 2011)	eutherian	Late Eocene
Henricosbornia	herbivore	folivore	1 kg-10 kg	(Croft 2024)	Calculated from molar dimensions of Zheng, Nanxiong et al. (1979) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Heteroglyphis	herbivore	folivore	10 kg-100 kg	(Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene

Heterolophodon	herbivore	herbivore	100 kg-1 tonne	(Palmer 1904)	Calculated from molar dimensions of Bostelmann, Le Roux et al. (2013) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Late Eocene
Homalostylops	herbivore	folivore	1 kg-10 kg	(Croft 2024)	(Elissamburu 2012, Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Hondonadia	herbivore	granivore	10 g-100 g	(Zimicz 2012, Zimicz 2014)	(Zimicz 2012, Zimicz 2014)	metatherian	Late Eocene
Hypodolops	herbivore	frugivore	100 g-1 kg	(Zimicz 2012, Chornogubsky 2021)	(Zimicz 2012, Chornogubsky 2021)	metatherian	Late Eocene
Indalecia	herbivore	folivore	1 kg-10 kg	(Cifelli and Soria 1983, Croft 2024)	Calculated from molar dimensions of Saade, García-López et al. (2023) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Isolophodon	herbivore	grazer	100 kg-1 tonne	(Billet, Patterson et al. 2007, Croft 2024)	(Vizcaíno, Cassini et al. 2012, Kramarz and Bond 2013, Defler 2019)	eutherian	Late Eocene
Isotemnus	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Lorente 2019)	eutherian	Late Eocene
Itaboraidelphys	carnivore	invertivore	100 g-1 kg	(Zimicz 2012, Rangel, Carneiro et al. 2019)	(Zimicz 2012)	metatherian	Late Eocene
Kramadolops	herbivore	herbivore	1 kg-10 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Lomaphorelus	carnivore	invertivore	10 kg-100 kg	Based on *Neoglyptatelus* (Vizcaíno, Rinderknecht et al. 2003, Croft 2016)	Based on *Proeutatus* (Ameghino 1902, Vizcaíno, Rinderknecht et al. 2003, Croft 2016)	eutherian	Late Eocene
Lumbreratherium	carnivore	invertivore	1 kg-10 kg	(Herrera, Powell et al. 2017)	Based on *Utaetus* and *Pucatherium* (Croft 2016, Herrera, Powell et al. 2017, Herrera, Esteban et al. 2019)	eutherian	Late Eocene
Machlydotherium	herbivore	grazer	100 kg-1 tonne	(Góis, Scillato-Yané et al. 2013, Defler 2019)	Based on *Yuruatherium* and hence *Pampatherium* (Vizcaíno, Cassini et al. 2012, Ciancio, Carlini et al. 2013)	eutherian	Late Eocene
Marmosopsis	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Martinmiguelia	herbivore	herbivore	100 kg-1 tonne	(Shockey, Flynn et al. 2012)	Calculated from molar dimensions of Bond and López (1995) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Late Eocene
Maxschlosseria	herbivore	folivore	1 kg-10 kg	(Croft 2016, Croft 2024)	(Elissamburu 2012)	eutherian	Late Eocene
Mazzoniphractus	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Compared via osteoderm dimensions to *Utaetus* (Carlini, Ciancio et al. 2010, Croft 2016)	eutherian	Late Eocene

Meteutatus	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Euphractus* and *Chaetophractus* (Robinson and Redford 1986, Farina and Vizcaino 1997, Carlini, Ciancio et al. 2010)	eutherian	Late Eocene
Nemolestes	carnivore	carnivore	1 kg-10 kg	(Prevosti and Forasiepi 2018, Rangel, Carneiro et al. 2019)	(Prevosti and Forasiepi 2018)	metatherian	Late Eocene
Notopithecus	herbivore	herbivore	1 kg-10 kg	(Croft 2016)	(Elissamburu 2012, Croft 2016)	eutherian	Late Eocene
Notorhinus	herbivore	herbivore	100 kg-1 tonne	(Cassini, Cerdeño et al. 2012)	Calculated from molar dimensions of Bostelmann, Le Roux et al. (2013) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Late Eocene
Notostylops	herbivore	herbivore	10 kg-100 kg	(Lorente, Gelfo et al. 2019)	(Elissamburu 2012, Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Oldfieldthomasia	herbivore	folivore	1 kg-10 kg	(Croft 2016, Croft 2024)	(Elissamburu 2012, Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Othnielmarshia	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Otrhonia	herbivore	herbivore	1 kg-10 kg	(Croft 2016)	(Croft 2016)	eutherian	Late Eocene
Paginula	herbivore	folivore	10 kg-100 kg	(Croft 2016, Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Palaeopeltis	herbivore	herbivore	100 kg-1 tonne	(Perea, Toriño et al. 2014, Gaudin and Croft 2015)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Palangania	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Pampahippus	herbivore	folivore	10 kg-100 kg	(Reguero, Candela et al. 2010, Croft 2016)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Pampatemnus	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Parastegosimpsonia	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on small *Dasypus* species (Farina and Vizcaino 1997, Ciancio, Carlini et al. 2013)	eutherian	Late Eocene
Parastrapotherium	herbivore	herbivore	1 tonne-10 tonnes	(Cassini, Cerdeño et al. 2012)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Parutaetus	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Zaedyus* (Farina and Vizcaino 1997, Carlini, Ciancio et al. 2010)	eutherian	Late Eocene
Pascualhyrax	herbivore	herbivore	1 kg-10 kg	(Ferro, García-López et al. 2023)	Calculated from molar dimensions of Ferro, García-López et al. (2023) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Patene	carnivore	carnivore	1 kg-10 kg	(Zimicz 2012, Prevosti and Forasiepi 2018, Rangel, Carneiro et al. 2019)	(Zimicz 2012, Prevosti and Forasiepi 2018)	metatherian	Late Eocene

Pauladelphys	omnivore	omnivore	100 g-1 kg	(Zimicz 2012, Gelfo, Goin et al. 2019)	(Zimicz 2012)	metatherian	Late Eocene
Paulogervaisia	omnivore	omnivore-herbivore	10 kg-100 kg	(Defler 2019)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Peripantostylops	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Periphragnis	herbivore	folivore	100 kg-1 tonne	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003, Elissamburu 2012)	eutherian	Late Eocene
Pharsophorus	carnivore	carnivore	10 kg-100 kg	(Zimicz 2012, Prevosti and Forasiepi 2018)	(Zimicz 2012, Prevosti and Forasiepi 2018)	metatherian	Late Eocene
Phoradiadius	herbivore	folivore	10 kg-100 kg	(Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Simpson, Minoprio et al. (1962) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Picunia	herbivore	folivore	100 kg-1 tonne	(Flynn, Wyss et al. 2003, Bostelmann, Le Roux et al. 2013)	(Flynn, Wyss et al. 2003, Bostelmann, Le Roux et al. 2013)	eutherian	Late Eocene
Pleurostylodon	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Elissamburu 2012)	eutherian	Late Eocene
Polyacrodon	herbivore	folivore	1 kg-10 kg	(Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Polydolops	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Polymorphis	herbivore	herbivore	10 kg-100 kg	(Cassini, Cerdeño et al. 2012, Croft 2024)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Prepidolops	omnivore	omnivore	10 g-100 g	(Zimicz 2012, Zimicz 2014, Babot, Rougier et al. 2020)	(Zimicz 2012, Zimicz 2014)	metatherian	Late Eocene
Proargyrolagus	herbivore	herbivore	10 g-100 g	(Sánchez-Villagra, Kay et al. 2000, Zimicz 2012)	(Sánchez-Villagra, Kay et al. 2000, Zimicz 2012)	metatherian	Late Eocene
Procladosictis	carnivore	carnivore	1 kg-10 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Proectocion	omnivore	omnivore-herbivore	1 kg-10 kg	(Defler 2019)	Calculated from molar dimensions of Ameghino (1904) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Proeocoleophorus	herbivore	herbivore	100 kg-1 tonne	Based on *Eocoleophorus* and thus to glyptodontoids (Oliveira, Ribeiro et al. 1997, Gaudin and Croft 2015, Sedor, Oliveira et al. 2017)	Based on *Eocoleophorus* and thus *Propaopus* (Farina and Vizcaino 1997, Oliveira, Ribeiro et al. 1997, Gaudin and Croft 2015)	eutherian	Late Eocene

Progarzonia	carnivore	invertivore	100 g-1 kg	Based on *Caenolestes* (Loomis 1921)	Calculated from molar dimensions of Simpson (1948) and the process of Gordon (2003) [pooled marsupials, *Caluromys* excluded]	metatherian	Late Eocene
Propyrotherium	herbivore	folivore	100 kg-1 tonne	(Hooker 2000)	Calculated from molar dimensions of Kramarz and Bond (2014) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Late Eocene
Prostegotherium	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Dasypus novemcinctus* and *hybridus* (Farina and Vizcaino 1997, Babot, López et al. 2012)	eutherian	Late Eocene
Protarchaeohyrax	herbivore	grazer	1 kg-10 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003)	eutherian	Late Eocene
Protodidelphis	herbivore	frugivore	1 kg-10 kg	(Goin, Oliveira et al. 1998, Zimicz 2012, Carneiro and Oliveira 2017, Carneiro 2018)	(Zimicz 2012)	metatherian	Late Eocene
Pseudeutatus	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Compared via osteoderm dimensions to *Utaetus* (Carlini, Ciancio et al. 2010, Croft 2016)	eutherian	Late Eocene
Pseudhyrax	herbivore	grazer	1 kg-10 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003)	eutherian	Late Eocene
Pseudoglyptodon	herbivore	grazer	1 kg-10 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003)	eutherian	Late Eocene
Pseudolops	omnivore	omnivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Pseudopachyrucos	herbivore	grazer	100 g-1 kg	(Simpson 1967)	Calculated from molar dimensions of Simpson (1967) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Pseudostegotherium	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Compared via osteoderm dimensions to *Utaetus* (Carlini, Ciancio et al. 2010, Croft 2016)	eutherian	Late Eocene
Pucatherium	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Dasypus novemcinctus* (Farina and Vizcaino 1997, Herrera, Esteban et al. 2019)	eutherian	Late Eocene
Puelia	herbivore	folivore	10 kg-100 kg	(Croft 2016)	(Croft 2016)	eutherian	Late Eocene
Punadolops	omnivore	omnivore	10 g-100 g	(Zimicz 2012, Zimicz 2014, Babot, Rougier et al. 2020)	(Zimicz 2012, Zimicz 2014)	metatherian	Late Eocene
Punahyrax	herbivore	grazer	10 kg-100 kg	(Croft 2024)	(Croft and Weinstein 2008, Reguero, Croft et al. 2008, Elissamburu 2012)	eutherian	Late Eocene
Punapithecus	herbivore	folivore	100 g-1 kg	(López and Bond 1995)	Calculated from molar dimensions of López and Bond	eutherian	Late Eocene

					(1995) and the process of Scarano, Carlini et al. (2011)		
Punatherium	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Chaetophractus* (Farina and Vizcaino 1997, Ciancio, Herrera et al. 2016)	eutherian	Late Eocene
Quirogalestes	omnivore	omnivore-invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012, Abello, Toledo et al. 2020)	metatherian	Late Eocene
Reigia	herbivore	herbivore	10 g-100 g	(Babot, Rougier et al. 2020)	Calculated from molar dimensions of Babot, Rougier et al. (2020) and the process of Gordon (2003) [pooled didelphids, *Caluromys* excluded]	metatherian	Late Eocene
Rhyphodon	herbivore	folivore	100 kg-1 tonne	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003)	eutherian	Late Eocene
Ricardolydekkeria	herbivore	folivore	1 kg-10 kg	(Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Riostegotherium	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Dasypus hybridus* (Farina and Vizcaino 1997, Oliveira and Bergqvist 1998)	eutherian	Late Eocene
Rosendolops	omnivore	omnivore-invertivore	10 g-100 g	(Zimicz 2012, Zimicz 2014)	(Zimicz 2012, Zimicz 2014)	metatherian	Late Eocene
Rutimeyeria	herbivore	herbivore	1 kg-10 kg	(Cassini, Cerdeño et al. 2012)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Saltatherium	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Punatherium* and *Parutaetus* (Farina and Vizcaino 1997, Carlini, Ciancio et al. 2010, Ciancio, Herrera et al. 2016, Fernicola, Zimicz et al. 2021)	eutherian	Late Eocene
Scaglia	herbivore	herbivore	100 kg-1 tonne	(Cassini, Cerdeño et al. 2012)	(Vizcaíno, Cassini et al. 2012, Kramarz and Bond 2013)	eutherian	Late Eocene
Sparnotheriodon	herbivore	folivore	100 kg-1 tonne	Based on *Notiolofos* (Gelfo 2016, Gelfo, Goin et al. 2019)	(Croft, Gelfo et al. 2020)	eutherian	Late Eocene
Stegosimpsonia	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on small *Dasypus* species (Farina and Vizcaino 1997, Ciancio, Carlini et al. 2013)	eutherian	Late Eocene
Suniodon	herbivore	folivore	1 kg-10 kg	(Croft 2016, Croft 2024)	Calculated from molar dimensions of López (1995) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Tarapotomys	herbivore	herbivore	10 g-100 g	(Boivin, Marivaux et al. 2019)	Calculated from molar dimensions of Boivin, Marivaux et al. (2018) and the process of Millien and Bovy (2010)	eutherian	Late Eocene

Teratopithecus	herbivore	herbivore	1 kg-10 kg	(Croft 2016, Croft 2024)	Calculated from molar dimensions of López, Gelfo et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Tetragonostylops	herbivore	herbivore	100 kg-1 tonne	(Cassini, Cerdeño et al. 2012)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Thomashuxleya	herbivore	folivore	10 kg-100 kg	(Croft 2016)	(Elissamburu 2012, Croft 2016, Carrillo and Asher 2017, Lorente 2019) [large variety of mass estimates – 100kg estimated here as compromise]	eutherian	Late Eocene
Transpithecus	herbivore	herbivore	1 kg-10 kg	(Hitz, Reguero et al. 2000)	Calculated from molar dimensions of Vera (2012) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Trigonolophodon	herbivore	folivore	10 kg-100 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003)	eutherian	Late Eocene
Trigonostylops	herbivore	herbivore	10 kg-100 kg	(Croft 2016)	(Croft 2016)	eutherian	Late Eocene
Trilobodon	herbivore	herbivore	10 kg-100 kg	(Palmer 1904)	Based on incisor width comparison with *Kobus kob* (Roth 1902, Janis and Ehrhardt 1988, De Iongh, De Jong et al. 2011)	eutherian	Late Eocene
Trimerostephanos	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Tsamnichoria	herbivore	folivore	1 kg-10 kg	(Croft 2016, Croft 2024)	Calculated from molar dimensions of Simpson (1967) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Ultrapithecus	herbivore	folivore	1 kg-10 kg	(Croft 2016, Croft 2024)	(Elissamburu 2012)	eutherian	Late Eocene
Utaetus	carnivore	invertivore	1 kg-10 kg	(Ciancio, Vieytes et al. 2014, Croft 2016)	(Croft 2016)	eutherian	Late Eocene
Victorlemoineia	herbivore	herbivore	100 kg-1 tonne	(Cassini, Cerdeño et al. 2012)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Wamradolops	herbivore	granivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Xenostephanus	herbivore	folivore	1 kg-10 kg	(Croft 2016, Croft 2024)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Xesmodon	herbivore	folivore	10 kg-100 kg	(Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Late Eocene
Abderites	herbivore	frugivore	100 g-1 kg	(Dumont, Strait et al. 2000, Abello, Ortiz-Jaureguizar et al. 2012)	(Dumont, Strait et al. 2000, Abello, Ortiz-Jaureguizar et al. 2012, Abello, Toledo et al. 2020)	metatherian	Oligocene

Acamana	herbivore	folivore	100 kg-1 tonne	(Croft 2024)	Calculated from molar dimensions of Simpson, Minoprio et al. (1962) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Acarechimys	herbivore	herbivore	100 g-1 kg	(Croft, Chick et al. 2011)	(Defler 2019)	eutherian	Oligocene
Acdestodon	herbivore	frugivore	100 g-1 kg	(Bown and Fleagle 1993)	(Rincón, Shockey et al. 2015)	metatherian	Oligocene
Acdestoides	herbivore	frugivore	100 g-1 kg	(Bown and Fleagle 1993)	(Dumont, Strait et al. 2000, Rincón, Shockey et al. 2015)	metatherian	Oligocene
Amblytatus	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Compared via osteoderm dimensions to *Utaetus* (Ciancio and Carlini 2008, Croft 2016)	eutherian	Oligocene
Anatrachytherus	herbivore	herbivore	10 kg-100 kg	(Croft and Weinstein 2008, Reguero, Candela et al. 2010, Ercoli and Armella 2021)	(Reguero, Candela et al. 2010)	eutherian	Oligocene
Anayatherium	herbivore	folivore	100 kg-1 tonne	(Croft 2016)	(Croft 2016)	eutherian	Oligocene
Ancylocoelus	herbivore	herbivore	100 kg-1 tonne	(Shockey, Flynn et al. 2012)	(Elissamburu 2012, Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene
Andemys	herbivore	herbivore	1 kg-10 kg	(Croft 2016, Álvarez, Ercoli et al. 2020)	(Croft 2016)	eutherian	Oligocene
Andinogale	carnivore	carnivore	1 kg-10 kg	(Hoffstetter and Petter 1983)	Calculated from molar dimensions of Hoffstetter and Petter (1983) and the process of Gordon (2003) [pooled marsupials, *Caluromys* excluded]	metatherian	Oligocene
Anisotemnus	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene
Antawallathentes	carnivore	invertivore	100 g-1 kg	(Rincón, Shockey et al. 2015)	(Rincón, Shockey et al. 2015, Abello, Toledo et al. 2020)	metatherian	Oligocene
Archaeohyrax	herbivore	grazer	10 kg-100 kg	(Croft and Weinstein 2008)	(Croft and Weinstein 2008, Elissamburu 2012)	eutherian	Oligocene
Archaeophylus	herbivore	herbivore	100 g-1 kg	(Reguero, Candela et al. 2010)	(Elissamburu 2012)	eutherian	Oligocene
Archaeotypotherium	herbivore	grazer	10 kg-100 kg	(Croft and Weinstein 2008)	(Croft and Weinstein 2008, Elissamburu 2012)	eutherian	Oligocene
Archaeutatus	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Compared via osteoderm dimensions to *Utaetus* (Carlini, Ciancio et al. 2010, Croft 2016)	eutherian	Oligocene
Argyrohippus	herbivore	grazer	10 kg-100 kg	(Shockey 1997)	(Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene
Argyrohyrax	herbivore	grazer	1 kg-10 kg	(Vera, Cerdeño et al. 2017)	Calculated from molar dimensions of Vera, Cerdeño et al. (2017) and the process of Scarano, Carlini et al. (2011)	eutherian	Oligocene

Ashaninkacebus	carnivore	invertivore	100 g-1 kg	(Marivaux, Negri et al. 2023)	(Marivaux, Negri et al. 2023)	eutherian	Oligocene
Asmodeus	herbivore	folivore	1 tonne-10 tonnes	(Cassini, Cerdeño et al. 2012, Hernández del Pino, Seoane et al. 2017, Croft 2024)	(Elissamburu 2012, Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene
Asteromys	herbivore	grazer	100 g-1 kg	(Álvarez, Ercoli et al. 2020)	Calculated from molar dimensions of Pérez, Arnal et al. (2019) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Astrapotherium	herbivore	herbivore	1 tonne-10 tonnes	(Cassini, Cerdeño et al. 2012)	(Vizcaíno, Cassini et al. 2012, Defler 2019)	eutherian	Oligocene
Australohyaena	carnivore	carnivore	10 kg-100 kg	(Prevosti and Forasiepi 2018)	(Prevosti and Forasiepi 2018)	metatherian	Oligocene
Baguatherium	herbivore	folivore	100 kg-1 tonne	(Hooker 2000)	Calculated from molar dimensions of Kramarz and Bond (2014) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Balsayacuy	herbivore	folivore	10 g-100 g	(Boivin, Marivaux et al. 2022)	Calculated from molar dimensions of Boivin, Marivaux et al. (2022) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Barrancatatus	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Zaedyus* and *Euphractus* (Robinson and Redford 1986, Farina and Vizcaino 1997, Carlini, Ciancio et al. 2010)	eutherian	Oligocene
Branisamys	herbivore	herbivore	1 kg-10 kg	(Álvarez, Ercoli et al. 2020, Rasia, Candela et al. 2021)	Calculated from molar dimensions of Patterson and Wood (1982) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Branisella	omnivore	omnivore-frugivore	100 g-1 kg	(Croft 2016, Defler 2019)	(Croft 2016, Kay, Gonzales et al. 2019)	eutherian	Oligocene
Brucemacfaddenia	herbivore	grazer	1 kg-10 kg	(Hitz, Billet et al. 2008)	Calculated from molar dimensions of Hitz, Billet et al. (2008) and the process of Scarano, Carlini et al. (2011)	eutherian	Oligocene
Cachiyacuy	herbivore	herbivore	10 g-100 g	(Defler 2019)	(Antoine, Marivaux et al. 2012)	eutherian	Oligocene
Canaanimico	herbivore	frugivore	1 kg-10 kg	(Marivaux, Adnet et al. 2016)	(Marivaux, Adnet et al. 2016)	eutherian	Oligocene
Canaanimys	herbivore	herbivore	10 g-100 g	(Defler 2019)	(Antoine, Marivaux et al. 2012)	eutherian	Oligocene
Canchadelphys	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Oligocene
Carlothentes	omnivore	omnivore	1 kg-10 kg	(Dumont, Strait et al. 2000, Zimicz 2012)	(Dumont, Strait et al. 2000, Zimicz 2012, Rincón, Shockey et al. 2015, Abello, Toledo et al. 2020)	metatherian	Oligocene
Cephalomyopsis	herbivore	grazer	100 g-1 kg	(Álvarez, Ercoli et al. 2020, Rasia, Candela et al. 2021)	Calculated from molar dimensions of Bond, López et	eutherian	Oligocene

					al. (1998) and the process of Millien and Bovy (2010)		
Cephalomys	herbivore	grazer	100 g-1 kg	(Vucetich, Dozo et al. 2015, Álvarez, Ercoli et al. 2020)	Calculated from molar dimensions of Vucetich, Dozo et al. (2015) and the process of Millien and Bovy (2010), additionally informed by Busker, Dozo et al. (2020)	eutherian	Oligocene
Chachapoyamys	herbivore	folivore	100 g-1 kg	(Boivin, Marivaux et al. 2022)	Calculated from molar dimensions of Boivin, Marivaux et al. (2022) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Chambiramys	herbivore	folivore	100 g-1 kg	(Boivin, Marivaux et al. 2017, Álvarez, Ercoli et al. 2020, Rasia, Candela et al. 2021)	Calculated from molar dimensions of Boivin, Marivaux et al. (2017) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Changquin	herbivore	grazer	100 g-1 kg	(Vucetich, Pérez et al. 2014)	Calculated from molar dimensions of Vucetich, Pérez et al. (2014) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Chilestylops	herbivore	folivore	10 kg-100 kg	(Croft 2024)	Calculated from molar dimensions of Bradham, Flynn et al. (2015) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Cholamys	herbivore	folivore	1 kg-10 kg	(Kramarz and Bellosi 2005)	Calculated from molar dimensions of Pérez, Arnal et al. (2019) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Chubutherium	herbivore	herbivore	100 kg-1 tonne	(Toledo, Bargo et al. 2015)	(Rincón, Solórzano et al. 2017)	eutherian	Oligocene
Chubutomys	herbivore	grazer	100 g-1 kg	(Álvarez, Ercoli et al. 2020)	Calculated from molar dimensions of Pérez, Vucetich et al. (2010) and Pérez, Krause et al. (2012) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Clenia	omnivore	omnivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Oligocene
Clypeotherium	carnivore	invertivore	100 g-1 kg	Based on *Neoglyptatelus* (Vizcaíno, Rinderknecht et al. 2003, Croft 2016)	Based on *Neoglyptatelus* (Vizcaíno, Rinderknecht et al. 2003, Croft 2016)	eutherian	Oligocene
Cochilius	herbivore	herbivore	1 kg-10 kg	(Billet, Patterson et al. 2007, Reguero, Candela et al. 2010, Croft 2024)	(Elissamburu 2012)	eutherian	Oligocene
Coniopternium	herbivore	herbivore	10 kg-100 kg	(Cassini, Cerdeño et al. 2012)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene

Coresodon	herbivore	grazer	10 kg-100 kg	(López, Ribeiro et al. 2010, Martínez, Dozo et al. 2021)	Calculated from molar dimensions of Loomis (1914) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Cramauchenia	herbivore	herbivore	10 kg-100 kg	(Cassini, Cerdeño et al. 2012)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Deseadognathus	herbivore	folivore	10 kg-100 kg	(Pujos, Gaudin et al. 2012)	Based on closely related *Hapalops* (Carlini and Scillato-Vane 2004, Vizcaíno, Cassini et al. 2012, Toledo, Cassini et al. 2014)	eutherian	Oligocene
Deseadomys	herbivore	folivore	100 g-1 kg	(Boivin, Marivaux et al. 2017)	Calculated from molar dimensions of Boivin, Marivaux et al. (2017) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Deuterotherium	herbivore	folivore	10 kg-100 kg	(Kramarz and Bond 2005, Mcgrath, Anaya et al. 2020)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Oligocene
Didolodus	omnivore	omnivore-herbivore	1 kg-10 kg	(Croft, Gelfo et al. 2020)	(Croft, Gelfo et al. 2020)	eutherian	Oligocene
Doellotatus	omnivore	omnivore-herbivore	1 kg-10 kg	(Vizcaíno and Bargo 1998, Defler 2019)	Based on armadillo jaws and osteoderm dimensions (Vizcaíno and Bargo 1998, Esteban, Nasif et al. 2001, Krmpotic, Ciancio et al. 2015)	eutherian	Oligocene
Draconomys	herbivore	folivore	100 g-1 kg	(Vucetich, Vieytes et al. 2010)	Calculated from molar dimensions of Vucetich, Vieytes et al. (2010) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Elmerriggsia	herbivore	herbivore	100 kg-1 tonne	(Shockey, Flynn et al. 2012)	Calculated from molar dimensions of Shockey, Flynn et al. (2012) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Eobranisamys	herbivore	herbivore	100 g-1 kg	(Frailey and Campbell Jr 2004)	Calculated from molar dimensions of Frailey and Campbell Jr (2004) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Eocoleophorus	herbivore	herbivore	10 kg-100 kg	Based on glyptodontoids (Oliveira, Ribeiro et al. 1997, Gaudin and Croft 2015)	Based on *Propaopus* (Farina and Vizcaino 1997, Oliveira, Ribeiro et al. 1997)	eutherian	Oligocene

Eodelphomys	herbivore	herbivore	1 kg-10 kg	(Frailey and Campbell Jr 2004)	Calculated from molar dimensions of Frailey and Campbell Jr (2004) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Eoespina	herbivore	herbivore	10 g-100 g	(Frailey and Campbell Jr 2004)	Calculated from molar dimensions of Frailey and Campbell Jr (2004) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Eoincamys	herbivore	herbivore	100 g-1 kg	(Álvarez, Ercoli et al. 2020, Rasia, Candela et al. 2021)	Calculated from molar dimensions of Frailey and Campbell Jr (2004) and Boivin, Marivaux et al. (2018) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Eomakhaira	carnivore	carnivore	1 kg-10 kg	(Engelman, Flynn et al. 2020)	(Engelman, Flynn et al. 2020)	metatherian	Oligocene
Eomicrobiotherium	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Oligocene
Eomorphippus	herbivore	herbivore	10 kg-100 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003, Elissamburu 2012)	eutherian	Oligocene
Eopachyrucos	herbivore	grazer	1 kg-10 kg	(Reguero, Ubilla et al. 2003)	(Reguero, Ubilla et al. 2003)	eutherian	Oligocene
Eopicure	herbivore	herbivore	100 g-1 kg	(Frailey and Campbell Jr 2004)	Calculated from molar dimensions of Frailey and Campbell Jr (2004) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Eopululo	herbivore	folivore	1 kg-10 kg	(Kramarz and Bellosi 2005)	Calculated from molar dimensions of Frailey and Campbell Jr (2004) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Eosachacui	herbivore	herbivore	10 g-100 g	(Frailey and Campbell Jr 2004)	Calculated from molar dimensions of Frailey and Campbell Jr (2004) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Eosallamys	herbivore	folivore	100 g-1 kg	(Pérez, Arnal et al. 2019)	Calculated from molar dimensions of Frailey and Campbell Jr (2004) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Eoviscaccia	herbivore	grazer	100 g-1 kg	(Álvarez, Ercoli et al. 2020)	Calculated from molar dimensions of Vucetich (1989) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Epiklohnia	herbivore	granivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Oligocene
Ethelomys	herbivore	herbivore	100 g-1 kg	(Vucetich, Dozo et al. 2015)	Calculated from molar dimensions of Vucetich, Dozo et al. (2015) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Eurygenium	herbivore	herbivore	10 kg-100 kg	(Shockey 1997)	(Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene

Evolestes	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012, Abello, Toledo et al. 2020)	metatherian	Oligocene
Federicoanaya	herbivore	herbivore	1 kg-10 kg	(Croft and Weinstein 2008)	(Croft and Weinstein 2008)	eutherian	Oligocene
Fieratherium	carnivore	invertivore	100 g-1 kg	(Forasiepi, Goin et al. 2014)	Calculated from molar dimensions of Forasiepi, Goin et al. (2014) and the process of Gordon (2003) [pooled marsupials, *Caluromys* excluded]	metatherian	Oligocene
Fredszalaya	carnivore	carnivore	10 kg-100 kg	(Prevosti and Forasiepi 2018)	(Prevosti and Forasiepi 2018)	metatherian	Oligocene
Galileomys	herbivore	herbivore	100 g-1 kg	(Kramarz and Bellosi 2005)	Calculated from molar dimensions of Vucetich, Kramarz et al. (2010) and the process of Millien and Bovy (2010), additionally informed by (Vucetich, Dozo et al. 2015)	eutherian	Oligocene
Glyptatelus	carnivore	invertivore	10 kg-100 kg	Based on *Neoglyptatelus* (Vizcaíno, Rinderknecht et al. 2003, Croft 2016)	Based on *Eocoleophorus* and thus *Propaopus* (Farina and Vizcaino 1997, Oliveira, Ribeiro et al. 1997)	eutherian	Oligocene
Griphodon	herbivore	folivore	100 kg-1 tonne	Based on *Pyrotherium* (Shockey and Daza 2004, Croft 2016)	Calculated from molar dimensions of Kramarz and Bond (2014) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Gualta	herbivore	herbivore	1 tonne-10 tonnes	(Cerdeño and Vera 2015)	Calculated from molar dimensions of Cerdeño and Vera (2015) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Guilielmoscottia	herbivore	folivore	10 kg-100 kg	(Simpson 1948, Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Simpson (1948) and the process of Scarano, Carlini et al. (2011)	eutherian	Oligocene
Hegetotheriopsis	herbivore	herbivore	1 kg-10 kg	(Billet, Patterson et al. 2007, Croft 2024)	Calculated from molar dimensions of Kramarz and Paz (2013) and the process of Scarano, Carlini et al. (2011)	eutherian	Oligocene
Hegetotherium	carnivore	invertivore	1 kg-10 kg	(Croft, Flynn et al. 2004, McCoy and Norris 2012)	(Cassini, Cerdeño et al. 2012, Elissamburu 2012)	eutherian	Oligocene
Henricofilholia	herbivore	herbivore	100 kg-1 tonne	(Shockey, Flynn et al. 2012, Cerdeño and Vera 2015)	Calculated from molar dimensions of Shockey, Flynn et al. (2012) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Homalodontotherium	herbivore	folivore	1 tonne-10 tonnes	(Cassini, Cerdeño et al. 2012, Seoane, Del Pino et al. 2017)	(Elissamburu 2012, Vizcaíno, Cassini et al. 2012, Seoane, Del Pino et al. 2017, Defler 2019)	eutherian	Oligocene

Hondonadia	herbivore	granivore	10 g-100 g	(Zimicz 2012, Zimicz 2014)	(Zimicz 2012, Zimicz 2014)	metatherian	Oligocene
Incadolops	herbivore	frugivore	10 g-100 g	(Zimicz 2012, Zimicz 2014)	(Zimicz 2012, Zimicz 2014)	metatherian	Oligocene
Incamys	herbivore	grazer	100 g-1 kg	(Álvarez, Ercoli et al. 2020, Rasia, Candela et al. 2021)	Calculated from molar dimensions of Busker and Dozo (2017) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Johnbell	herbivore	herbivore	1 kg-10 kg	(Hitz, Flynn et al. 2006)	Calculated from molar dimensions of Hitz, Flynn et al. (2006) and the process of Scarano, Carlini et al. (2011)	eutherian	Oligocene
Kichkasteiromys	herbivore	folivore	100 g-1 kg	(Boivin, Marivaux et al. 2018)	Calculated from molar dimensions of Boivin, Marivaux et al. (2018) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Kirutherium	carnivore	invertivore	1 g-10 g	(Campbell Jr 2004, Zimicz 2012)	(Zimicz 2012)	metatherian	Oligocene
Kiruwamaq	carnivore	invertivore	1 g-10 g	(Campbell Jr 2004)	Calculated from molar dimensions of Goin and Candela (2004) and the process of Gordon (2003) [pooled marsupials, *Caluromys* excluded]	metatherian	Oligocene
Klohnia	herbivore	granivore	10 g-100 g	(Zimicz 2012)	(Flynn, Wyss et al. 2003, Croft, Flynn et al. 2008, Zimicz 2012)	metatherian	Oligocene
Kramadolops	herbivore	herbivore	1 kg-10 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Oligocene
Kuntinaru	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on closely related *Priodontes* (Billet, Hautier et al. 2011, Carter, Superina et al. 2016)	eutherian	Oligocene
Lambdaconus	herbivore	folivore	10 kg-100 kg	(Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Oligocene
Lapazomys	herbivore	herbivore	100 g-1 kg	(Pérez, Arnal et al. 2019)	Calculated from molar dimensions of Pérez, Arnal et al. (2019) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Leontinia	herbivore	herbivore	100 kg-1 tonne	(Shockey, Flynn et al. 2012)	(Elissamburu 2012, Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene
Leucokephalos	herbivore	folivore	100 g-1 kg	(Pérez, Arnal et al. 2019)	Calculated from molar dimensions of Vucetich, Dozo et al. (2015) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Liarthrus	herbivore	herbivore	1 tonne-10 tonnes	Based on closely related *Parastrapotherium* (Kramarz and Bond 2008, Cassini, Cerdeño et al. 2012)	Based on closely related *Parastrapotherium* (Kramarz and Bond 2008, Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene

Litodontomys	herbivore	herbivore	100 g-1 kg	(Álvarez, Ercoli et al. 2020, Rasia, Candela et al. 2021)	Calculated from molar dimensions of Loomis (1914) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Llitun	herbivore	folivore	100 g-1 kg	(Vucetich, Dozo et al. 2015)	Calculated from molar dimensions of Vucetich, Dozo et al. (2015) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Loncolicu	herbivore	grazer	100 g-1 kg	(Álvarez, Ercoli et al. 2020, Rasia, Candela et al. 2021)	Calculated from molar dimensions of Vucetich, Dozo et al. (2015) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Loretomys	herbivore	folivore	10 g-100 g	(Boivin, Marivaux et al. 2017)	Calculated from molar dimensions of Boivin, Marivaux et al. (2017) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Machlydotherium	herbivore	grazer	100 kg-1 tonne	(Góis, Scillato-Yané et al. 2013, Defler 2019)	Based on *Yuruatherium* and hence *Pampatherium* (Vizcaíno, Cassini et al. 2012, Ciancio, Carlini et al. 2013)	eutherian	Oligocene
Maddenia	herbivore	grazer	10 kg-100 kg	(Kramarz and Bond 2009, Cassini, Cerdeño et al. 2012)	Calculated from molar dimensions of Kramarz and Bond (2009) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Mayomys	herbivore	folivore	10 g-100 g	(Boivin, Marivaux et al. 2019)	Calculated from molar dimensions of Boivin, Marivaux et al. (2018) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Medistylus	herbivore	herbivore	1 kg-10 kg	(Billet, Patterson et al. 2007, Croft 2024)	Based on *Prosotherium* (Reguero, Dozo et al. 2007, Elissamburu 2012)	eutherian	Oligocene
Mendozahippus	herbivore	herbivore	10 kg-100 kg	(Martínez, Dozo et al. 2021)	Calculated from molar dimensions of Cerdeño and Vera (2010) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Meteutatus	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Euphractus* and *Chaetophractus* (Robinson and Redford 1986, Farina and Vizcaino 1997, Carlini, Ciancio et al. 2010)	eutherian	Oligocene
Microbiotherium	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Oligocene
Migraveramus	herbivore	folivore	100 g-1 kg	(Pérez, Arnal et al. 2019)	Calculated from molar dimensions of Pérez, Arnal et al. (2019) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Moqueguahippus	herbivore	grazer	100 kg-1 tonne	(López, Ribeiro et al. 2010)	Calculated from molar dimensions of Shockey, Salas et al. (2006) and the averaged	eutherian	Oligocene

					processes of Damuth (1990) and Janis (1990)		
Morphippus	herbivore	herbivore	10 kg-100 kg	(López, Ribeiro et al. 2010)	(Elissamburu 2012)	eutherian	Oligocene
Neoglyptatelus	carnivore	invertivore	10 kg-100 kg	(Croft 2016)	(Croft 2016)	eutherian	Oligocene
Neoreomys	herbivore	herbivore	1 kg-10 kg	(Álvarez, Ercoli et al. 2020)	(Defler 2019)	eutherian	Oligocene
Nesodon	herbivore	herbivore	100 kg-1 tonne	(Townsend and Croft 2008, Cassini, Cerdeño et al. 2012)	(Elissamburu 2012, Vizcaíno, Cassini et al. 2012, Croft 2016)	eutherian	Oligocene
Notodiaphorus	herbivore	herbivore	100 kg-1 tonne	(Loomis 1914, Carroll 1988) [compromise between Edwardian prediction of diet and implicit litoptern classification]	Calculated from femur dimensions of Loomis (1914) and the process of Campione and Evans (2012)	eutherian	Oligocene
Notogale	carnivore	carnivore	1 kg-10 kg	(Zimicz 2012, Prevosti and Forasiepi 2018)	(Zimicz 2012, Prevosti and Forasiepi 2018)	metatherian	Oligocene
Notostylops	herbivore	herbivore	10 kg-100 kg	(Lorente, Gelfo et al. 2019)	(Elissamburu 2012, Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene
Octodontotherium	herbivore	herbivore	100 kg-1 tonne	(Shockey and Anaya 2011, Kalthoff and Green 2018)	(Shockey and Anaya 2011)	eutherian	Oligocene
Orophodon	herbivore	herbivore	100 kg-1 tonne	(Kalthoff and Green 2018)	(Shockey and Anaya 2011, Kalthoff and Green 2018)	eutherian	Oligocene
Palaeopeltis	herbivore	herbivore	100 kg-1 tonne	(Perea, Toriño et al. 2014, Gaudin and Croft 2015)	(Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene
Palaeosteiromys	herbivore	folivore	100 g-1 kg	(Kramarz and Bellosi 2005)	Calculated from molar dimensions of Boivin, Marivaux et al. (2017) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Palaeothentes	omnivore	omnivore	100 g-1 kg	(Dumont, Strait et al. 2000)	(Dumont, Strait et al. 2000, Abello, Toledo et al. 2020)	metatherian	Oligocene
Parabderites	omnivore	omnivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012, Rincón, Shockey et al. 2015, Abello, Toledo et al. 2020)	metatherian	Oligocene
Paraborhyaena	carnivore	carnivore	10 kg-100 kg	(Zimicz 2012, Prevosti and Forasiepi 2018)	(Zimicz 2012, Prevosti and Forasiepi 2018)	metatherian	Oligocene
Parastegosimpsonia	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on small *Dasypus* species (Farina and Vizcaino 1997, Ciancio, Carlini et al. 2013)	eutherian	Oligocene
Parastrapotherium	herbivore	herbivore	1 tonne-10 tonnes	(Cassini, Cerdeño et al. 2012)	(Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene
Paroctodontotherium	herbivore	grazer	10 kg-100 kg	(Shockey and Anaya 2011)	(Shockey and Anaya 2011)	eutherian	Oligocene
Parutaetus	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Zaedyus* (Farina and Vizcaino 1997, Carlini, Ciancio et al. 2010)	eutherian	Oligocene
Pascualihippus	herbivore	grazer	100 kg-1 tonne	(Shockey 1997)	Calculated from molar dimensions of Shockey (1997)	eutherian	Oligocene

					and the averaged processes of Damuth (1990) and Janis (1990)		
Patagonhippus	herbivore	herbivore	10 kg-100 kg	(López, Ribeiro et al. 2010)	(López, Ribeiro et al. 2010)	eutherian	Oligocene
Patene	carnivore	carnivore	1 kg-10 kg	(Zimicz 2012, Prevosti and Forasiepi 2018, Rangel, Carneiro et al. 2019)	(Zimicz 2012, Prevosti and Forasiepi 2018)	metatherian	Oligocene
Paulacoutomys	herbivore	folivore	1 kg-10 kg	(Kramarz and Bellosi 2005)	Calculated from molar dimensions of Ribeiro (2010) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Peltephilus	herbivore	herbivore	10 kg-100 kg	(Vizcaíno and Fariña 1997)	(Vizcaíno, Bargo et al. 2006, Croft 2016)	eutherian	Oligocene
Periakros	herbivore	granivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Oligocene
Periphragnis	herbivore	folivore	100 kg-1 tonne	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003, Elissamburu 2012)	eutherian	Oligocene
Perulestes	herbivore	frugivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012, Abello, Toledo et al. 2020)	metatherian	Oligocene
Perupithecus	omnivore	omnivore	100 g-1 kg	(Bond, Tejedor et al. 2015)	(Kay, Gonzales et al. 2019)	eutherian	Oligocene
Pharsophorus	carnivore	carnivore	10 kg-100 kg	(Zimicz 2012, Prevosti and Forasiepi 2018)	(Zimicz 2012, Prevosti and Forasiepi 2018)	metatherian	Oligocene
Pilchenia	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012, Abello, Toledo et al. 2020)	metatherian	Oligocene
Platypittamys	herbivore	folivore	10 g-100 g	(Defler 2019)	Calculated from molar dimensions of Wood (1949) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Plesiosteiromys	herbivore	folivore	100 g-1 kg	(Boivin, Marivaux et al. 2017)	Calculated from molar dimensions of Boivin, Marivaux et al. (2017) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Pleurostylodon	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Elissamburu 2012)	eutherian	Oligocene
Polydolops	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Oligocene
Pozomys	herbivore	herbivore	100 g-1 kg	(Boivin, Marivaux et al. 2017)	Calculated from molar dimensions of Boivin, Marivaux et al. (2017) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Praedens	carnivore	invertivore	1 g-10 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Oligocene
Proadiantus	herbivore	folivore	1 kg-10 kg	(Simpson and Minoprio 1949, Croft 2024)	Calculated from molar dimensions of Loomis (1914) and the process of Scarano, Carlini et al. (2011)	eutherian	Oligocene
Proadinotherium	herbivore	herbivore	100 kg-1 tonne	(Croft, Radic et al. 2003)	(Elissamburu 2012, Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene
Proargyrohyrax	herbivore	grazer	1 kg-10 kg	(Hitz, Reguero et al. 2000)	(Scarano, Carlini et al. 2011)	eutherian	Oligocene

Proargyrolagus	herbivore	herbivore	10 g-100 g	(Sánchez-Villagra, Kay et al. 2000, Zimicz 2012)	(Sánchez-Villagra, Kay et al. 2000, Zimicz 2012)	metatherian	Oligocene
Proborhyaena	carnivore	carnivore	100 kg-1 tonne	(Zimicz 2012, Prevosti and Forasiepi 2018)	(Zimicz 2012, Prevosti and Forasiepi 2018)	metatherian	Oligocene
Proeuphractus	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Based on *Chaetophractus* and *Euphractus* (Robinson and Redford 1986, Farina and Vizcaino 1997, Scillato-Yané, Góis et al. 2013)	eutherian	Oligocene
Progaleopithecus	herbivore	grazer	1 kg-10 kg	(Vera, Cerdeño et al. 2017)	(Scarano, Carlini et al. 2011)	eutherian	Oligocene
Prohegetotherium	herbivore	herbivore	1 kg-10 kg	(Billet, Patterson et al. 2007, Croft 2024)	(Elissamburu 2012)	eutherian	Oligocene
Promylophis	omnivore	omnivore	10 kg-100 kg	(Shockey, White et al. 2022)	(Shockey, White et al. 2022)	eutherian	Oligocene
Propachyrucos	herbivore	herbivore	1 kg-10 kg	(Billet, Patterson et al. 2007, Croft 2024)	(Elissamburu 2012)	eutherian	Oligocene
Proplatyarthrus	herbivore	herbivore	100 kg-1 tonne	(Shockey and Anaya 2011, Kalthoff and Green 2018)	(Shockey and Anaya 2011, Kalthoff and Green 2018)	eutherian	Oligocene
Prosotherium	herbivore	herbivore	1 kg-10 kg	(Billet, Patterson et al. 2007, Croft 2024)	(Elissamburu 2012)	eutherian	Oligocene
Protacaremys	herbivore	grazer	100 g-1 kg	(Álvarez, Ercoli et al. 2020)	Calculated from molar dimensions of Vucetich, Kramarz et al. (2010) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Protarchaeohyrax	herbivore	grazer	1 kg-10 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003)	eutherian	Oligocene
Proterotherium	herbivore	folivore	10 kg-100 kg	(Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the process of Scarano, Carlini et al. (2011)	eutherian	Oligocene
Protheosodon	herbivore	folivore	10 kg-100 kg	(Mcgrath, Anaya et al. 2020, Croft 2024)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Protosteiromys	herbivore	folivore	1 kg-10 kg	(Kramarz and Bellosi 2005)	Calculated from molar dimensions of Pérez, Arnal et al. (2019) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Protypotherium	herbivore	grazer	1 kg-10 kg	(Townsend and Croft 2008, Cassini, Cerdeño et al. 2012)	(Cassini, Cerdeño et al. 2012, Elissamburu 2012)	eutherian	Oligocene
Prozaedyus	omnivore	omnivore-invertivore	1 kg-10 kg	(Vizcaíno, Bargo et al. 2006, Defler 2019)	(Vizcaíno, Bargo et al. 2006)	eutherian	Oligocene
Pseudeutatus	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Compared via osteoderm dimensions to *Utaetus*	eutherian	Oligocene

					(Carlini, Ciancio et al. 2010, Croft 2016)		
Pseudhalmarhiphus	carnivore	invertivore	10 g-100 g	Based on *Stilotherium* (Dumont, Strait et al. 2000, Goin, Candela et al. 2009)	Based on *Stilotherium* (Dumont, Strait et al. 2000, Goin, Candela et al. 2009)	metatherian	Oligocene
Pseudhyrax	herbivore	grazer	1 kg-10 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003)	eutherian	Oligocene
Pseudoglyptodon	herbivore	grazer	1 kg-10 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003)	eutherian	Oligocene
Pseudohegetotherium	herbivore	herbivore	10 kg-100 kg	(Croft 2024)	Based on *Hemihegetotherium* (Bond and López 1997, Elissamburu 2012, Croft 2016)	eutherian	Oligocene
Pseudoplohophorus	herbivore	grazer	100 kg-1 tonne	(Tambusso and Fariña 2015)	(Tambusso and Fariña 2015)	eutherian	Oligocene
Pseudorophodon	herbivore	herbivore	100 kg-1 tonne	Based on glyptodontoids and folivorans (Hoffstetter 1969, Perea, Toriño et al. 2014, Gaudin and Croft 2015)	Based on *Palaeopeltis* (Hoffstetter 1969, Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene
Pseudostegotherium	omnivore	omnivore-invertivore	1 kg-10 kg	(Defler 2019)	Compared via osteoderm dimensions to *Utaetus* (Carlini, Ciancio et al. 2010, Croft 2016)	eutherian	Oligocene
Pternoconius	herbivore	herbivore	10 kg-100 kg	(Cassini, Cerdeño et al. 2012)	Calculated from molar dimensions of Mcgrath, Anaya et al. (2020) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Puelia	herbivore	folivore	10 kg-100 kg	(Croft 2016)	(Croft 2016)	eutherian	Oligocene
Pyrotherium	herbivore	folivore	1 tonne-10 tonnes	(Croft 2016)	(Croft 2016, Croft, Gelfo et al. 2020)	eutherian	Oligocene
Rhynchippus	herbivore	herbivore	10 kg-100 kg	(Shockey 1997)	(Elissamburu 2012, Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene
Rhyphodon	herbivore	folivore	100 kg-1 tonne	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003)	eutherian	Oligocene
Ronwolffia	herbivore	herbivore	10 kg-100 kg	Based on *Peltephilus* (Vizcaíno and Fariña 1997, Shockey and Vlachos 2017)	Based on *Peltephilus* (Vizcaíno, Bargo et al. 2006, Croft 2016, Shockey and Vlachos 2017)	eutherian	Oligocene
Rosendo	herbivore	herbivore	1 kg-10 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003)	eutherian	Oligocene
Rosendolops	omnivore	omnivore-invertivore	10 g-100 g	(Zimicz 2012, Zimicz 2014)	(Zimicz 2012, Zimicz 2014)	metatherian	Oligocene
Rumiodon	carnivore	carnivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Oligocene
Sallacyon	carnivore	carnivore	1 kg-10 kg	(Zimicz 2012, Prevosti and Forasiepi 2018)	(Zimicz 2012, Prevosti and Forasiepi 2018)	metatherian	Oligocene
Salladolodus	omnivore	omnivore-herbivore	10 kg-100 kg	(Defler 2019)	Calculated from molar dimensions of Gelfo 2006 and the process of Scarano, Carlini et al. (2011)	eutherian	Oligocene

Sallamys	herbivore	folivore	100 g-1 kg	(Pérez, Arnal et al. 2019)	Calculated from molar dimensions of Pérez, Arnal et al. (2019) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Sallatherium	herbivore	herbivore	1 kg-10 kg	(Billet, Patterson et al. 2007, Croft 2024)	Calculated from molar dimensions of Reguero and Cerdeño (2005) and the process of Scarano, Carlini et al. (2011)	eutherian	Oligocene
Santiagorothia	herbivore	grazer	1 kg-10 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003, Scarano, Carlini et al. 2011)	eutherian	Oligocene
Sasawatsu	herbivore	frugivore	100 g-1 kg	(Campbell Jr 2004, Zimicz 2012)	(Zimicz 2012)	metatherian	Oligocene
Scarrittia	herbivore	herbivore	1 tonne-10 tonnes	(Defler 2019)	(Elissamburu 2012)	eutherian	Oligocene
Scleromys	herbivore	grazer	1 kg-10 kg	(Álvarez, Ercoli et al. 2020)	(Defler 2019)	eutherian	Oligocene
Scotamys	herbivore	herbivore	100 g-1 kg	(Álvarez, Ercoli et al. 2020, Rasia, Candela et al. 2021)	Calculated from molar dimensions of Loomis (1914) and the process of (Millien and Bovy 2010)	eutherian	Oligocene
Selvamys	herbivore	folivore	10 g-100 g	(Boivin, Marivaux et al. 2018)	Calculated from molar dimensions of Boivin, Marivaux et al. (2018) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Shapajamys	herbivore	folivore	100 g-1 kg	(Boivin, Marivaux et al. 2019)	Calculated from molar dimensions of Boivin, Marivaux et al. (2018) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Similhapalops	herbivore	herbivore	10 kg-100 kg	Based on *Hapalops* (Pujos, Ciancio et al. 2021, Melki, de Souza Barbosa et al. 2022)	Based on *Hapalops* (Toledo, Cassini et al. 2014, Pujos, Ciancio et al. 2021)	eutherian	Oligocene
Steiromys	herbivore	herbivore	1 kg-10 kg	(Croft 2016, Álvarez, Ercoli et al. 2020)	(Croft 2016, Defler 2019)	eutherian	Oligocene
Stenotatus	omnivore	omnivore	1 kg-10 kg	(Vizcaíno, Bargo et al. 2006, Defler 2019)	(Vizcaíno, Bargo et al. 2006)	eutherian	Oligocene
Szalatavus	omnivore	omnivore-grazer	100 g-1 kg	(Defler 2019)	Based on *Leontopithecus rosalia* (Rosenberger, Hartwig et al. 1991, Dietz, Baker et al. 1994)	eutherian	Oligocene
'Tacheria'	herbivore	herbivore	10 kg-100 kg	Based on modern caviomorphs (Krapovickas and Nasif 2011, Álvarez, Ercoli et al. 2020)	Based on closely related *Dinomys* (Krapovickas and Nasif 2011, Álvarez, Arévalo et al. 2017)	eutherian	Oligocene
Tarapotomys	herbivore	herbivore	10 g-100 g	(Boivin, Marivaux et al. 2019)	Calculated from molar dimensions of Boivin, Marivaux et al. (2018) and the process of Millien and Bovy (2010)	eutherian	Oligocene

Taubatherium	herbivore	herbivore	100 kg-1 tonne	(Shockey, Flynn et al. 2012)	(Ribeiro 2015)	eutherian	Oligocene
Termastherium	herbivore	folivore	100 kg-1 tonne	(Wyss, Flynn et al. 2018)	Calculated from molar dimensions of Wyss, Flynn et al. (2018) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Teushentherium	herbivore	herbivore	100 kg-1 tonne	(Martínez, Dozo et al. 2021)	Calculated from molar dimensions of Martínez, Dozo et al. (2021) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Thadanius	herbivore	herbivore	1 kg-10 kg	(Cifelli and Soria 1983)	Calculated from molar dimensions of Cifelli and Soria (1983) and the process of Scarano, Carlini et al. (2011)	eutherian	Oligocene
Trachytherus	herbivore	herbivore	100 kg-1 tonne	(Croft and Weinstein 2008, Ercoli and Armella 2021)	(Croft and Weinstein 2008, Elissamburu 2012)	eutherian	Oligocene
Trelewthentes	carnivore	invertivore	100 g-1 kg	(Dumont, Strait et al. 2000)	(Dumont, Strait et al. 2000, Abello, Toledo et al. 2020)	metatherian	Oligocene
Tricoelodus	herbivore	grazer	1 kg-10 kg	(Loomis 1914)	Calculated from molar dimensions of Cifelli and Soria (1983) and the process of Scarano, Carlini et al. (2011)	eutherian	Oligocene
Trigonolophodon	herbivore	folivore	10 kg-100 kg	(Flynn, Wyss et al. 2003)	(Flynn, Wyss et al. 2003)	eutherian	Oligocene
Trigonostylops	herbivore	herbivore	10 kg-100 kg	(Croft 2016)	(Croft 2016)	eutherian	Oligocene
Trimerostephanos	herbivore	folivore	10 kg-100 kg	(Croft 2024)	(Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene
Ucayalimys	herbivore	herbivore	1 kg-10 kg	(Boivin, Marivaux et al. 2017)	Calculated from molar dimensions of Boivin, Marivaux et al. (2017) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Ucayalipithecus	herbivore	frugivore	100 g-1 kg	(Seiffert, Tejedor et al. 2020)	(Seiffert, Tejedor et al. 2020)	eutherian	Oligocene
Urotherium	herbivore	herbivore	100 kg-1 tonne	(Vizcaíno, Cassini et al. 2011)	(Vizcaíno, Cassini et al. 2012)	eutherian	Oligocene
Uruguaytherium	herbivore	herbivore	1 tonne-10 tonnes	(Cassini, Cerdeño et al. 2012)	Calculated from molar dimensions of Goillot, Antoine et al. (2011) and the averaged processes of Damuth (1990) and Janis (1990)	eutherian	Oligocene
Vallehermosomys	herbivore	herbivore	100 g-1 kg	(Vucetich, Vieytes et al. 2010)	Calculated from molar dimensions of Vucetich, Vieytes et al. (2010) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Vucetichimys	herbivore	folivore	10 g-100 g	(Arnal, Pérez et al. 2022)	Based on *Canaanimys* (Antoine, Marivaux et al. 2012, Arnal, Pérez et al. 2022)	eutherian	Oligocene
Wamradolops	herbivore	granivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Oligocene

Wirunodon	carnivore	invertivore	1 g-10 g	(Campbell Jr 2004)	Calculated from molar dimensions of Goin and Candela (2004) and the process of Gordon (2003) [pooled marsupials, *Caluromys* excluded]	metatherian	Oligocene
Xylechimys	herbivore	herbivore	100 g-1 kg	(Patterson and Pascual 1968)	Calculated from molar dimensions of Patterson and Pascual (1968) and the process of Millien and Bovy (2010)	eutherian	Oligocene
Yuruatherium	herbivore	grazer	100 kg-1 tonne	(Ciancio, Carlini et al. 2013)	(Vizcaíno, Cassini et al. 2012, Ciancio, Carlini et al. 2013)	eutherian	Oligocene

Table A1 – Every metatherian and eutherian genus from Palaeogene South America considered, each accompanied with relevant ecological information and sources. Diagnosis of diet is based on direct academic reference, dental condition (e.g. hypsodonty vs brachydonty), taxonomic identity or comparison to similar taxa. Diagnosis of body mass is based on direct academic reference, molar/osteological/scute measurements or comparison to similar taxa. Notable or exceptional assumptions are described in writing.

Genus	Diet classification	Fine diet classification	Body mass	Diet source	Body mass source	Metatherian or eutherian	Time bin
Archaeonothos	carnivore	invertivore	10 g-100 g	(Beck, Godthelp et al. 2008, Beck 2013)	(Beck 2013)	metatherian	Ypresian
Chulpasia	omnivore	omnivore-frugivore	100 g-1 kg	(Beck 2013)	(Beck 2013)	metatherian	Ypresian
Djarthia	carnivore	invertivore	10 g-100 g	(Beck, Godthelp et al. 2008)	(Beck 2013)	metatherian	Ypresian
Thylacotinga	omnivore	omnivore-frugivore	1 kg-10 kg	(Beck 2013)	(Beck 2013)	metatherian	Ypresian
Tingamarra	herbivore	herbivore	100 g-1 kg	(Halliday, Upchurch et al. 2017, Defler 2019)	Calculated from molar dimensions of Godthelp, Archer et al. (1992) and the process of Scarano, Carlini et al. (2011)	eutherian	Ypresian
Ankotarinja	carnivore	invertivore	10 g-100 g	Based on *Antechinus* (Archer 1976, Hall 1980)	Calculated from molar dimensions of Archer (1976) and the process of Gordon	metatherian	Oligocene

					(2003) [pooled dasyurids]		
Ayekaye	herbivore	folivore	1 kg-10 kg	(Palmer 2023)	Calculated from molar dimensions of Megirian, Murray et al. (2004) and the process of Myers (2001) [diprotodont equation] [used upper premolar as proxy for molar]	metatherian	Oligocene
Badjcinus	carnivore	carnivore	1 kg-10 kg	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Balbaroo	herbivore	folivore	1 kg-10 kg	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Barguru	herbivore	herbivore	100 g-1 kg	(Schwartz 2006, Wheat 2023)	Calculated from molar dimensions of (Schwartz 2006) and the process of (Myers 2001) [diprotodont equation]	metatherian	Oligocene
Bulungamaya	omnivore	omnivore	1 kg-10 kg	(Janis, Damuth et al. 2016)	(Palmer 2023)	metatherian	Oligocene
Bulungu	omnivore	omnivore	100 g-1 kg	(Wheat 2023)	(Palmer 2023)	metatherian	Oligocene
Burramys	omnivore	omnivore-herbivore	10 g-100 g	(Wilman, Belmaker et al. 2014)	(Palmer 2023)	metatherian	Oligocene
Chunia	herbivore	frugivore	100 g-1 kg	(Wheat 2023)	(Palmer 2023)	metatherian	Oligocene
Cookeroo	herbivore	folivore	1 kg-10 kg	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Dasylurinja	carnivore	invertivore	10 g-100 g	(Wroe 1999, Amador and Giannini 2021)	Based on *Wakamatha,* and thus *Sminthopsis* (Archer and Rich 1979, Nagy, Lee et al. 1988, Muirhead and Archer 1990, Wroe 1997)	metatherian	Oligocene
Djilgaringa	omnivore	omnivore-herbivore	100 g-1 kg	(Black, Archer et al. 2012, Wheat 2023)	(Palmer 2023)	metatherian	Oligocene
Ekaltadita	omnivore	omnivore-carnivore	1 kg-10 kg	(Black, Archer et al. 2012)	(Palmer 2023)	metatherian	Oligocene
Ektopodon	herbivore	frugivore	1 kg-10 kg	(Wheat 2023)	(Palmer 2023)	metatherian	Oligocene
Eocuscus	herbivore	herbivore	1 kg-10 kg	(Wheat 2023)	Calculated from molar dimensions of Case, Meredith et al. (2008) and the process of Myers (2001) [diprotodont equation]	metatherian	Oligocene
Galadi	carnivore	carnivore	100 g-1 kg	(Travouillon, Gurovich et al. 2010)	(Palmer 2023)	metatherian	Oligocene
Galanarla	herbivore	folivore	1 kg-10 kg	(Janis, Damuth et al. 2016, Butler, Travouillon et al. 2021)	(Butler, Travouillon et al. 2018, Palmer 2023)	metatherian	Oligocene
Ganawamaya	herbivore	folivore	1 kg-10 kg	(Janis, Damuth et al. 2016)	(Palmer 2023)	metatherian	Oligocene
Gumardee	herbivore	folivore	1 kg-10 kg	(Janis, Damuth et al. 2016)	(Palmer 2023)	metatherian	Oligocene
Ilaria	herbivore	herbivore	100 kg-1 tonne	(Munson 1992)	(Beck, Louys et al. 2020)	metatherian	Oligocene
Keeuna	carnivore	invertivore	10 g-100 g	Based on *Antechinus* (Archer 1976, Hall 1980)	Calculated from molar dimensions of Archer (1976) and the process of Gordon (2003) [pooled dasyurids]	metatherian	Oligocene
Kuterintja	herbivore	folivore	10 kg-100 kg	(Black, Archer et al. 2012)	(Palmer 2023)	metatherian	Oligocene
Kutjamarcoot	carnivore	invertivore	100 g-1 kg	(Chamberlain, Travouillon et al. 2016)	(Chamberlain, Travouillon et al. 2016)	metatherian	Oligocene

Kyeema	omnivore	omnivore	1 kg-10 kg	(Janis, Damuth et al. 2016)	(Janis, Damuth et al. 2016)	metatherian	Oligocene
Lekaneleo	carnivore	carnivore	1 kg-10 kg	(Yates 2015)	(Palmer 2023)	metatherian	Oligocene
Litokoala	herbivore	folivore	1 kg-10 kg	(Amador and Giannini 2021)	(Palmer 2023)	metatherian	Oligocene
Lumakoala	herbivore	folivore	1 kg-10 kg	(Amador and Giannini 2021)	(Crichton, Beck et al. 2023)	metatherian	Oligocene
Madakoala	herbivore	folivore	1 kg-10 kg	(Amador and Giannini 2021)	(Black, Price et al. 2014)	metatherian	Oligocene
Madju	carnivore	invertivore	100 g-1 kg	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Marada	herbivore	folivore	10 kg-100 kg	(Crichton, Worthy et al. 2023, Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Marlu	herbivore	folivore	100 g-1 kg	(Wheat 2023)	(Palmer 2023)	metatherian	Oligocene
Miralina	herbivore	herbivore	1 kg-10 kg	(Wheat 2023)	Based on *Durudawiri* (Crosby 2002)	metatherian	Oligocene
Mukupirna	herbivore	herbivore	10 kg-100 kg	(Crichton, Worthy et al. 2023)	(Crichton, Worthy et al. 2023)	metatherian	Oligocene
Muramura	herbivore	herbivore	10 kg-100 kg	(Pledge 2003)	(Beck, Louys et al. 2020)	metatherian	Oligocene
Nambaroo	herbivore	herbivore	1 kg-10 kg	(Janis, Damuth et al. 2016, Butler, Travouillon et al. 2021, Palmer 2023)	Calculated from molar dimensions of Flannery and Rich (1986) and the process of Myers (2001) [diprotodont equation]	metatherian	Oligocene
Namilamadeta	herbivore	folivore	10 kg-100 kg	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Neohelos	herbivore	folivore	100 kg-1 tonne	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Ngamaroo	herbivore	folivore	1 kg-10 kg	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Ngapakaldia	herbivore	folivore	100 kg-1 tonne	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Nimbacinus	carnivore	carnivore	1 kg-10 kg	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Nimbadon	herbivore	frugivore	10 kg-100 kg	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Nimiokoala	herbivore	folivore	1 kg-10 kg	(Amador and Giannini 2021)	(Palmer 2023)	metatherian	Oligocene
Paljara	herbivore	folivore	100 g-1 kg	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Perikoala	herbivore	folivore	1 kg-10 kg	(Amador and Giannini 2021)	(Black, Price et al. 2014)	metatherian	Oligocene
Pildra	herbivore	folivore	100 g-1 kg	(Wheat 2023)	(Palmer 2023)	metatherian	Oligocene
Pilkipildra	omnivore	omnivore-herbivore	1 kg-10 kg	(Black, Archer et al. 2012, Wheat 2023)	Calculated from molar dimensions of Archer, Tedford et al. (1987) and the process of Myers (2001) [diprotodont equation]	metatherian	Oligocene
Propalorchestes	herbivore	folivore	10 kg-100 kg	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Purtia	herbivore	folivore	1 kg-10 kg	(Palmer 2023)	Calculated from molar dimensions of Case (1984) and the process of Myers (2001) [diprotodont equation]	metatherian	Oligocene
Raemeotherium	herbivore	folivore	10 kg-100 kg	(Palmer 2023)	Calculated from molar dimensions of Rich and Archer (1978) and the process of Myers (2001) [diprotodont equation]	metatherian	Oligocene
Rhizophascolonus	herbivore	grazer	100 kg-1 tonne	(Palmer 2023)	Calculated from molar dimensions of Brewer, Archer et al. (2008) and the process of Myers (2001)	metatherian	Oligocene

					[diprotodont equation]		
Silvabestius	herbivore	folivore	10 kg-100 kg	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Wabularoo	herbivore	folivore	1 kg-10 kg	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Wakaleo	carnivore	carnivore	10 kg-100 kg	(Yates 2015)	(Palmer 2023)	metatherian	Oligocene
Wakamatha	carnivore	invertivore	10 g-100 g	(Archer and Rich 1979)	Based on *Sminthopsis* (Archer and Rich 1979, Nagy, Lee et al. 1988)	metatherian	Oligocene
Wakiewakie	herbivore	folivore	1 kg-10 kg	(Palmer 2023)	Calculated from molar dimensions of Woodburne (1984) and the process of Myers (2001) [diprotodont equation]	metatherian	Oligocene
Wururoo	herbivore	folivore	1 kg-10 kg	(Palmer 2023)	(Palmer 2023)	metatherian	Oligocene
Wynyardia	herbivore	folivore	1 kg-10 kg	(Palmer 2023)	Based on *Felis catus* (Macphail 1996, Mattern and McLennan 2000)	metatherian	Oligocene
Yalkaparidon	carnivore	invertivore	100 g-1 kg	(Black, Archer et al. 2012)	(Palmer 2023)	metatherian	Oligocene
Yarala	carnivore	invertivore	10 g-100 g	(Travouillon, Gurovich et al. 2010)	(Palmer 2023)	metatherian	Oligocene

Table A2 – Every metatherian and eutherian genus from Palaeogene Australia considered, each accompanied with relevant ecological information and sources. Diagnosis of diet is based on direct academic reference, dental condition (e.g. hypsodonty vs brachydonty), taxonomic identity or comparison to similar taxa. Diagnosis of body mass is based on direct academic reference, molar measurements or comparison to similar taxa. Notable or exceptional assumptions are described in writing.

Genus	Diet classification	Fine diet classification	Body mass	Diet source	Body mass source	Metatherian or eutherian	Time bin
Antarctodolops	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Antarctodon	herbivore	folivore	10kg-100kg	(Gelfo, Goin et al. 2019)	(Gelfo, Goin et al. 2019)	eutherian	Ypresian
Derorhynchus	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Marambiotherium	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Notiolofos	herbivore	folivore	100kg-1 tonne	(Gelfo, Goin et al. 2019)	(Gelfo, Goin et al. 2019)	eutherian	Ypresian
Pauladelphys	omnivore	omnivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Perrodelphys	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Polydolops	herbivore	frugivore	100 g-1 kg	(Zimicz 2012, Croft 2016)	(Zimicz 2012, Croft 2016)	metatherian	Ypresian
Pujatodon	omnivore	omnivore	100 g-1 kg	(Gelfo, Goin et al. 2019)	(Gelfo, Goin et al. 2019)	metatherian	Ypresian
Woodburnodon	herbivore	frugivore	1 kg-10 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Xenostylos	omnivore	omnivore-invertivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Ypresian
Antarctodolops	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene

Antarctodon	herbivore	folivore	10kg-100kg	(Gelfo, Goin et al. 2019)	(Gelfo, Goin et al. 2019)	eutherian	Late Eocene
Derorhynchus	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Marambiotherium	carnivore	invertivore	10 g-100 g	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Notiolofos	herbivore	folivore	100kg-1 tonne	(Gelfo, Goin et al. 2019)	(Gelfo, Goin et al. 2019)	eutherian	Late Eocene
Pauladelphys	omnivore	omnivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Perrodelphys	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Polydolops	herbivore	frugivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene
Trigonostylops	herbivore	herbivore	10 kg-100 kg	(Croft 2016)	(Croft 2016)	eutherian	Late Eocene
Victorlemoineia	herbivore	herbivore	100 kg-1 tonne	(Cassini, Cerdeño et al. 2012)	(Vizcaíno, Cassini et al. 2012)	eutherian	Late Eocene
Xenostylos	omnivore	omnivore-invertivore	100 g-1 kg	(Zimicz 2012)	(Zimicz 2012)	metatherian	Late Eocene

Table A3 – Every metatherian and eutherian genus from Palaeogene Antarctica considered, each accompanied with relevant ecological information and sources. The taxon list is derived from the Palaeobiology Database [https://paleobiodb.org/]. Diagnosis of diet and body mass is based on direct academic reference. Notable or exceptional assumptions are described in writing.

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Genus	Diet classification	Fine diet classification	Body mass	Metatherian or eutherian	Continent
Abrawayaomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Abrocoma	herbivore	herbivore	100 g-1 kg	eutherian	South America
Abrothrix	herbivore	herbivore	10 g-100 g	eutherian	South America
Aconaemys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Aepeomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Akodon	carnivore	invertivore	10 g-100 g	eutherian	South America
Alouatta	herbivore	folivore	1 kg-10 kg	eutherian	South America
Amphinectomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Andalgalomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Andinomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Anotomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Aotus	herbivore	herbivore	100 g-1 kg	eutherian	South America
Ateles	herbivore	frugivore	1 kg-10 kg	eutherian	South America

Atelocynus	carnivore	carnivore	1 kg-10 kg	eutherian	South America
Auliscomys	omnivore	omnivore	10 g-100 g	eutherian	South America
Bassaricyon	herbivore	frugivore	1 kg-10 kg	eutherian	South America
Bibimys	herbivore	grazer	10 g-100 g	eutherian	South America
Blarinomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Blastocerus	herbivore	herbivore	10 kg-100 kg	eutherian	South America
Brachyteles	herbivore	folivore	10 kg-100 kg	eutherian	South America
Bradypus	herbivore	folivore	1 kg-10 kg	eutherian	South America
Brucepattersonius	carnivore	invertivore	10 g-100 g	eutherian	South America
Cabassous	carnivore	invertivore	1 kg-10 kg	eutherian	South America
Cacajao	herbivore	frugivore	1 kg-10 kg	eutherian	South America
Caenolestes	carnivore	invertivore	10 g-100 g	metatherian	South America
Callicebus	herbivore	frugivore	1 kg-10 kg	eutherian	South America
Callimico	herbivore	frugivore	100 g-1 kg	eutherian	South America
Callistomys	herbivore	frugivore	100 g-1 kg	eutherian	South America
Callithrix	herbivore	herbivore	100 g-1 kg	eutherian	South America
Calomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Caluromys	herbivore	herbivore	100 g-1 kg	metatherian	South America
Caluromysiops	herbivore	herbivore	100 g-1 kg	metatherian	South America
Calyptophractus	carnivore	invertivore	100 g-1 kg	eutherian	South America
Carterodon	herbivore	herbivore	100 g-1 kg	eutherian	South America
Catagonus	herbivore	folivore	10 kg-100 kg	eutherian	South America
Cavia	herbivore	herbivore	100 g-1 kg	eutherian	South America
Cebus	omnivore	omnivore-frugivore	1 kg-10 kg	eutherian	South America
Cerdocyon	carnivore	carnivore	1 kg-10 kg	eutherian	South America
Chaetomys	herbivore	granivore	1 kg-10 kg	eutherian	South America
Chaetophractus	carnivore	invertivore	1 kg-10 kg	eutherian	South America
Chelemys	herbivore	herbivore	10 g-100 g	eutherian	South America
Chibchanomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Chilomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Chinchilla	herbivore	herbivore	100 g-1 kg	eutherian	South America
Chinchillula	herbivore	herbivore	100 g-1 kg	eutherian	South America
Chironectes	carnivore	invertivore	100 g-1 kg	metatherian	South America
Chiropotes	herbivore	frugivore	1 kg-10 kg	eutherian	South America
Chlamyphorus	carnivore	invertivore	10 g-100 g	eutherian	South America
Choloepus	herbivore	folivore	1 kg-10 kg	eutherian	South America
Chrysocyon	carnivore	carnivore	10 kg-100 kg	eutherian	South America
Clyomys	herbivore	grazer	100 g-1 kg	eutherian	South America
Coendou	herbivore	folivore	1 kg-10 kg	eutherian	South America
Conepatus	carnivore	invertivore	1 kg-10 kg	eutherian	South America
Cryptotis	carnivore	carnivore	1 g-10 g	eutherian	South America
Ctenomys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Cuniculus	herbivore	herbivore	1 kg-10 kg	eutherian	South America
Cuscomys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Cyclopes	carnivore	invertivore	100 g-1 kg	eutherian	South America
Dactylomys	herbivore	folivore	100 g-1 kg	eutherian	South America

Dasyprocta	herbivore	herbivore	1 kg-10 kg	eutherian	South America
Dasypus	carnivore	invertivore	1 kg-10 kg	eutherian	South America
Delomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Deltamys	herbivore	herbivore	10 g-100 g	eutherian	South America
Didelphis	omnivore	omnivore-carnivore	1 kg-10 kg	metatherian	South America
Dinomys	herbivore	herbivore	10 kg-100 kg	eutherian	South America
Diplomys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Dolichotis	herbivore	herbivore	1 kg-10 kg	eutherian	South America
Dromiciops	carnivore	invertivore	10 g-100 g	metatherian	South America
Dusicyon	carnivore	carnivore	10 kg-100 kg	eutherian	South America
Echimys	herbivore	frugivore	100 g-1 kg	eutherian	South America
Echinoprocta	herbivore	folivore	100 g-1 kg	eutherian	South America
Eira	carnivore	carnivore	1 kg-10 kg	eutherian	South America
Eligmodontia	herbivore	granivore	10 g-100 g	eutherian	South America
Euneomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Euphractus	omnivore	omnivore	1 kg-10 kg	eutherian	South America
Euryzygomatomys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Galea	herbivore	grazer	100 g-1 kg	eutherian	South America
Galenomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Galictis	carnivore	carnivore	1 kg-10 kg	eutherian	South America
Geoxus	carnivore	invertivore	10 g-100 g	eutherian	South America
Glironia	omnivore	omnivore	100 g-1 kg	metatherian	South America
Gracilinanus	carnivore	invertivore	10 g-100 g	metatherian	South America
Graomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Handleyomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Heteromys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Hippocamelus	herbivore	folivore	10 kg-100 kg	eutherian	South America
Holochilus	herbivore	herbivore	100 g-1 kg	eutherian	South America
Hoplomys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Hydrochoerus	herbivore	grazer	10 kg-100 kg	eutherian	South America
Hyladelphys	carnivore	invertivore	10 g-100 g	metatherian	South America
Ichthyomys	carnivore	invertivore	10 g-100 g	eutherian	South America
Irenomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Isothrix	herbivore	herbivore	100 g-1 kg	eutherian	South America
Isthmomys	carnivore	invertivore	100 g-1 kg	eutherian	South America
Juliomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Juscelinomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Kannabateomys	herbivore	folivore	100 g-1 kg	eutherian	South America
Kerodon	herbivore	folivore	100 g-1 kg	eutherian	South America
Kunsia	herbivore	herbivore	100 g-1 kg	eutherian	South America
Lagidium	herbivore	herbivore	1 kg-10 kg	eutherian	South America
Lagostomus	herbivore	grazer	1 kg-10 kg	eutherian	South America
Lagothrix	herbivore	frugivore	1 kg-10 kg	eutherian	South America
Lama	herbivore	herbivore	100 kg-1 tonne	eutherian	South America
Lenoxus	herbivore	herbivore	10 g-100 g	eutherian	South America
Leontopithecus	omnivore	omnivore	100 g-1 kg	eutherian	South America

Leopardus	carnivore	carnivore	1 kg-10 kg	eutherian	South America
Lestodelphys	carnivore	carnivore	10 g-100 g	metatherian	South America
Lestoros	carnivore	invertivore	10 g-100 g	metatherian	South America
Lonchothrix	herbivore	herbivore	100 g-1 kg	eutherian	South America
Lontra	carnivore	carnivore	10 kg-100 kg	eutherian	South America
Loxodontomys	omnivore	omnivore	10 g-100 g	eutherian	South America
Lundomys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Lutreolina	carnivore	carnivore	100 g-1 kg	metatherian	South America
Lycalopex	carnivore	carnivore	1 kg-10 kg	eutherian	South America
Lyncodon	carnivore	carnivore	100 g-1 kg	eutherian	South America
Makalata	herbivore	frugivore	100 g-1 kg	eutherian	South America
Marmosa	omnivore	omnivore	10 g-100 g	metatherian	South America
Marmosops	omnivore	omnivore	10 g-100 g	metatherian	South America
Mazama	herbivore	folivore	10 kg-100 kg	eutherian	South America
Megaoryzomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Melanomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Mesomys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Metachirus	carnivore	carnivore	100 g-1 kg	metatherian	South America
Micoureus	carnivore	invertivore	100 g-1 kg	metatherian	South America
Microakodontomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Microcavia	herbivore	herbivore	100 g-1 kg	eutherian	South America
Microryzomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Microsciurus	herbivore	herbivore	10 g-100 g	eutherian	South America
Monodelphis	omnivore	omnivore	10 g-100 g	metatherian	South America
Mustela	carnivore	carnivore	100 g-1 kg	eutherian	South America
Myocastor	herbivore	herbivore	1 kg-10 kg	eutherian	South America
Myoprocta	herbivore	herbivore	100 g-1 kg	eutherian	South America
Myrmecophaga	carnivore	invertivore	10 kg-100 kg	eutherian	South America
Nasua	herbivore	frugivore	1 kg-10 kg	eutherian	South America
Nasuella	herbivore	frugivore	1 kg-10 kg	eutherian	South America
Neacomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Necromys	carnivore	invertivore	10 g-100 g	eutherian	South America
Nectomys	omnivore	omnivore-carnivore	100 g-1 kg	eutherian	South America
Neotomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Nesoryzomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Neusticomys	carnivore	invertivore	10 g-100 g	eutherian	South America
Noronhomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Notiomys	carnivore	invertivore	10 g-100 g	eutherian	South America
Octodon	herbivore	herbivore	100 g-1 kg	eutherian	South America
Octodontomys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Octomys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Odocoileus	herbivore	herbivore	10 kg-100 kg	eutherian	South America
Oecomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Olallamys	herbivore	folivore	100 g-1 kg	eutherian	South America
Oligoryzomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Oreonax	herbivore	frugivore	1 kg-10 kg	eutherian	South America

Orthogeomys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Oryzomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Oxymycterus	carnivore	invertivore	10 g-100 g	eutherian	South America
Ozotoceros	herbivore	herbivore	10 kg-100 kg	eutherian	South America
Panthera	carnivore	carnivore	10 kg-100 kg	eutherian	South America
Paralomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Pearsonomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Pecari	herbivore	herbivore	10 kg-100 kg	eutherian	South America
Phaenomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Philander	carnivore	carnivore	100 g-1 kg	metatherian	South America
Phyllomys	herbivore	frugivore	100 g-1 kg	eutherian	South America
Phyllotis	herbivore	herbivore	10 g-100 g	eutherian	South America
Pipanacoctomys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Pithecia	herbivore	herbivore	1 kg-10 kg	eutherian	South America
Podoxymys	herbivore	herbivore	10 g-100 g	eutherian	South America
Potos	herbivore	frugivore	1 kg-10 kg	eutherian	South America
Priodontes	carnivore	invertivore	10 kg-100 kg	eutherian	South America
Procyon	carnivore	invertivore	1 kg-10 kg	eutherian	South America
Proechimys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Pseudoryzomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Pteronura	carnivore	carnivore	10 kg-100 kg	eutherian	South America
Pudu	herbivore	folivore	1 kg-10 kg	eutherian	South America
Puma	carnivore	carnivore	10 kg-100 kg	eutherian	South America
Punomys	herbivore	grazer	10 g-100 g	eutherian	South America
Reithrodon	herbivore	grazer	10 g-100 g	eutherian	South America
Reithrodontomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Rhagomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Rhipidomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Rhyncholestes	carnivore	invertivore	10 g-100 g	metatherian	South America
Saguinus	herbivore	herbivore	100 g-1 kg	eutherian	South America
Saimiri	herbivore	herbivore	100 g-1 kg	eutherian	South America
Salinoctomys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Salinomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Scapteromys	carnivore	invertivore	100 g-1 kg	eutherian	South America
Sciurillus	herbivore	herbivore	10 g-100 g	eutherian	South America
Sciurus	herbivore	granivore	100 g-1 kg	eutherian	South America
Scolomys	omnivore	omnivore	10 g-100 g	eutherian	South America
Sigmodon	omnivore	omnivore	100 g-1 kg	eutherian	South America
Sigmodontomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Spalacopus	herbivore	herbivore	100 g-1 kg	eutherian	South America
Speothos	carnivore	carnivore	1 kg-10 kg	eutherian	South America
Sphiggurus	herbivore	folivore	1 kg-10 kg	eutherian	South America
Sylvilagus	herbivore	herbivore	1 kg-10 kg	eutherian	South America
Tamandua	carnivore	invertivore	1 kg-10 kg	eutherian	South America
Tapecomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Tapirus	herbivore	folivore	100 kg-1 tonne	eutherian	South America

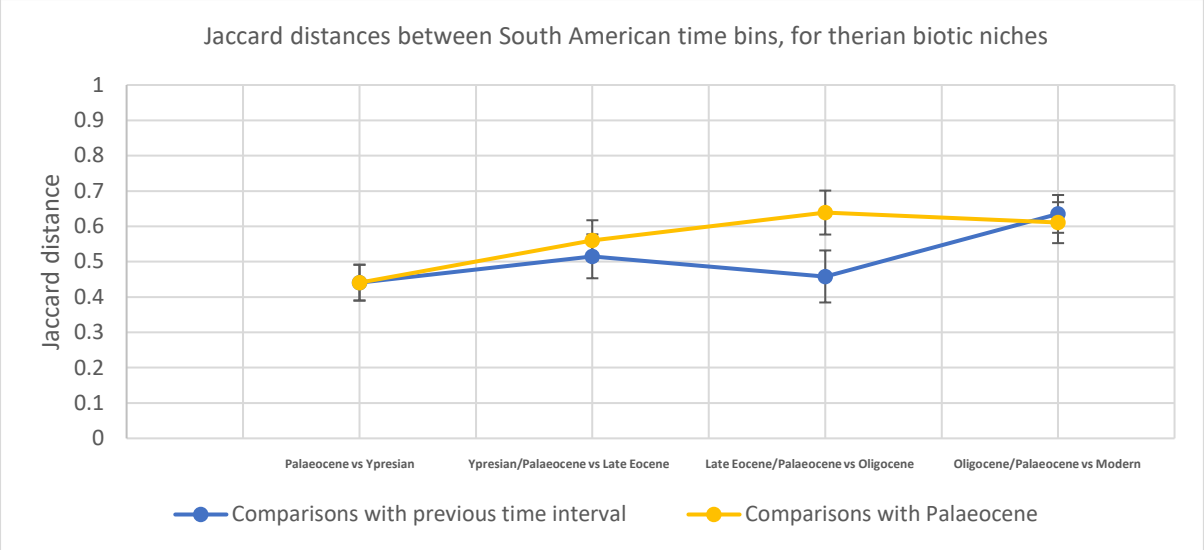
Tayassu	herbivore	herbivore	10 kg-100 kg	eutherian	South America
Thalpomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Thaptomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Thomasomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Thrichomys	herbivore	frugivore	100 g-1 kg	eutherian	South America
Thylamys	carnivore	invertivore	10 g-100 g	metatherian	South America
Tolypeutes	carnivore	invertivore	1 kg-10 kg	eutherian	South America
Tremarctos	herbivore	frugivore	100 kg-1 tonne	eutherian	South America
Trinomys	herbivore	herbivore	100 g-1 kg	eutherian	South America
Tylomys	herbivore	granivore	100 g-1 kg	eutherian	South America
Tympanoctomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Urocyon	omnivore	omnivore	1 kg-10 kg	eutherian	South America
Vicugna	herbivore	herbivore	10 kg-100 kg	eutherian	South America
Wiedomys	omnivore	omnivore	10 g-100 g	eutherian	South America
Wilfredomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Zaedyus	carnivore	invertivore	1 kg-10 kg	eutherian	South America
Zygodontomys	herbivore	herbivore	10 g-100 g	eutherian	South America
Acrobates	carnivore	invertivore	10 g-100 g	metatherian	Australia
Aepyprymnus	herbivore	grazer	1 kg-10 kg	metatherian	Australia
Antechinomys	carnivore	invertivore	10 g-100 g	metatherian	Australia
Antechinus	carnivore	invertivore	10 g-100 g	metatherian	Australia
Bettongia	herbivore	folivore	1 kg-10 kg	metatherian	Australia
Burramys	omnivore	omnivore-herbivore	10 g-100 g	metatherian	Australia
Caloprymnus	herbivore	grazer	100 g-1 kg	metatherian	Australia
Cercartetus	herbivore	herbivore	10 g-100 g	metatherian	Australia
Chaeropus	herbivore	grazer	100 g-1 kg	metatherian	Australia
Conilurus	herbivore	herbivore	100 g-1 kg	eutherian	Australia
Dactylopsila	carnivore	invertivore	100 g-1 kg	metatherian	Australia
Dasycercus	carnivore	carnivore	10 g-100 g	metatherian	Australia
Dasykaluta	carnivore	invertivore	10 g-100 g	metatherian	Australia
Dasyuroides	carnivore	carnivore	100 g-1 kg	metatherian	Australia
Dasyurus	carnivore	invertivore	1 kg-10 kg	metatherian	Australia
Dendrolagus	herbivore	herbivore	1 kg-10 kg	metatherian	Australia
Echymipera	carnivore	invertivore	1 kg-10 kg	metatherian	Australia
Gymnobelideus	omnivore	omnivore	100 g-1 kg	metatherian	Australia
Hemibelideus	herbivore	folivore	100 g-1 kg	metatherian	Australia
Hydromys	carnivore	invertivore	100 g-1 kg	eutherian	Australia
Hypsiprymnodon	carnivore	invertivore	100 g-1 kg	metatherian	Australia
Isoodon	carnivore	invertivore	100 g-1 kg	metatherian	Australia
Lagorchestes	herbivore	grazer	1 kg-10 kg	metatherian	Australia
Lagostrophus	herbivore	herbivore	1 kg-10 kg	metatherian	Australia
Lasiorhinus	herbivore	grazer	10 kg-100 kg	metatherian	Australia
Leggadina	herbivore	herbivore	10 g-100 g	eutherian	Australia
Leporillus	herbivore	herbivore	100 g-1 kg	eutherian	Australia
Macropus	herbivore	grazer	10 kg-100 kg	metatherian	Australia
Macrotis	carnivore	invertivore	100 g-1 kg	metatherian	Australia

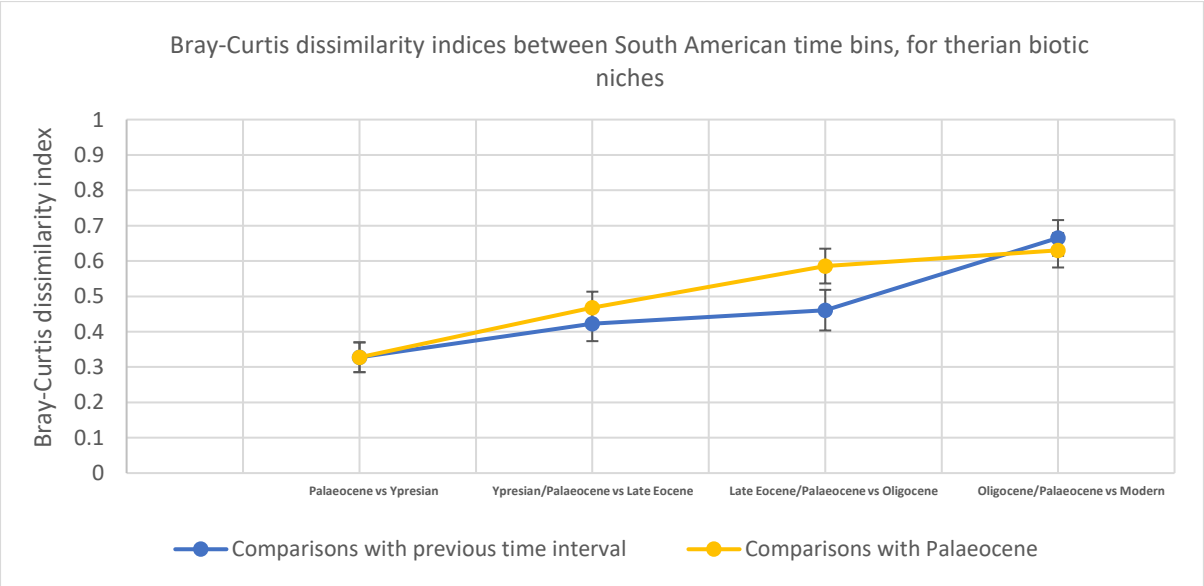
Mastacomys	herbivore	grazer	100 g-1 kg	eutherian	Australia
Melomys	herbivore	frugivore	10 g-100 g	eutherian	Australia
Mesembriomys	herbivore	herbivore	100 g-1 kg	eutherian	Australia
Myrmecobius	carnivore	invertivore	100 g-1 kg	metatherian	Australia
Ningaui	carnivore	invertivore	1 g-10 g	metatherian	Australia
Notomys	herbivore	herbivore	10 g-100 g	eutherian	Australia
Notoryctes	carnivore	invertivore	10 g-100 g	metatherian	Australia
Onychogalea	herbivore	folivore	1 kg-10 kg	metatherian	Australia
Parantechinus	carnivore	invertivore	10 g-100 g	metatherian	Australia
Perameles	carnivore	invertivore	100 g-1 kg	metatherian	Australia
Petauroides	herbivore	folivore	1 kg-10 kg	metatherian	Australia
Petaurus	herbivore	herbivore	100 g-1 kg	metatherian	Australia
Petrogale	herbivore	folivore	1 kg-10 kg	metatherian	Australia
Petropseudes	herbivore	folivore	1 kg-10 kg	metatherian	Australia
Phalanger	herbivore	herbivore	1 kg-10 kg	metatherian	Australia
Phascogale	carnivore	carnivore	100 g-1 kg	metatherian	Australia
Phascolarctos	herbivore	folivore	10 kg-100 kg	metatherian	Australia
Planigale	carnivore	carnivore	1 g-10 g	metatherian	Australia
Pogonomys	herbivore	herbivore	10 g-100 g	eutherian	Australia
Potorous	herbivore	folivore	1 kg-10 kg	metatherian	Australia
Pseudantechinus	carnivore	invertivore	10 g-100 g	metatherian	Australia
Pseudocheirus	herbivore	folivore	100 g-1 kg	metatherian	Australia
Pseudochirops	herbivore	folivore	1 kg-10 kg	metatherian	Australia
Pseudochirulus	herbivore	folivore	1 kg-10 kg	metatherian	Australia
Pseudomys	herbivore	herbivore	10 g-100 g	eutherian	Australia
Rattus	herbivore	herbivore	100 g-1 kg	eutherian	Australia
Sarcophilus	carnivore	carnivore	1 kg-10 kg	metatherian	Australia
Setonix	herbivore	grazer	1 kg-10 kg	metatherian	Australia
Sminthopsis	carnivore	invertivore	10 g-100 g	metatherian	Australia
Spilocuscus	herbivore	herbivore	1 kg-10 kg	metatherian	Australia
Tarsipes	herbivore	herbivore	1 g-10 g	metatherian	Australia
Thylacinus	carnivore	carnivore	10 kg-100 kg	metatherian	Australia
Thylogale	herbivore	folivore	1 kg-10 kg	metatherian	Australia
Trichosurus	herbivore	herbivore	1 kg-10 kg	metatherian	Australia
Uromys	herbivore	frugivore	100 g-1 kg	eutherian	Australia
Vombatus	herbivore	grazer	10 kg-100 kg	metatherian	Australia
Wallabia	herbivore	folivore	10 kg-100 kg	metatherian	Australia
Wyulda	herbivore	folivore	1 kg-10 kg	metatherian	Australia
Xeromys	omnivore	omnivore-carnivore	10 g-100 g	eutherian	Australia
Zyzomys	herbivore	herbivore	10 g-100 g	eutherian	Australia

Table B – Every modern metatherian and eutherian genus from South America and Australia considered, each accompanied with relevant ecological information. Taxon lists for each continent are based on the Mammal Diversity Database

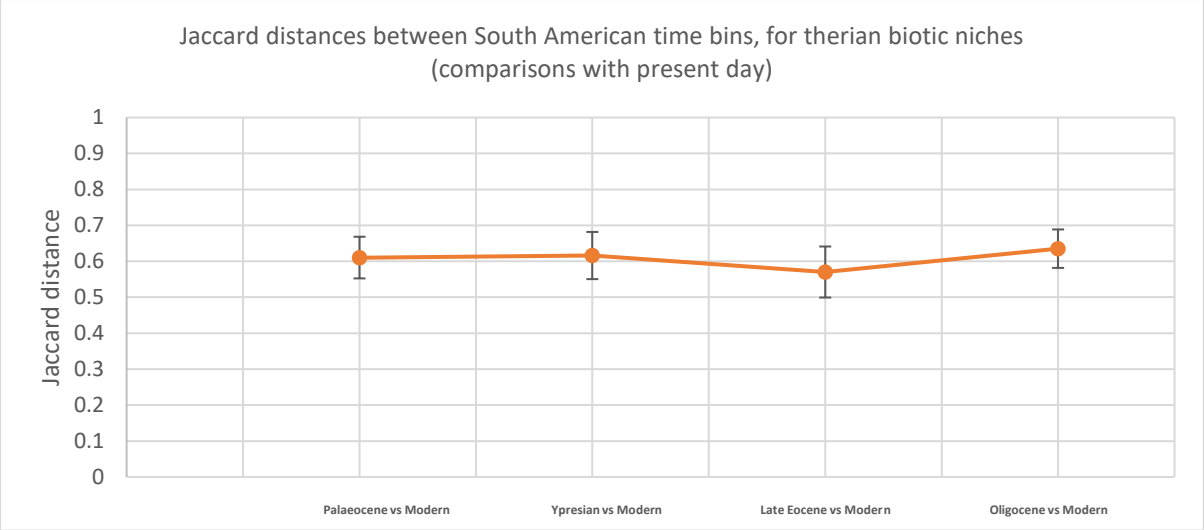
[https://www.mammaldiversity.org/index.html] (Burgin, Colella et al. 2018) while diagnosis of diet and body mass is largely based on EltonTraits (Wilman, Belmaker et al. 2014).

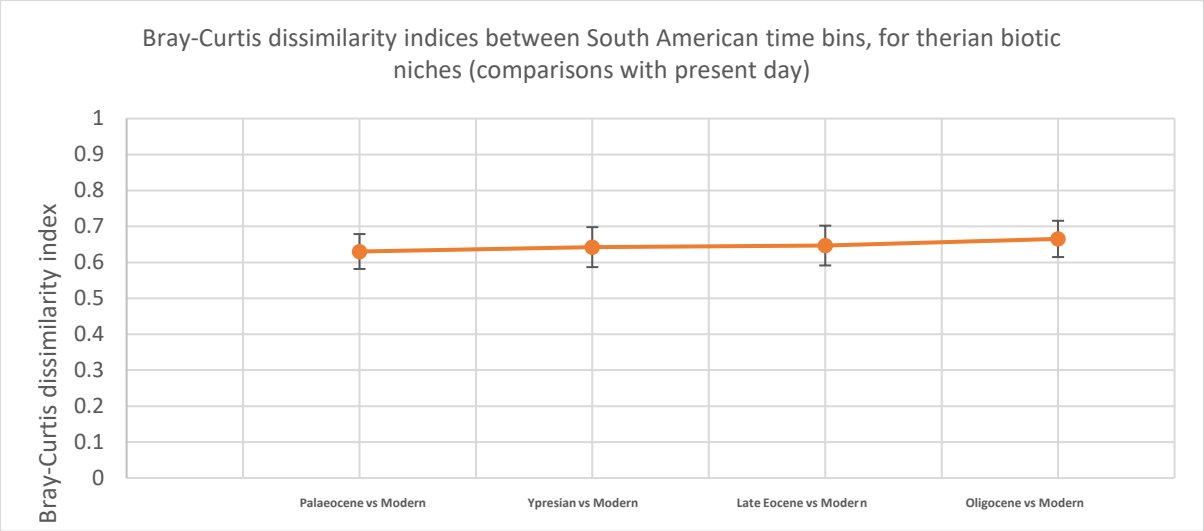
3.3



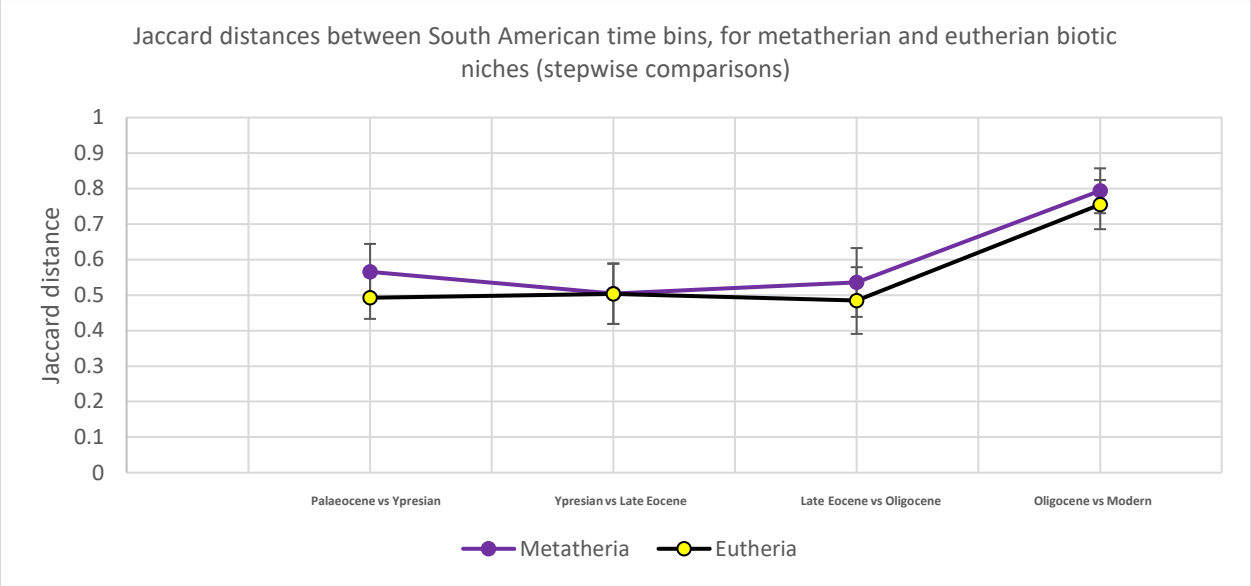


Figures A1 and A2. The mean (±SD) Jaccard distances and Bray-Curtis dissimilarity indices for comparison between time bins, for South American therian biotic niches, using a stepwise approach (blue) and comparisons with the Palaeocene baseline (yellow). Means and SD are calculated from 100 bootstrap replicates. This figure is based on Figures 2 and 6 in Cribb et al. (2023).





Figures B1 and B2. The mean (±SD) Jaccard distances and Bray-Curtis dissimilarity indices for comparisons between the present-day time bin and other time bins, for South American therian biotic niches. Means and SD are calculated from 100 bootstrap replicates. This figure is based on Figures 2 and 6 in Cribb et al. (2023).



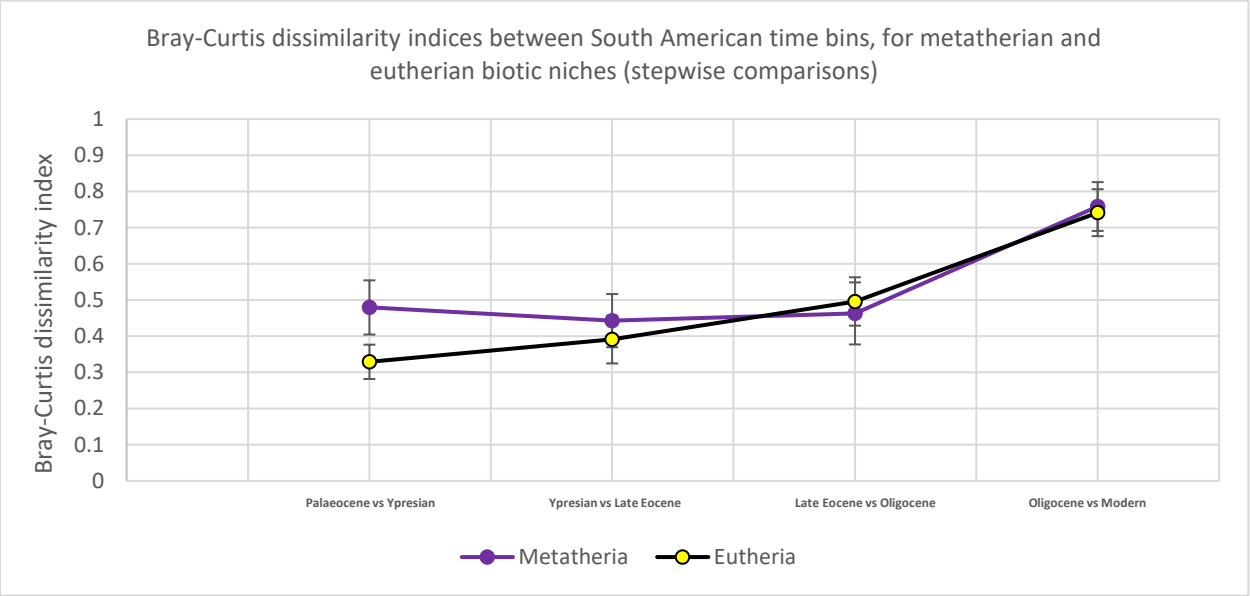
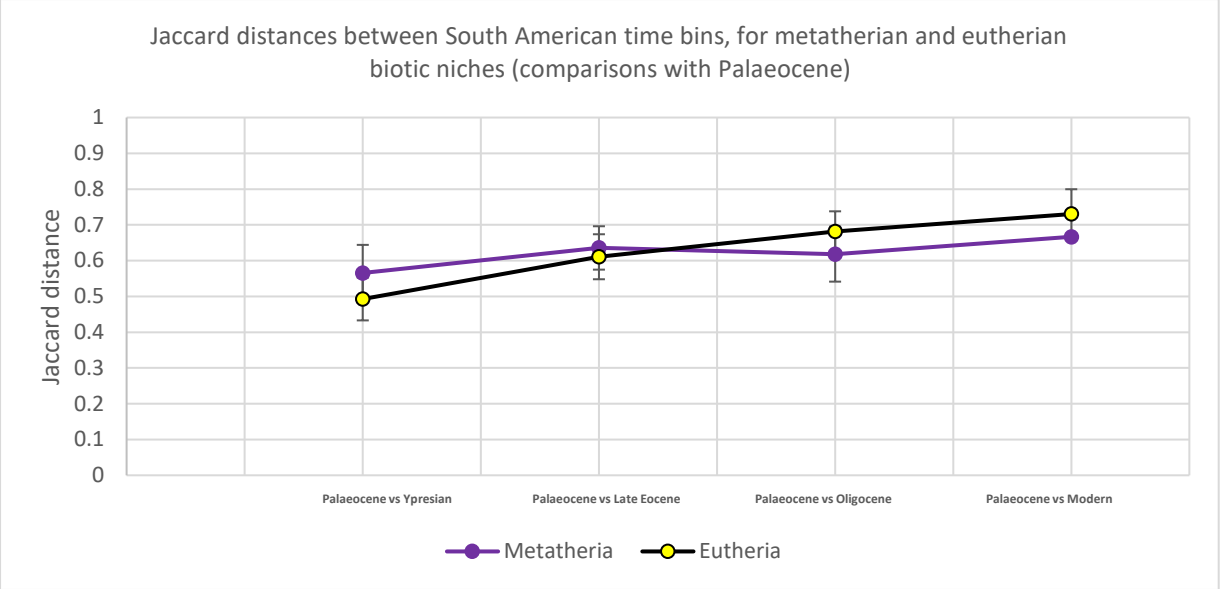


Figure C1 and C2. The mean (±SD) Jaccard distances and Bray-Curtis dissimilarity indices for stepwise comparisons, for South American metatherian and eutherian biotic niches. Means and SD are calculated from 100 bootstrap replicates. This figure is based on Figures 2 and 6 in Cribb et al. (2023).



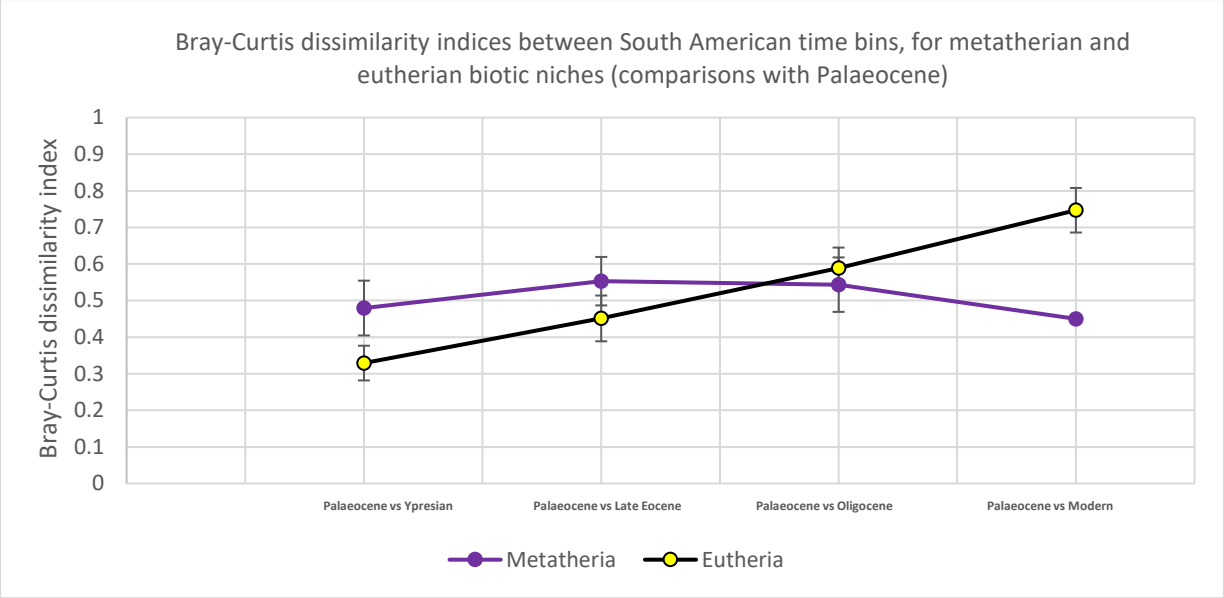
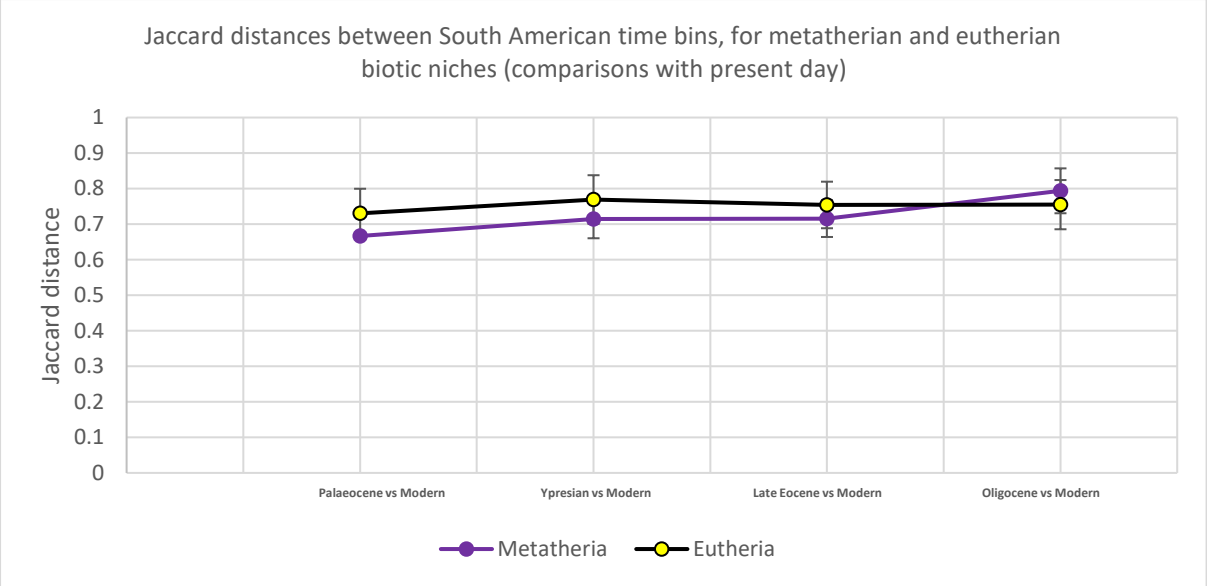


Figure D1 and D2. The mean (±SD) Jaccard distances and Bray-Curtis dissimilarity indices for comparison between the Palaeocene time bin and other time bins, for South American metatherian and eutherian biotic niches. Means and SD are calculated from 100 bootstrap replicates. This figure is based on Figures 2 and 6 in Cribb et al. (2023).



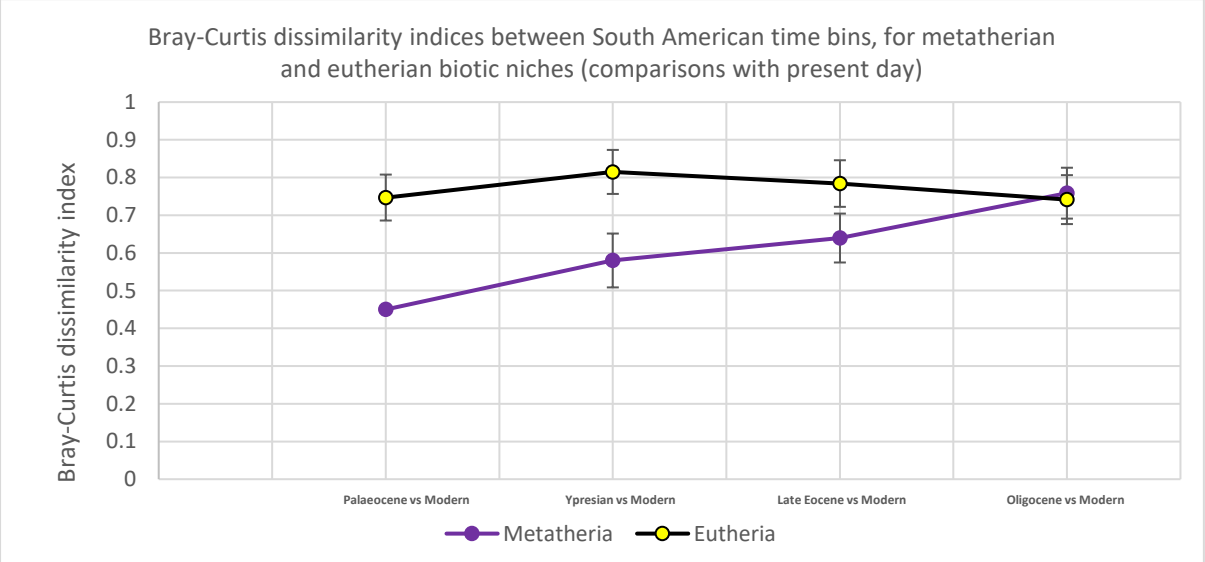


Figure E1 and E2. The mean (±SD) Jaccard distances and Bray-Curtis dissimilarity indices for comparison between the present-day time bin and other time bins, for South American metatherian and eutherian biotic niches. Means and SD are calculated from 100 bootstrap replicates. This figure is based on Figures 2 and 6 in Cribb et al. (2023).

3.4

Clade	Palaeocene [66-56 Ma]	Ypresian [56-47.8 Ma]	Late Eocene [47.8-33.9 Ma]	Oligocene [33.9-23.03 Ma]	Present day [0 Ma]
***Microbiotheria* (monito del monte)**	**Invertivore/10g-100g** [?*Khasia*]	**Invertivore/10g-100g** [*Eomicrobiotherium, Marambiotherium*], **Invertivore/100g-1kg** [?*Mirandatherium*], **Frugivore/10g-100g** [?*Monodelphopsis*], **Frugivore/1kg-10kg** [*Woodburnodon*]	**Invertivore/10g-100g** [*Eomicrobiotherium, Marambiotherium*]	**Invertivore/1g-10g** [?*Kirutherium*], **Invertivore/10g-100g** [*Eomicrobiotherium, Microbiotherium*], **Omnivore/10g-100g** [*Clenia*]	**Invertivore/10g-100g** [*Dromiciops*]
***Paucituberculata* (shrew opossums)**	No described genera	**Invertivore/10g-100g** [*Bardalestes*], **Invertivore/100g-1kg** [*Riolestes*]	**Invertivore/10g-100g** [*Bardalestes*]	**Invertivore/10g-100g** [*Evolestes, Pseudhalmarhiphus*], **Invertivore/100g-1kg** [*Antawallathentes, Fieratherium, Trelewthentes*], **Omnivore-invertivore/10g-100g** [*Quirogalestes*], **Omnivore/10g-100g** [*Parabderites*], **Omnivore/100g-1kg** [*Palaeothentes*], **Omnivore/1kg-10kg** [*Carlothentes*], **Frugivore/10g-100g** [*Perulestes*], **Frugivore/100g-1kg** [*Abderites, Acdestodon, Acdestoides, Pilchenia, Sasawatsu*]	**Invertivore/10g-100g** [*Caenolestes, Lestoros, Rhyncholestes*]
***Dasyuromorphia* (Australian carnivorous marsupials)**	No described genera	No described genera	No described genera	**Invertivore/10g-100g** [*Dasylurinja*], **Carnivore/1kg-10kg** [*Badjcinus, Nimbacinus*]	**Invertivore/1g-10g** [*Ningaui*], **Invertivore/10g-100g** [*Antechinomys, Antechinus, Dasykaluta, Notoryctes, Parantechinus, Pseudantechinus, Sminthopsis*], **Invertivore/100g-1kg** [*Myrmecobius*], **Invertivore/1kg-10kg** [*Dasyurus*], **Carnivore/1g-10g** [*Planigale*], **Carnivore/10g-100g** [*Dasycercus*], **Carnivore/100g-1kg** [*Dasyuroides, Phascogale*], **Carnivore/1kg-10kg** [*Sarcophilus*], **Carnivore/10kg-100kg** [*Thylacinus*]
***Peramelemorphia* (bandicoots and bilbies)**	No described genera	No described genera	No described genera	**Omnivore/100g-1kg** [*Bulungu*], **Carnivore/100g-1kg** [*Galadi*], **Invertivore/10g-100g** [*Yarala*], **Invertivore/100g-1kg** [*Kutjamarcoot, Madju*]	**Invertivore/100g-1kg** [*Isoodon, Macrotis, Perameles*], **Invertivore/1kg-10kg** [*Echimypera*], Grazer [*Chaeropus*]

Macropodiformes (kangaroos and kin)	No described genera	No described genera	No described genera	**Herbivore/1kg-10kg** [*Nambaroo*], **Folivore/1kg-10kg** [*Balbaroo, Cookeroo, Galanarla, Ganawamaya, Gumardee, Ngamaroo, Purtia, Wabularoo, Wakiewakie, Wururoo*], **Omnivore/1kg-10kg** [*Bulungamaya, Kyeema*], **Omnivore-carnivore/1kg-10kg** [*Ekaltadita*],	**Invertivore/100g-1kg** [*Hypsiprymnodon*], **Herbivore/1kg-10kg** [*Dendrolagus, Lagostrophus*], **Folivore/1kg-10kg** [*Bettongia, Onychogalea, Petrogale, Potorous, Thylogale*], **Folivore/10kg-100kg** [*Wallabia*], **Grazer/100g-1kg** [*Caloprymnus*], **Grazer/1kg-10kg** [*Aepyprymnus, Lagorchestes, Setonix*], **Grazer/10kg-100kg** [*Macropus*]
Phalangeroidea (phalangeroid possums)	No described genera	No described genera	No described genera	**Herbivore/100g-1kg** [*Barguru*], **Herbivore/1kg-10kg** [*Eocuscus, Miralina*], **Frugivore/100g-1kg** [*Chunia*], **Frugivore/1kg-10kg** [*Ektopodon*], **Omnivore-herbivore/10g-100g** [*Burramys*]	**Omnivore-herbivore/10g-100g** [*Burramys*], **Herbivore/10g-100g** [*Cercartetus*], **Herbivore/1kg-10kg** [*Phalanger, Spilocuscus, Trichosurus*], **Folivore/1kg-10kg** [*Wyulda*]
Petauroidea (petauroid possums)	No described genera	No described genera	No described genera	**Omnivore-herbivore/100g-1kg** [*Djilgaringa*], **Omnivore-herbivore/1kg-10kg** [*Pilkipildra*], **Folivore/100g-1kg** [*Marlu, Pildra*]	**Invertivore/10g-100g** [*Acrobates*], **Invertivore/100g-1kg** [*Dactylopsila*], **Omnivore/100g-1kg** [*Gymnobelideus*], **Herbivore/1g-10g** [*Tarsipes*], **Herbivore/100g-1kg** [*Petaurus*], **Folivore/100g-1kg** [*Hemibelideus, Pseudocheirus*], **Folivore/1kg-10kg** [*Petauroides, Petropseudes, Pseudochirulus, Pseudochirops*]
Vombatiformes (wombats, koalas and kin)	No described genera	No described genera	No described genera	**Carnivore/1kg-10kg** [*Lekaneleo*], **Carnivore/10kg-100kg** [*Wakaleo*], **Herbivore/10kg-100kg** [*Mukupirna, Muramura*], **Herbivore/100kg-1 tonne** [*Ilaria*], **Frugivore/10kg-100kg** [*Nimbadon*], **Folivore/1kg-10kg** [*Ayekaye, Litokoala, Lumakoala, Madakoala, Nimiokoala, Perikoala*], **Folivore/10kg-100kg** [*Kuterintja, Marada, Namilamadeta, Propalorchestes, Raemeotherium, Silvabestius*], **Folivore/100kg-1 tonne** [*Neohelos, Ngapakaldia*], **Grazer/100kg-1 tonne** [*Rhizophascolonus*]	**Folivore/10kg-100kg** [*Phascolarctos*], **Grazer/10kg-100kg** [*Lasiorhinus, Vombatus*]

Cingulata (armadillos)	No described genera	**Invertivore/1kg-10kg** [*Astegotherium, Utaetus*], **Omnivore-invertivore/1kg-10kg** [*Coelutaetus, Noatherium, Prostegotherium, Pucatherium, Riostegotherium*]	**Invertivore/1kg-10kg** [*Astegotherium, Lumbreratherium, Utaetus*], **Invertivore/10kg-100kg** [*Glyptatelus, Lomaphorelus*], **Omnivore-invertivore/1kg-10kg** [*Barrancatatus, Mazzoniphractus, Meteutatus, Parastegosimpsonia, Parutaetus, Prostegotherium, Pseudeutatus, Pseudostegotherium, Pucatherium, Punatherium, Riostegotherium, Saltatherium, Stegosimpsonia*], **Herbivore/100kg-1 tonne** [*Palaeopeltis, Proeocoleophorus*], **Grazer/100kg-1 tonne** [*Machlydotherium*]	**Invertivore/100g-**1kg [*Clypeotherium*], **Invertivore/10kg-100kg [***Glyptatelus, Neoglyptatelus*], **Omnivore/1kg-10kg** [*Stenotatus*], **Omnivore-invertivore/1kg-10kg** [*Amblytatus, Archaeutatus, Barrancatatus, Kuntinaru, Meteutatus, Parastegosimpsonia, Parutaetus, Proeuphractus, Prozaedyus, Pseudeutatus, Pseudostegotherium*], **Omnivore-herbivore/1kg-10kg** [*Doellotatus*], **Herbivore/10kg-100kg** [*Eocoleophorus, Peltephilus, Ronwolffia*], **Herbivore/100kg-1 tonne** [*Palaeopeltis, Proplatyarthrus, ?Pseudorophodon, Urotherium*], **Grazer/100kg-1 tonne** [*Machlydotherium Pseudoplohoplophorus, Yuruatherium*]	**Invertivore/10g-100g**[*Chlamyphorus*], **Invertivore/100g-1kg [***Calyptophractus*], **Invertivore/1kg-10kg [***Cabassous,Chaetophractus, Dasypus, Euphractus, Tolypeutes, Zaedyus*], **Invertivore/10kg-100kg [***Priodontes*]
Folivora (sloths)	No described genera	No described genera	**Grazer/1kg-10kg** [*Pseudoglyptodon]*	**Herbivore-10kg-100kg [***Similhapalops*], **Herbivore/100kg-1 tonne** [*Octodontotherium, Orophodon, Proplatyarthrus, ?Pseudorophodon*], **Folivore/10kg-100kg** [*Deseadognathus*], **Grazer/1kg-10kg** [*Pseudoglyptodon],* **Grazer/10kg-100kg** [*Paroctodontotherium*]	**Folivore/1kg-10kg** [*Bradypus, Choloepus*]
Caviomorpha	No described genera	No described genera	**Herbivore/10g-100g** [*Cachiyacuy, Canaanimys, Eoespina, Tarapotomys*], **Herbivore/100g-1kg** [*Eobranisamys, Eoincamys*], **Folivore/10g-100g** [*Balsayacuy*], **Folivore/100g-1kg** [*Chachapoyamys*]	**Herbivore/10g-100g** [*Cachiyacuy, Canaanimys, Eoespina, Eosachacui, Tarapotomys*], **Herbivore/100g-1kg** [*Acarechimys, Eobranisamys, Eoincamys, Eopicure, Ethelomys, Galileomys, Lapazomys, Litodontomys, Pozomys, Scotamys, Vallehermosomys, Xylechimys*], **Herbivore/1kg-10kg** [*Andemys, Branisamys, Eodelphomys, Neoreomys, Steiromys, Ucayalimys*], **Herbivore/10kg-100kg** [*'Tacheria'*], **Folivore/10g-100g** [*Balsayacuy, Loretomys, Mayomys, Platypittamys, Selvamys, Vucetichimys*],	**Invertivore/10g-100g** [*Akodon, Brucepattersonius, Geoxus, Ichthyomys, Necromys, Neusticomys, Notiomys, Oxymycterus*], **Invertivore/100g-1kg** [*Isthmomys, Scapteromys*], **Omnivore/10g-100g** [*Auliscomys, Loxodontomys, Scolomys, Wiedomys*], **Omnivore/100g-1kg** [*Sigmodon*], **Omnivore-carnivore/100g-1kg** [*Nectomys*], **Herbivore/10g-100g** [*Abrawayaomys, Abrothrix, Aepeomys, Amphinectomys, Andalgalomys, Andinomys, Anotomys, Blarinomys, Calomys, Chelemys, Chibchanomys, Chilomys, Delomys, Deltamys, Euneomys, Galenomys, Graomys, Handleyomys, Irenomys, Juliomys, Juscelinomys, Lenoxus, Megaoryzomys, Melanomys, Microakodontomys, Microryzomys, Microsciurus]*

Caviomorpha (cntd.)				**Folivore/100g-1kg** [*Chachapoyamys, Chambiramys, Deseadomys, Draconomys, Eosallamys, Kichkasteiromys, Leucokephalos, Llitun, Migraveramus, Palaeosteiromys, Plesiosteiromys, Sallamys, Shapajamys*], **Folivore/1kg-10kg** [*Cholamys, Eopululo, Paulacoutomys, Protosteiromys*], **Grazer/100g-1kg** [*Asteromys, Cephalomyopsis, Cephalomys, Changquin, Chubutomys, Eoviscaccia, Incamys, Loncolicu, Protacaremys*], **Grazer/1kg-10kg** [*Scleromys*]	**Herbivore/10g-100g (cntd.)** [*Neacomys, Neotomys, Nesoryzomys, Noronhomys, Oecomys, Oligoryzomys, Oryzomys, Paralomys, Pearsonomys, Phaenomys, Phyllotis, Podoxymys, Pseudoryzomys, Reithrodontomys, Rhagomys, Rhipidomys, Salinomys, Sciurillus, Sigmodontomys, Tapecomys, Thalpomys, Thaptomys, Thomasomys, Tympanoctomys, Wilfredomys, Zygodontomys*], **Herbivore/100g-1kg** [*Abrocoma, Aconaemys, Carterodon, Cavia, Chinchilla, Chinchillula, Ctenomys, Cuscomys, Diplomys, Euryzygomatomys, Heteromys, Holochilus, Hoplomys, Isothrix, Kunsia, Lonchothrix, Lundomys, Mesomys, Microcavia, Myoprocta, Octodon, Octodontomys, Octomys, Orthogeomys, Pipanacoctomys, Proechimys, Salinoctomys, Spalacopus, Trinomys*], **Herbivore/1kg-10kg** [*Lagidium, Dolichotis, Dasyprocta, Cuniculus, Myocastor*], **Herbivore/10kg-100kg** [*Dinomys*], **Grazer/10g-100g** [*Bibimys, Punomys, Reithrodon*], **Grazer/100g-1kg** [*Clyomys, Galea*], **Grazer/1kg-10kg** [*Lagostomus*], **Grazer/10kg-100kg** [*Hydrochoerus*], **Granivore/10g-100g** [*Eligmodontia*], **Granivore/100g-1kg** [*Sciurus, Tylomys*], **Granivore/1kg-10kg** [*Chaetomys*], **Frugivore/100g-1kg** [*Phyllomys, Callistomys, Echimys, Makalata, Thrichomys*], **Folivore/100g-1kg** [*Dactylomys, Kannabateomys, Olallamys, Echinoprocta, Kerodon*], **Folivore/1kg-10kg** [*Coendou, Sphiggurus*]
Anthropoidea	No described genera	No described genera	No described genera	**Invertivore/100g-1kg [***Ashaninkacebus*], **Omnivore/100g-1kg [***Perupithecus*], **Omnivore-frugivore/100g-1kg** [*Branisella*], **Omnivore-grazer/100g-1kg [***Szalatavus*], **Frugivore/100g-1kg** [*Ucayalipithecus*], **Frugivore/1kg-10kg [***Canaanimico*],	**Omnivore/100g-1kg** [*Leontopithecus*], **Omnivore-frugivore/1kg – 10kg** [*Cebus*], **Herbivore/100g – 1kg** [*Aotus, Callithrix, Saguinus, Saimiri*], **Herbivore/1kg – 10kg** [*Pithecia*], **Frugivore/100g-1kg** [*Callimico*], **Frugivore/1kg-10kg** [*Ateles, Cacajao, Callicebus, Chiropotes, Lagothrix, Oreonax*], **Folivore/1kg-10kg** [*Alouatta*], **Folivore/10kg-100kg** [*Brachyteles*]

Table C. Gondwanan therian clades, their genera, and their diets and body masses across the Palaeogene and in the modern day. Didelphimorphia (opossums) and Myrmecophagidae (anteaters) is not included as their fossil records begin in the Miocene (Dunn, Madden et al. 2013, Goin and Abello 2013, Gaudin and Croft 2015).

4.1

Species	Optimal model combination	TSS	CBI	AUC	Most significant variable (% contribution)
Dromiciops gliroides	5-qh	0.96575	0.862	0.98925	Maximum temperature of the warmest month (47.8%)
Chusquea culeou	0.1-lq	0.9451	0.715	0.998855	Minimum temperature of the coldest month (52.1%)
Nothofagus dombeyi	0.8-lt	0.92905	0.980	0.97835	Maximum temperature of the warmest month (37.4%)
Tristerix corymbosus	0.1-lqp	0.903	0.866	0.9661	Minimum temperature of the coldest month (62.4%)

Table A – The four extant species considered in this study, their most suitable niche models built around a biogeographically informed calibration region as selected by kuenm (Cobos, Peterson et al. 2019), and some associated model metrics. All models have a TSS and CBI over 0.5, and an AUC over 0.7, and were included in further analysis, following previous literature (Pearce and Ferrier 2000, Coetzee, Robertson et al. 2009, Farrell, Wang et al. 2019).

4.2

Areas of suitable Antarctic abiotic conditions (excluding extrapolation)	Threshold method	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***	Total Antarctic area (km^2)
Danian [66-61.6 Ma]	95% LTP	72750	502287	1365079	26027	13079315
	maxSSS	203318	880977	2525981	47731	
Selandian [61.6-59.2Ma]	95% LTP	70286	701462	1735204	24176	13238898
	maxSSS	255616	1196128	3314605	44180	
Ypresian [56-47.8Ma]	95% LTP	195926	1672633	1973434	44103	13784981
	maxSSS	450402	2730216	4694165	70139	
Priabonian [37.71-33.9Ma]	95% LTP	34043	1444895	2741223	55905	13956406
	maxSSS	250335	2606814	5929413	93907	
Rupelian [33.9-27.82 Ma]	95% LTP	0	0	0	0	14126946
	maxSSS	0	0	1434	0	
Chattian [27.82-23.03Ma]	95% LTP	0	1820	38258	0	14241288
	maxSSS	777	158009	183189	0	

Areas of suitable Antarctic abiotic conditions (including extrapolation)	Threshold method	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***	Total Antarctic area (km^2)
Danian [66-61.6 Ma]	95% LTP	72750	502287	6264686	26027	13079315
	maxSSS	203318	880977	9383110	47731	
Selandian [61.6-59.2Ma]	95% LTP	70286	701462	6448076	24176	13238898
	maxSSS	255616	1196128	10280372	44180	
Ypresian [56-47.8Ma]	95% LTP	195926	1672633	2828314	44103	13784981
	maxSSS	450402	2730216	6329084	70139	
Priabonian [37.71-33.9Ma]	95% LTP	34043	1444895	4830392	55905	13956406
	maxSSS	250335	2606814	10774196	93907	
Rupelian [33.9-27.82 Ma]	95% LTP	0	0	0	0	14126946
	maxSSS	0	0	21308	0	
Chattian [27.82-23.03Ma]	95% LTP	0	1820	102962	0	14241288
	maxSSS	777	158009	492602	0	

***Table B1 and B2 – The area of suitable Antarctic abiotic conditions (km^2) in Antarctica, as predicted for* Dromiciops gliroides, Chusquea culeou, Nothofagus dombeyi *and* Tristerix corymbosus.**

4.3

Danian [66-61.6Ma] projections thresholded by 95% LTP	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***
Dromiciops gliroides	n/a	72750 (100% of *Dromiciops*, 14.4% of *Chusquea*)	72750 (100% of *Dromiciops*, 5.3% of *Nothofagus* [1.2% including extrap.])	7938 (10.9% of *Dromiciops,* 30.5% of *Tristerix*)
Chusquea culeou	72750 (100% of *Dromiciops*, 14.4% of *Chusquea*)	n/a	420566 (83.7% of *Chusquea,* 30.8% of *Nothofagus* [6.7% including extrap.])	18966 (3.8% of *Chusquea*, 72.9% of *Tristerix*)
Nothofagus dombeyi	72750 (100% of *Dromiciops*, 5.3% of *Nothofagus* [1.2% including extrap.])	420566 (83.7% of *Chusquea,* 30.8% of *Nothofagus* [6.7% including extrap.])	n/a	22682 (1.7% of *Nothofagus* [0.3% including extrap.], 87.1% of *Tristerix*)
Tristerix corymbosus	7938 (10.9% of *Dromiciops,* 30.5% of *Tristerix*)	18966 (3.8% of *Chusquea*, 72.9% of *Tristerix*)	22682 (1.7% of *Nothofagus* [0.3% including extrap.], 87.1% of *Tristerix*)	n/a

Danian [66-61.6Ma] projections thresholded by maxSSS	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***
Dromiciops gliroides	n/a	203318 (100% of Dromiciops, 23.1% of Chusquea)	203318 (100% of Dromiciops, 8% of Nothofagus [2.2% including extrap.])	43508 (21.4% of Dromiciops, 91.2% of Tristerix)
Chusquea culeou	203318 (100% of Dromiciops, 23.1% of Chusquea)	n/a	858419 (97.4% of Chusquea, 34% of Nothofagus [9.1% including extrap.])	47092 (5.3% of Chusquea, 98.7% of Tristerix)
Nothofagus dombeyi	203318 (100% of Dromiciops, 8% of Nothofagus [2.2% including extrap.])	858419 (97.4% of Chusquea, 34% of Nothofagus [9.1% including extrap.])	n/a	47377 (99.3% of Tristerix, 1.9% of Nothofagus [0.5% including extrap.])
Tristerix corymbosus	43508 (21.4% of Dromiciops, 91.2% of Tristerix)	47092 (5.3% of Chusquea, 98.7% of Tristerix)	47377 (99.3% of Tristerix, 1.9% of Nothofagus [0.5% including extrap.])	n/a

Selandian [61.6-59.2Ma] projections thresholded by 95% LTP	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***
Dromiciops gliroides	n/a	70286 (100% of Dromiciops, 10% of Chusquea)	70286 (100% of Dromiciops, 4.1% of Nothofagus [1.1% including extrap.])	7516 (10.7% of Dromiciops, 31.1% of Tristerix)
Chusquea culeou	70286 (100% of Dromiciops, 10% of Chusquea)	n/a	508408 (72.5% of Chusquea, 29.3% of Nothofagus [7.9% including extrap.])	19463 (2.8% of Chusquea, 80.5% of Tristerix)
Nothofagus dombeyi	70286 (100% of Dromiciops, 4.1% of Nothofagus [1.1% including extrap.])	508408 (72.5% of Chusquea, 29.3% of Nothofagus [7.9% including extrap.])	NA	21830 (90.3% of Tristerix, 1.3% of Nothofagus [0.3% including extrap.])
Tristerix corymbosus	7516 (10.7% of Dromiciops, 31.1% of Tristerix)	19463 (2.8% of Chusquea, 80.5% of Tristerix)	21830 (90.3% of Tristerix, 1.3% of Nothofagus [0.3% including extrap.])	n/a

Selandian [61.6-59.2Ma] projections thresholded by maxSSS	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***
Dromiciops gliroides	n/a	255616 (100% of Dromiciops, 21.4% of Chusquea)	255616 (100% of Dromiciops, 7.7% of Nothofagus [2.5% including extrap.])	39232 (15.3% of Dromiciops, 88.8% of Tristerix)
Chusquea culeou	255616 (100% of Dromiciops, 21.4% of Chusquea)	n/a	1121500 (93.8% of Chusquea, 33.8% of Nothofagus [10.9% including extrap.])	43565 (3.6% of Chusquea, 98.6% of Tristerix)
Nothofagus dombeyi	255616 (100% of Dromiciops, 7.7% of Nothofagus [2.5% including extrap.])	1121500 (93.8% of Chusquea, 33.8% of Nothofagus [10.9% including extrap.])	n/a	44180 (100% of Tristerix, 1.3% of Nothofagus [0.4% including extrap.])
Tristerix corymbosus	39232 (15.3% of Dromiciops, 88.8% of Tristerix)	43565 (3.6% of Chusquea, 98.6% of Tristerix)	44180 (100% of Tristerix, 1.3% of Nothofagus [0.4% including extrap.])	n/a

Ypresian [56-47.8Ma] projections thresholded by 95% LTP	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***
Dromiciops gliroides	n/a	195926 (100% of Dromiciops, 11.7% of Chusquea)	193342 (98.7% of Dromiciops, 9.8% of Nothofagus [6.8% including extrap.])	29212 (14.9% of Dromiciops, 66.2% of Tristerix)
Chusquea culeou	195926 (100% of Dromiciops, 11.7% of Chusquea)	n/a	1021844 (61.1% of Chusquea, 51.8% of Nothofagus [36.1% including extrap.])	40662 (2.4% of Chusquea, 92.2% of Tristerix)
Nothofagus dombeyi	193342 (98.7% of Dromiciops, 9.8% of Nothofagus [6.8% including extrap.])	1021844 (61.1% of Chusquea, 51.8% of Nothofagus [36.1% including extrap.])	n/a	41313 (93.7% of Tristerix, 2.1% of Nothofagus [1.5% including extrap.])
Tristerix corymbosus	29212 (14.9% of Dromiciops, 66.2% of Tristerix)	40662 (2.4% of Chusquea, 92.2% of Tristerix)	41313 (93.7% of Tristerix, 2.1% of Nothofagus [1.5% including extrap.])	n/a

Ypresian [56-47.8Ma] projections thresholded by maxSSS	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***
Dromiciops gliroides	n/a	450402 (100% of Dromiciops, 16.5% of Chusquea)	442567 (98.3% of Dromiciops, 9.4% of Nothofagus [7% including extrap.])	54962 (12.2% of Dromiciops, 78.4% of Tristerix)
Chusquea culeou	450402 (100% of Dromiciops, 16.5% of Chusquea)	n/a	2267494 (83.1% of Chusquea, 48.3% of Nothofagus [35.8% including extrap.])	67952 (2.5% of Chusquea, 96.9% of Tristerix)
Nothofagus dombeyi	442567 (98.3% of Dromiciops, 9.4% of Nothofagus [7% including extrap.])	2267494 (83.1% of Chusquea, 48.3% of Nothofagus [35.8% including extrap.])	n/a	68394 (97.5% of Tristerix, 1.5% of Nothofagus [1.1% including extrap.])
Tristerix corymbosus	54962 (12.2% of Dromiciops, 78.4% of Tristerix)	67952 (2.5% of Chusquea, 96.9% of Tristerix)	68394 (97.5% of Tristerix, 1.5% of Nothofagus [1.1% including extrap.])	n/a

Priabonian [37.71-33.9Ma] projections thresholded by 95% LTP	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***
Dromiciops gliroides	n/a	34043 (100% of Dromiciops, 2.4% of Chusquea)	34043 (100% of Dromiciops, 1.2% of Nothofagus [0.7% including extrap.])	4889 (14.4% of Dromiciops, 8.7% of Tristerix)
Chusquea culeou	34043 (100% of Dromiciops, 2.4% of Chusquea)	n/a	830138 (57.5% of Chusquea, 30.3% of Nothofagus [17.2% including extrap.])	33457 (2.3% of Chusquea, 59.8% of Tristerix)
Nothofagus dombeyi	34043 (100% of Dromiciops, 1.2% of Nothofagus [0.7% including extrap.])	830138 (57.5% of Chusquea, 30.3% of Nothofagus [17.2% including extrap.])	n/a	34739 (62.1% of Tristerix, 1.3% of Nothofagus [0.7% including extrap.])
Tristerix corymbosus	4889 (14.4% of Dromiciops, 8.7% of Tristerix)	33457 (2.3% of Chusquea, 59.8% of Tristerix)	34739 (62.1% of Tristerix, 1.3% of Nothofagus [0.7% including extrap.])	n/a

Priabonian [37.71-33.9Ma] projections thresholded by maxSSS	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***
Dromiciops gliroides	n/a	250335 (100% of Dromiciops, 9.6% of Chusquea)	250335 (100% of Dromiciops, 4.2% of Nothofagus [2.3% including extrap.])	47677 (19% of Dromiciops, 50.8% of Tristerix)
Chusquea culeou	250335 (100% of Dromiciops, 9.6% of Chusquea)	n/a	2404626 (92.2% of Chusquea, 40.6% of Nothofagus [22.3% including extrap.])	70726 (2.7% of Chusquea, 75.3% of Tristerix)
Nothofagus dombeyi	250335 (100% of Dromiciops, 4.2% of Nothofagus [2.3% including extrap.])	2404626 (92.2% of Chusquea, 40.6% of Nothofagus [22.3% including extrap.])	n/a	88783 (94.5% of Tristerix, 1.5% of Nothofagus [0.8% including extrap.])
Tristerix corymbosus	47677 (19% of Dromiciops, 50.8% of Tristerix)	70726 (2.7% of Chusquea, 75.3% of Tristerix)	88783 (94.5% of Tristerix, 1.5% of Nothofagus [0.8% including extrap.])	n/a

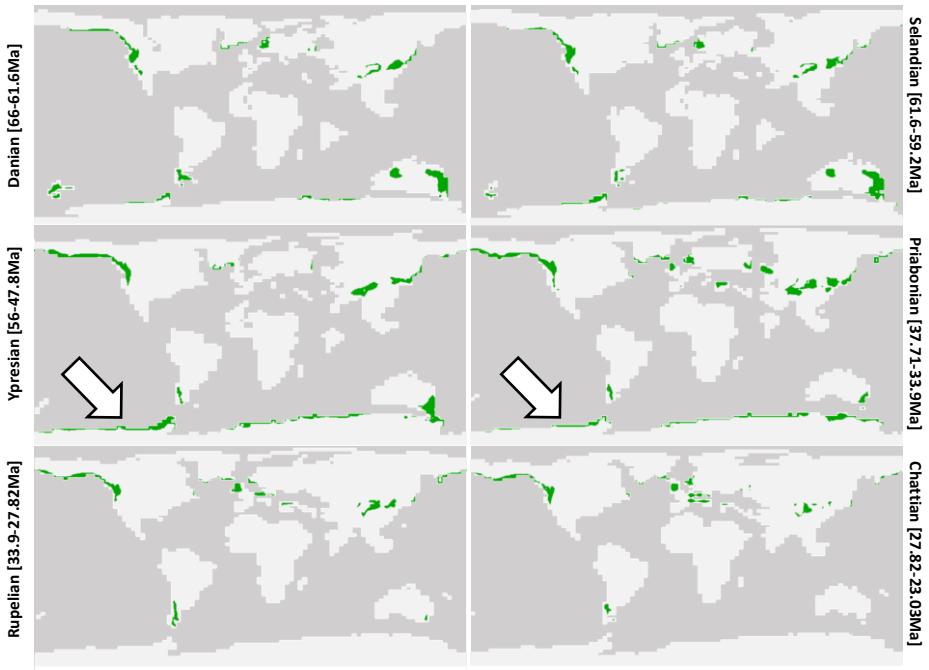
Chattian [27.82-23.03Ma] projections thresholded by 95% LTP	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***
Dromiciops gliroides	n/a	0	0	0
Chusquea culeou	0	n/a	1066 (58.6% of Chusquea, 2.8% of Nothofagus [1% including extrap.])	0
Nothofagus dombeyi	0	1066 (58.6% of Chusquea, 2.8% of Nothofagus [1% including extrap.])	n/a	0
Tristerix corymbosus	0	0	0	n/a

Chattian [27.82-23.03Ma] projections thresholded by maxSSS	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***
Dromiciops gliroides	n/a	777 (100% of Dromiciops, 0.5% of Chusquea)	777 (100% of Dromiciops, 0.4% of Nothofagus [0.2% including extrap.])	0
Chusquea culeou	777 (100% of Dromiciops, 0.5% of Chusquea)	n/a	75708 (47.9% of Chusquea, 41.3% of Nothofagus [15.4% including extrap.])	0
Nothofagus dombeyi	777 (100% of Dromiciops, 0.4% of Nothofagus [0.2% including extrap.])	75708 (47.9% of Chusquea, 41.3% of Nothofagus [15.4% including extrap.])	n/a	0
Tristerix corymbosus	0	0	0	n/a

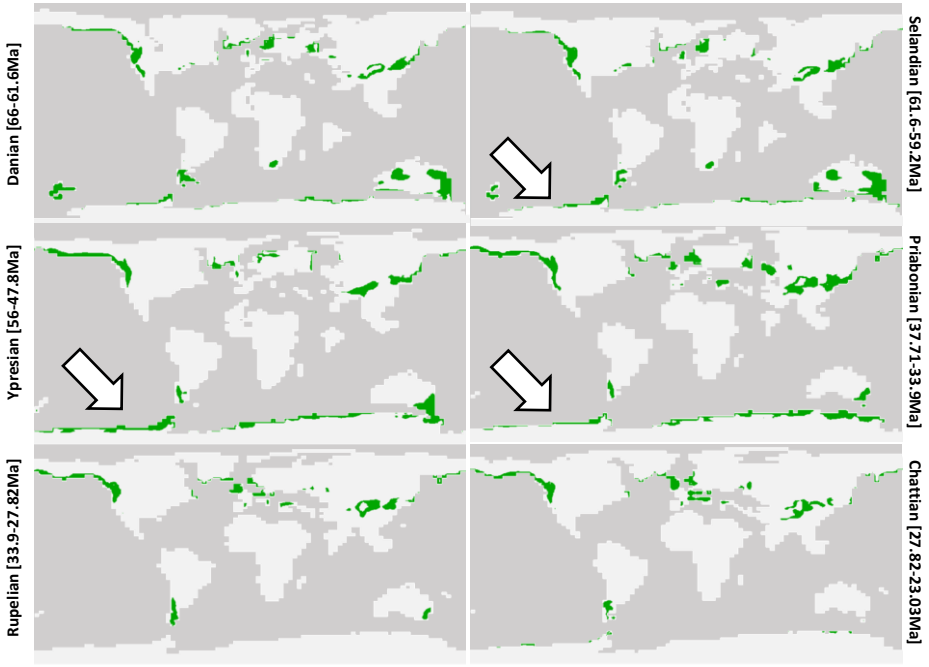
Table C1-C10 – The overlapping area of suitable abiotic conditions (km^2) in Antarctica between* Dromiciops gliroides, Chusquea culeou, Nothofagus dombeyi *and* Tristerix corymbosus. *The areas of overlap between species were same whether or not extrapolative suitable area was included. The percentage of each genus' suitable Antarctic area that is overlap is given in brackets. The Rupelian is not included here as there is no overlap during this time interval.

4.4

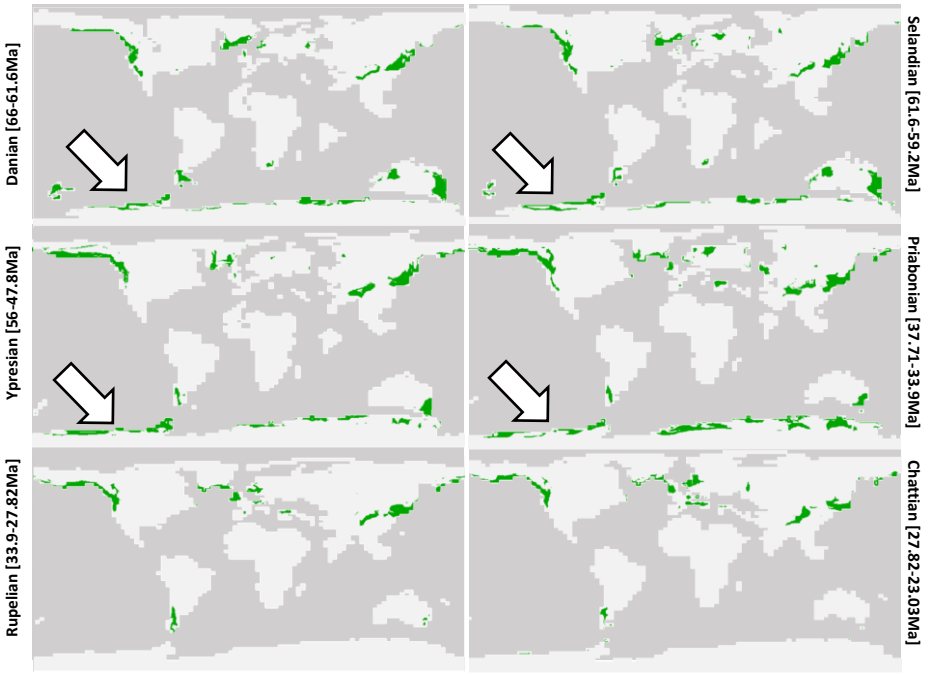
CHUSQUEA CULEOU (95% LTP THRESHOLDED MODELS)



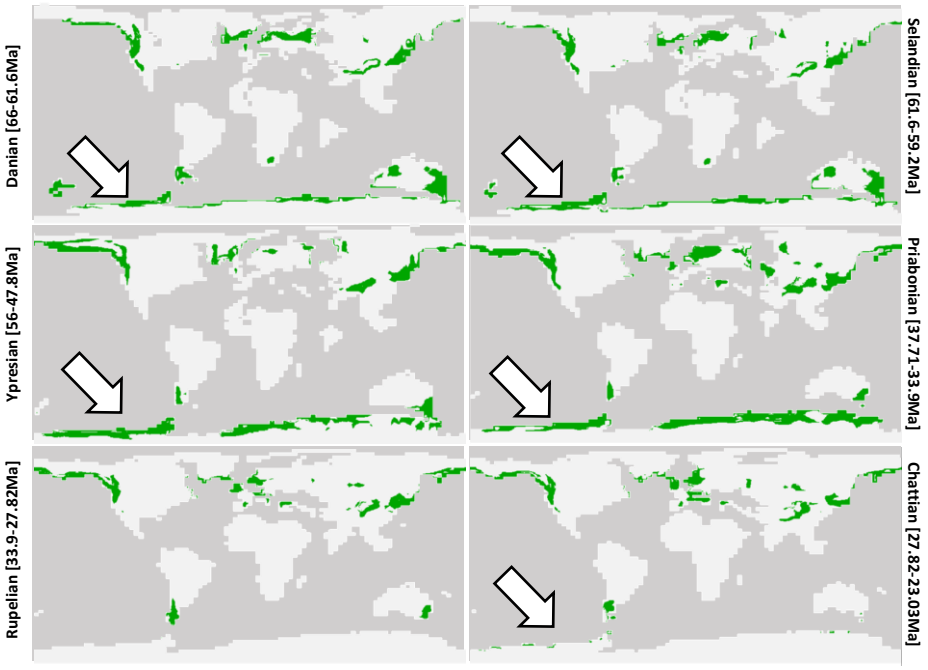
CHUSQUEA CULEOU (maxSSS LTP THRESHOLDED MODELS)



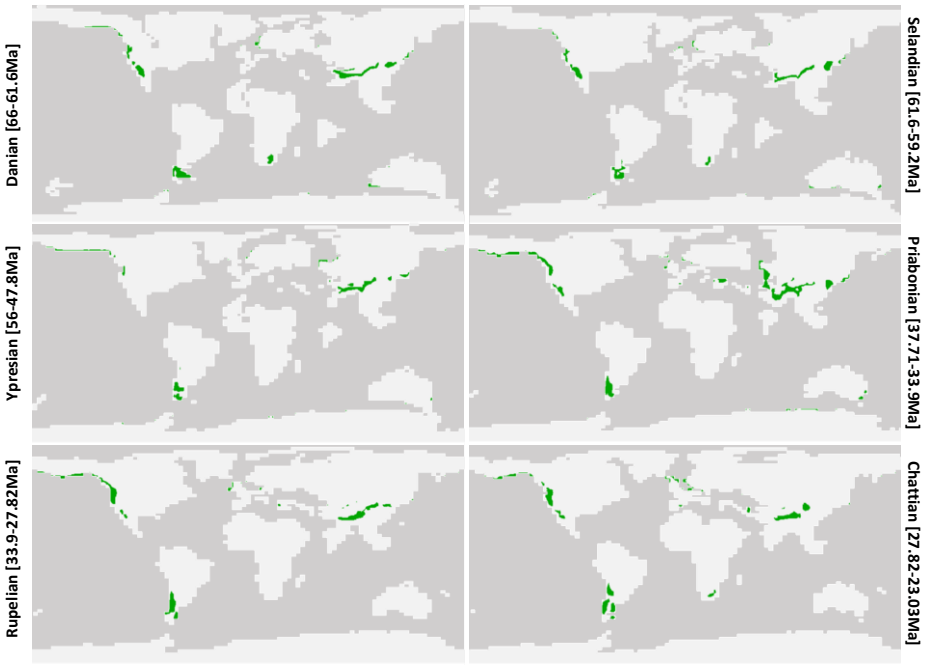
NOTHOFAGUS DOMBEYI (95% LTP THRESHOLDED MODELS)



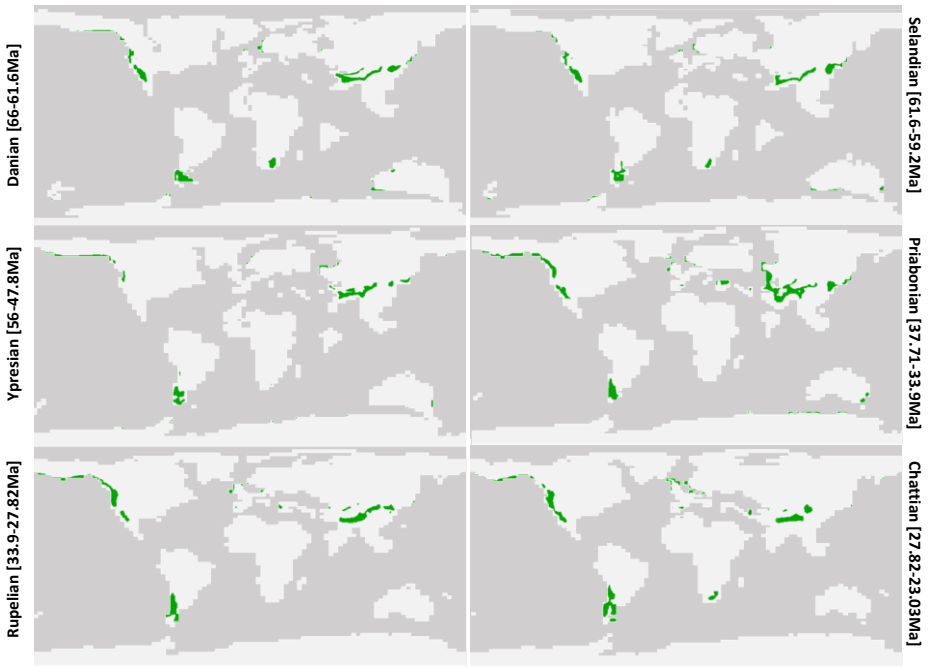
NOTHOFAGUS DOMBEYI (maxSSS LTP THRESHOLDED MODELS)



TRISTERIX CORYMBOSUS (95% LTP THRESHOLDED MODELS)



TRISTERIX CORYMBOSUS (maxSSS LTP THRESHOLDED MODELS)



Figures A1-A6 – Regions of suitable conditions projected onto Palaeogene time intervals for a niche model built using present-day occurrences of Valdivian plant species. Models used the entire South America as a calibration region. Areas of suitable, non-extrapolative climatic conditions are shown in green. An arrow on the projections indicates the position of the hypothesised 'dispersal corridor' of suitable climatic conditions, along Antarctica's Pacific coast. *Dromiciops gliroides*'s niche projections can be found in Supplementary Information 2.10.

4.5

Changes to PBDB records of *Nothofagus.* are as follows:

- *Nothofagidites* presences from the Danian sites of Cerro Bororo and Bajada de Hansen are added (Romero 1973).
- The Berwick Quarry site in Australia is categorised as Chattian (Pole, Hill et al. 1993).
- The Loy Yang M1A and Y sites, along with the Chenque Formation, are categorised as Miocene and are subsequently excluded from study (Korasidis, Wallace et al. 2018, Carmona, Mángano et al. 2020).
- The S-11 and S-13 Antarctic stratigraphic sections intersect multiple time intervals (Danian/Selandian and Selandian/Ypresian respectively) and are subsequently excluded from study (Hall 1977).

4.6

NOTHOFAGUS NICHE PROJECTION TYPE	Danian with maxSSS threshold	Danian with 95% LTP threshold	Ypresian with maxSSS threshold	Ypresian with 95% LTP threshold	Priabonian with maxSSS threshold	Priabonian with 95% LTP threshold	Rupelian with maxSSS threshold	Rupelian with 95% LTP threshold	Chattian with maxSSS threshold	Chattian with 95% LTP threshold
Non-extrapolated suitable abiotic conditions only	5/6, p<0.025 **[6/6, p<0.025]**	5/6, p<0.025 **[6/6, p<0.025]**	1/4, p>0.025 **[3/4, p<0.025]**	0/4, p>0.025 **[1/4, p>0.025]**	2/8, p>0.025 **[3/8, p>0.025]**	1/8, p>0.025 **[2/8, p>0.025]**	2/5, p>0.025 **[3/5, p<0.025]**	0/5, p>0.025 **[2/5, p<0.025]**	2/8, p>0.025 **[5/8, p<0.025]**	0/8, p>0.025 **[4/8, p<0.025]**
Extrapolated and non-extrapolated suitable abiotic conditions	5/6, p<0.025 **[6/6, p<0.025]**	5/6, p<0.025 **[6/6, p<0.025]**	1/4, p>0.025 **[3/4, p<0.025]**	0/4, p>0.025 **[1/4, p>0.025]**	2/8, p>0.025 **[3/8, p>0.025]**	1/8, p>0.025 **[2/8, p>0.025]**	2/5, p>0.025 **[3/5, p>0.025]**	0/5, p>0.025 **[2/5, p>0.025]**	2/8, p>0.025 **[5/8, p<0.025]**	0/8, p>0.025 **[4/8, p<0.025]**

Table D – The proportion of* Nothofagus*'s fossil sites predicted by its niche models projected onto Palaeogene palaeoclimate rasters, and the statistical significance of this capacity as calculated via binomial test with Bonferroni correction [p<0.025] - excluding areas of extrapolated suitable conditions. Models described here were built from a biogeographically informed calibration region. Square brackets show equivalent information if fossils within 150km of suitable abiotic conditions are considered to be 'predicted'. The results shown here are based on fossil locality coordinates rotated to reflect the mid-point of the geological age considered.

4.7

Environmental variable	PC1 (59.26%)	PC2 (27.34%)
Maximum temperature of the warmest month	1	0.7349871
Minimum temperature of the coldest month	0.73498711	1
Precipitation of the wettest month	0.40189148	0.7378228
Precipitation of the driest month	-0.04121057	0.2659145

Table E – The two principal component axes which explain most environmental variation in Chapter 4's ecological analyses and the relative importance of abiotic variables for each (Fick and Hijmans 2017).

4.8

Niche overlap with *Dromiciops* (Schoener's D)	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***
Dromiciops gliroides	n/a	0.724	0.781	0.675
Chusquea culeou	0.724	n/a	0.667	0.471
Nothofagus dombeyi	0.781	0.667	n/a	0.726
Tristerix corymbosus	0.675	0.471	0.726	n/a

Niche similarity (p-value)	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***
Dromiciops gliroides	n/a	0.02	0.01	0.01
Chusquea culeou	0.03	n/a	0.059	0.04
Nothofagus dombeyi	0.02	0.05	n/a	0.01
Tristerix corymbosus	0.03	0.04	0.01	n/a

Niche expansion beyond *Dromiciops*	***Dromiciops gliroides***	***Chusquea culeou***	***Nothofagus dombeyi***	***Tristerix corymbosus***
Dromiciops gliroides	n/a	0.087	0.122	0.462
Chusquea culeou	0.038	n/a	0.077	0.303
Nothofagus dombeyi	0.004	0.012	n/a	0.251
Tristerix corymbosus	0.003	0.044	0.055	n/a

Table F1, F2 and F3 – Metrics used to assess the differences between the ecological niches of* Dromiciops gliroides, Chusquea culeou, Nothofagus dombeyi *and* Tristerix corymbosus. *Our choices and calculation of metrics mirrors that of Silva, Vilela et al. (2016), in turn based on Broennimann, Fitzpatrick et al. (2012) and functions within the ecospat v.4.0 R package (Di Cola, Broennimann et al. 2017). Table E2 consists of p-values derived from comparing the niche overlap between the species in the column x row, and the overlap between the species in the column x a randomised niche (see Methods: Niche comparison metrics). Table E3 consists of the proportion of the niche of the species in the row that extends beyond the niche of the species in the column.

X

Myrmecobius - GBIF.org (17 September 2021) GBIF Occurrence Download
https://doi.org/10.15468/dl.xygz5e
Notoryctes - GBIF.org (17 September 2021) GBIF Occurrence Download
https://doi.org/10.15468/dl.mk2x6r
Phascolarctos - GBIF.org (18 September 2021) GBIF Occurrence Download
https://doi.org/10.15468/dl.yamgjc
Trichosurus - GBIF.org (18 September 2021) GBIF Occurrence Download
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Wallabia - GBIF.org (18 September 2021) GBIF Occurrence Download
https://doi.org/10.15468/dl.3gy6rf
Tlacuatzin - GBIF.org (11 May 2022) GBIF Occurrence Download
https://doi.org/10.15468/dl.ymbxzg
Macropus - GBIF.org (01 July 2022) GBIF Occurrence Download
https://doi.org/10.15468/dl.7p9rng
Notamacropus - GBIF.org (01 July 2022) GBIF Occurrence Download
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Osphranter - GBIF.org (1 July 2022) GBIF Occurrence Download
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Caenolestes - GBIF.org (08 July 2022) GBIF Occurrence Download
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Chlamyphorus - GBIF.org (5 December 2022) GBIF Occurrence Download
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Nothofagus dombeyi - GBIF.org (20 May 2024) GBIF Occurrence Download
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https://doi.org/10.15468/dl.svtv46
Chusquea culeou - GBIF.org (20 May 2024) GBIF Occurrence Download
https://doi.org/10.15468/dl.ym3ggs
Tristerix corymbosus - GBIF.org (20 May 2024) GBIF Occurrence Download
https://doi.org/10.15468/dl.av669c
All others (derived dataset) - GBIF.org (8 October 2024) Filtered export of GBIF occurrence data
https://doi.org/10.15468/dd.dr6crw [*dataset keys are listed alongside occurrences*]

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Pictured – *The Kongouro from New Holland*, by George Stubbs [1772]. This piece, now in the National Maritime Museum in Greenwich, London, is probably the first painting of an Australian marsupial ever produced by a European artist. In a 1770 journal entry, Sir Joseph Banks (ship botanist of 'HMB' *Endeavour*, reporting to Captain Cook) wrote of the kangaroo '*To compare it to any European animal would be impossible as it has not the least resemblance of any one I have seen***'. The very next sentence, he appears to give up on this sentiment, trying to convince the reader that kangaroos are basically just giant hopping rats.**

I hope that my thesis was more biologically illuminating than this, as well as more respectful to both kangaroos and rats.

Jack McMinn, October 2024