**Material and Methods**

Additional methodological details are provided in the *SI Appendix*.

**Fossil data compilation and analytical framework.** We downloaded and cleaned all genus-level South American terrestrial mammal occurrences from *The Paleobiology Database* (<https://paleobiodb.org/>) spanning the late Paleocene to the early Miocene (60-16 Ma) (3,384 occurrences; *SI Appendix, Extended Materials and Methods*). Cleaning consisted of a manual revision of the taxonomic name (e.g., synonymies, missing open nomenclature elements, typos) and time range of each occurrence, the latter often being imprecise (*SI Appendix,***Fig. S4** and *Extended Materials and Methods*). Using paleocoordinate reconstructions (75) and paleobiome maps (76), we assigned each occurrence a tropical or extratropical affinity, and collapsed their associated dental ecomorphotype-derived trophic classes into four categories: carnivorous, herbivorous, omnivorous, insectivorous (**Table 1**).

We analyzed our database using PyRate v.3 (77), and approximated the posterior distribution of the origination and extinction times (Ts and Te, respectively) of each genus and the rate of the preservation process using the RJMCMC algorithm. We then used these Ts and Te to estimate the underlying diversification process (origination and extinction rates) with the Birth-Death model with Constrained Shifts (BDCS) (78) (*SI Appendix, Extended Materials and Methods*).

We ran the RJMCMC model for 50 million generations and sampled every 50,000, with a time-dependent preservation process allowing for rate shift between geological stages (*SI Appendix,* **Fig. S5-6** and *Extended Materials and Methods*). We allowed for a gamma-distributed preservation heterogeneity across lineages. We ran the BDCS model for 10 million generations, sampled every 10,000, and allowed diversification (i.e. origination and extinction) rates to vary between each geological sub-Epochs (*SI Appendix,* **Fig. S1**). Diversification analyses were replicated 20 times after randomly drawing fossil ages between their upper and lower age boundaries, and posterior estimates across all replicates were combined. To test the robustness of our macroevolutionary inference, we conducted sensitivity analyses by either removing singletons or subsampling our fossil database to unique locality-lineage combinations *(SI Appendix,* *Extended Materials and Methods*). We assessed the convergence of each parameter with the pymc 5.9.2 python library (79). We considered parameters achieved convergence if their Effective Sample Size (ESS) was above 200.

Subsequent data manipulation and visualization was performed in R v4.4.0 (80), relying on the Tidyverse suite of R packages (81), the palaeoverse (82), deeptime (83), and rphylopic (84) R packages.

**Age-dependent Extinction (ADE) model.** We assessed the effect of taxon age on its extinction probability by fitting the ADE model to our genus-level occurrence data (56). We ran the model for 100 million generations and sampled every 50,000, with preservation rates varying between geological stages and across lineages according to a *Gamma* model. We focused on the shape (𝜙) of the Weibull distribution, knowing that 𝜙 < 1 indicates a decreasing extinction probability with increasing taxon age and 𝜙 > 1 indicates an increasing extinction probability with increasing taxon age (no effect if 𝜙 = 1). We performed 20 independent ADE analyses of randomized datasets before and after the increase in turnover to assess the age selectivity of this taxonomic renewal (*SI Appendix,* **Fig. S8-11** and *Extended Materials and Methods*). We monitored parameter convergence with the pymc 5.9.2 python library, and parameters were considered convergent if their ESS was above 200.

**Selection of environmental variables.** To investigate possible environmental correlates for the changes in SAM diversification dynamics over the Eocene-Oligocene interval, we selected two global (i.e., atmospheric temperature and sea level) and four continental-scale (i.e., Andean uplift, Neotropical plant diversity, forest density and habitat openness) variables (*SI Appendix,* **Table S2**). Temperature is known for influencing macroevolutionary processes across several groups, including mammals (63, 85), and sea level has a direct effect on the connectivity of habitats. Even in its early phase, the Andean uplift was evidenced as a major diversification driver for many South American groups (68). Diversity of SAM, in particular herbivorous taxa, can be controlled by plant diversity. Finally, relative Leaf Area Index (proxy for forest density, 71) and patterns of relative abundance of open habitats (34, 41, 86) are both indicators of the relative abundance of grasslands, which has long been regarded as shaping herbivore diversity (35). As highlighted by Weppe et al. (22), it is important to consider regional-scale variables because environmental changes across the Eocene-Oligocene were shown to be regionally heterogeneous (65, 87).

**Multivariate Birth-Death (MBD) model.** We carried out environment-dependent diversification analyses involving the aforementioned variables by running the MBD model included in PyRate (88). This model carries out two independent correlations involving a set of environmental covariates and diversification rates (*λ* and *μ)* newly-estimated from empirical *Ts* and *Te*. Each variable is assigned to two correlation coefficients, one for the correlation with *λ* (Gi,λ, where *i* is the index of the variable in the set of covariates) and the other for the correlation with *μ* (Gi,μ). An MCMC algorithm jointly estimates baseline origination and extinction rates and all the Gλ and Gµ, while controlling for over-parameterization. Each Gλ and Gµ is assigned a shrinkage weight (*w*(Gλ) or *w*(Gµ)), ranging between 0 and 1, testing the significance of the correlation. A correlation of coefficient Gλ,i is considered significant if *w*(Gλ,i) > 0.5 and if a sufficiently high proportion (i.e., >90%) of its posterior density does not overlap with 0. Each set of MBD analyses was run across 10 million iterations, sampling every 10,000. We carried out exponential correlations. Parameter convergence (i.e., ESS > 200) was assessed using the *pymc* 5.9.2Python library (79).

**Data, Materials, and Software Availability**

All the occurrence and outputs data used in this study are available on a Figshare repository (XXX), and all the data analysis and visualization codes have been deposited in GitHub (<https://github.com/Buffan3369/Neotropical_mammals.git> and <https://github.com/Alexis-Marion/CorsaiR.git>).

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