Supplementary Material - Detailed Methods

Data Analysis

All data analysis was done with the R Statistical Language [1] using the packages sp [2,3], rgdal [4] maptools [5], PBSmapping [6], and geosphere [7]. The full R code, including the full set of polygons and areal values for each polygon and during each time period, is available on Dryad [8].

The SAR was first described as a power function [9], although it is often expressed in its double logarithmic form [10] of

$$logS = logk + zlogA$$

where S is the number of species, A is the area, z is the slope of the relationship, and k is a constant. For the primary analysis, the interprovincial land mammal SAR formula from Wright [11] of

$$logS = 2.01 + 0.478 * logA$$

was used to calculate the predicted number of species for each individual land mass.

In addition to the SAR value given by Wright [11], I gathered several other interprovincial SAR equations, both additional estimates for terrestrial mammals [12,13] as well as terrestrial birds [11]. Volant and marine groups were excluded from would not have been affected to as great a degree due to their ability to more readily cross large bodies of water, and so were not included. In the case of the data in both Flessa [12] and Smith and colleagues [13], I had to use their available data to calculate the SAR using a linear model in R. For the Smith et al. [13] dataset, there were a larger number of recognized species of mammals (3094 vs 3850), but the SAR calculated from this dataset actually had a lower slope ($z = 0.384\pm0.063$; adjusted $R^2 = 0.859$; $P = 0.00167$; $c = 2.29$). Additionally, Flessa [12]

provides values for generic, though not species level, occurrence data for the continents that can be used to construct an SAR. Here again, the z value is lower than that of Wright [11] ($z = 0.325 \pm 0.049$; adjusted $R^2 = 0.825$; $P \ll 0.01$, $c = 1.89$), although the generic SAR is difficult to directly compare with the species level SAR. Either of these lower z values would further amplify the increase through time, however I used the Wright [11] formula, as other terrestrial vertebrate groups[14] (e.g. land birds, amphibians) have been estimated to have higher z values. Because the exact equation used will change the estimate of standing diversity, biodiversity values had to be standardised in order to be compared to one another. To standardize the estimates through time, biodiversity was scaled between 0 and 1, with 0 being no taxa and 1 being the maximum observed number of species. While there is some minor variation in the scaled biodiversity values between the different SAR calculations, the overall pattern of biodiversity is very similar (fig S2).

It is important to note that the curve to be used needs to represent an interprovincial curve, rather than an intraprovincial one [15–17]. Some previously published estimates for the SAR of different groups have used methods which divide larger, contiguous land masses into smaller ones (i.e. Gaston and Hudson [18] in Collins *et al.* [14]) or use only a portion of a land mass [17], both of which appear to provide higher z values than those based on geographically defined provinces.

Each land mass was assumed to have a unique biota, with no shared taxa between regions. Although it is highly unlikely that every single species during the Mesozoic was entirely restricted to a single landmass, based on the dataset of modern mammals from Smith et al. [13], the proportion of endemic taxa on each isolated landmass is somewhere above 90%. Though never previously quantified to my knowledge, discussions of species ranges [19] have noted that very few species have ranges as large as the continent they inhabit, and qualitative discussions of diversity between continents [16] have noted large amounts of turnover between biotic provinces. While changing the proportion of endemic taxa on each land mass from 100% to 90% would result in a lower estimate of biodiversity, the relative pattern of diversity would be mathematically identical. In modern ecosystems, particularly on islands,

patterns of endemism are correlated with degree of isolation and size of landmass [20]. However, understanding the relative importance of temperature, landmass size, and historical changes in geography on the variation in endemism at continental scales is still an unresolved question.

Palaeocoastline Map Sources

For this study, I used the maps of Smith et al. [21], which provide a large number of consistent global maps that could be readily digitized. Other sources, including more recent references, do not provide a consistent set of maps covering the entire Mesozoic or Earth, meaning that multiple sources would be needed to compile a set of palaeocoastline maps. Using multiple sources with different methods as well as different geographic projections then introduces increased sources of error for each map relative to one another. As well, this study is primarily concerned with large scale, overall trends in terrestrial vertebrate biodiversity through the Mesozoic, rather than individual, precise estimates for any given time period. The maps of Smith et al. [21] accurately capture the large scale patterns of continental break-up and inland flooding that took place, and though variation in precise ages for specific events (i.e. the subdivision of North America into multiple, independent land masses) will have an effect on biodiversity for a given set of areas, the overall effect on the Mesozoic-wide trend is negligible.

Supplementary Figure Captions

**Figure S1.** Number of individual landmasses through time.

Figure S2. Comparison of biodiversity curves using different SAR equations. **Mammals**, SAR equation for land mammals from Wright [11]; **Smith**, SAR equation derived from dataset of [13]; **birds**, SAR equation for land birds from Wright [11]; **Flessa**, SAR equation derived from values for generic mammal diversity in [12].

Supplementary References

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Figure S1 – Number of individual land masses through time
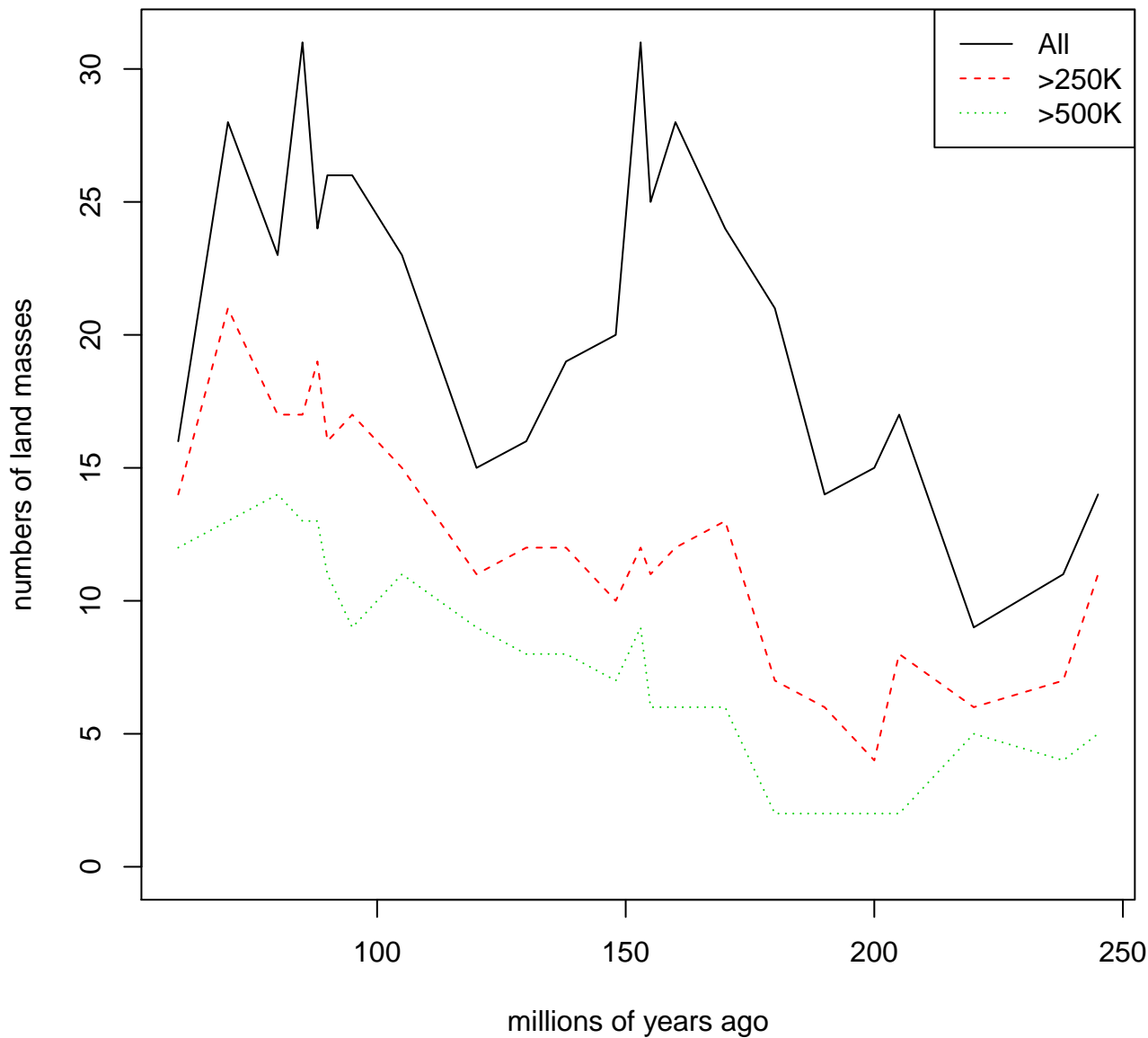
Figure S2 – Comparison of SAR equations