

Cosmopolitan and provincialism dynamics of North American terrestrial mammals across the Cenozoic

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Abstract

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1 Introduction

Evolutionary paleoecology is the study of how ecological traits expressed at any level affect the macroevolutionary process, or long term patterns in speciation and extinction (Kitchell, 1985). Community structure plays a fundamental roll in determining which biotic interactions are possible at a given time. The importance of biotic interactions in understanding evolutionary dynamics

2 Materials and Methods

Mammalian occurrence information was obtained from the Paleobiology Database (PBDB; <http://www.paleodb.org>). Occurrence information was restricted to terrestrial mammals from the North American fossil record of the Cenozoic. For each occurrence, the locality information was also recorded, most importantly formation name and estimated age. Hierarchical taxonomic information was recorded for each taxon. All partially, ambiguously, or incompletely identified genera or species (e.g. aff., cf., ?) were excluded from analysis.

For each taxon, dietary and life habit information recorded in the PBDB was gathered. Dietary information was then simplified into three categories: herbivore, omnivore, and carnivore. Herbivorous taxa were the amalgam of the PBDB classifications herbivore, grazer, browser, folivore, and granivore. Omnivorous taxa were the amalgam of frugivores and omnivores.

Finally, carnivores were the amalgam of all carnivores and insectivores. These three categories were chosen because they represent coarse groups which are identifiable from most mammalian teeth which are the primarily mammalian fossil material. Additionally, these groupings have been used in prior analysis of the effect of ecology on site similarity (Jernvall and Fortelius, 2004).

Temperature information was estimated using the δO^{18} isotope information from the benthic foram record for the entire Cenozoic (Zachos et al., 2008). An increase in δO^{18} levels are associated with a decrease in atmospheric temperature (Zachos et al., 2008, 2001). Benthic foram δO^{18} information has been used previously as climatic information in studies of mammalian macroevolutionary patterns (Alroy et al., 2000; Figueirido et al., 2012; Rose et al., 2011).

Taxonomic presence-absence was recorded for each formation. Abundance information was not included in this analysis, though it is possible (Sidor et al., 2013), because the highly variable preservation conditions not just between formations but across the Cenozoic may not accurately record abundance information (Damuth, 1982).

Bipartite biogeographic networks were constructed, following Sidor et al. (2013) and Vilhena et al. (2013), with species as the taxonomic occurrence and formation as the locality of interest. As explained in Sidor et al. (2013), biogeographic networks have many advantages over ordination based methods that are frequently used in numerical ecology (Legendre and Legendre, 2012). Principally, both taxonomic and locality information are preserved in analysis which allows for a more complete understanding of community structure. For each temporal bin biogeographic networks were constructed for all taxonomic information, individually for each dietary category and each locomotor category.

Four measures of biogeographic network structure were used to asses community change: code length as measured via the map equation (Rosvall et al., 2010; Rosvall and Bergstrom, 2007, 2008), biogeographic connectedness, average number of locality occurrences per taxon, and average number of endemics per site. Biogeographic connectedness is defined

$$BC = \frac{O - N}{LN - N} \quad (1)$$

where O is the number of edges or number of occurrences in the biogeographic network, N is the number of taxa, and L is the number of localities (Sidor et al., 2013). All four of these measures have previously been used to assess cosmopolitan and endemism dynamics (Sidor et al., 2013). The four measures of biogeographic network were then calculated for each temporal bin for the total network, each of the dietary networks, and each of the locomotor category networks.

Network analysis, including calculation of network code length, was done using the **igraph** package (Csardi and Nepusz, 2006) for the R language (R Core Team, 2013).

3 Results

4 Discussion

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