

Phylogenetic community assembly over time in Eurasian Plio-Pleistocene mammals

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Keywords: phylogenetic turnover metric, large mammal, paleocommunity evolution, EA PCOM

ABSTRACT

Phylogenetic community structure and assembly is a burgeoning field in the discipline of community ecology. An array of statistical techniques have been developed in order to study whether or not local assemblages of species are a phylogenetically random, overdispersed, or clustered subset of the regional species pool to which they belong. Phylogenetic clustering or overdispersion depends on aspects of species evolutionary ecology, such as habitat preference, limits of similarity among closely related species, and how traits are inherited in ancestor-descendant relationships. Here I applied the first analysis of phylogenetic community structure and assembly to Plio-Pleistocene large mammal communities of western Eurasia, with the additional goal of verifying if the existing statistics are suitable to be used with fossil data. The results demonstrate that (1) the use of phylogeny in the study of community evolution is feasible with a number of diverse metrics, (2) phylogenetic distance between fossil communities provides an important addition to classic turnover metrics, and (3) the phylogenetic structure of Eurasian Ice-Age mammal communities changed significantly around 1 Ma, when these communities were filled with closely related species from both carnivore and herbivore clades.