Taxonomic and numerical sufficiency in a Lower and Middle Miocene molluscan metacommunity of the Central Paratethys

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Among the most important questions in quantitative palaeoecology is how taxonomic and numerical resolution affect the analysis of community and metacommunity patterns. A species-abundance data set (10 localities, 213 bulk samples, 478 species, > 49,000 shells) from Burdigalian, Langhian and Serravallian benthic marine molluscan assemblages of the Central Paratethys was studied for this purpose.

Assemblages are from two nearshore habitats (estuarine and marine intertidal) and three subtidal habitats (estuarine, fully marine sandy, and fully marine pelitic), which represent four biozones and four 3rd order depositional sequences over more than three million years, and are developed along the same depth-related environmental gradient.

Double-standardized data subsampled to 19 samples per habitat, each with a minimum of 50 specimens, were used to calculate R^2-values from PERMANOVA as a measure of differences between habitats at three taxonomic levels (species, genera and families) and at five levels of data transformation (raw abundances, percentages, square-root transformed percentages, fourth-root transformed percentages, presence-absence data).

Species discriminate better between habitats than genera and families, but the differences between taxonomic levels are much stronger in the subtidal, where genera and families have more species than than in the intertidal. When all habitats are compared percentages and square-root transformed percentages discriminate equally well and perform better than higher levels of data transformation. Among nearshore and among subtidal habitats, however, the ability to discriminate between habitats increases with the level of data transformation (i.e. it is best for fourth-root transformed percentages and presence-absence data). The impact of decreasing taxonomic resolution is of minor importance in nearshore habitats, which are characterized by similar assemblages showing strong dominance of few widely distributed species, and many families represented by only one species (77.9%). Consequently, the differentiation between nearshore habitats is much weaker compared to subtidal assemblages. The latter are characterized by more distinct, relatively even assemblages with comparatively few families represented by only one species (64.2%) and many rare taxa, whose importance is emphasized by higher levels of data transformation.