



## **Taxonomic and numerical sufficiency in depth- and salinity-controlled marine paleocommunities**

Martin Zuschin (1), Rafal Nawrot (1), Mathias Harzhauser (2), Oleg Mandic (2), and Adam Tomašových (3)

(1) University of Vienna, Institut für Paläontologie, Vienna, Austria (martin.zuschin@univie.ac.at), (2) Department of Geology and Palaeontology, Natural History Museum Vienna, Vienna, Austria, (3) Earth Science Institute, Slovak Academy of Sciences, Bratislava, Slovak Republic

Numerical and taxonomic resolution of compositional data sets affects investigators' abilities to detect and measure relationships between communities and environmental factors. We test whether varying numerical (untransformed, square-root- and fourth-root-transformed relative abundance, and presence-absence data) and taxonomic (species, genera, families) resolutions reveals different insights into early to middle Miocene molluscan communities along bathymetric and salinity gradients. The marine subtidal has a more even species-abundance distribution, a higher number of rare species, and higher species:family and species:genus ratios than the three habitats with higher fluctuations in salinity and other physical parameters (marine and estuarine intertidal, estuarine subtidal). Taxonomic aggregation and numerical transformation of data result in very different ordinations, although all habitats differ significantly from one another at all taxonomic and numerical levels. Rank correlations between species-level and higher-taxon, among-sample dissimilarities are very high for proportional abundance and decrease strongly with increasing numerical transformation, most notably in the two intertidal habitats. The proportion of variation explained by depth is highest for family-level data, decreases gradually with numerical transformation, and is higher in marine than in estuarine habitats. The proportion of variation explained by salinity is highest for species-level data, increases gradually with numerical transformation, and is higher in subtidal than in intertidal habitats. Therefore, there is no single best numerical and taxonomic resolution for the discrimination of communities along environmental gradients: the "best" resolution depends on the environmental factor considered and the nature of community response to it. Different numerical and taxonomic transformations capture unique aspects of metacommunity assembly along environmental gradients that are not detectable at a single level of resolution. We suggest that simultaneous analyses of community gradients at multiple taxonomic and numerical resolutions provide novel insights into processes responsible for spatial and temporal community stability.