



## **Palaeocommunity dynamics across the Lower to Middle Miocene 3rd order sequence boundary of the Central Paratethys**

Martin Zuschin (1), Mathias Harzhauser (2), and Oleg Mandic (2)

(1) Department of Palaeontology, University of Vienna, Althanstrasse 14, A-1090 Vienna, Austria  
(martin.zuschin@univie.ac.at), (2) Natural History Museum Vienna, Burggring 7, A-1010 Vienna, Austria

The 3rd order sequence boundary from the Lower to the Middle Miocene of the Paratethys is characterized by a well-known major change of the molluscan fauna. This change was mainly studied based on regional species lists, which suggest a transition from low-diversity Karpatian (Upper Burdigalian) to highly diverse Badenian (Langhian and Lower Serravallian) assemblages. Here, we present quantitative data from 4 Karpatian and 6 Badenian localities to capture the anatomy of this faunal transition by comparing species-abundance patterns of local assemblages. 223 bulk samples, comprising more than 65,000 shells, were taken from shell beds; all molluscs > 1mm were studied quantitatively and sorted into 496 species. Independent sources (e.g., palaeogeographic position of localities and environmental data from foraminifera) suggest a water depth ranging from the intertidal to several tens of meters for the studied assemblages. Ordination methods indicate that benthic assemblages in the study area developed along the same depth-related environmental gradient across the 3rd order sequence boundary. Due to strong facies shifts at the boundary, the Karpatian faunas are mostly preserved in nearshore settings, but the Badenian faunas range from intertidal to shelf depth. Statistical analyses indicate that differences between the total of Karpatian and the total of Badenian assemblages are smaller than any differences among individual localities. The striking differences among the studied localities are most likely due to heterogeneous environments present on the Lower and Middle Miocene shelf of the Central Paratethys. Clearly, the immigration of several thermophilic molluscan families and superfamilies (e.g., Strombidae, Tonnaidea, Isognomonidae, and Carditidae) reflects climatic changes at the onset of the Langhian transgression. Our quantitative approach, however, favours the strong facies shift at the Lower / Middle Miocene boundary as the main reason for the pretended faunal turnover observed from regional species lists, because species abundance patterns from local assemblages indicate largely persisting palaeocommunities.