

The evolutionary origins of abyssal biodiversity — new ideas from biogeography and habitat mapping

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The abyss is a homogeneous and barrier-free sediment habitat. At least that is what the text books say. Yet, at the same time we know that abyssal communities are locally highly diverse. It appears contradictory that a seafloor habitat free of barriers and poor in heterogeneity can host a rich biodiversity. Likewise the evolutionary origins of this diversity remain in the dark, although it has been proposed that the organisms we encounter at abyssal depth originated from the much more heterogeneous bathyal zone.

During the interdisciplinary Vema-TRANSIT project, biological, bathymetrical, and geological data were collected in the North Atlantic. Following the Vema Fracture Zone and crossing the Mid-Atlantic Ridge, abyssal habitats and communities were studied.

Using high-resolution bathymetric scans in conjunction with rock sampling and video surveys, we encountered a surprisingly high habitat heterogeneity. From the spreading axis to a crustal age of over 90 Ma, the seafloor represented a patchwork of sediment (dominating) and bare rock formations. Furthermore, taxonomic, phylogenetic and population genetic data for isopod crustaceans, one of the most abundant macrofaunal elements in abyssal soft sediments, suggests that bathymetric features, such as the Mid-Atlantic Ridge, contribute to genetic differentiation in some benthic species. Interspecific differences seemed to be connected in dispersal capacity. We present these new insights and discuss their implications for our understanding of the origins of abyssal biodiversity.

We conclude: the abyssal seafloor is much more heterogeneous than commonly assumed and seafloor topography is a limiting factor for dispersal thus contributing to diversity.