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TITLE: Biodiversity of the Deep-Sea Continental Margin Bordering the Gulf of Maine (NW Atlantic): Relationships among Sub-Regions and to Shelf Systems

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## ABSTRACT:

In contrast to the well-studied continental shelf region of the Gulf of Maine, fundamental questions regarding the diversity, distribution, and abundance of species living in deep-sea habitats along the adjacent continental margin remain unanswered. Lack of such knowledge precludes a greater understanding of the Gulf of Maine ecosystem and limits development of alternatives for conservation and management. We use data from the published literature, unpublished studies, museum records and online sources, to: (1) assess the current state of knowledge of species diversity in the deep-sea habitats adjacent to the Gulf of Maine (39-43°N, 63-71°W, 150-3000 m depth); (2) compare patterns of taxonomic diversity and distribution of megafaunal and macrofaunal species among six distinct sub-regions and to the continental shelf; and (3) estimate the amount of unknown diversity in the region. Known diversity for the deep-sea region is 1,671 species; most are narrowly distributed and known to occur within only one sub-region. The number of species varies by sub-region and is directly related to sampling effort occurring within each. Fishes, corals, decapod crustaceans, molluscs, and echinoderms are relatively well known, while most other taxonomic groups are poorly known. Taxonomic diversity decreases with increasing distance from the continental shelf and with changes in benthic topography. Low similarity in faunal composition suggests the deep-sea region harbours faunal communities distinct from those of the continental shelf. Non-parametric estimators of species richness suggest a minimum of 50% of the deep-sea species inventory remains to be discovered. The current state of knowledge of biodiversity in this deep-sea region is rudimentary. Our ability to answer questions is hampered by a lack of sufficient data for many taxonomic groups, which is constrained by sampling biases, life-history characteristics of target species, and the lack of trained taxonomists.

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