

# Divergence and zoogeography of mole crabs, *Emerita* spp. (Decapoda: Hippidae), in the Americas

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## Abstract

Six of the nine described species of the mole crab genus *Emerita* are distributed in the Americas, two [*E. analoga* (Stimpson, 1857) and *E. rathbunae* Schmitt, 1935] on the west coast, and four [*E. benedicti* Schmitt, 1935, *E. brasiliensis* Schmitt, 1935, *E. portoricensis* Schmitt, 1935 and *E. talpoida* (Say, 1817)] on the east. The presence of an extended planktonic larval stage in all *Emerita* species suggests high dispersal potential and the possibility of extensive gene flow among conspecific populations. Two taxa were sampled to study the extent of gene flow between widely separated conspecific populations: *E. analoga* (California and Chile) and *E. talpoida* (Massachusetts, South Carolina, and the west coast of Florida), while all other taxa were characterized from a single location. Portions of two mitochondrial genes, cytochrome oxidase I (COI) and 16S ribosomal RNA (16S rRNA) were sequenced. For data analysis, approximately 500 bp (COI) and 400 bp (16S rRNA) were examined. Estimated genetic divergence of 5.41% in COI between *E. talpoida* populations sampled from the Gulf of Mexico and the Atlantic coast, and 3.47% between *E. analoga* sampled in Chile and California, indicates that in both cases there has been no recent gene flow between disjunct populations. Additional molecular and morphological studies are necessary to decide whether disjunct populations should be accorded specific status. We predict that many marine invertebrates with antitropical distributions similar to *E. analoga* may consist of sibling species. In contrast to relationships inferred earlier from distribution patterns, parsimony analyses of both COI and 16S rRNA data yield similar phylogenetic trees in which *E. analoga* is separated from a clade composed of other species in the Americas; a bootstrap value (67%) in the COI inferred tree marginally supports the separation, but the same tree topology with a higher bootstrap value (84%) is obtained with 16S rRNA sequence data. Genetic divergence among the taxa indicates that the *Emerita* species constitute an old group and that distribution of species has been modified by past climatic and geological events.