

Investigation of gene flow and migration across the global range of *Riftia pachyptila* using six molecular markers

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Riftia pachyptila represents a single species within its own family (Riftiidae) that ranges from the Guaymas Basin (27°N) to 32°S along the Eastern Pacific Rise, as well as the Galapagos Rift. This span of 6475 km is one of the widest ranges of hydrothermal vent endemic species. We used six molecular markers to examine the population structure, migration, and gene flow between *R. pachyptila* vent populations. This is the first study to incorporate samples from the entire range of *R. pachyptila* and a suite of five nuclear loci and one mitochondrial locus. We employ sequence data from four anonymous nuclear loci, two nuclear introns, and one mitochondrial locus. Preliminary results from this study suggest a stepping stone model of dispersal, with geographically adjacent populations being more genetically similar than remote populations. There is also evidence of an equatorial break of gene flow and significant differences between the Galapagos Rift population and the Eastern Pacific Rise populations. This research lays the groundwork for understanding the mechanisms of larval dispersal in general as well as life history characteristics specific to this species. Characterizing migration and gene flow in *R. pachyptila* populations is the first step in understanding its role in colonization and biological succession of hydrothermal vents. Coupling this work with biogeochemical data would lend valuable insight into parameters for larval settlement and development.

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