

Brachyuran Tree of Life Illuminates the Origin and Biogeography of Hydrothermal Vent Crabs

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Organisms associated with hydrothermal vents are of great interest as their adaptation to this extreme environment is considered to be evolutionary novelty. The origin and biogeography of hydrothermal vent fauna are, however, poorly known except for several well studied taxa. We construct the most comprehensive tree of life for the brachyuran crabs using a dataset of eight molecular markers (two mitochondrial rRNA genes and six nuclear protein-coding genes) from more than 320 species in 93 families (representing ~90% of the 104 brachyuran families), including 13 of the 14 species from the hydrothermal vent crab family Bythograeidae, to determine the evolutionary origin and biogeography of Bythograeidae. The divergence times for different clades were estimated and superimposed with biogeographic reconstruction in order to reveal the evolutionary history of vent crabs. The inferred phylogeny reveals the polyphyletic nature of Bythograeidae, with one lineage closely related to Hypothalassidae, and members from Mathildellidae and Oziidae, and the other to Progeryonidae. Divergence time estimation suggests Paleogene origins for both lineages. Biogeographic analyses reveal independent invasions to the East Pacific deep water hydrothermal vent habitat, with one lineage subsequently colonized the other oceans whilst the remaining one diversified but restricted to East Pacific. The high morphological similarities of the two vent crab lineages are likely the result of convergence. Future analysis will focus on functional genes expressed in the two lineages to elucidate convergent evolution with respect to genetic and physiological adaptation.

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