

GENETIC POPULATION STRUCTURE IN THE SOLITARY CORAL *BALANOPHYLLIA ELEGANS*: HISTORY STOMPS ON STEPPING-STONES

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New species arise when genetic variation within a species is parceled into divisions whose constituents cannot interbreed. Understanding the mechanisms shaping the geographical distribution of intraspecific genetic variants may yield clues as to what forces have rendered such incipient species from their progenitors. Paleontological data can help inform this search for mechanism by revealing when and where a species first arose and how its geographical distribution has changed through time. In my talk, I will provide an example of this interplay between paleontological data and the interpretation of genetic population structure from my work on *Balanophyllia elegans*, a solitary coral often sought by paleontologists for dating NE Pacific Pleistocene marine terraces using $^{230}\text{Th}/^{234}\text{U}$ ratios. The larvae of this coral crawl only about a meter from their mothers before settling. Such limited dispersal may provide an important mechanism for generating genetic differentiation in the absence of physical barriers to movement among populations. At a spatial scale of 1-50 km, levels of gene flow (inferred from the distribution of protein electromorphs) correlated strongly with the distance separating populations, consistent with expectations for populations at equilibrium in which gene flow occurs only between adjacent populations. Over a broader (50-3000 km) geographical scale, however, the relationship between gene flow and distance in this species was far weaker. The fossil record suggests Pleistocene climatic fluctuations have repeatedly shifted the geographic ranges of benthic marine invertebrates in this region. In addition, northern populations of *B. elegans* showed relatively low genetic diversity. Together, these findings suggest that although geographic distance facilitates the accumulation of genetic differences within *B. elegans* at smaller spatial scales, at larger spatial scales, genetic drift and gene flow will have insufficient time to equilibrate following latitudinal shifts in geographic range caused by Pleistocene climatic fluctuations.