

Hellberg, M. E. 1995. Stepping-stone gene flow in the solitary coral *Balanophyllia elegans*: equilibrium and nonequilibrium at different spatial scales. Mar. Biol. 123: 573-581.

Limited dispersal should result in genetic differences between populations proportional to geographic distances of separation. This association between gene flow and distance can be disrupted by (1) continuing genetic exchange among distant populations, (2) historical changes in gene flow, and (3) physical barriers or corridors to dispersal. The movements of larvae are thought to determine dispersal capability in benthic marine invertebrates. The solitary scleractinian *Balanophyllia elegans* Verrill possesses crawling larvae capable of only limited dispersal. Paradoxically, however, inferred levels of gene flow between pairs of localities spread over much of the 4000 km range of *B. elegans* exhibited a weaker relationship with geographical separation than that expected for a linear array of populations in which all genetic exchange takes place between adjacent populations. In this paper, I examined the pattern of gene flow (inferred from the frequencies of eight polymorphic allozyme loci) in *B. elegans* at a smaller (1 to 50 km) spatial scale to determine (1) whether gene flow at this spatial scale conformed to the expectations of the stepping-stone model, and (2) whether continuing long-distance gene flow or historical changes in gene flow were responsible for the weak relationship between gene flow and distance observed previously at the rangewide spatial scale. Between May and August 1992, I collected 75 adults from each of 18 localities along the coast of Sonoma County, California, USA. These populations of *B. elegans* were significantly subdivided both among localities separated by 1 to 50 km ($F_{LT} = 0.053$, $SE = 0.0075$) and among patches separated by 4 to 8 m ($F_{PL} = 0.026$, $SE = 0.0023$). The observed slope and correlation ($r^2 = 0.54$) between inferred levels of gene flow and the geographic distance at the 1 to 50 km spatial scale conformed to equilibrium expectations (obtained by simulation) for a linear stepping-stone model, although those from the rangewide spatial scale did not. This implies that the mechanisms conferring patterns of inferred genetic differentiation between localities in *B. elegans* differ fundamentally with spatial scale. At a scale of 1 to 50 km, continuing gene flow and drift have equilibrated and the process of isolation-by-distance may facilitate local adaptive change. At a broader spatial scale, historical changes in gene flow, perhaps affected by late Pleistocene climatic fluctuations, disrupt the equilibration of gene flow and genetic drift, so that genetic differentiation may not increase continuously with separation between populations.