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When the dispersal capability of a species is considerably less than its geographic range, genetic differences between populations should increase with the distance separating those populations. This pattern should be most evident in linearly distributed species. The sessile solitary cup coral *Balanophyllia elegans* lives along nearly the entire Pacific coast of North America, yet its crawling larvae usually settle within 4O cm of their birthplace. In this paper, I document geographic patterns of allozyme differentiation within and among populations of *B. elegans* and estimate the proportion of observed geographic pattern attributable to gene flow between adjacent populations. Genetic subdivision among localities separated by up to 3OOO km was high (F_{ST} = O.283, SE = O.O38). Inferred gene flow between pairs of localities (M, individuals per generation) correlated inversely with the geographic distance between those localities, consistent with the pattern expected for a species at equilibrium in which gene flow occurred exclusively between adjacent localities. Within localities, patches separated by 4 to 3O m were also significantly subdivided, but genetic differentiation between patches did not vary significantly with the distance separating them. Simulations revealed that the power to detect genetic pattern expected from gene flow between adjacent populations increased with both the number of loci used to infer gene flow and the heterozygosity of those loci. Simulations also verified that when geographic distance poorly approximated the number of steps between populations, reduced major-axis regression more accurately portrayed the structural relationship between gene flow and separation than did ordinary least-squares regression. Attenuation of gene flow with distance explained 15% of the between-locality pattern of genetic differentiation in *B. elegans.* The remaining variation appeared to be due to neither natural selection nor a recent rangewide recolonization. Loci from the northern sampled localities, however, had fewer alleles than those from the remainder of the range, suggesting these localities had been recolonized recently following Pleistocene cooling.