

Genetic Analysis of Recruitment and Dispersal Patterns in the Porcelain Shore Crab, *Petrolisthes*  
*cinctipes*

BY

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## Abstract

Understanding the role of planktonic larval dispersal remains one of the major hurdles facing marine population biologists. Using microsatellite markers, I characterized genetic structure within and among 12 geographic populations that span nearly the entire species range (from Morro Bay, CA to Neah Bay, WA.) of the porcelain shore crab, *Petrolisthes cinctipes*. Retention zones associated with headlands (the upwelling-relaxation flow hypothesis) cannot account for the pattern of genetic structure observed among geographic populations of *P. cinctipes*. Inferred levels of effective gene flow among populations decrease with geographic distance of separation between sites, but this relationship appears nonlinear. This curvilinear relationship suggests that pelagic larvae of *P. cinctipes* settle with greatest frequency at an intermediate distance from the site of release.

Estimates of population subdivision (using both  $F_{ST}$  and  $U$ ) among northern California sites from collections made in each of 1997, 1998, and 1999 are significant and consistent. However, these single-year estimates appear misleading relative to the overall data set in which the observed genetic variance is partitioned by sampling year, site, and age class (recruits, subadults and adults). Geographic population structure changes from year-to-year in such a way that the overall estimate of population subdivision among sites (pooling the three sampling years) is not significantly different from zero. Instead, collection year and age class appear to account for the significant differentiation among samples. This result argues that evolutionary inferences drawn from single-time samples of *P. cinctipes* are unreliable. If this pattern proves to be a general phenomenon among marine invertebrates with planktonic larvae, studies of the genetic structure of marine organisms that sample populations only once through time should be viewed with caution.

These data are consistent with genetic structure in *P. cinctipes* being a combined result of 1) variation in the source of larval recruits across years, 2) individual variation in reproductive success, and 3) temporally and spatially variable natural selection. Further understanding will require refined theoretical expectations for marine populations that are far from equilibrium, linked by complex patterns of dispersal, and in which a variety of contemporary and historical

processes are likely acting synergistically.

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