

**POPULATION GENETICS, LARVAL DISPERSAL, AND DEMOGRAPHIC
CONNECTIVITY IN MARINE SYSTEMS**

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Abstract

Population connectivity plays significant roles on both evolutionary and ecological time-scales, however efforts at constraining the magnitude and pattern of demographic exchange between populations of marine organisms has been encumbered by the difficulty of tracking the trajectory and fate of propagules. I survey 300 published studies to synthesize life-history and population genetic structure data from a broad array of marine taxa to determine how well pelagic larval duration (PLD) correlates with population genetic estimates of dispersal for benthic organisms. Expanding on earlier studies, I further explore other potential biophysical correlates of population substructure (genetic marker class, habitat type, and larval swimming ability) that have not been considered previously. In contrast to previous studies concluding that longer planktonic periods confer greater dispersal ability, average PLD was poorly correlated with population connectivity (F_{ST}) except among species in intertidal ecosystems. For species in which minimum, maximum and mean PLD were available, both minimum and maximum PLD are better correlated with F_{ST} than is the mean estimate. Furthermore, even this weak correlation appears to be anchored by non-pelagic dispersal, because removal of species that lack a pelagic phase entirely (the zero PLD class) from the analysis resulted in a non-significant relationship between F_{ST} and mean estimated PLD. A 3-way ANCOVA instead reveals that differences among genetic marker classes (mtDNA, allozymes, and microsatellites) are responsible for most of the variation in F_{ST} ($F = 7.113$, $df = 2$, $p = 0.001$), while neither habitat nor swimming ability were significant factors. In contrast to the general expectation that microsatellite-based studies should provide the finest resolution of population structure, this survey finds that significantly

higher values of F_{ST} are obtained with mtDNA than with either microsatellites or allozymes (which were not significantly different). Useful predictors of the pattern and scale of dispersal play a central role in both ecological and evolutionary studies, but as yet remain elusive; this study suggests that mean PLD is at best a weak predictor of population genetic structure and that estimates of dispersal in the sea will need to encompass both behavioral and physical transport processes.