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### PROJECT TITLE: Measuring connectivity of reserve networks in Puget Sound using genetic tools

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#### Abstract:

Most marine reserves are too small to sustain self-seeding populations of marine species that have widely dispersive planktonic larvae, such as most fish and commercially harvested invertebrates. As a result, larvae settling within a reserve are generally thought to be derived from populations outside, either from other reserves or from intervening, exploited populations. In addition, the impact of reserves within broad regional ecosystems depends on whether the reserves export eggs, larvae, juveniles or adults into surrounding areas. Thus, the connectivity of reserves within a reserve network and to the ecosystem is a critical feature of successful network function. Measuring connectivity directly is difficult because of the distances between most marine reserves, but genetic tools have proven useful in discerning hidden barriers to dispersal and in measuring average dispersal of target taxa.

We propose to begin study of the population genetic differences among populations of reserves in Washington State in order to understand the ability of the current reserves to form a functional network and to begin to test for significant barriers to dispersal among reserves. Recent establishment of a series of reserves in Puget Sound sets the stage for the first measurements of connectivity in this area, and allows the integration of genetic and ecological data into management decisions. Because we are currently studying the dispersal and population genetics of intertidal barnacles (*Balanus glandula*), because this species shows unexpected dispersal barriers among the 800 individuals already sequenced from the outer coasts of Washington, Oregon and California (E. Sotka and S. Palumbi, unpubl.), we propose to begin with this model species in the first year. Prior work in Washington State has suggested strong selective differences in settlement cues between southern and northern Puget Sound, and there is some indication of local adaptation across this range (Strathmann et al. 1981). Thus there is a strong possibility of discovering significant differentiation among reserve localities in the southern vs northern Sound.. Other advantages of this species include their commonness within and right outside existing reserves. As a result, we can sample populations adjacent to each reserve studied without violating the protection afforded by the reserves but also without compromising our study.

We will collect 50-100 adult *Balanus glandula* from areas near five reserves throughout Puget Sound and amplify and sequence a 700 base pair section of the Cytochrome Oxidase I gene using techniques already established for this species (Sotka and Palumbi, unpubl., Wares and Cunningham, 2001). Comparison of sequences among localities will reveal levels of genetic differentiation. Comparison to simulation models (Palumbi, in press) will allow us to estimate the average dispersal among localities. Further work in subsequent years will allow us to fill in more localities and assay more loci, which will enhance the accuracy of these measurements.

The larval phase of barnacles include a 2-4 week dispersal phase, similar to, but generally shorter than most fish. Because of this difference, we will also develop molecular tools to examine population structure in ling cod and *Sebastes* rockfish, species that have formed the focus of a great deal of study in the oldest Puget Sound reserve - the Edmonds Underwater Park. A fuller picture of fish connectivity will be completed in later years in order to enhance the wildlife focus of the MEH program.