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**Title**: Area or Ancestry: Does Habitat or Population Origin Have a Greater Effect on Fitness of Outplanted Olympia Oysters?

**Background**: As part of the Washington Shellfish Initiative, the native Olympia oyster is undergoing extensive restorations efforts in attempt to bring their populations back to early 1900’s levels within the Puget Sound. Most restoration practices include the outplanting of viable larvae or seed oysters into bays with known or historically referenced populations. It is assumed that these populations are isolated from one another via geographic or oceanographic features and thus have very little genetic mixing occurring via larval dispersal and spawning. It is also inferred, due to this assumption, that the phenomena of local adaptation may be present within self sustaining populations. The theory of local adaptation claims that animals within unique habitat types will be better suited for their habitat than all others. If this is true, then it would have significant ramifications for restoration practices within the state of Washington as well as around the world. Luckily, local adaptation appears to occur on a case to case basis depending on species and selected traits. To test whether the effect of local adaptation is in play with Olympia oysters, we performed a reciprocal transplant experiment using geographically separated populations of Olympia oysters. Broodstock were collected from three bays along a latitudinal axis by PSRF then conditioned and bred under common garden conditions. Larvae produced were also raised under common garden conditions until August 2013 at which point equal subsets of each population were transplanted at the three origin bays as well as a fourth outlier site. For one year, the animals were monitored via three key metrics for fitness: Survival, Growth, Reproduction.

**Questions for Analysis**:

When comparing all the descriptors of fitness after one year, do the outplanted subsets still cluster with their original parent populations?

Which descriptor is affected most/least significantly by outplant site? By origin population?

**Source of the Data**: In field counts of mortality/survivors, ImageJ Size Analysis for growth, subsampled measurements for whole body weight, weekly reproductive activity assessments in the field, field measurements of brooder size

**Data Structure**

*Sample Unit*--N individuals in each population for each sampling

*Data Matrix*--Population/Site;#ofSurvivors(out of 480);AVG Size (mm);AVG weight (g);Total number of brooders

*Hierarchical Structure*--3 Parent Populations;4 sites;4 replicate trays equaling 480 total animals at each site for each population