A Genetic Survey of English Sole Populations in the Salish Sea

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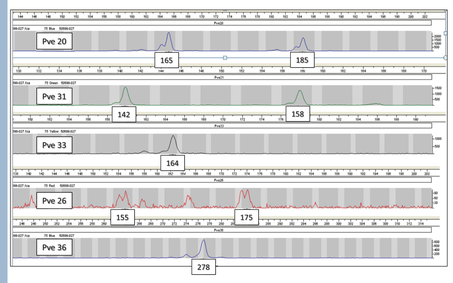
Why Survey English Sole?

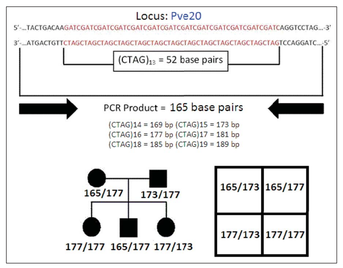
English Sole is one of the dominant species of flatfish that inhabits the Salish Sea, the marine ecosystem that includes Puget Sound, Strait of Juan de Fuca, and the Strait of Georgia. Although English sole have been used extensively to monitor pollution levels, biologists do not know if fish inhabiting different locales are genetically distinctive. A genetic survey using microsatellite markers was initiated in the genetics laboratory at NOAA's Mukilteo Field Station. The assumption is that genetically distinctive populations or stocks may respond differently to changes in the environment, whether the changes are natural (e.g., climate change) or man-made (e.g., pollution).

The goal: to evaluate if genetically distinctive groups of English Sole can be recognized in the Salish Sea. Unique populations may have unique adaptive and/or evolutionary backgrounds.

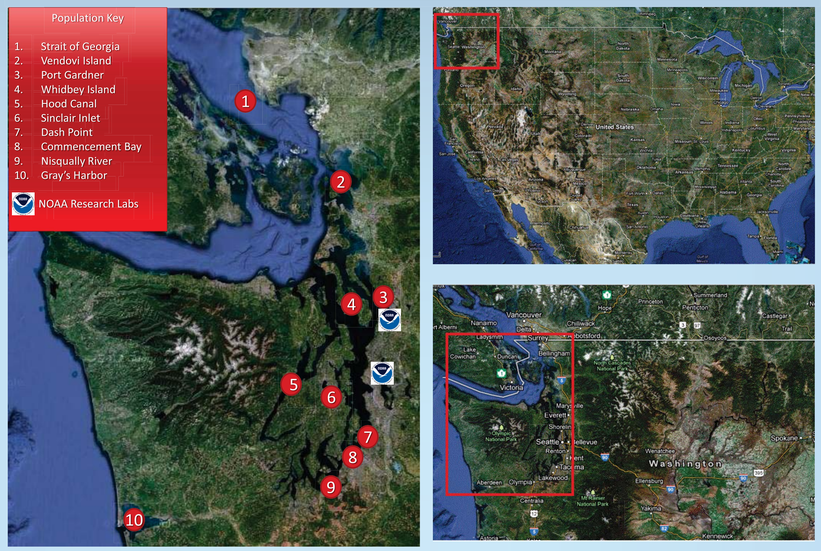
Microsatellite (mSAT) Analysis

In this type of study, we identify genetic variants or **alleles** at mSAT traits (gene **loci**) and look for differences in frequency of occurrence of alleles among the collections. This summer, we amplified mSATs at 5 loci: Pve20, Pve26, Pve31, Pve33, Pve36. Electropherograms from fish #027 from the Hood Canal population are shown (left below). On the right is a model of mSAT inheritance.



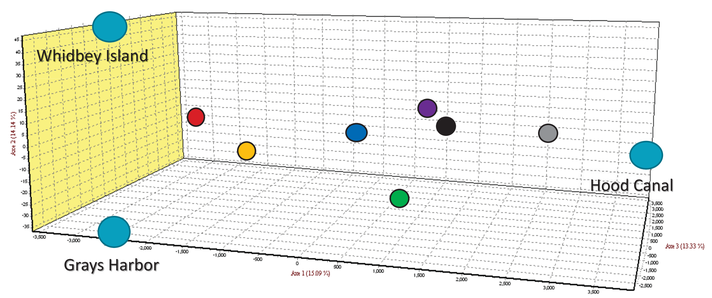


Populations Surveyed



Ten populations in the southern Salish Sea were surveyed.

Patterns of Variability



Factorial correspondence analysis was performed over 163 total alleles across the 5 loci. The graph is a plot of mean collection values along the three major axes of allelic variation. Significant differences were seen among three collections: Grays Harbor, Whidbey Island, and Hood Canal.

Data Interpretation

The factorial correspondence analysis suggests that three of ten populations surveyed are significantly different from one another genetically. Although suggestive, these data are preliminary. We are developing and will employ at least ten more microsatellite markers before drawing any conclusions on the genetic variation of English Sole in the Salish Sea. Further, we hope to obtain collections from the Canadian Salish Sea to complete our picture of variability in the Salish Sea ecosystem.

What's Next?

NOAA and The Salish Sea project would like to continue their genetic surveys to include:

- principal forage fish (Pacific herring, sand lance, and surf smelt)
- eel grass inhabitants (sculpins, surfperch, sand dollar, kelp crab, *Pandalus* shrimp)
- eel grass *Zostera*
- pelagic invertebrates (squid and moon jellyfish) that are affected directly by changes in water chemistry and freshwater input
- More flatfish and ratfish species
- six gill shark

The vision is to incorporate the results from genetic surveys for a large number of ecologically important marine species into one data base. Multispecies data can be used to:

- monitor patterns and levels of genetic variability across taxa and habitats in the Salish Sea
- select representative populations for experimental work re. pollution, ocean acidification, and/or climate change
- contribute to managing the ecosystem biodiversity
- make informed decisions about marine protected areas (MPA).

Grant No. 0952013

This material is based upon work supported by the S.D. Bechtel, Jr. Foundation and by the National Science Foundation under Grant No. 0952013. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the S.D. Bechtel, Jr. Foundation or the National Science Foundation. This project has also been made possible with support of the National Marine Sanctuary Foundation. The STAR program is administered by the Cal Poly Center for Excellence in Science and Mathematics Education (CESaME) on behalf of the California State University (CSU).