

# A Genetic Survey of English Sole Populations in the Salish Sea

### 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

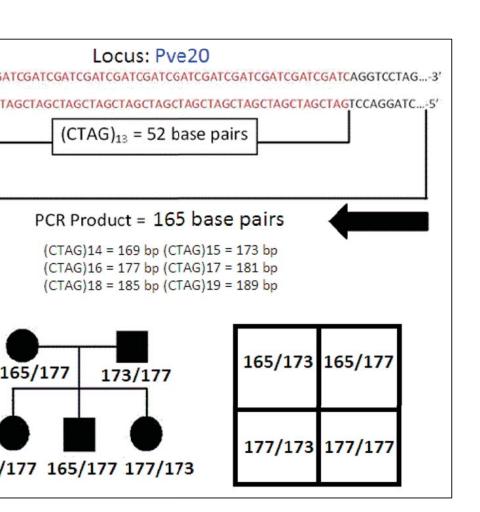
In this type of study, we identify genetic variants or **alleles** at mSAT traits (gene **loci**) and look for differences in frequency of occurrence of alleles among the collections. This summer, we amplified mSATs at 5 loci: Pve20, Pve26, Pve31, Pve33, Pve36. Electropherograms from fish #027 from the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

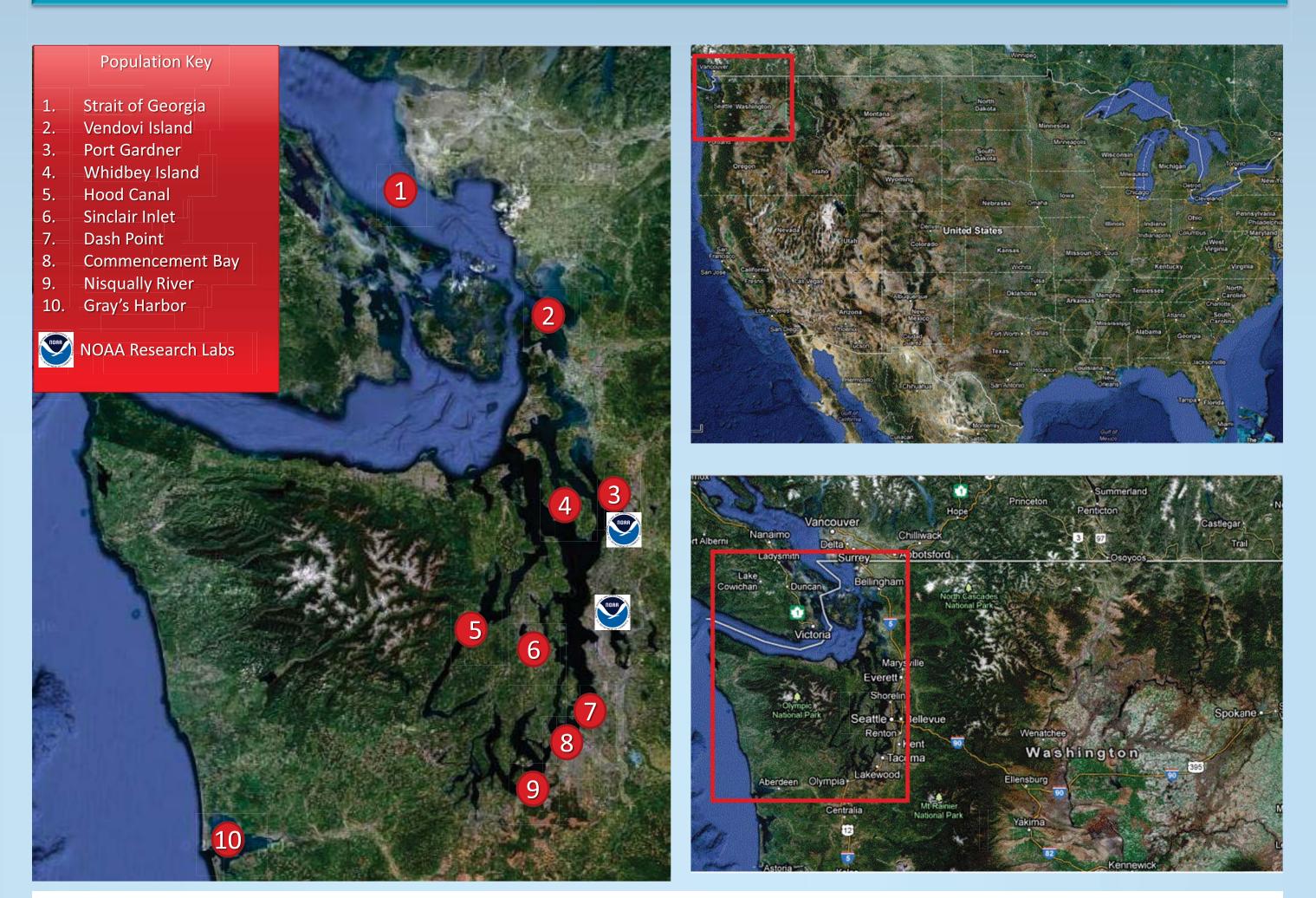
144 148 148 150 152 154 156 158 160 162 164 166 168 170 172 174 176 178 180 182 184 186 188 190 192 194 196 198 200 202	
Pve20  09-027.fsa 75 Blue 50899-027	
Pve 20	5'TACT 3'ATG/
165 185	
130 132 134 130 138 140 142 144 146 148 150 152 154 166 160 162 164 166 168 170	
Pve31	
150 152 154 156 158 142 164 166 168 170 172 174 176 158 150 182 184 186 188 160	
Pve33 09-027.fsa 75 Yellon 50899-027	
Pve 33	
164	
138 140 142 144 146 148 150 152 154 156 155 160 562 154 166 165 170 172 174 176 178 150 182 184 156 188 160 192 194 195 198 200 202 Pre25	
99-027.193 75 Red 50099-027 Pve 26	
155 266 268 270 272 274 276 278 280 28 Pve36	
Pve 36	



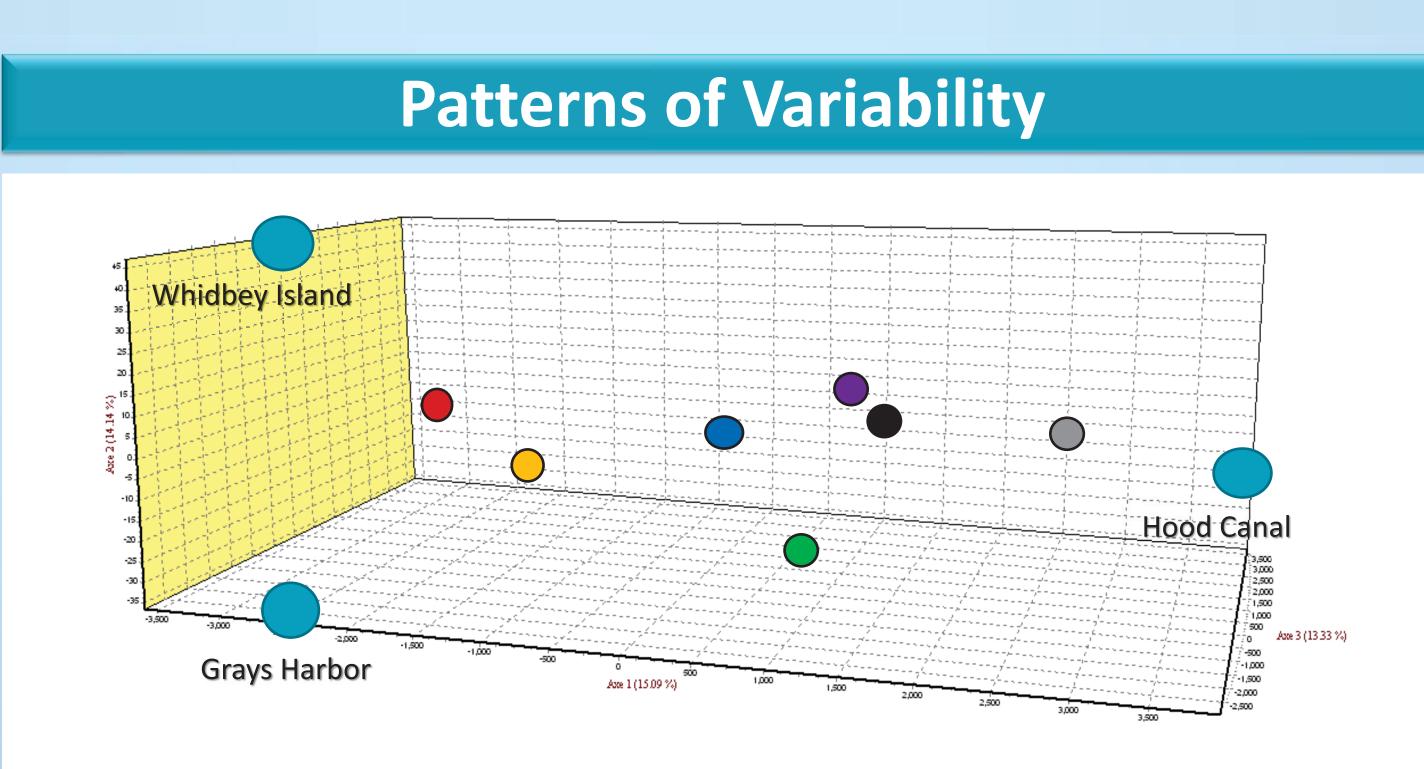
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Ten populations in the southern Salish Sea were surveyed.



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.

### **Populations Surveyed**

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.

# genetic surveys to include:

- 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

- 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
- areas (MPA).



### **Data Interpretation**

## What's Next?

- NOAA and The Salish Sea project would like to continue their
- principal forage fish (Pacific herring, sand lance, and surf

- 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:
- make informed decisions about marine protected



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