

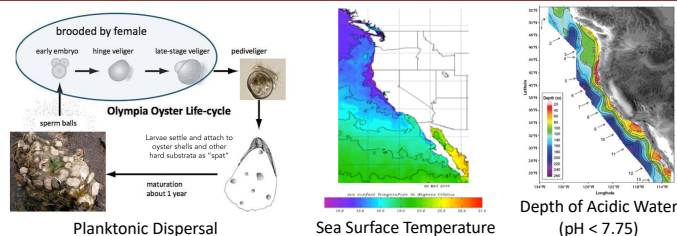


Genetic and Phenotypic Differentiation in the Olympia Oyster (*Ostrea lurida*)

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Local adaptation in the face of gene flow?

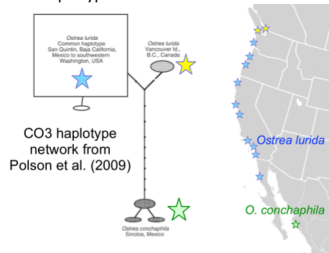


But first...demographic population structure

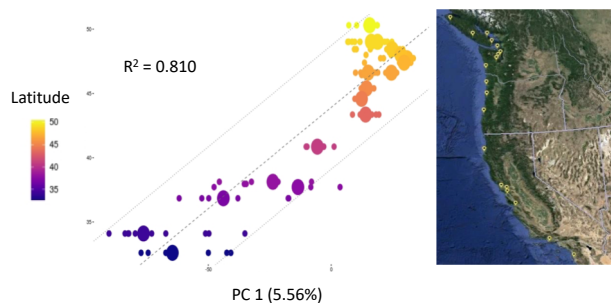
Phylogeographic break in mitochondrial haplotypes at Strait of Juan de Fuca

Genotype-by-sequencing approach

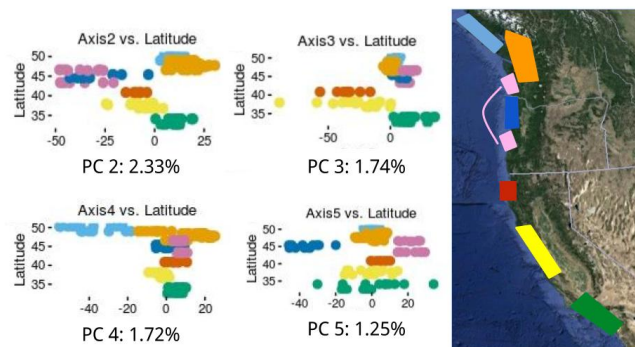
- 20 sampling sites, ~8 individuals per site
- 8 *Ostrea conchaphila* samples from 4 sites in Mexico
- Assembly with *ipyrad* – determined optimal clustering threshold
- 338,835 total loci
- 9,170 "unlinked" SNPs, 137 individuals (*O. lurida*)
- 9,322 SNPs, 145 individuals (+8 *O. conchaphila*)
- Filtered for excess heterozygosity, departure from H-W equilibrium, sample coverage, minor allele freq > 0.025, outliers identified in Bayescan and OutFLANK



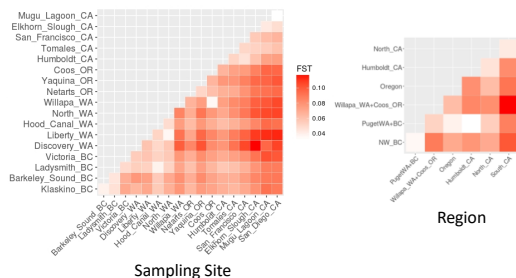
PC 1 represents latitudinal structure



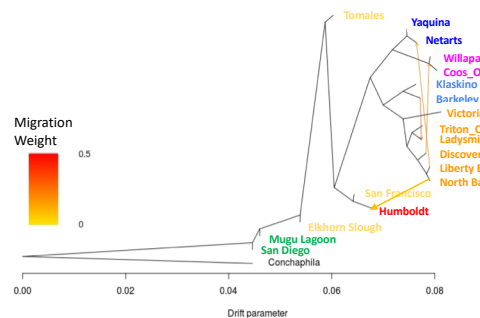
PCs 2-5 represent regional structure



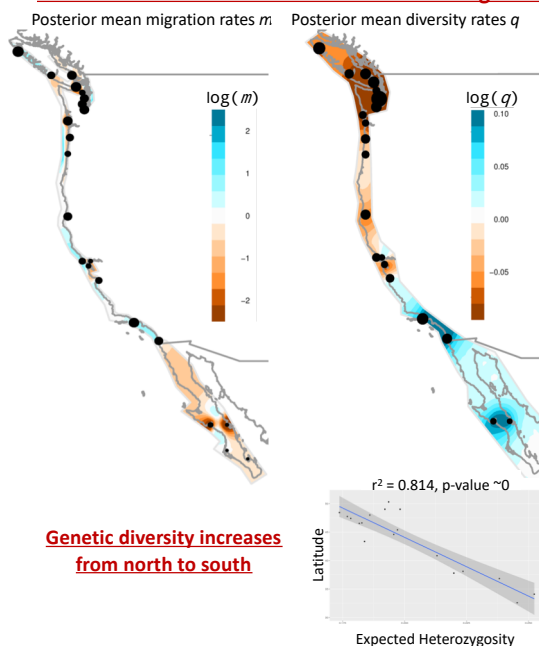
Pairwise F_{ST} (W&C 1984) indicates isolation by distance, with some irregularities



Treemix suggests migration events out of Puget Sound



EEMS identifies areas of reduced effective migration



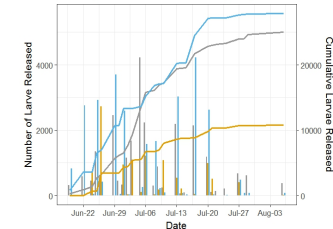
Genetic diversity increases from north to south

Phenotypic variation in growth and reproduction on a small spatial scale



- Common garden experiment with 1st (G1) and 2nd (G2) generation, commonly reared oysters from 3 populations in Puget Sound, WA
- Reproduction (G1): Larval output counted every day or so, with buckets of oysters treated as independent replicates
- Larvae growth (G2): ~700 larvae raised in 1 L beakers for 2 weeks; 3 reps per population, shell length measured 3x
- Juvenile growth (G2): Larvae >224µm set on 10cm x 10cm PVC tiles; hung off dock Aug. 2015 - Nov. 2015; shell area measured 3x

Timing of Larvae Release by Population



A. The total number of larvae released over 7 weeks by G1 oysters, with daily larvae counts on the left axis and cumulative larvae counts on the right axis. B. Cumulative larvae released within replicate buckets. C. Calendar day of first observed larval release.

Significance Codes: *** 0.001 ** 0.01 * 0.05 . 0.1

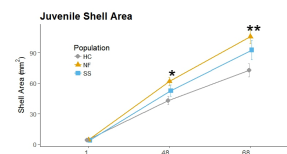
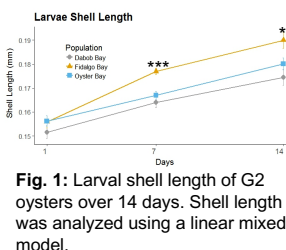
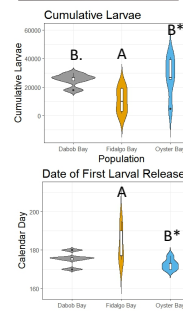


Fig. 1: Larval shell length of G2 oysters over 14 days. Shell length was analyzed using a linear mixed model.

Fig. 2: Juvenile shell area of G2 oysters over 9 weeks, analyzed using a linear mixed model.

Discussion and Future Directions

Population genomics

- Multiple lines of evidence for population genetic structure in *Ostrea lurida* on a regional scale
- Variation in effective migration rates suggests a more complex demographic scenario than pure isolation by distance
 - Phylogeographic "breaks" at Strait of Juan de Fuca and San Francisco Bay
 - Confounding impact of human-assisted "migration"
- Future directions: Use environmental data and Bayenv to detect putative loci under selection

Common garden experiment

- Observed significant differences in growth rate at both larval and juvenile life stages in 2nd generation commonly reared oysters from 3 populations in Puget Sound, consistent with previous experiments (Heare et al. 2017. *Marine Ecology*)
- The population with fastest growth also exhibited delayed and reduced reproduction activity, indicating a potential adaptive trade-off
- Future directions: 2bRAD genotyping and MBD-BS (methylation) coupled with newly sequenced genome to understand molecular mechanisms underlying phenotypic variation