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Genetic structure of the bull-kelp Nereocystis luetkeana in the Salish Sea

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Genetic structure of the Bull-Kelp Nereocystis luetkeana in the Salish Sea

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Why study genetic connectivity?

• Low connectivity between populations decreases genetic diversity
• Small and fragmented populations are at risk for local extinction
• Important to conserve well connected populations and keep individual numbers high to prevent inbreeding
Bull Kelp
Nereocystis luetkeana

- Brown algae in the order Laminariales
- Found from Alaska to Central California
- Dominant canopy forming kelp in Salish Sea

Kidder, 2006
Bull Kelp history in the Puget Sound

- Puget Sound populations are fragmented with small population size
- Recent declines
- Genetic markers used to estimate gene flow between populations
- Isolated populations at risk of going locally extinct

Berry, 2017
Hypotheses

• Because spores cannot travel far, genetic differentiation will be high in Bull Kelp

• Alternatively, because kelp fragments can raft at the will of sea surface currents genetic differentiation will be correlated with oceanographic distance

• Due to spore limited dispersal, inbreeding will be high within populations.
Methods

- Seven microsatellite markers
- Alleles scored in STRand
Microsatellite allele distribution across sites

- Allele frequencies
- Genetic diversity is a measure of allelic richness and frequencies
• 58 sites from Alaska to central California
Bull Kelp genetic diversity

Allelic richness

Genetic co-ancestry
In summary

• Four genetic co-ancestry groups spanning over 3,500 kilometers
• Lowest allelic richness in Puget Sound and Strait of Georgia
• Juan de Fuca is a genetic break
• Strait of Georgia and Puget Sound share similar environments & similar genetic background
• Distance over water is a poor predictor of differentiation
• A large proportion of sites had significant positive FIS suggesting inbreeding
What drives Bull Kelp genetic differentiation in the Salish Sea?
Isolation by oceanographic distance

- Long distance dispersal events of rafting
- Oceanographic transport can extend dispersal of spores
GNOME (General NOAA Operational MODEL Environment) and the Salish Sea Model

- Uses sea surface current data to map trajectory of oil spills
- Particles were tracked for 14 days
- Thirteen dates of release from July to December 2014
Stepping stone connectivity

• Historical Bull-Kelp distribution in the Salish Sea
• Generated 42 pseudo-sites to model stepping stone connectivity using network analysis
• Oceanographic distance is defined as the network path of least resistance, i.e., the minimum sum of -logProb of transport across all paths
Network Analysis

Genetic differentiation (Jost’s D)  Hydrodynamic transport probability
Exploring isolation by environment

- If there is local adaptation, migrants will have lower fitness.
- Nine environmental variables.
  - Taken from NASA’s MODIS AQUIS.
Modeling genetic differentiation as a function of ocean currents and environmental variables

Jost’s D ~ \textit{Isolation by distance} + \textit{isolation by oceanographic transport} + \textit{isolation by environment}

Jost’s D ~ \textit{Sea surface spatial distance} + \textit{oceanographic distance} + \textit{kd490} + \textit{Chla} + \textit{Summer SST}

\[
\text{Adj. } r^2 = 0.388
\]
Conclusions

• Dispersal may not be as limited as previously thought

• Oceanographic distance explains variation in genetic differentiation better than spatial distance and environmental distance

• Partial support for isolation by environment
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