Background

The ascidian chordate *Didemnum vexillum*, or Dvex, also known as the “carpet sea squirt” or “sea vomit” is an invasive species that was first documented in the San Francisco Bay area in 1993. Its ability to overgrow and smother native organisms has made it a great ecological and economical concern. *D. vexillum* poses a serious threat to aquaculture and benthic communities, both of which have a significant economic impact.

Why estimate genetic diversity?

The genetic diversity of a population can indicate how long it has been established, its ability to further expand, and can illustrate a pattern of dispersal by identifying potential geographic origins. Understanding diversity patterns of *D. vexillum* will serve management purposes and policy implementation for the prevention of further invasions.

Research Goal

Our goal was to obtain and analyze mitochondrial gene sequences from the cytochrome oxidase 1 (CO1) locus and compare them to an existing global database to determine relative levels of genetic diversity. We focused on Eastern Pacific invasive populations along the west coast of North America, namely Sitka, Alaska and San Francisco Bay area populations, in comparison to native Japan population samples. Western Atlantic populations in Connecticut and Maine were also examined in comparison to Japan and United States west coast.

D. vexillum Global Distribution

Examples DNA sequence data visualization: (LEFT) Electropherogram data from a gene sequence visualized by the DNA sequencing software program Sequencher. (RIGHT) An example (not *D. vexillum*) of an aligned gene sequence from 19 individuals.

D. vexillum Global Distribution

Global distribution of *D. vexillum* (Dvex): Dvex is native to Japan, and has colonized regions of Europe, New England, and more recently the west coast of the United States. Whiting Harbor in Sitka, Alaska is the most recently discovered location of invasion.

Predictions

- As the most recent, and geographically limited population, Alaska will have the lowest level of genetic diversity
- As the native source population, Japan will have the highest level of genetic diversity
- The San Francisco Bay area populations will have a level of genetic diversity comparable to Japan due to being multiplied-sourced by high marine traffic

Analysis & Preliminary Results

Hardy-Weinberg Equilibrium F-statistics are commonly used in population genetic analysis, but are not necessarily the best metric for an invasive species. We used Bayesian inference, which quantifies population parameter uncertainties based on conditional probabilities, to estimate population parameters. The program MIGRATE-n (Beerli, 2010) was used on the sequence data to estimate various population genetic parameters using a Bayesian inference model. We used the estimated theta (θ) values, which is given by the formula 4N_e μ where N_e is the effective population size and μ is the mutation rate, as our main measure of genetic diversity in each population.

Future Research

- Longer, repeated MIGRATE-n runs with varying search strategies to test robustness of our initial promising results.
- More numerous and variable loci (i.e. microsatellites) will provide more robust estimates of both genetic diversity and levels of directional migration among populations.
- More San Francisco Bay and other west coast sites to estimate local patterns of diversity and gene flow
- Larger sample sizes for some populations.

References


Acknowledgements

Thanks to the following people and groups for their assistance, support, and encouragement throughout the summer: Darragh Clancy, Benson Chow, Carrie Craig, Danielle Demet, Addie Ewan, Veronica Guerra, Vanessa Willer Gru, Beth Sheves, Joseph Spaulding, The Cohen Lab, The Cal Poly STAR Program and Fellows, The Romberg Tiburon Center and San Francisco State, and NSF, and all sources of funding for the STAR program. SPFU RTG gene lab use thanks to NSF FSML Grant 0435033 (CSC).