
How Do We Distinguish between Different Populations?

Population genetics is a field of biology that studies the genetic composition of biological populations and the changes in genetic composition that result from various factors, including natural selection. It is related to the study of evolution and is often regarded as the theoretical cornerstone of modern Darwinism.

Natural selection occurs when members of a population out-reproduce other members, as a result of being better adapted to the environment, or 'fitter'. It is one of the most important factors that can affect a population's genetic composition.

Fixation index (F_{ST}) is a measure of population differentiation based on genetic polymorphism data, such as Single nucleotide polymorphisms (SNPs) or microsatellites. It is a special case of F -statistics, the concept developed in the 1920s by Sewall Wright. This statistic compares the genetic variability within and between populations and is frequently used in the field of population genetics. In population genetics, an $F_{ST} = 0$ means that there is no genetic difference between the populations, indicating high gene flow between them.

The spread of lobster shell disease: genetic and social barriers

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Objectives of the Research:

We propose to study the population genetics and behavioral ecology of lobsters and their impact on the spread of shell disease. Our specific goals include the following:

- Characterize lobster stocks and map the levels of genetic exchange between lobster populations
- Develop easy to use morphometric parameters for identification of lobster stocks from different regions.
- Determine if social barriers could lead to stock segregation through behavioral interactions
- Determine if diseased males of different stocks are at a disadvantage in social dominance, and access to shelter
- Determine if the severity of the disease affects social interactions
- Examine difference between epizootic and impoundment shell disease in its effects on social behavior

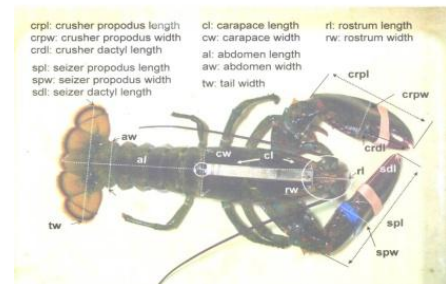
Methodology:

Population genetics

Pleopod samples for DNA analysis are collected from different geographic locations. We use our newly developed SSR-EST markers to test for genetic differences between populations. Size differences in PCR products of SSR-EST markers are analyzed by a capillary automated sequencer Beckman (CEQ 2000).

Development of morphometric parameters

Lobster parts are measured relative to other anatomical measurements. We expanded our list of characters used to describe adult stock differences, sampling males and females from all of our sites. We used principal component analysis to separate stocks and correlate the results with genetics.



Behavioral Ecology

We will measure avoidance, attraction, and dominance between healthy and diseased individuals of same & different lobster stocks. We use a choice flume tank to test female choice between

male pairs. Pairings include: healthy/ diseased, different stocks, dominant/subordinate and combinations of these attributes. In other experiments we measure dominance fights and shelter possession between shell-diseased and healthy males from same and foreign stocks. We determine the severity of disease required to become socially non-interactive.

Results to Date:

Significant differences between Maine and Rhode Island lobster populations were found based on 4 markers with one marker being the most informative. All markers amplified DNA and showed between 4 and 15 alleles per locus. The mean F_{ST} value = 0.035 shows significant difference between the two populations strongly driven by one locus that has an F_{ST} value of 0.117.

Both males and females showed significant differences in their morphology between sites in Maine and Rhode Island ($p < 0.0001$). The males in Maine have longer rostrums, wider abdomens and longer wider tails than RI males. RI males have larger claws and longer walking legs. Maine female lobsters have wider tails. RI female lobsters have a wider carapace and abdomen, longer walking legs and a longer tail. Discriminant analysis showed highly significant stock differences predicting stock membership 100% for these sized animals. Not surprisingly given their proportionally larger claws, RI males won significantly more fights than ME males when paired together. Females showed a trend towards favoring males from their own stock before a fight, but after the fight, the female preferred the dominant (in this case RI) males.

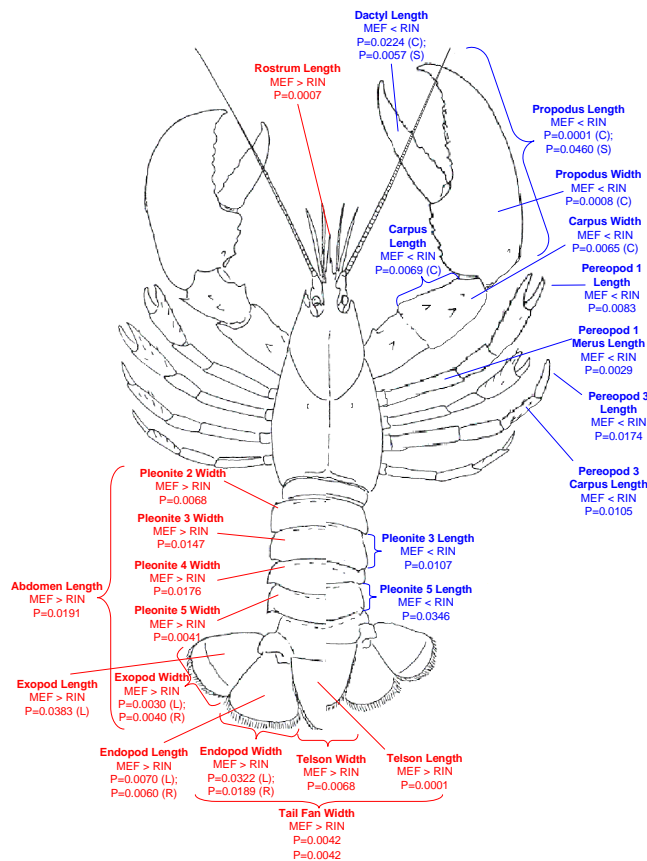


Figure 1. Morphometry of Males. Significant differences between Maine Frenchman Bay (MEF) population and Rhode Island Narragansett Bay (RIN) population. Red characters: MEF>RIN, Blue characters: MEF<RIN. C=crusher claw, S=seizer claw, L=left side, R=right side.

Jelle, Roxanna, Steven and Gabriele are all either visiting or adjunct scientists at the Marine Resource Center at the Marine Biological Laboratory in Woods Hole, Massachusetts. All have their own laboratories but are collaborating on this effort.

