Population Genetics of Invasive Green Crab, *Carcinus maenas*, in the Gulf of Maine

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Abstract

One of the most successful marine invaders, *Carcinus maenas* has established populations on all temperate coasts. The past few years have seen a surge in the abundance of *C. maenas* and their impacts on coastal communities from Long Island to Nova Scotia, which may reflect a new strain of *C. maenas* introduced into the region from Northern Europe. As a marker of genetic diversity and gene flow between populations, I studied haplotypes caused by silent mutations of the mitochondrial cytochrome c oxidase I (COI) gene. I found the highest genetic diversity in the northern sites (NS: h=0.7619). Pairwise comparisons show Nova Scotia and Mt. Desert populations are genetically more differentiated from the other populations (NS: F_{ST}=0.4201, MDI: F_{ST}=0.1448) likely caused by the recent invasion to Nova Scotia, which has subsequently spread south.

Background

- **Characteristics of Good Invaders**: high fecundity, dispersal, tolerance to salinity, temperature changes, and desiccation.
- **Ecological Impact**: *C. maenas* feeds on species of commercial importance including soft-shell clams and lobsters, and ecosystem engineers such as eelgrass.
- **Population Genetics**: analysis of DNA polymorphisms show patterns of population structure and the spread of different lineages. Mitochondrial DNA shows the recent migration history of a species.
- **Genetic Paradox**: an invader should suffer from reduced genetic diversity and reduced adaptability, however, high propagule pressure, rapid population expansion and multiple invasion events allow them to prosper.
- **First arrived to New York in 1817, C. maenas reached the Gulf of Maine 100 years later.** Invasion in the 1980’s to Nova Scotia introduced many new haplotypes, which are moving southwards into the established populations.

How much population structure exists in the Gulf of Maine?  
How much diversity is found in Nova Scotia and what is the southern range of these haplotypes?

Results and Conclusions

- The highest haplotype diversity was found in the northern populations, and the predominant haplotype (1) was found in all populations (Fig. 2 and 3).
- All haplotypes were caused by variants at 5 polymorphic sites (Fig. 3) and three components explain 93.5% of the sequence variation (Fig. 4).
- There is a positive correlation between geographic distance and genetic differentiation (Fig. 5) though little population structure exists at the southern sites, likely due to high rates of larval dispersal connecting the populations.
- Based on comparisons to the previous study (Pringle et al 2011), the haplotypes from Nova Scotia have migrated south approximately one third of the coast of Maine in one generation.

Methods

Fifteen adult crabs sampled were from each of 9 sites in the NW Atlantic. DNA was isolated from muscle tissue (Qiagen Tissue Kit), and the COI gene was sequenced (Sanger technology). Sequence analysis included: haplotype diversity (h), haplotype frequencies, pairwise distances between populations (F_{ST}) and number of migrants (Nm) (Hudson et al 1992; in DNA SP), and Polymorphic loci diversity by principle component analysis (JMP Genomics).

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