

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.

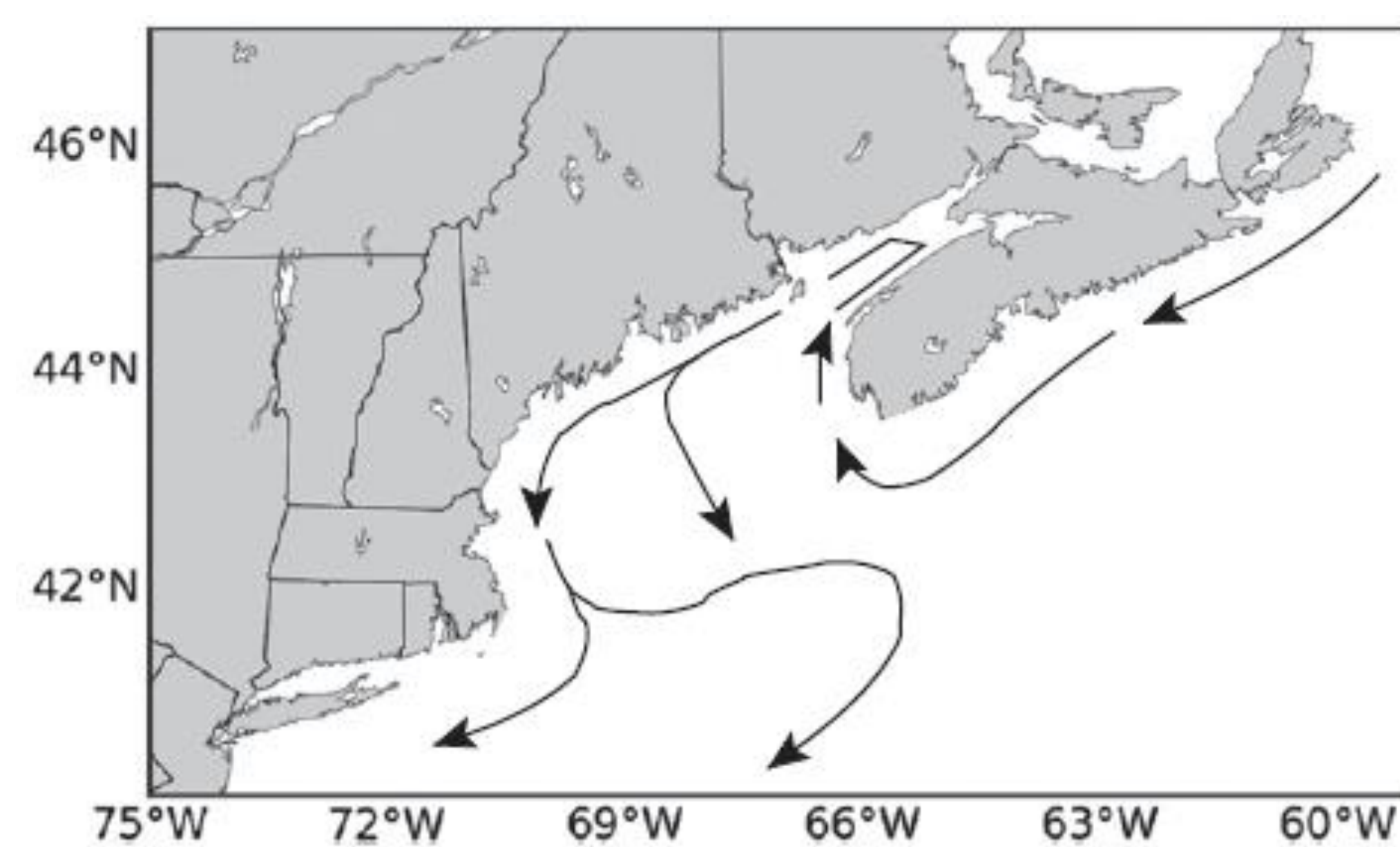


Figure 1. Map of coastal currents in the northwestern Atlantic. (Figure from Pringle *et al* 2011)

Research Questions

- 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?



Carcinus maenas

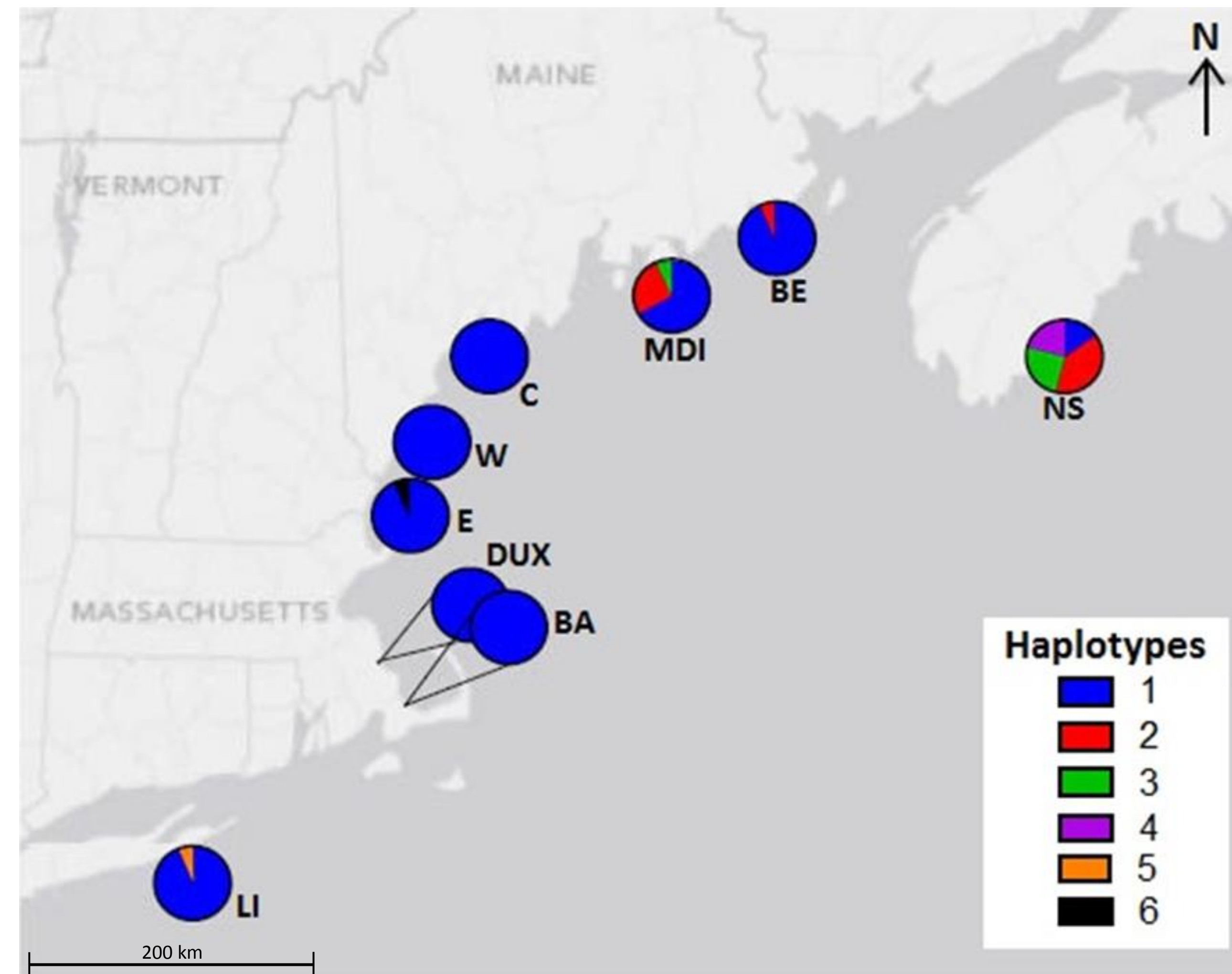


Figure 2. Haplotype frequencies of a 400 bp region of the cytochrome oxidase I gene ($n=15$ per site). Pie charts indicate proportion of haplotypes found from each population.

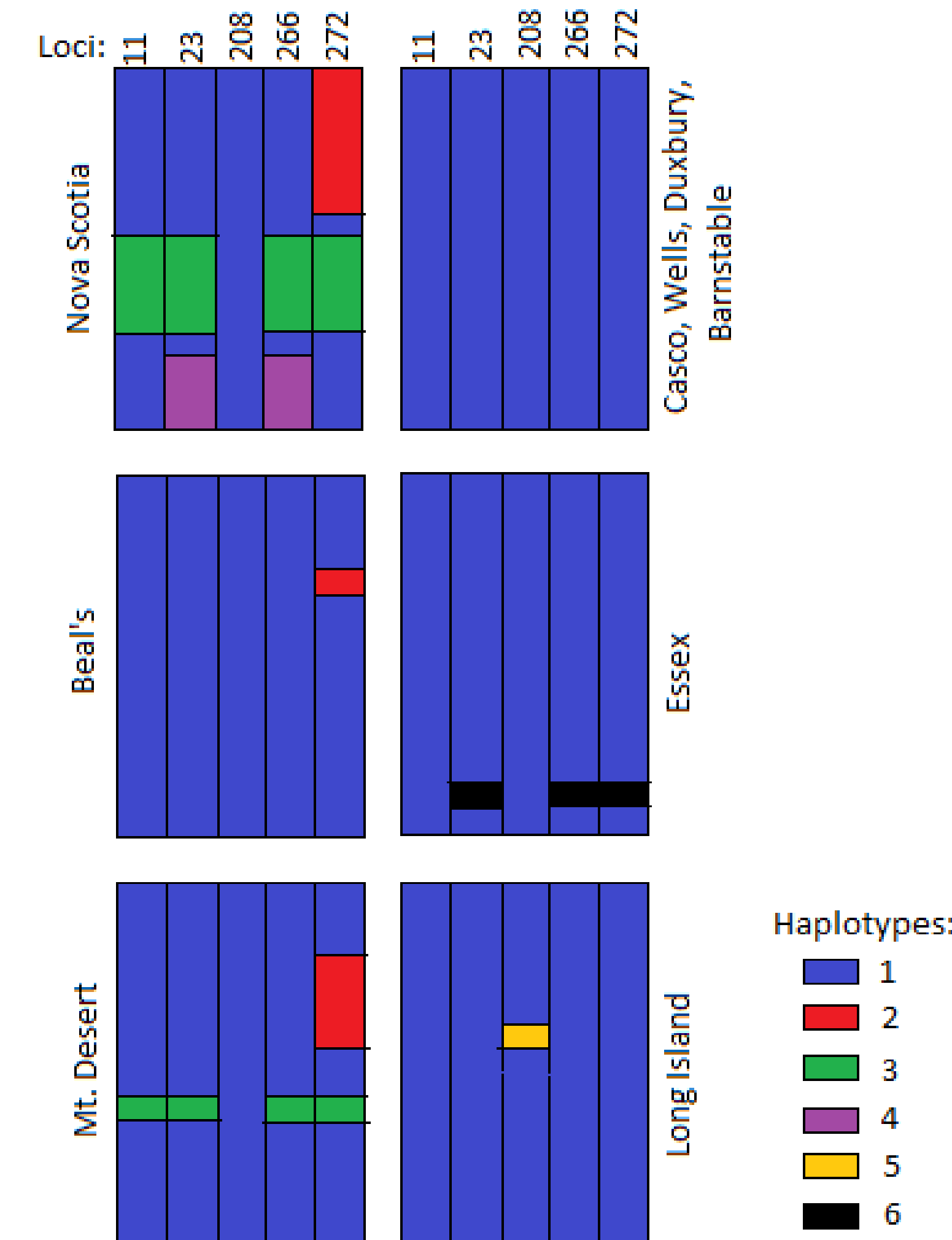


Figure 3. Cell plot of 5 polymorphic loci. Individuals are represented in rows, and colored cells represent a nucleotide change from the predominant haplotype (1). Among all haplotypes, there were two variants per polymorphic site.

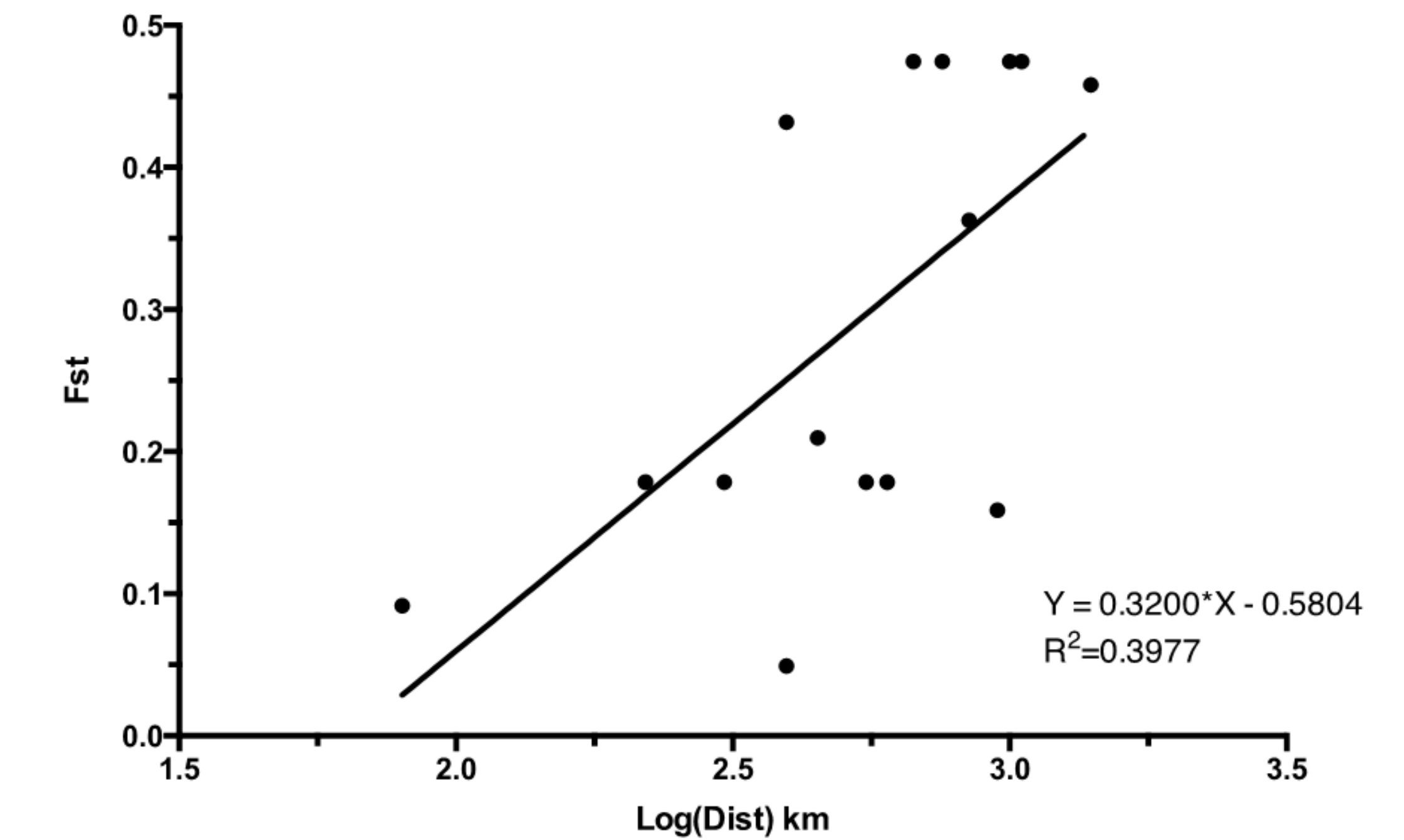


Figure 5. Linear regression of non-zero pairwise comparisons of haplotype diversity (F_{ST}) as a factor of the log of the distance between sites. There is a positive correlation between geographic distance and genetic differentiation ($p=0.01$). Population pairs with non-zero F_{ST} values include: Nova Scotia with all other populations and Mt. Desert with all other populations.

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 (N_m) (Hudson *et al* 1992; in DNA SP), and Polymorphic loci diversity by principle component analysis (JMP Genomics).

Acknowledgements

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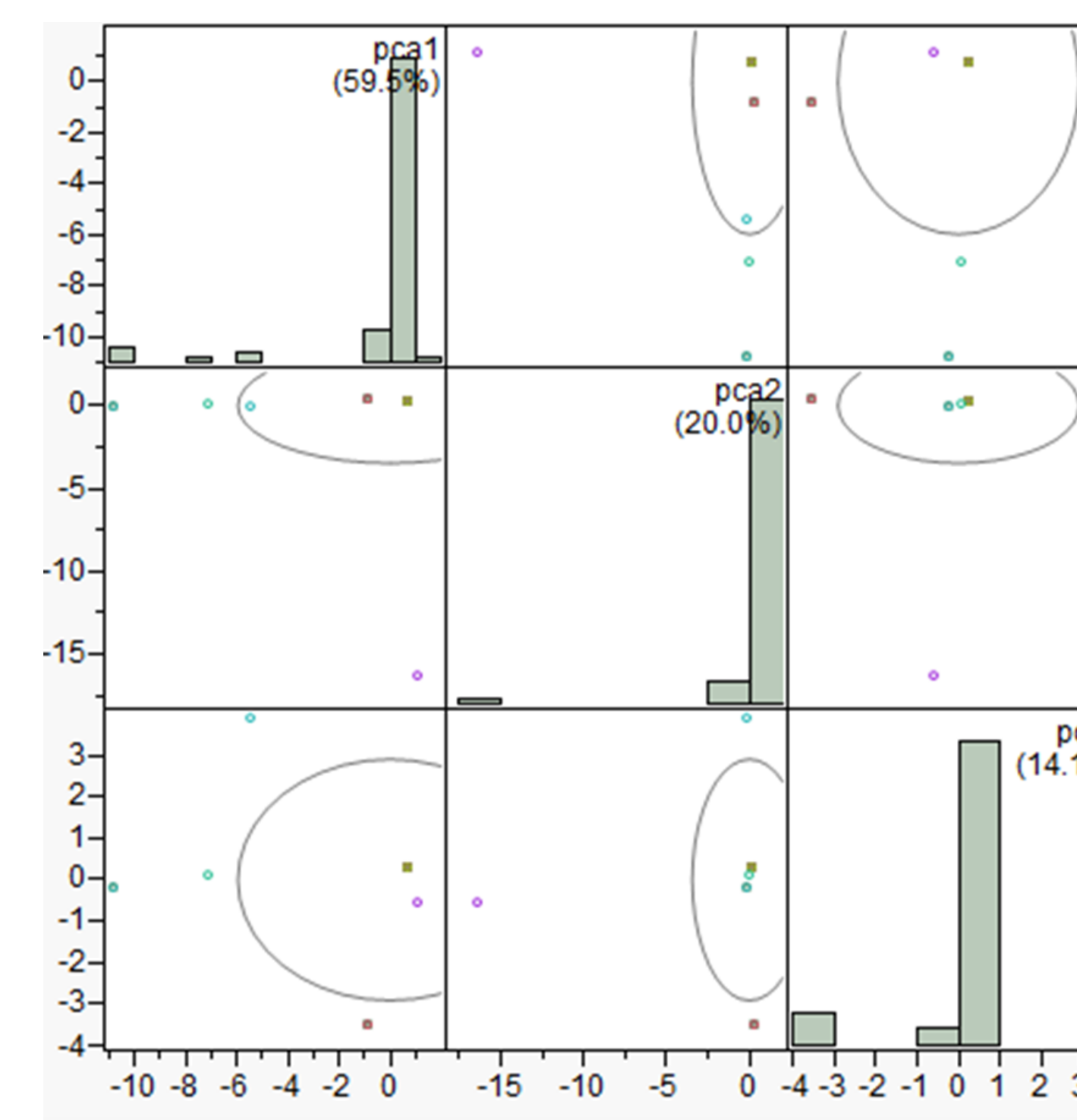


Figure 4. Principal component analysis of the five polymorphic sites, each caused by two possible variants, found in a 400 bp region of the *C. maenas* *COI* gene.