

Genetic variation within and between populations of the invasive skeleton shrimp, *Caprella mutica*, from Maine to Long Island Sound and beyond



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Introduction

- The skeleton shrimp, *Caprella mutica* (Figures 1 and 2), is native to northeast Asia, but has been widely introduced in the Northern Hemisphere and has significantly increased in these non-native regions over the last 40 years (Ashton et al., 2008).
- Our project goal was to document the genetic variation within non-native *C. mutica* populations on the scale of 100's of kilometers from the Gulf of Maine to Long Island Sound (Figure 1) as well as to compare genetic variation with other non-native populations and native populations using data from Ashton et al. (2008).
- We report here on our progress utilizing PCR protocols for amplifying the mitochondrial DNA marker (cytochrome *c* oxidase subunit 1 gene) of *C. mutica* from samples collected from Outer Island, CT (OI) (41.24°N, 72.76°W), Harpswell Cove, ME (BM) (43.79°N, 69.96°W), and Scituate, MA (SCI) (42.2°N, 70.73°W) as well as subsequent genetic analyses.

Methods

- DNA was extracted using Red Extract-N-Amp Tissue PCR kit (Sigma Aldrich) followed by standard PCR protocols to sequence the cytochrome *c* oxidase subunit 1 mitochondrial gene using forward and reverse primers (see Ashton et al. 2008).
- GenElute PCR Clean Up Kit (Sigma Aldrich) was used to clean up the PCR products after which samples were sequenced.
- Sequences were aligned and ambiguities were checked against complementary fragments using Geneious Prime.
- Arlequin 3.5 was used to calculate pairwise F_{ST} measures between collection sites and Φ -statistics to compare genetic differentiation among geographic regions using AMOVA. We specifically tested 1) native vs. non-native, 2) ocean basin, and 3) coastline.



Figure 1. *Caprella mutica* female.

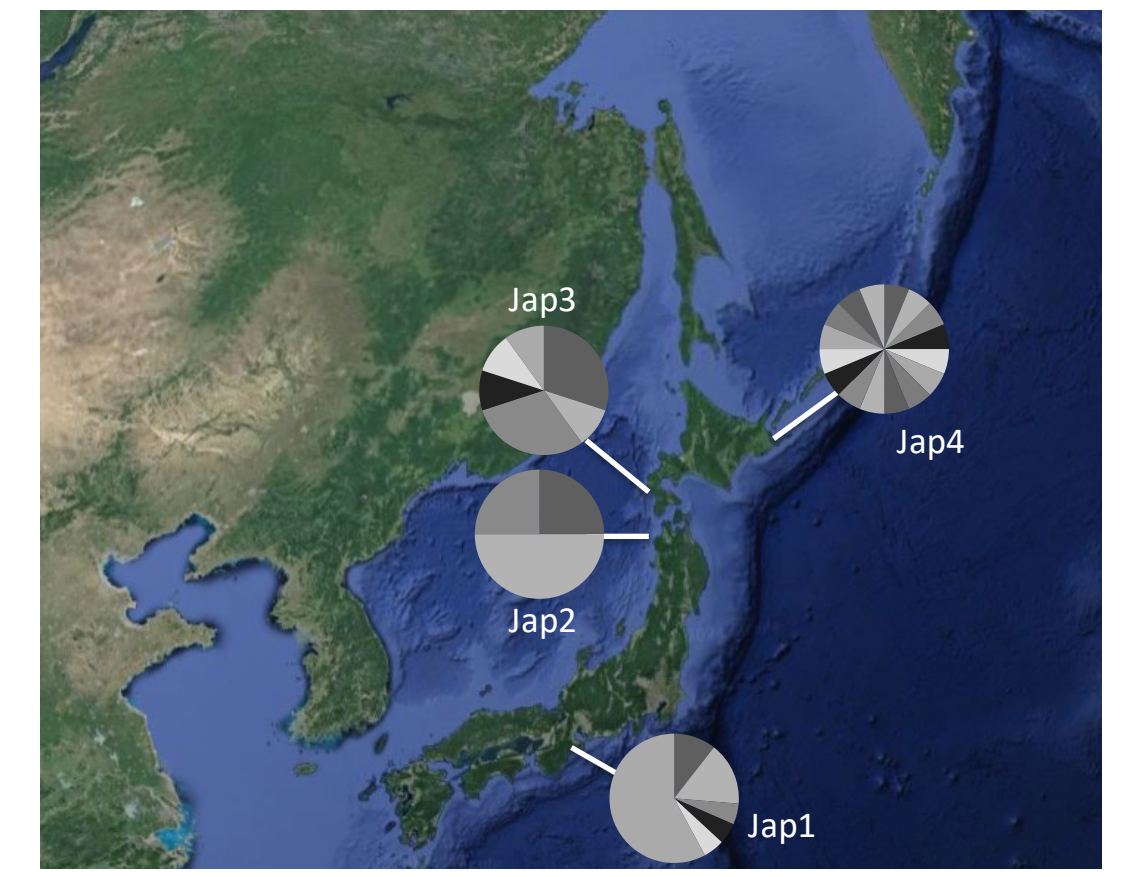
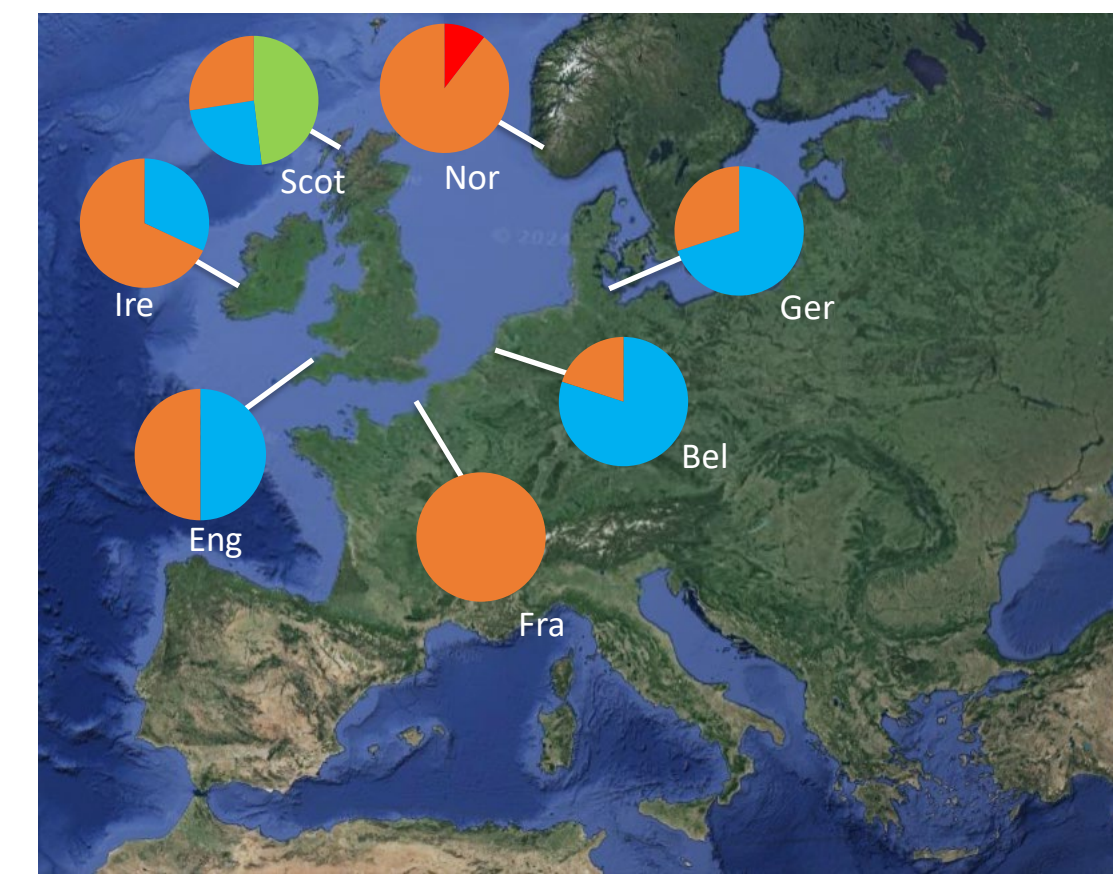


Figure 2. *Caprella mutica* male.

References

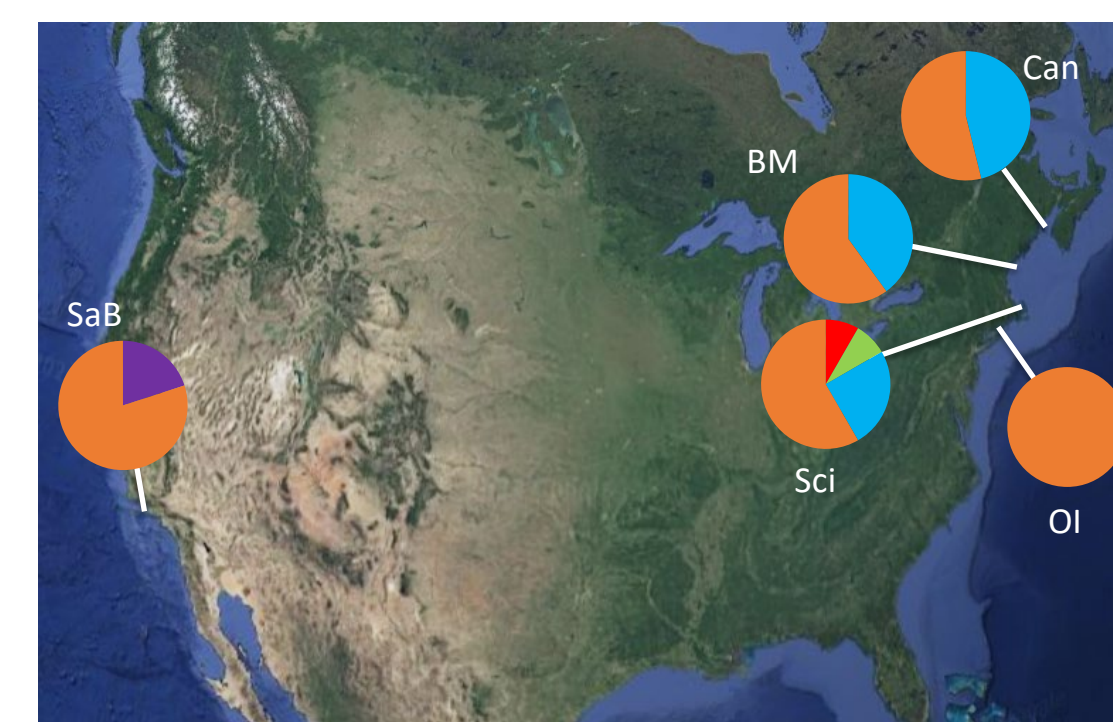
Ashton, G. V., Stevens, M. I., Hart, M. C., Green, D. H., Burrows, M. T., Cook, E. J., & Willis, K. J. (2008). *Molecular Ecology*, 17(5), 1293-1303.

Results



○ Unique Haplotypes in Native Region
● Haplotype A ● Haplotype B
● Haplotype C ● Haplotype D ● Haplotype E

Figure 3. Locations and proportions of *Caprella mutica* haplotypes from Ashton et al. (2008) in combination with data from Outer Island, CT, Scituate, MA, and Harpswell Cove, ME. N=2 (England) to 102 (Scotland). Native populations each had several unique haplotypes. (■ = h39, ■ = h38) haplotypes dominated the non-native populations



| | SCOT | NOR | IRE | GER | FRA | ENG | BEL | CAN | BM | SCI | OI | SAB | J1 | J2 | J3 | J4 | |
|------|------|-----|-----|-----|-----|-----|-----|-----|----|-----|----|-----|----|----|----|----|---|
| SCOT | | + | + | + | + | - | + | + | - | + | + | + | + | + | + | + | + |
| NOR | + | | + | + | + | - | + | + | - | - | - | - | - | - | - | - | - |
| IRE | + | + | | + | + | - | + | - | - | - | - | + | + | + | + | + | + |
| GER | + | + | + | | + | - | - | - | - | + | + | + | + | + | + | + | + |
| FRA | + | - | + | + | | + | + | + | + | + | - | + | + | + | + | + | + |
| ENG | - | - | - | - | - | | - | - | - | - | - | - | - | - | - | - | - |
| BEL | + | + | + | - | + | - | | - | - | + | + | + | + | + | + | + | + |
| CAN | + | + | - | + | - | - | - | | - | - | + | + | + | + | + | + | + |
| BM | - | - | - | + | - | - | - | - | | - | - | + | + | + | + | + | + |
| SCI | + | - | - | + | + | - | + | + | - | | - | - | + | + | + | + | + |
| OI | + | - | - | + | + | - | + | + | - | - | | - | + | + | + | + | + |
| SAB | + | - | + | + | + | + | + | + | + | + | + | | + | + | + | + | + |
| J1 | + | + | + | + | + | + | + | + | + | + | + | + | | - | - | - | - |
| J2 | + | + | + | + | + | + | + | + | + | + | + | + | + | | - | - | - |
| J3 | + | + | + | + | + | + | + | + | + | + | + | + | + | + | | - | - |
| J4 | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | | - |

Table 1. Matrix of F_{ST} p values (+: $p > 0.05$; -: $p \leq 0.05$). ■ highlights significant genetic differentiation between Native and Non-native populations. ■ highlights lack of genetic differentiation among samples from Long Island Sound, Massachusetts Bay, and the Gulf of Maine (present study). ■ highlights lack of genetic differentiation among samples in our study and populations in Norway, Ireland, England, and Santa Barbara. ■ highlights lack of genetic differentiation among Canada, Maine, and Massachusetts populations and genetic differentiation between Canada and Long Island Sound populations.

| Source of variation | d.f. | Sum of squares | Variance components | Percentage of variation |
|---------------------------------|------|----------------|---------------------|-------------------------|
| Among groups | 1 | 160.830 | 1.76678 Va | 42.50 |
| Among populations within groups | 14 | 179.419 | 0.59866 Vb | 14.40 |
| Within populations | 307 | 550.184 | 1.79213 Vc | 43.11 |
| Total | 322 | 890.433 | 4.15756 | |

Table 2. Largest percent variation (42.5%) was explained when comparing Native and Non-native populations (AMOVA). AMOVA results for Ocean Basin (N=3) and Coastline (N=4) explained less of the observed variation.

Discussion

- Our samples from Harpswell ME, Scituate, MA, and Outer Island, CT revealed no genetic differentiation among these populations.
- These findings could result from a single introduction followed by rapid expansion or separate introductions from the same native population.
- As described by Ashton et al. (2008), and reconfirmed in our present study, genetic differentiation among Native and Non-native populations explains at least 42% of the variation observed. We are unable to identify native population origins for the three non-native populations in our study.

Acknowledgements

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