Research Notes

Lack of diversity in phylogeographic analysis of the limpet *Tectura testudinalis*

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Much has been learned through phylogeographic analysis about the recolonization of formerly glaciated regions. A regional case that has received much attention has been the intertidal community of the northwestern Atlantic. Vermeij (1991) and Ingólfsson (1992) detailed the biogeographic signal for extirpation of these populations along the New England coast and Canadian Maritimes, along with the signal for recolonization from European and more southern American populations of the same taxa. Since then, the study of intraspecific genetic diversity has been used to more accurately date and reconstruct the dynamics of these recolonization events (Wares and Cunningham 2001; Turon et al. 2003; Hickerson and Cunningham 2005; Maggs et al. 2008). As more species can be included in such analyses, greater statistical power is available to begin identifying ecological or natural history traits that play deterministic roles in community persistence and/or re-assembly (Ilves et al. 2010).

There still exists, of course, a bias in the literature toward the treatment of species that harbor sufficient genetic diversity at the mitochondrial COI gene region for easy analysis. With few resources available for exploring greater sample sizes or more rapidly-evolving portions of the genome, a number of species have not yet been included in the overall reconstruction of post-glacial dynamics in the North Atlantic.

One of these amphi-Atlantic taxa is the patellogastropod limpet *Tectura testudinalis*. Distributed across the entire range that was covered in Wares and Cunningham (2001), with extremely limited dispersal (Willcox 1905), this species is of interest because it could be a good candidate for identifying additional population structure for phylogeographic analysis. Here, a small data set from the mitochondrial COI gene region is reported and analyzed within the context of expected levels of variation for the Patellogastropoda and more inclusive molluscan data sets.

Methods

Individuals (n=31) of *T. testudinalis* were collected in 1997 and 1998 by JPW at the same European and North American sites as reported in Wares and Cunningham (2001). Here, all sites in North America are grouped together, all European sites are grouped together, and Icelandic collections are reported separately. DNA isolation, PCR, and sequencing protocols were identical to those reported in Wares and Cunningham (2001).

Sequence data were aligned using CodonCode Aligner; the final alignment was evaluated for population genetic diversity using COMPUTE (Thornton 2003) and a haplotype network generated from the maximum-parsimony phylogram reconstructed using PAUP*4.0b10 (Swofford 2002).

Contextual information was provided by searching Genbank for all population studies using the same locus in the Patellogastropoda and Gastropoda, using script software detailed in Wares (2010).

Results

The haplotypes generated for *T. testudinalis* are available in Genbank (AF242036-242066). Wares (2000) reconstructed a substitution rate $\mu = 2.6 \times 10^8$ based on comparison with a presumed Pacific progenitor species. Nucleotide diversity $\pi = 0.00158$ for *T. testudinalis*, with Tajima's D = 0.432. There were no differences in haplotype diversity between the North American and European populations (including Iceland in the 'European' category; 0.648 North America, 0.664 Europe). This is largely because only 4 haplotypes were recovered from this sample (Figure 1). The only singleton haplotype was found in an individual from Maine (USA).

The mean value of π for the Patellogastropoda from Genbank (n=52 data sets, 29 named species) is 0.0140, with a mean D of -0.473. The same values for the Gastropoda overall (see Wares 2010) are 0.0301, with mean D of -0.540. This suggests that the recovered diversity for *T. testudinalis* is quite low for the taxon, and in this small sample there is an excess of common alleles relative to other population data sets in the inclusive clades.

Discussion

Given the importance of limpets in benthic marine ecology (Johnson and Black 1984; Vermeij et al. 1987), it is of value to ensure inclusion of this and as many other distinct taxa as possible when reconstructing the likely history of a community (Maggs et al. 2008). Although little information is provided by the genetic data recovered from this sample of *T. testudinalis*, they may be useful in larval/juvenile barcoding efforts and it may in fact be of interest to identify the larger number of species which are poorly reported in the literature or that have evinced little interest because of the low genetic diversity recovered in preliminary assays. As noted by Bazin et al. (2006), it is likely that some species will harbor low diversity for demographic reasons, and others may harbor low diversity due to genomic transitions such as selective sweeps. Only by accounting for as many species as possible in a community can we begin to identify the stochastic, biological, and historical factors that have influenced that community (Haydon et al. 1994).

Acknowledgments

Figure 1. Parsimony haplotype network for the 4 haplotypes recovered in *Tectura testudinalis.* Sample sizes for the shared haplotypes, from left to right, are n=7, n=13, n=10.
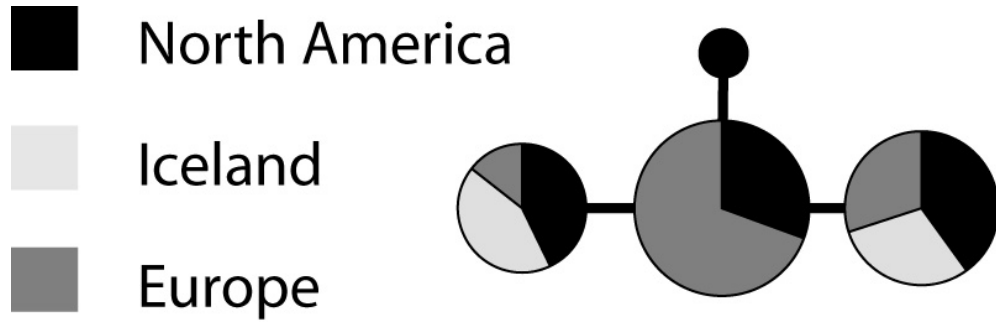
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