

Origins of North American populations of the invasive faucet snail, *Bithynia tentaculata*

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Abstract

Since the introduction of the faucet snail, *Bithynia tentaculata*, into the Upper Mississippi River (UMR) in 2002, there have been yearly die-offs of 15 species of waterfowl. *B. tentaculata* completes the life cycle of several invasive parasitic trematodes causing the waterfowl deaths. The objectives of this project are to determine the origin and spread of invasive *B. tentaculata* populations in the U.S. which will be used to implement better prevention of colonization routes. Since 16s mtDNA sequences show little to no variation between U.S. *B. tentaculata* populations, microsatellite analysis is used to more accurately show variation. Seventeen microsatellite loci (tandem base repeats) from *B. tentaculata* were characterized through a collaboration with the Savannah River Ecology Laboratory. These loci should provide more relevant data than mitochondrial DNA sequences due to the high polymorphism rate associated with the non-coding microsatellites regions.

Introduction

The invasive faucet snail, *Bithynia tentaculata* (Fig. 1), is transmitting parasitic trematodes to Upper Mississippi River (UMR) waterfowl which are causing wide-scale mortality (1). *B. tentaculata* is both the primary and secondary intermediate host for two invasive parasitic trematodes (Fig.2), *Cyathocotyle bushiensis* and *Sphaeridiotrema globulus* (4). *B. tentaculata* was first introduced into the Great Lakes from Europe in the early 1870's from the ballasts of trade ships (2). Since that time, it has spread throughout the Great Lakes region, and has also been found on the East Coast and Montana (3). Genetic differentiation between populations can help to determine the origin(s) of the U.S. *B. tentaculata* populations and determine colonization routes within U.S. lakes and rivers. This knowledge could facilitate management actions to deter further spread of this invasive species.

Methods

- Collection – Snails collected from the three invaded regions in the US and from Hungary in the native range (Fig. 5).
- DNA Extraction – CTAB followed by Phenol/Chloroform.
- PCR – Nuclear DNA: 17 microsatellite loci.
- Microsatellite fragment analysis – ABI 3730xl at Biotech facility at UW-Madison using GeneMarker(Fig.3)

FIG. 1. *Bithynia tentaculata*



FIG. 2. Trematode life cycle.

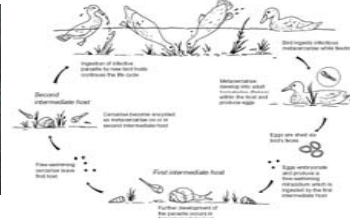
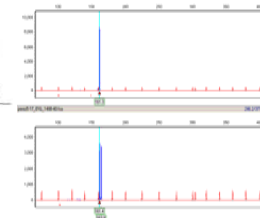
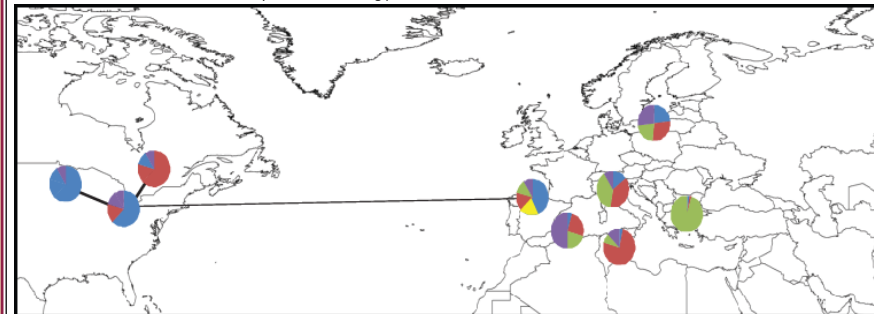


FIG. 3. Microsatellite data.



Small scale initial invasion with secondary invasions showing probable founder effects.



Large scale initial invasion with secondary invasions showing probable founder effects.

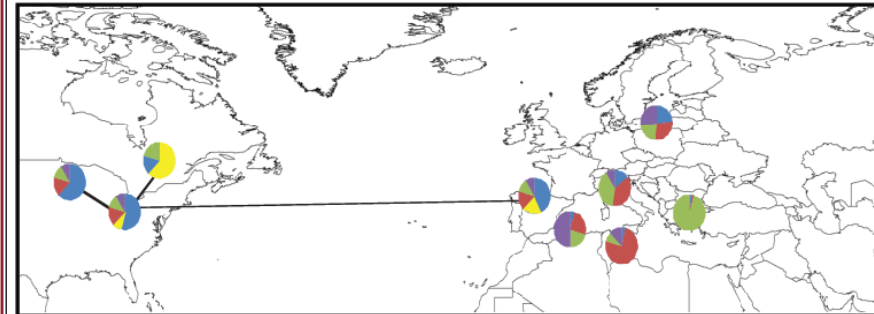
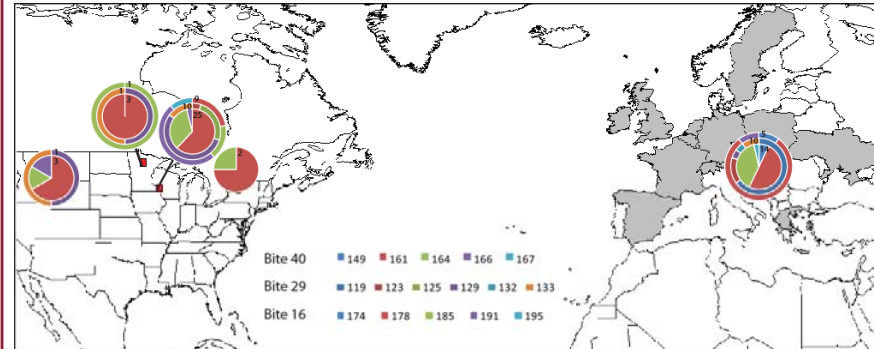


FIG. 5. Current Data and collection sites



Results & Discussion

Allele sizes are determined through microsatellite analysis (Fig. 3). Six of the 17 developed microsatellite loci have been worked with at this point in the project. Though the data collection process is still in its beginning stages, the current data suggests that the invasion likely was not from the Danube watershed of Hungary (Fig. 5). Alleles are present in the Hungarian samples that aren't in the U.S. samples. While this alone would not exclude it from being the origin, because of the possibility of a founder effect (Fig. 4), it is in conjunction with alleles being present in the U.S. samples that aren't in the Hungarian samples. Therefore, the founder effect can't explain the differences and the Danube is likely not the origin of the U.S. populations. Though most of the U.S. samples are still in preliminary stages, the current data suggests that the UMR was the first spread point after the Great Lakes. The other populations appear to be subsets of the UMR population with different founder effects influencing their allele distributions. Since the populations have different allele frequencies, it is assumed, at this time, that little ongoing mixing of the populations is occurring or initial colonizing populations were very small. This preliminary data supports a single introduction of *B. tentaculata* from its native range followed by subsequent colonization within North America.

Future Work

At this time, only about 6 of the 17 microsatellite loci have been used for <100 individuals. We need to explore the rest of the loci with the DNA that we currently have. In addition, samples will need to be obtained from a much wider area within the *B. tentaculata* native distribution in order to determine the origin(s) of the introduction(s). We also need samples from the Great Lakes as the site of the initial introduction.

Acknowledgements

Funding sources: The River Studies Center, USGS, UW System Institute on Race and Ethnicity.

Other project partners: Greg Sandland, Rebecca Coles, Roger Haro, Ben Walker,
Thanks to: Adam Ladwig, Cody Haro, Kirk Gallant, Yer Lor, Josh Laurila, Rachelle Amundson and Chris Lynum.

References

1. Wilkins, K.A., & M.C. Otto. 2006. Preliminary report: Trends in duck breeding populations, 1955-2006. U.S. Fish and Wildlife Service, Division of Migratory Bird Management. 19 p.
2. Mills, E.L., J.H. Leach, J.T. Carlton, & C.L. Seacor. 1993. Exotic species in the Great Lakes: a history of biotic crises and anthropogenic introductions: J Great Lakes Res 19:1-54.
3. J.S. Sauer, R.A. Cole, and J.M. Nissen. USGS. 2007. Open File Report 1065.
4. Hermann, K.K. & R. E. Sorensen. 2009. Seasonal dynamics of two mortality-related trematodes using an introduced snail. Journal of Parasitology 95(4):823-828.