Genetics Provide New Hope for Endangered Freshwater Mussels

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WELLSBORO, Pa. — A piece of the restoration puzzle to save populations of endangered freshwater mussels may have been found, according to a recent U.S. Geological Survey led study. Local population losses in a river may not result in irreversible loss of mussel species; other mussels from within the same river could be used as sources to restore declining populations.

Though they serve a critical role in rivers and streams, freshwater mussels are threatened by habitat degradation such as dams, alteration to river channels, pollution and invasive species. Mussels filter the water and provide habitat and food for algae, macroinvertebrates, and even fish, which are necessary components of aquatic food webs.

“Few people realize the important role that mussels play in the ecosystem," said USGS research biologist Heather Galbraith, lead author of the study. "Streams and rivers with healthy mussel populations tend to have relatively good water quality which is good for the fish and insects that also inhabit those systems."

Mussels in general are poorly understood and difficult to study. Because of this lack of knowledge, population genetics has become a useful tool for understanding their ecology and guiding their restoration.

More than 200 of the nearly 300 North American freshwater mussel species are imperiled, with rapidly dwindling populations. Researchers are providing information to resource managers, who are working to reverse this trend. USGS led research suggests that re-introducing mussels within the same river could reverse population declines without affecting the current genetic makeup of the population.

The research shows that patterns in the genetic makeup of a population occurs within individual rivers for freshwater mussels; and that in the study area, mussels from the same river could be used for restoration.

“That genetic structuring is occurring within individual rivers is good news, because it may be a means of protecting rare, threatened and endangered species from impending extinction,” said Galbraith. “Knowing the genetic structure of a freshwater mussel population is necessary for restoring declining populations to prevent factors such as inbreeding, high mutation rates and low survivorship.”

Knowing that mussels in the same river are similar genetically opens up opportunities for augmenting declining populations or re-introducing mussels into locations where they were historically found. The genetics also highlight the importance of not mixing populations among rivers without additional studies to verify the genetic compatibility of mussels within those rivers.

The international team of researchers from Canada and the United States working to understand mussel genetics found similar genetic patterns among common and endangered mussel species. This is important information for mussel biologists because studying endangered species can be difficult, and researchers may be able to study the genetic structure of common mussels and generalize the patterns to endangered mussels.

Although understanding the genetic structure of mussel populations is important for restoration, genetic tools do have limitations. Researchers found that despite drastic reductions in freshwater mussel populations, there was little evidence of this population decline at the genetic level. This may be due to the extremely long lifespan of mussels, some of which can live to be more than 100 years old.

“Genetics, it turns out, is not a good indicator of population decline; by the time we observe a genetic change, it may be too late for the population,” said Galbraith.

By way of comparison, in fruit flies, which have short lifespans, genetic changes show up quickly within a few generations. Mussels, on the other hand, are long lived animals; therefore it may take decades to see changes in their genetic structure within a population.

The study examined six species of freshwater mussels in four Great Lakes Tributaries in southwestern Ontario. The species are distributed across the eastern half of North America and range in status from presumed extinct to secure. The six mussels were the snuffbox, *Epioblasma triquetra*;

kidneyshell, *Ptychobranchus fasciolaris*; mapleleaf, *Quadrula quadrula*; wavy-rayed lampmussel,*Lampsilis fasciola*; Flutedshell *Lasmigona costata*; and the threeridge mussel *Amblema plicata.*

The study, “Comparative analysis of riverscape genetic structure in rare, threatened and common freshwater mussels” is available online in the journal *Conservation Genetics*.

Mapleleaf mussel, Quadrula quadrula, collected from the Great Lakes region of Canada.
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Collecting a DNA sample from a native freshwater mussel's muscular foot.
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