Using Population Genetics to Inform Fisheries and Wildlife Conservation

> Dr Eric Hallerman Dr Jess Jones



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Conservation can be difficult work on an ever-changing planet, where human activity often runs counter to the needs of endangered species. When budgets and resources are limited, it is critical that conservation plans are designed to be as effective as possible. **Dr Eric Hallerman** and **Dr Jess Jones** use population genetics to help conservationists develop management plans that protect the genetic diversity of aquatic organisms while bolstering their populations.

Worldwide, the effects of climate change and habitat loss have led to declines in the populations of many organisms, and every year an increasing number of plants and animals appear on the International Union for Conservation of Nature's Red List for imperilled species. This is particularly true of aquatic life in the southeast United States, where many freshwater and marine animals are rapidly declining due to factors such as overfishing, agricultural runoff and industrial pollution, dams, and the withdrawal of water for human activities.

However, designing effective conservation programs can be complicated work, particularly for species whose natural population structure is poorly understood. While habitat restoration and species reintroduction can be good strategies, it is the genetic diversity of a species that helps it to survive in a changing world, and makes it most likely to persist once conservation efforts have ceased. Without a good understanding of the genetic variation present across a species, where some groups might be specially adapted with unique traits, it is easy for well-intended efforts to accidentally lead to inbred populations at high risk for disease or less suited to their once-native homes.

Dr Eric Hallerman of Virginia Tech University and Dr Jess Jones of the US Fish and Wildlife Service, who is stationed at Virginia Tech, apply the tools of population genetics to conservation biology to help save aquatic animals in the southeast US. Their research has helped to restore numerous fish and mussel populations and provided frameworks for others to follow when planning effective conservation efforts.

Keeping it Local

Among the greatest difficulties when embarking upon a conservation effort is understanding the best way to manage the remaining natural populations. Often it is assumed that all the members of a species are similar enough to be treated the same and even interbred with little consequence, but in reality, this is seldom the case.

Species are often divided into populations – distinct groups of the same species that live in the same area, experience similar challenges, and primarily interact with and mate with one another. While members of different populations are still the same species, and can produce offspring together if they meet by chance, often the different conditions that they experience lead to minor changes in their genetics and fitness-related traits, known as 'local adaptation'. When members of a locally adapted population are transplanted to the conditions experienced by a different population, they may not fare as well.

Conservation efforts that fail to recognise local variation between populations may fall flat. However, this variation can be difficult to detect by observation alone, particularly





for small aquatic creatures such as freshwater mussels. Fortunately, modern genetics tools offer a window into local adaptation that can help researchers parse out which populations might be unique.

Drs Jones and Hallerman have developed the use of genetic data to inform conservation decisions into an art. Using modern molecular genetics techniques, they routinely identify where the variation in populations lies, and use this information to advise conservation agencies in how to manage species to both protect the uniqueness of locally adapted populations and preserve genetic variation across the species.





The habitat of a threatened Virginia fish, the Roanoke logperch, has been heavily fragmented by the damming of its native rivers, creating a patchwork of dam-divided populations across the region. In 2013, Dr Hallerman's lab completed a comprehensive survey of the current populations of the fish, in an effort to determine how their numbers could be restored. They found that the fragmentation had led to a loss of genetic variation in certain areas, and recommended that to restore the Roanoke logperch, it would be necessary to reconnect certain isolated populations. Similarly, a research team led by Dr Jones set out to characterise the genetic structure of remaining populations of the endangered rough pigtoe mussel, found in rivers in Tennessee and Kentucky. First, they determined that the rough pigtoe is indeed a unique species, distinct from its close relatives. Then they found that populations from the two states are similar enough to be considered a single species. Although they are the same species, the two populations are genetically distinct, and Dr Jones recommended that they should be managed as distinct units. Though not imperilled, the horseshoe crab is of high ecological and economic importance to the Eastern seaboard, due to its unusual copper-based blood which is harvested for medical applications. However, habitat loss and harvesting have led to a steady decline in horseshoe crab populations. Recently, Dr Hallerman's team sampled crabs along the shore from Maine to Mexico, and found that there are regional differences between populations. This supports the formation of a region-based management system that can maintain demographically viable crab populations.

Drawing Lines Between Species

In addition to characterising known species, Dr Hallerman and Dr Jones often find evidence for new species in their work.

Mussel species can be particularly difficult to distinguish by assessing their shells alone. During his work on the highly endangered *Epioblasma* genus of mussels, they found that one group of the small creatures was indeed a unique species, while another with a slightly different shell qualified as a subspecies.

Another group of critically endangered mussels, the Cumberland bean and Tennessee bean, have highly similar shells but with different colours – white and pinkish purple on the inside, respectively. It was



believed that the two overlapped in habitat, making management decisions for their conservation difficult. When the team investigated, they instead found that the two are not only distinct species, but that their ranges do not overlap at all. Rather, white-shelled mussels that had previously been identified as Cumberland beans, were actually just another colour variation of the Tennessee bean mussel. Although the white shells of the two species are not distinguishable by eye, their genetics tell another story.

The Hatchery Problem

One of the most common means of conservation intervention for endangered aquatic animals is hatchery-based rearing with subsequent release into the wild. While this may seem like a straightforward enough task, without a careful program design that helps preserve genetic variation, hatcheries are at risk of negatively altering the genetic makeup of the populations they are trying to preserve.

This most commonly happens through unintentional artificial selection. Artificial selection occurs when only plants or animals with a particular trait are allowed to breed – this is the method by which most of our modern crops and domesticated animals have come to exist in the forms we recognise. Pure-bred dogs are among the most familiar examples – there is only one species of dog, but through breeding for a specific trait, such as short legs in the dachshund, humans have created a myriad of dog breeds that look nothing like their wolf ancestors.

When artificial selection occurs in hatcheries, it is often less obvious, and is more likely to be due to the conditions in the hatchery itself or the conditions under which the breeders for the hatchery were collected. In the first case, conditions in the hatchery may be different than those in the wild and cause young animals sensitive to those conditions to survive at lower rates.

For example, imagine that the water temperature in a hatchery is a few degrees cooler than what animals would normally experience in their native stream. Very young offspring that are cold-hardy would be likely to survive to adulthood, while those that need warmer waters die off. However, when returned to their natural habitat, the individuals that thrived in the hatchery may struggle to deal with warmer water.

In the second case, many animals breed over the course of a season, with some individuals that preferentially breed early and those that preferentially breed late. If well-intending conservationists only collect breeders during one time point of the season, they are likely to exclude genetic variants unique to early and late breeders.

In both of these situations, artificial selection has occurred, which may impede the success of any reintroduction programs.

Innovation in Hatchery Conservation

Dr Jones and Dr Hallerman have made strides in improving hatchery programs for both mussels and fish, and helped others prevent common errors that put hatchery conservation at risk of failure. As population geneticists, their chief goal is to build restocking programs that maintain the genetic diversity of the original population.

As part of his extensive research in captive mussel propagation, Dr Jones has developed a comprehensive set of guidelines that can inform other programs. He posits that first and foremost, there should be a habitat to introduce the animals back into. Next, it should be determined what the current genetic variability of a target population is, and what the plans are for collecting and maintaining this genetic diversity. Throughout the entire hatchery rearing process, Dr Jones's team is initiating a program to ensure that genetically diverse progeny are stocked into the wild.

It is critical for conservationists to be aware of subpopulations that may have their own genetic structure and may have unique traits that would be diluted or lost by interbreeding with larger populations. Breeders should be collected from the same areas that their progeny will be returned to, ideally during multiple points in the season and periodically rotating out breeding adults. Hatchery habitats should mimic natural ones as closely as possible, providing variation in temperature and other factors that offspring will face when returned to the wild. And finally, release programs should be carefully designed and monitored to identify which factors facilitate the most successful boosts to wild populations.

Following these guidelines, Dr Jones and Dr Hallerman were able to lead a program in Virginia that successfully bolstered the population of endangered oyster mussels and identified the best release methods for this particular species.

These methods have also helped to bolster the populations of sport fisheries. The walleye is a popular and economically important sport fish in the eastern US, but the population of these fish crashed after hydroelectric dams were constructed in the New River of Virginia. Initial stocking programs introduced fish from other locations, but this practice was suspended in 1997 when it was realised that this process conflicted with the conservation of native walleye.

Through genetic testing, Dr Hallerman and his colleagues were able to first identify native individuals, and then develop a breeding program to focus on restoring their numbers. Over 17 years, the team was able to successfully restore the population to historical numbers, while simultaneously increasing the frequency of native walleye. By marrying genetics and conservation, Dr Hallerman's team has been able to ensure that these fish will retain their natural variation while remaining available for sport fishing.

A Future for Aquatic Conservation

As more aquatic species face endangered status and budgets tighten, it is becoming ever more critical to identify the best approaches to population management. Through the work of Dr Hallerman and Dr Jones, fisheries managers now have a better understanding of how to plan and implement cost-effective conservation strategies that are proven to work.





Meet the researchers

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Dr Eric Hallerman is a professor in applied population genetics and biotechnology. His research interests include genetics of fish and wildlife species, genetic improvement of aquaculture stocks, animal biotechnology and related public policy, and genetics education. He completed his BS in environmental science in 1977 and his MS in biology in 1980 at the University of Illinois at Champaign-Urbana, followed by a PhD in fisheries and aquaculture at Auburn University in 1984. He then worked as a post-doctoral fellow at Hebrew University of Jerusalem, and as a research scientist at the University of Minnesota. He joined the faculty at Virginia Tech in 1989, where he maintains an active molecular genetics laboratory. He was also head of the department between 2007 and 2013.

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Dr Jess W. Jones is a restoration biologist with the US Fish & Wildlife Service and director of the Freshwater Mollusk Conservation Center. He is also an associate professor in the Department of Fish and Wildlife Conservation at Virginia Tech. His research focuses on conservation biology of freshwater mussels, with an emphasis on: conservation aquaculture; restoration ecology and monitoring of populations; aquatic ecotoxicology; and conservation genetics. He is particularly interested in improving field and laboratory techniques to restore mussel populations to enhance the capability of the Department of Interior's Natural Resource and Damage Assessment and Restoration (NRDAR) program. This work includes applying small- and large-scale mesocosms to improve captive growing and experimental conditions for endangered mussels and fishes. He earned his BS in 1996, his MS in 2004 and a PhD in 2009, all in fisheries science at Virginia Polytechnic Institute and State University.

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