

Little genes, big conservation: Scientists study genetic rescue

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A new paper by UM scientists examines the potential and uncertainties of attempting genetic rescue. Credit: University of Montana



At first glance, there aren't many similarities between westslope cutthroat trout in Montana, wolves on Isle Royale National Park in Michigan and Australia's mountain pygmy possum, a mouse-sized alpine marsupial.

With all three, though, managers have attempted or explored the possibility of genetic <u>rescue</u>, a conservation approach that involves moving a small number of individual animals from one population to another to reduce genetic problems and decrease extinction risk.

Now, a new paper by University of Montana scientists examines the potential and uncertainties of attempting genetic rescue. The peer-reviewed paper, published this month in the journal *Trends in Ecology and Evolution*, is a synthesis and summary of the state of genetic rescue. In this opinion piece, the authors focus on what is unknown about genetic rescue and where research could go in the future.

The authors define genetic rescue as a decrease in population extinction probability owing to gene flow, best measured as in increase in population growth.

"Inbreeding can cause genetic defects that lower survival," said Donovan Bell, paper co-author and a doctoral candidate in UM's W.A. Franke College of Forestry and Conservation. "In small populations, every individual becomes closely related and the resulting genetic problems put these populations at a higher risk of extinction. With genetic rescue, introducing unrelated individuals from another population can alleviate these genetic problems."

"It allows natural selection to increase the amount of beneficial genetic material introduced by managers," said co-author Zak Robinson, also a doctoral candidate in the forestry college. "It increases individual survival and lifetime reproductive success, which can increase the



population's size and health."

As human development increases, so does fragmentation, and animal populations are increasingly splintered into smaller, isolated populations, the authors say.

"Even if fragmentation was to stop today, there are already millions of populations that are limited to small habitats," Robinson said. "In order to address issues with small, fragmented populations and maintain biodiversity, we're going to have to find ways to mitigate the impacts of inbreeding and the genetic problems it brings."

That's where genetic rescue comes in.

"Habitat fragmentation is incredibly common, and it's a huge problem for conservation," Bell said. "There are a few research groups that are strongly advocating that we start implementing genetic rescue in a much more widespread manner to address issues with habitat fragmentation. We think that genetic rescue is very valuable, but there is a lot left to understand about genetic rescue."

In their paper, Bell, Robinson and their co-authors focus on what is still unknown about genetic rescue and areas where future research could prove beneficial. Some of those big questions include: how long the effects of genetic rescue will last; under what conditions potential negative consequences could occur, including genetic swamping (the loss of unique local adaptations), and outbreeding depression (reduced fitness of offspring with evolutionarily divergent parents); how populations and individuals should be selected for genetic rescue attempts; and how advances in genomics—the study of genomes—fits into the whole picture.

The authors also draw attention to the relationships between genetic



rescue and boots-on-the-ground conservation efforts—a pairing emphasized by successful genetic rescue stories like the Florida panther or Australia's mountain pygmy possum.

"Genetic rescue is unlikely to be a conservation silver bullet on its own, but instead needs to be attempted as part of a broader conservation strategy that includes habitat improvements," Bell said.

"Genetics and ecology are fundamentally intertwined," Robinson said.
"There's a complex relationship between the genetic composition of a population and extinction. We need to understand this better in order to mitigate the part of extinction risk that's associated with the genetic composition of a population."

The synthesis closely ties to Bell and Robinson's ongoing research efforts. As part of their wildlife biology doctoral programs, each is running a genetic rescue experiment testing the conservation approach on wild fish populations.

In partnership with Montana Fish, Wildlife and Parks and with funding from the National Science Foundation, Bell is studying westslope cutthroat trout in Montana—Big Sky Country's state fish and currently listed as at-risk in Montana. On the east side of the Continental Divide, most of the populations that haven't hybridized with rainbow trout are isolated in small headwater streams, and there are concerns that these populations could suffer from genetic problems, Bell said.

Robinson's project, also funded by NSF, encompasses similar research on Eastern brook trout in his home state of Virginia, research he originally embarked on as an undergraduate student.

They hope these projects will help answer some of the questions they acknowledge in their latest paper.



"These are tests. We want to see how it works and see if it's ready for popular consumption for the state agencies managing isolated trout populations," Robinson said. "What we want to do is understand genetic rescue well enough so that managers can prioritize their activities and weigh it against other competing strategies on a limited budget."

"Attempting genetic rescue is a really promising conservation strategy, but there are still uncertainties we need to address in order to make it as useful as possible for conservation and also to increase confidence in using the strategy," Bell said. "It's actually implemented very rarely right now."

More information: Donovan A. Bell et al, The Exciting Potential and Remaining Uncertainties of Genetic Rescue, *Trends in Ecology & Evolution* (2019). DOI: 10.1016/j.tree.2019.06.006

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