

Genetic analysis of the American eel helps explain its decline

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American Eels of the upper St. Lawrence grow slowly but attain larger sizes (top) compared with eels in coastal areas (bottom). Credit: Guy Verreault/*Current Biology* 2015

The American eel has been a concern for the U.S. Fish and Wildlife Service since 2007, when it was first considered for, but failed to receive, Endangered Species Act protection. The numbers of these slender, slimy, ancient fish in freshwater areas have been decreasing rapidly due to dams, pollution, and overfishing, but scientists have been puzzled as to why the fish can't recolonize. Now, a new look at eel



genetics published on May 28 in *Current Biology* finds that there are differences between eels that feed in freshwater and eels that feed in brackish environments that were previously thought to be genetically interchangeable.

Both freshwater and brackish American <u>cels</u> are the same species, but they vary in size and have very different growth rates and life spans. Once a year, sexually mature eels from both groups migrate thousands of miles to spawn in the Sargasso Sea (located in the North Atlantic Ocean east of Bermuda). The offspring are carried off by the current to their new homes. It's been thought that young American eels can detect whether they've ended up in brackish or freshwater habitats and acclimate accordingly. But this new study suggests that eels are predisposed to survive in these environments, depending on what genes they inherited.

"People have considered these differences in growth and age to be 100 percent due to phenotypic plasticity, independent of the genotype," says lead author Scott Pavey, a postdoctoral fellow at the Integrated Biology Institute of Laval University in Quebec, Canada. "But what we found is that genes affect whether an eel can survive freshwater or brackish environments." This helps explain why some conservation efforts to preserve the freshwater eel haven't been successful, as more plentiful brackish eels cannot easily change their traits to survive in freshwater environments.

Pavey, in collaboration with ecologist Louis Bernatchez and colleagues, used new sequencing technologies to screen the eel genome in 45,000 places. The analysis identified 99 genes that differ between <u>freshwater</u> and brackish eels, including those associated with growth rate, heart development, and smell. It's unknown whether this type of genetic differentiation exists in other, non-eel marine species with high levels of <u>phenotypic plasticity</u>.



The question remains, though, as to why eels would have such a strange approach to survival. The fish is considered evolutionarily ancient, so they must be doing something right. "It's a different strategy, a kind of hedging your bets," speculates Pavey. His team is now working to publish and release the entire genome of the eel. This will provide an important tool for other researchers to conduct similar studies on different aspects of eel ecology.

More information: *Current Biology*, Pavey et al.: "RAD-sequencing highlights polygenic discrimination of habitat ecotypes in the panmictic American Eel" <u>www.cell.com/current-biology/a</u>... <u>0960-9822(15)00548-5</u>

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