

Genomic correlates of disease recovery in natural populations of mountain yellow-legged frogs

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Abstract

In our rapidly changing world, evolution is likely to play an important role in facilitating the resilience of wildlife populations. The mountain yellow-legged frog (*Rana muscosa*/*Rana sierrae*) provides a rare example of recovery following severe declines caused by the amphibian chytrid fungus (*Batrachochytrium dendrobatidis*). However, the role of evolution in facilitating this recovery remains circumstantial. In this study, we sought to gain insights into the potential role of evolution by comparing genomes of frogs from naïve and recovering populations located in relatively close proximity. Using multiple methods to scan frog genomes for signatures of selection, our study reveals several genomic variants associated with frog recovery. Specifically, we identify gene variants in interferon-related genes and genes associated with the complement system and major histocompatibility complex (MHC). Additionally, we identify a recovery-associated variant in *RIN3*, a gene that may play a critical role in disease defense and wound healing. Finally, we report no differences in genetic diversity between naïve and recovering populations. We provide a rare example from natural populations that suggests that evolution can produce individuals that harbor adaptive alleles and allow population recovery in a novel environment. These findings complement recent research on amphibian immune evolution and provide mechanistic hypotheses for how individuals from populations can recover from disease.

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