Investigating the Genomic Diversity among Lineages of the Imperiled Gila Trout (*Oncorhynchus gilae*) using RADseq Data: A Conservation Management Perspective

David Camak[1], Megan Osborne[1], and Thomas Turner[1]

[1]University of New Mexico

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Abstract

Many salmonid species exist in highly structured and isolated populations, and are susceptible to habitat fragmentation and disturbances. Gila Trout (*Oncorhynchus gilae*) is a threatened species found in the Southwestern United States. Gila trout is managed to preserve remnant populations (i.e. lineages) distributed across a fragmented landscape. We evaluated genomic variation within and among remaining lineages of Gila Trout using RADseq to assess how drift and selection have structured populations using neutral and outlier loci. We also examined whether a signature of hybridization was evident in relict populations. Despite Gila Trout lineages being significantly differentiated and highly structured with low effective population sizes, we found that most lineages maintained genomic diversity and were potentially locally adapted. Hybridization with non-native Rainbow Trout (*O. mykiss*) was not detected in any lineage. Some lineages may have experienced recent population bottlenecks perhaps associated with mortality from drought and severe wildfires. Current management strategies should be reevaluated and adapted to better account for long-term effects of climate change. Specifically, we suggest reconnecting some populations via dendritic stream networks to facilitate natural dispersal in a metapopulation context. This would allow natural genetic mixing on the landscape and potentially increase adaptive potential. Furthermore, genetic rescue should be implemented to preserve integrity of the unique Spruce Creek lineage that is currently compromised by extremely low diversity.

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