

Multilocus genetic analysis of North American common loon populations using “RAD-tag” second-generation sequence data

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Common loons (*Gavia immer*) breed on lakes in the mid- and high-latitudes of North America and winter on the Pacific and Atlantic near-coastal waters. Establishing linkages between breeding populations, migratory routes and overwintering regions is important for providing a comprehensive understanding of threats to loon populations. Using second-generation DNA sequencing technology on samples from breeding, migrating and overwintering loons from across North America, we created single-nucleotide-polymorphism (SNP) genetic profiles based on hundreds of loci.

Analysis of this large dataset provides evidence that, 1) common loon populations show patterns of genetic diversity consistent with isolation by distance, 2) the North American Great Lakes are an important migratory stopover site for birds that breed across a greater range than previously described, and 3) these genetic markers provide enough resolution to assign wintering individuals back to their breeding populations. These results improve our understanding of common loon demographics and conservation. Further, they demonstrate the dramatic power of second-generation sequencing data for informing studies of loon populations.