

Resource Summary Report

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Protocols from: Invasion genetics of the silver carp (*Hypophthalmichthys molitrix*) across North America: Differentiation of fronts, introgression, and eDNA detection

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Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.u6zezf6>

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Summary: This protocol describes the data collection and analysis performed in "Invasion genetics of the silver carp (*Hypophthalmichthys molitrix*) across North America: Differentiation of fronts, introgression, and eDNA detection". Published in PLOS One, 2018. The invasive silver carp *Hypophthalmichthys molitrix* escaped from southern U.S. aquaculture during the 1970s to spread throughout the Mississippi River basin and steadily moved northward, now reaching the threshold of the Laurentian Great Lakes. The silver carp is native to eastern Asia and is a large, prolific filter-feeder that decreases food availability for fisheries. The present study evaluates its population genetic variability and differentiation across the introduced range using 10 nuclear DNA microsatellite loci, sequences of two mitochondrial genes (cytochrome b and cytochrome c oxidase subunit 1), and a nuclear gene (ribosomal protein S7 gene intron 1). Populations are analyzed from two invasion fronts threatening the Great Lakes (the Illinois River outside Lake Michigan and the Wabash River, leading into the Maumee River and western Lake Erie), established areas in the southern and central Mississippi River, and a later Missouri River colonization. Results discern considerable genetic diversity and some significant population differentiation, with greater mtDNA haplotype diversity and unique microsatellite alleles characterizing the southern populations. Invasion fronts significantly differ, diverging from the southern Mississippi River population. About 3% of individuals contain a unique and very divergent mtDNA haplotype (primarily the southerly populations and the Wabash River), which may stem from historic introgression in Asia with female largescale silver carp *H. harmandi*. Nuclear microsatellites and S7 sequences of the

introgressed individuals do not significantly differ from silver carp. MtDNA variation is used in a high-throughput sequence assay that identifies and distinguishes invasive carp species and their population haplotypes (including *H. molitrix* and *H. harmandi*) at all life stages, in application to environmental (e)DNA water and plankton samples. We discerned silver and bighead carp eDNA from 10 bait shops in the Great Lakes watershed, indicating that release from retailers comprises another likely vector. Our findings provide key baseline population genetic data for understanding and tracing the invasion's progression, facilitating detection, and evaluating future trajectory and adaptive success.

Associated Publications: Stepien CA, Snyder MR, Elz AE (2019) Invasion genetics of the silver carp *Hypophthalmichthys molitrix* across North America: Differentiation of fronts, introgression, and eDNA metabarcode detection. PLoS ONE 14(3): e0203012. doi: [10.1371/journal.pone.0203012](https://doi.org/10.1371/journal.pone.0203012)

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