

A Nuclear DNA Perspective on Delineating Evolutionarily Significant Lineages in Polyploids:  
The Case of the Endangered Shortnose Sturgeon (*Acipenser brevirostrum*)

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Abstract

The Shortnose Sturgeon, *Acipenser brevirostrum*, oft considered a phylogenetic relic, is listed as an “endangered species threatened with extinction” in the US and “Vulnerable” on the IUCN Red List. Effective conservation of *A. brevirostrum* depends on understanding its diversity and evolutionary processes, yet challenges associated with the polyploid nature of its nuclear genome have heretofore limited population genetic analysis to maternally inherited haploid characters. We developed a suite of polysomic microsatellite DNA markers and characterized a sample of 561 *A. brevirostrum* collected from major extant populations along the North American Atlantic coast. The 181 alleles observed at 11 loci were scored as binary loci and the data were subjected to multivariate ordination, Bayesian clustering, hierarchical partitioning of variance, and among-population distance metric tests. The methods uncovered moderately high levels of gene diversity suggesting population structuring across and within three metapopulations (Northeast, Mid-Atlantic, and Southeast) that encompass seven demographically discrete and evolutionarily distinct lineages. The predicted groups are consistent with previously described behavioral patterns, especially dispersal and migration, supporting the interpretation that *A. brevirostrum* exhibit adaptive differences based on watershed. Combined with results of prior genetic (mitochondrial DNA) and behavioral studies, the current work suggests that dispersal is an important factor in maintaining genetic diversity in *A. brevirostrum* and that the basic unit for conservation management is arguably the local population.