Transitioning Atlantic Sturgeon from Population Genetics to Population Genomics

King, T.[1], D. Kazyak[1], M. Eackles[1], R. Johnson[1], J.E. Kahn[2], and M. Rasser[3]

[1]US Geological Survey, Leetown Science Center, Kearneysville, WV;
[2]National Oceanic and Atmospheric Administration, Silver Springs, MD;
[3]Bureau of Ocean Energy Management, Sterling, VA

USGS-Leetown Science Center (LSC) in conjunction with NOAA-Fisheries has genotyped in excess of 1,500 Atlantic Sturgeon sampled from the St. Lawrence River, Canada to southern Georgia at 12-20 microsatellite DNA markers. This information has assisted resource managers by clarifying population structuring, identifying appropriate management units, and allowing assignment of individuals intercepted as bycatch or other anthropogenic activities to river or DPS of origin. As three putative metapopulations have been identified, fine-scale population resolution is required as well as the identification of adaptive features. To address this research need we have begun a transition from population genetics (12 microsatellite markers screened across 124 chromosomes) to population genomics (screen thousands of markers across the genome) by employing genotype by sequence (GBS). This research has allowed the identification and contrasting of large numbers of neutral and non-neutral markers among collections interspersed across the species range to further assess functional (meta)population assemblages, identification of evolutionary significant lineages, and provided data for modeling adaptive resiliency. Genomic shotgun sequencing has allowed the assembly and annotation of the complete mitochondrial genome. GBS sequences mapped to this genome have identified a large number of polymorphic sites distributed throughout the mtDNA molecule. In addition, LSC has generated approximately 40X coverage of the Atlantic Sturgeon transcriptome in the form of 394,482 contigs (genome segments) using contemporary genomic sequencing (RNA-Seq). Variant detection in these contigs have yielded in excess of 1 million SNPs. We are currently in the process of annotating the transcriptome; the most complete of any Acipenseridae species. This transcriptome will provide an important resource for future studies of physiological and immunological processes in this species, and help delineate adaptive differentiation which ultimately could promote resiliency in the context of environmental change.