

Identifying the fundamental unit of management and characterizing historical demographic patterns in the Atlantic Sturgeon: A genetic perspective

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The issue of defining appropriate units of management becomes acute when taxa under consideration are threatened or endangered and protection relies on proof of distinction of the units. Sturgeons present significant challenges for investigating the evolutionary processes shaping the nuclear genomes of extant species due to the presence of polyploidy ranging in a series from 4N-8N times the haploid number. We will present the results of a range-wide survey of 12 disomic nDNA markers in >1,500 river-resident juvenile and adult Atlantic Sturgeon (*Acipenser oxyrinchus*; 4N) sampled from 13 river systems. Results from a series of statistical analyses indicate that most, if not all, subpopulations are statistically differentiated based on allelic frequencies, AMOVA, F_{ST} (and F'_{ST}) and allocation analyses and that the river system should be considered the fundamental unit of management. While nDNA analyses detected statistically significant differences in allelic frequencies between most river systems, regional zones of genetic discontinuity were detected in the patterns of genetic variation across the range that likely delineate evolutionarily significant differentiation and adaptive potential for this species. These regions, demarcated by zones of genetic discontinuity, represented deeper levels of genetic differentiation, perhaps a higher degree of reproductive isolation than that usually attributable to population-level differentiation. These zones of discontinuity delineate populations or groups of populations that likely warrant greater conservation considerations. We propose the designation of at least six evolutionarily significant lineages: 1) St. Lawrence and St. John; 2) Gulf of Maine (Kennebec), 3) New York Bight (Hudson R., Delaware R.) 4) Chesapeake Bay (James R., York R.), 5) Carolina (Albemarle Sound), and 6) South Atlantic (Edisto, Savannah, Ogeechee, and Altamaha). This level of molecular differentiation has allowed assignment of individuals sampled from near-shore mixed-stocked collections to river or lineage of origin. While a statistically significant, positive correlation exists between the measures of population differentiation (F_{ST}) for nDNA and the maternally inherited mitochondrial DNA (mtDNA), differences of opinion exist as to what constitutes a Distinct Population Segment for Atlantic Sturgeon. Comparisons will be made with patterns observed by other researchers.