

Speciation, hybridization, and conservation of musk turtles in the southeastern United States

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Conservation of biodiversity is contingent on a thorough understanding of species level diversity and the relationships between species as well as understanding the demographic history of genes across the landscape. The southeastern United States, and especially Alabama, is a hotspot of aquatic biodiversity, but it is also a highly imperiled ecological region. This gives added urgency to understanding evolutionary history of species in this region, especially for threatened organisms as robust inference of species limits and interspecific relationships is necessary to ensure management efforts are conducted in a meaningful way. Here musk turtles (*Sternotherus*) are used as a model to understand processes of speciation and lineage diversification across riverine systems in the southeastern US. *Sternotherus* has had a historically turbulent taxonomic history, plagued in part by constraints due to background rates of evolution in turtles. Reduced representation genomic sequencing is used to test species limits and understand evolutionary relationships within *Sternotherus*. Once a firm taxonomic background is established, hybridization and resulting genomic clines between two species are analyzed to understand how selection may be influencing the shape and direction of genomic introgression, especially in relation to a federally imperiled species: the flattened musk turtle. Lastly, a complete reassessment of the status of the flattened musk turtle is discussed, which highlights best practice to ensure the species survival. Overall, this work highlights one of the first studies to use genomic-scale data to infer evolutionary histories of species inhabiting a major, yet under-researched, biodiversity hotspot and provides a new framework for hypotheses on mechanisms shaping biodiversity in this region to be tested.