POPULATION STRUCTURE AND GENE FLOW IN THE SHEEPNOSE MUSSEL (*PLETHOBASUS CYPHYUS*) AND THEIR IMPLICATIONS FOR CONSERVATION

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Abstract

North American freshwater mussel species have experienced substantial range fragmentation and population reductions. These impacts have the potential to reduce genetic connectivity among populations and increase the risk of losing genetic diversity. Thirteen microsatellite loci and an 883 bp fragment of the mitochondrial ND1 gene were used to assess genetic diversity, population structure, contemporary and historical migration rates, and population size changes across the range of the Sheepnose mussel (*Plethobasus cyphus*). Population structure analyses reveal five populations, three in the Upper Mississippi River Basin and two in the Ohio River Basin. Sampling locations exhibit a high degree of genetic diversity and contemporary migration estimates indicate that migration between populations within river basins is occurring, although at low rates. but no migration is occurring between the Ohio and Mississippi river basins. No evidence of bottlenecks was detected, and almost all locations exhibited the signature of population expansion. Our results indicate that although anthropogenic activity has altered the landscape across the range of the Sheepnose, these activities have yet to be reflected in losses of genetic diversity. Efforts to conserve sheepnose populations should focus on maintaining existing habitats and fostering genetic connectivity between extant demes to conserve remaining genetic diversity for future viable Sheepnose populations.

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