

PhD Dissertation
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Title: Population Genetic Structure of The Red-Spotted Newt (*Notophthalmus Viridescens*) In Virginia

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ABSTRACT

The red-spotted newt (*Notophthalmus viridescens viridescens*) is ubiquitous throughout eastern North America. Despite its commonness, gaps exist in our understanding of its population structure. The hypothesis, first proposed in the 1970's, that the red-spotted newt exists as an intrametapopulation panmixis dependent on high levels of connectivity for its long-term persistence has not been adequately tested using the genetic tools developed since that time. Instead, genetic analyses to date have focused on the population structures of the rarer subspecies of *N. viridescens* or on the phylogenetic relationships between these subspecies. This is the first study of population structure conducted specifically on the red-spotted newt.

To evaluate the genetic population structure, I collected sequence data on the mitochondrial D-loop and the flanking tRNA Pro and tRNA Phe genes from nine populations of newts located in the Shenandoah Mountains west of Harrisonburg, Virginia and in the Massanutten Mountains. The lack of sequence differentiation between these populations indicates a collection of breeding populations connected through gene flow, supporting the premise of a metapopulation structure. This connectivity was maintained even though the ponds were located on separate mountain ridges. Presumably the contiguous, forested habitat between ponds allowed unimpeded dispersal between ponds. The detection of unique haplotypes in an

isolated Massanutten Mountain pond may indicate a recent disruption in gene flow and warrants further investigation. The level of habitat disturbance seen in the Shenandoah Valley isolating this pond would be prohibitive to dispersal.

An evaluation of microsatellite markers previously published and those developed for this study revealed the likelihood of polyploidy in these populations. Triploidy in *N. viridescens* had been observed previously through cytogenetic analysis; however, the tetraploidy observed in this study had not previously been documented. It is unknown whether this is unique to the populations in this study.

The long-term survival of the red-spotted newt is dependent on the connectivity of the sub-populations of the regional metapopulation. As such, conservation efforts should focus on maintaining connectivity between populations. This study has called attention to the need for further genetic research to identify populations at risk of genetic isolation.