

NORTHERN ILLINOIS UNIVERSITY

**THE EVOLUTIONARY SIGNIFICANCE OF MELANISM IN  
THE COMMON GARTER SNAKE,  
*THAMNOPHIS SIRTALIS***

A DISSERTATION SUBMITTED TO THE GRADUATE SCHOOL  
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ABSTRACT

Evolution is defined as a change in gene frequency over time and occurs via several mechanisms, including natural selection, genetic drift, gene flow, and mutation. This study investigates the first three mechanisms in populations of the common garter snake, *Thamnophis sirtalis*. High levels of melanism (black coloration) occur in island and mainland populations in the western basin of Lake Erie. The frequency of melanism varies among populations but is stable within populations. Color pattern is probably determined at one locus with melanism recessive to normal coloration. Dorsal coloration may influence natural selection in two ways. Melanism may be advantageous if dark coloration increases heating rates or equilibrium temperatures. However, melanism may be detrimental if reduced crypsis leads to greater detection by predators.

To determine how melanistic snakes differ from normal snakes, I tested for associations of color pattern with morphology, growth, and behavior and found melanism may be associated with a greater number of subcaudal scales, a slower growth rate in mass, and a longer latency to move. To determine whether melanistics differ in thermal properties, I measured heating rates and equilibrium temperatures in matched pairs of normal and melanistic snakes. I found no thermal differences among neonates or subadults, suggesting that if melanism provides a thermal advantage, it is restricted to larger body sizes. To determine whether melanistics are subject to greater predation, I measured predation intensity using clay models. I found no difference in attack rate between normal and melanistic snake models.

In addition to these selection hypotheses, I also examined the role of population size, gene flow, and genetic drift. Estimation of population sizes suggests that some populations are small enough for genetic drift to influence allele frequencies. However,

estimation of gene flow from patterns of molecular variation using  $F_{ST}$ - and coalescent-based approaches suggests that gene flow is high (greater than 3 migrants per generation). If estimated gene flow rates are correct, genetic drift should be swamped by migration, and variance in morph frequency among populations is better explained by differences in selective regimes. However, if these rates overestimate contemporary gene flow, drift may be primarily responsible for this variance.