DANIEL L. PITTS, ZACHARY J. LOUGHMAN, & NICOLE L. GARRISON, Dept of Biological Sciences, West Liberty University, West Liberty, WV, 26074. How much information is phylogenetically informative: investigations with single and multilocus analyses of garter snake (*Thamnophis*) taxonomy.

Garter snakes *(Thamnophis)* are a diverse group of North American natricid snakes. Previous studies have used single and multilocus analyses to investigate the relationships between members of this genus. Varying amounts of information used in these analyses have yielded different results, which have been used as evidence for and against speciation, potentially impacting conservation efforts. This study aimed to assess the quantity of genetic information needed to draw conclusions on species and subspecies-level relationships. Publicly available mitochondrial DNA sequences from four mitochondrial genes for each available *Thamnophis* species and the outgroup, water snakes (*Nerodia*), were gathered. Sequences were aligned and trimmed to generate maximum likelihood phylogenies with ultrafast bootstrap values for single gene and multiple gene concatenated trees. Seven total trees were generated: 3 single gene trees, 2 two gene trees, a three gene tree, and a four gene tree. Cytochrome B trees of *T. elegans* and members of the northern clade were made to investigate the paraphyly of *T. elegans*. Results indicate that some individuals of *T. atratus* were possibly misidentified as *T. e. terrestris*. Three broad clades conforming to the results of previous studies were retrieved across multiple gene trees. Trees using multiple genes had higher bootstrap support but sampled fewer species. The polyphyly of *T. cyrtopsis* and *T. pulchrilatus* were retrieved in previous studies, however, the authors did not offer any comment on the results, warranting further investigation. This research provides a starting point for further investigation into species and subspecies delineation in *Thamnophis*.