HOW FAR HAVE THEY SLITHERED? GENETIC VARIATION AMONG GARTER SNAKES IN WESTERN MONTANA

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Snake gene flow across wide geographic regions is poorly understood. Limited sampling opportunities and the challenges posed by microsatellite analysis often prevent researchers from assessing the impact of topographic barriers and the influence of human settlement on the genetics of snake populations. Last year we demonstrated that SNPs significantly improve our understanding of Isolation by Distance for both species of garter snake in Western Montana. Since then we have initially analyzed larger sample sets of Wandering Garters (N=192) and Common Garters (N=160). These samples were obtained at 77 sites during the 2014-2017 seasons. With these samples we hope to initially understand gene flow on both sides of the Continental Divide. Moreover, herpetologists traditionally assumed that the Continental Divide instigated a subspecies barrier for Common Garters. We hope to determine the efficacy of this assumption in the initial analysis of our data.