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# Genetic Connectivity of Eastern Massasauga Rattlesnakes in Michigan*

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Migration can be the mechanism through which gene flow occurs allowing for increased genetic diversity (Slatkin, 1985). When habitats are fragmented, genetic diversity between populations declines because of the inability of migrants to disperse between populations (Manier, 2005). Loss and fragmentation of suitable habitat, resulting in isolation of populations, has contributed to the decline and subsequent listing of the eastern massasauga rattlesnake as a threatened species by the U.S. Fish and Wildlife Service in September of 2016 (Chiucchi, 2010; Johnson, 1995; Mierzwa, 1993; Szymanski, 1998; United States Fish and Wildlife Service, 2016). Wetlands are a crucial environment for hibernation and reproduction of eastern massasaugas (Johnson, 2000). The loss and fragmentation of 50% of these lands, due to increased agriculture and building, in Michigan has led to declines in population size (Szymanski, 1998).

Eastern massasaugas (EMRs) have relatively limited dispersal and small home ranges (Weatherhead, 1992). As a result, population subdivision can occur, despite geographic proximity of populations (Ray, 2013; Andre, 2003; Gibbs, 1997). Previous studies have shown that EMR's occur in distinct populations, each containing an average of 23% unique alleles (Gibbs, 1997). This demonstrates isolation and lack of migration (Gibbs, 1997). We expand on previous studies by examining the level of genetic connectivity between eastern massasauga rattlesnake populations in Michigan.

We compared populations from seven sample sites across six Michigan counties. Samples were genotyped using polymerase chain reactions of 16 published microsatellites. We performed a STRUCTURE analysis and used GENEPOP v 4.6 (Rousset, 2008) and Genalex to calculate $F_{IS}$ and $F_{ST}$ as laid out by Weir and Cockerham (1984). A preliminary analysis resulted in an overall $F_{ST}$ value of 0.115. Moderate levels of inbreeding were found on Bois Blanc Island with an $F_{IS}$ value of 0.175. Additionally, a preliminary STRUCTURE analysis produced K=7, indicating seven distinct genetic clusters.

Our preliminary results indicate isolation of Michigan populations with little gene flow between them. Despite this isolation, most populations do not indicate inbreeding and signs of inbreeding depression are not evident. A possible explanation for this is that EMR's long history of living in small isolated populations has allowed them to adapt to slight levels of inbreeding (Chucchi, 2010). Additionally, if EMRs can recognize kin, like other snake species, they would be able to avoid mating with relatives, even in close proximity (Clark, 2004). Although most current populations do not indicate inbreeding, the Bois Blanc Island population is an example of extreme isolation and is the only population to show signs of inbreeding. This may be where mainland populations are headed if habitat loss and fragmentation continues leading to further isolation. Currently, EMRs are protected from harm under the Endangered Species Act. Our study helps to better understand mating pattern distribution of massasaugas. Using the conclusions of our study we hope to help optimize the success of future management plans by protecting critical massasauga habitat and restore connectivity of EMR populations in Michigan.

*This scholar and faculty mentor have requested that only an abstract be published.