1. Significance of the Study

The Neosho Smallmouth Bass (*M. d. velox*) potentially constitutes a significant portion of black bass diversity in the Interior Highlands of Missouri, Oklahoma, and Arkansas despite its restricted natural range. Although this subspecies has been morphologically distinguished from the conspecific Northern Smallmouth Bass (*M. d. dolomieu*; Hubbs and Bailey 1940), and although multiple studies have revealed genetic differentiation between these variants (Stark 1995; Stark and Echelle 1998), we have yet to validate its taxonomic status by synthesizing morphometric and genomic data. Taylor et al. (2016) detected introgression of non-native genes into native *M. d. velox* populations; with this information, they inferred three distinct genetic clusters that could serve as potential broodstock for stocking Grand Lake o’ the Cherokees (Taylor et al. 2016). However, their study was focused primarily on the Oklahoma portion of the range of M. d. velox and the waters in which non-native stocks had been introduced. Therefore, they are not fully reflective of *M. d. velox’* distinction from *M. d. dolomieu* and other congeners, especially in Missouri. Further, their study used microsatellite loci, which have limited power to detect hybridization and backcrossing. Validating the taxonomic status of *M. d. velox* is vital for strengthening our understanding of fish community diversity in the Interior Highlands. It may also shed light on the effects of inter- and intraspecific hybridization.

Largely due to its popularity as a sportfish, Smallmouth Bass have been ubiquitously stocked outside their native range (Robins and MaCrimmon 1974). They are known to hybridize with non-native congeners (Morizot et al. 1991; Whitmore 1983; Edwards 1979; Whitmore and Butler 1982; Turner et al. 1991; Pipas and Bulow 1998; Wheat et al. 1971; Whitt et al. 1971; Beaty and Childers 1980; Buck and Hooe 1986; Whitmore and Hellier 1998; Pierce and Van Den Avyle 1997; Pflieger and Fajen 1975; Koppelman 1994; Avise et al. 1997), so introducing individuals into new habitats can often lead to uncontrolled intermixing. Subsequent genetic introgression among related taxa can dilute the gene pool, potentially eliminating local adaptations, increasing vulnerability to disease (Hallerman 2003; Goldberg et al. 2005), or reducing overall diversity. Without a comprehensive understanding of smallmouth bass taxonomy, the continued implementation of stocking programs could severely alter their genetic and morphological diversity. If *M. d. velox* indeed represents a distinct smallmouth variant, its conservation as a unique subspecies is warranted. Taxonomic validation of *M. d. velox* is therefore necessary to preserve valuable biodiversity in the Interior Highlands.

Whether subspecies status is established or dismissed, resolving the taxonomic relationship between *M. d. velox* and *M. d. dolomieu* would offer conclusion to a 76-year-old taxonomic question (Hubbs and Bailey 1940). It would offer vital information on the protection of a unique subspecies through increased conservation and management efforts. These efforts, in turn, could generate opportunities for anglers and stimulate local economic growth. Furthermore, *M. dolomieu* is known to be a top predator, a host for many macroinvertebrates, and a bioaccumulator of anthropogenic contaminants (Brewer and Orth 2015). Increased monitoring of this species, including both subspecies, may be crucial for sustaining ecosystem structure and function.

*M. dolomieu* is only one of nine currently recognized *Micropterus* species endemic to North America (Shaw 2015).Classification for these taxa remains an imperfect process; species and subspecies nomenclature have been in near-constant flux since Hubbs and Bailey’s original descriptions 76 years ago (Hubbs and Bailey 1940). Validating the taxonomic status of *M. d. velox* using genomic methods could lay the groundwork for further morphological and genetic resolution across this historically and economically important genus.