SUMMARY OF GENETIC STUDIES RELATED TO *NOTROPIS TOPEKA* (TOPEKA SHINER)

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Several genetic studies have been conducted on *Notropis topeka* using a variety of analytical approaches. These genetic studies include the use of allozymes (coded enzymes, Bruce, 1988), ribosomal RNA (Bergstrom and Holtsford, 1999), mitochondrial DNA (Michels, 2000), microsatellite DNA (Bergstrom and Holtsford, 1999; Anderson and Sarver, 2008; Blank et al., 2011) and genetic markers for major histocompatibility (MHC, Anderson and Sarver, 2008) genes to detect polymorphism (variant forms of a gene responsible for immune system protection). Essentially all of these techniques are using some defined genetic marker to distinguish differences between or among populations. The later methods mentioned above are newer and tend to reveal greater levels of genetic diversity than the older method of allozyme analysis, thus making it easier to assess genetic differentiation between populations. Unfortunately, no systematic and comprehensive study of *N. topeka* across its range using sufficiently large sample sizes to estimate genetic diversity has ever been completed. Of the five genetic studies conducted on this species, all used different methods, different sample sizes, and fish from different locations. Because of this, making definitive statements about the genetic diversity and relationships among populations of this species across its range is difficult. However, enough work has been completed to make some general statements about the genetic relationships among *N. topeka* populations across spatial scales.

At the large river basin scale, significant genetic differences exist among the major river basins of the Missouri and Arkansas rivers. Moreover, significant differences exist within the Missouri River basin and among its major drainage basins (Bruce, 1988; Michels, 2000; Anderson and Sarver, 2008). Genetic differentiation is significant between the lower Missouri River (Kansas and Missouri) and upper Missouri River (South Dakota, Minnesota, and Iowa) populations, and among the Big Sioux, Vermillion, James, and Des Moines rivers. Essentially, the populations of *N. topeka* in the northern part of its range are significantly different from the southern part of its range *and* populations among the major drainages are distinct from one another. In addition to genetic differences between the upper and lower portions of the Missouri River, overall genetic diversity appears to be higher in the lower portion of the basin than in the upper portion (Michels, 2000; Blank et al., 2011). But, as a whole, *N. topeka* across its range appears to have lower levels of overall genetic diversity compared to the average measured genetic diversity of other freshwater fishes (DeWoody and Avise, 2000). The reason for this is difficult to ascertain given the complete lack of studies addressing this issue. Is this lower genetic diversity a result of recent post-glacial evolution or of a lack of genetic exchange due to anthropogenic modification of the landscape? Further studies are needed to address this question.

Finally, the issue of genetic differentiation among small watersheds is a bit more difficult to determine. Because no single genetic testing methodology was used in the various studies, conclusions regarding the genetic diversity and population structural differences among individual streams vary depending upon the methods used and conclusion drawn from it. But remember, all of these methods are accomplishing the same task, using a genetic marker to determine genetic relationships. Although the markers may have been different, the overall conclusion from the various studies seems to indicate that *most* of the sampling localities (i.e., individual streams) are genetically distinct. Exceptions to this include: two streams in Kansas which appears to lack significant genetic differentiation and could be treated as one population based on the work of two studies (Michels, 2000; Anderson and Sarver, 2008); and two streams in Min-

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nesota could be treated as one population but distinct from the other Big Sioux River populations under one study (Anderson and Sarver, 2008), yet another study finds these two streams could be treated as one population, but they are not distinct from others within the Big Sioux drainage (Michels, 2000). In addition, potential fine-scale population structure may exist among tributaries of the Vermillion and James rivers, respectively, in South Dakota (Blank et al., 2011). Clearly, additional research is needed to thoroughly understand genetic diversity throughout the range of *N. topeka*. For now, the precautionary principle should guide conservation managers to treat each stream with *N. topeka* as having the potential to harbor a unique genome, enabling this species to persist and remain resilient in the face of further anthropogenic landscape changes as well as climate change.

References

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