



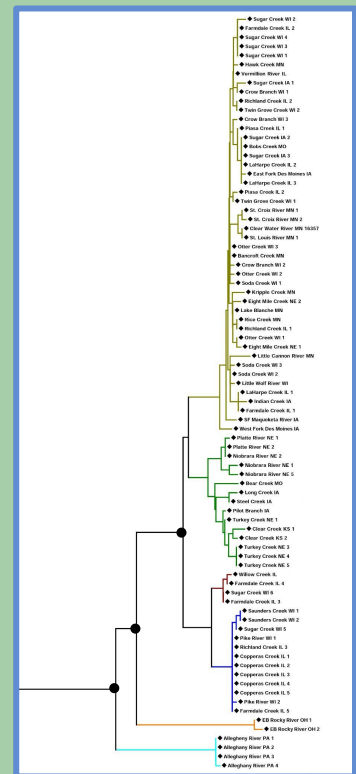
# Molecular Genetics and Phylogeography of *Notropis dorsalis*



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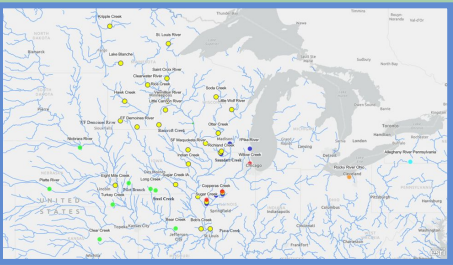


Allegheny River-Ohio River Clade Lake Erie Missouri River  
Illinois-Wisconsin 1 Illinois-Wisconsin 2 Iowa-Minnesota

Fig 3. Neighbor-Joining Phylogeny using a Jukes-Cantor distance matrix in MEGA v7.0.26

## Introduction/Background

North American river systems exhibit highly diverse fish species due to impacts of Pleistocene glaciation on geography<sup>1</sup>. The Bigmouth Shiner, *Notropis dorsalis*, is broadly distributed and may be comprised of multiple morphologically similar, but genetically divergent lineages<sup>2</sup>. We hypothesized that geographically separate drainage systems would contain genetically distinct clades. Cytochrome B is an 1140 base-pair mitochondrial gene with a moderate rate of mutation, making it an effective gene for inexpensive phylogeny construction.<sup>4</sup>



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Fig 1. Map of sample locations constructed in Power BI with ArcGIS

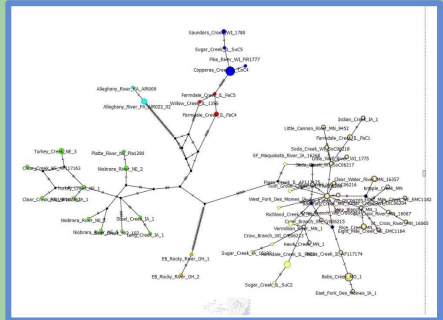


Fig 2. Minimum Spanning Network of sequence data for each sample. Constructed in PopART.

## Impact of the Data

- Provides insight into the distributions of freshwater species.
- Displays evolutionary history of *N. dorsalis*
- Aids in development of conservation management plans.
- Aids in future predictions of the biogeographical history of Mississippi river drainages.

## Methods

- Mitochondrial and Nuclear DNA was extracted using Qiagen Dneasy Blood and Tissue Columns.
- Cyt B gene regions were isolated using primers and PCR Amplified.<sup>3</sup>
- PCR products were purified using AMPure bead cleanup procedure, products were packaged and sent to the MU DNA core for sequencing.
- Sanger sequences were assembled in Geneious Prime v2022.0.1.
- Neighbor-Joining phylogenetic tree was constructed using Jukes-Cantor distance matrix in MEGA 7.0.26.

## Conclusions

Six clades were well supported, each represented by a colored branch on the phylogeny (Fig. 3). Three major population splits were observed (black dots). Generally, the western portion of the species range is less diverse, exhibiting only two closely related clades. These lineages diverged after the pleistocene.<sup>5</sup> The eastern populations were the most genetically distinct. These lineages diverged prior to the pleistocene and were dispersed as a result of glaciation events.

## Acknowledgements

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## References

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