



# A Bug's Life: DNA Barcoding of the Johnson Creek Site 5 Caddisfly Specimens

Aljabiry, H.; Ayodeji, Y.; Burt, D.; Moore, T.; Thomas, B.  
Natural Sciences Department, Marygrove College, Detroit, MI 48221

## Hypothesis

If there is a variety or diversity of macroinvertebrates within Johnson Creek, then the river is of good health and/or quality.

## Introduction

### DNA Barcoding

- uses the information of one or a few gene regions to identify all species of life
- aids in identifying species based on DNA sequences and compares the entire genome structure and expression of the specie
- valuable in helping to generate and characterize all species on the planet by comparing DNA

### Caddisfly

- common macroinvertebrate that can be found in streams, lakes, and ponds
- important because they indicate the quality of the water in the location that they are found in

We were able to identify the caddisflies' taxonomic group and compare the relationship of the specimens to other close relatives.



Johnson Creek Site 5  
volunteer team  
Marygrove/WSU



Johnson Creek River  
Rochester, MI

## Methods

- Gathered specimens from Johnson Creek (Rochester, MI)
- Sorted and Identified specimens
- Dissected and started DNA extraction of caddisfly
- Amplified specimen DNA using PCR
- Applied gel electrophoresis and PCR clean up
- DNA sequencing done through Wayne State University
- DNA Barcoding: sequence editing, chromatograms, contig building, BLAST, sequence alignment, and tree building

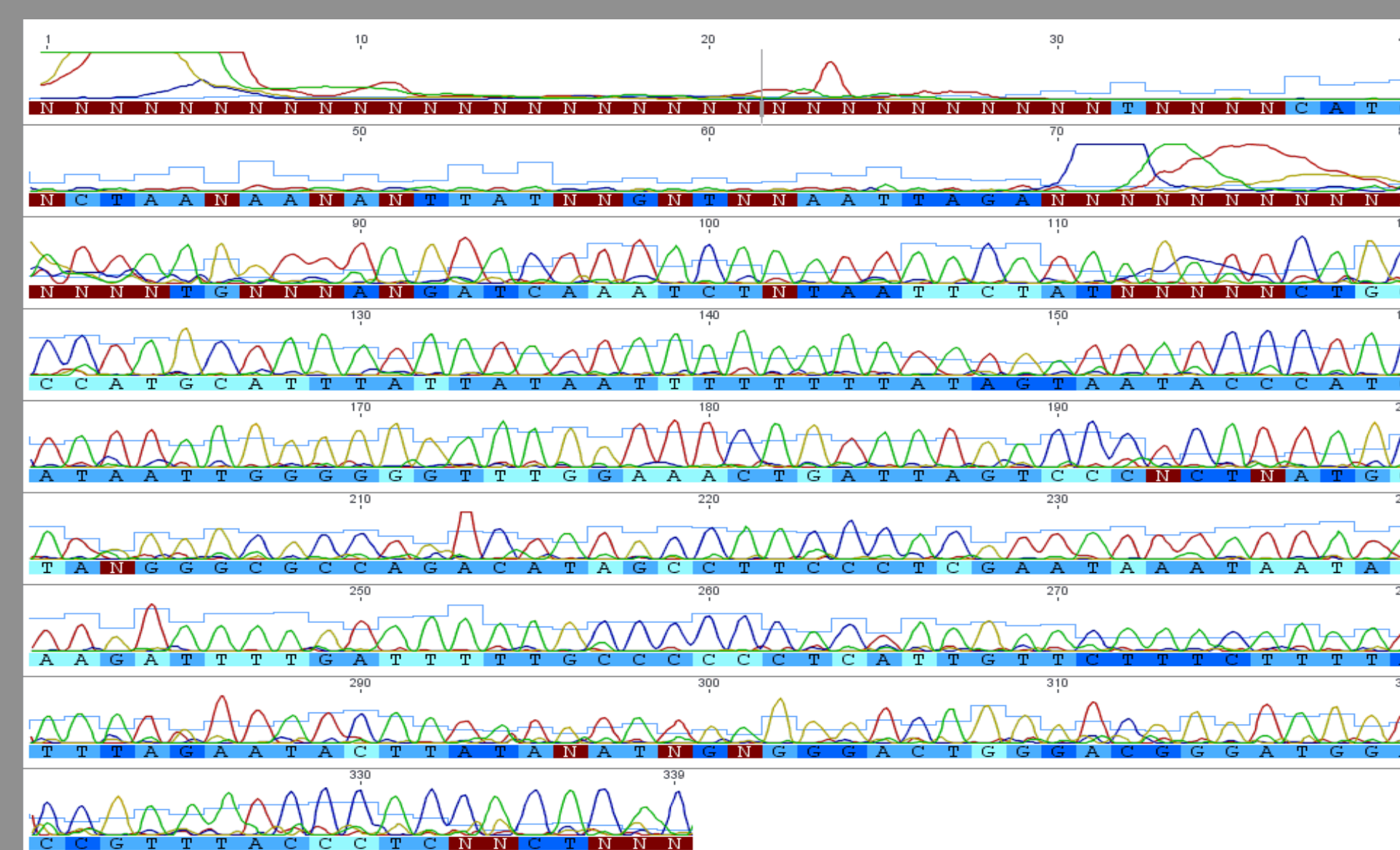
## A Bug's Life Cycle (Methods)



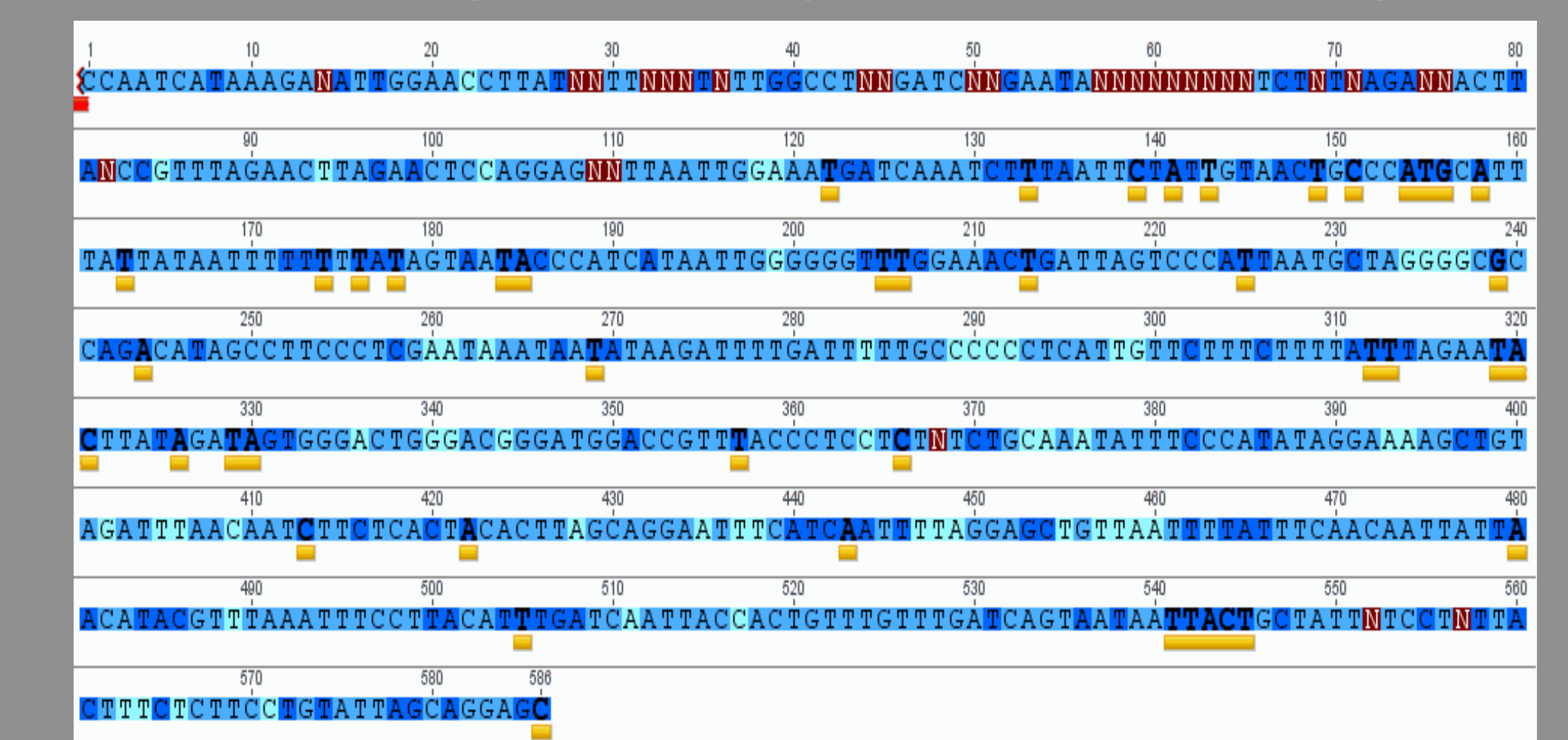
## Results

### Geneious

- to edit the DNA sequences of the specimen
- editing was done through the chromatogram of the specimen
- sequences required several edits within both the forward and reverse sequences

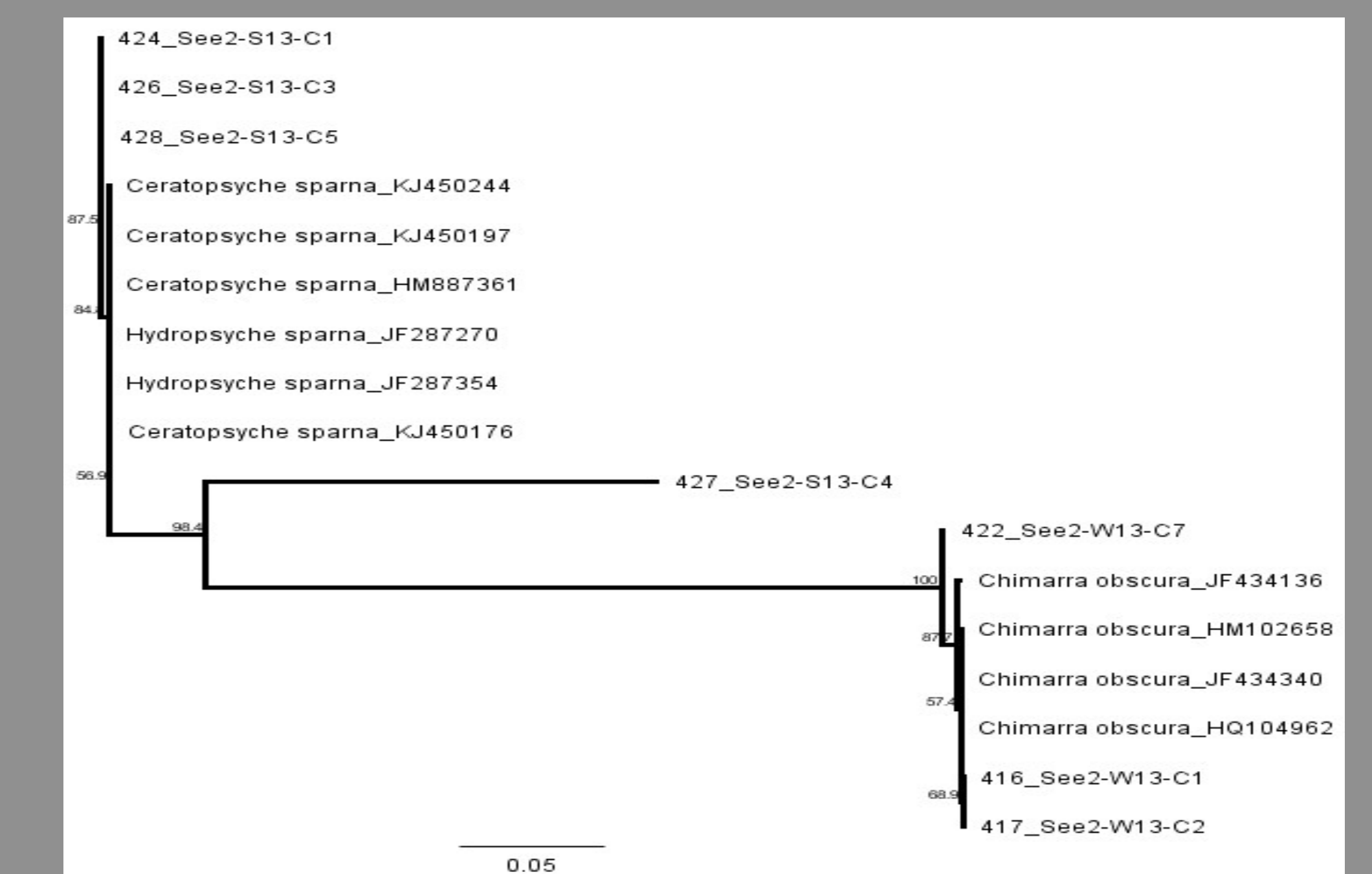


- for correct sequence alignments, we had to do reverse compliment(s) for the reversed sequences
- forward sequences were paired with their reverse compliments and then pairwise aligned forming a full nucleotide alignment



### Geneious Tree Builder Program

- to construct a phylogeny tree
- to compare the caddisflies that we collected to any other species that may be related
- We found a variety of biodiversity within our species!



## Conclusion

- The river had a vast amount of biodiversity within the macroinvertebrates which means that the Johnson Creek is of good health and quality.
- DNA barcoding has the potential of being a very helpful tool to biologists, and it is comprehensive for phylogenetic trees. It can be used to determine the evolutionary history for species and to identify species.
- DNA barcoding has proven to be a great advancement in the identification of species, and this method is cost effective and very efficient.

## References

- Fusaro, A. 2016. "Aquatic Ecosystems" slides. BIO 151, Marygrove College, Detroit, MI.
- Kress, JW, Garcia-Robledo C, Uriarte M, Erickson DL. DNA barcodes for ecology, evolution, and conservation. 2015. Trends in Ecology and Evolution 30: 25-36.