



Identification of Ant species through DNA Barcoding along the Forge River

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Abstract

The overall trend of biodiversity in the Forge River is decreasing due to duck farms and industrialized agriculture. Due to these historical anthropogenic events, this environment has become hypoxic. Hypoxia in the Forge River negatively affects biodiversity as the decrease in oxygen in an area lowers the life that inhabits it (Swanson, 2010). Analyzing ant biodiversity given the historical state of the sediments within the Forge River is crucial because ants increase soil quality (Harvard, 2011). Barcoding; a method used to compare genetic sequences in organisms is more accurate than identifying species specifically on phenotype and will be used to analyze the ants collected. An expected outcome is a relationship would be evident between pollutants in the sediments and the species of ants found.

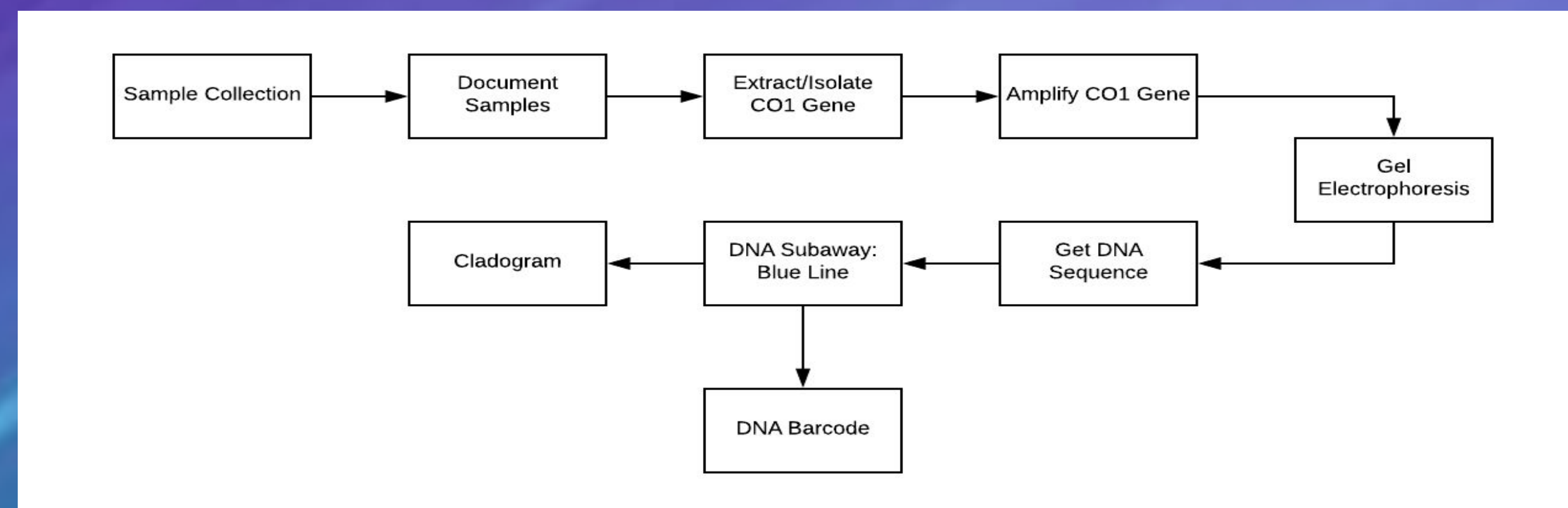
Introduction

Research question: are novel sequences present in the gene sequence of ants collected along the Forge River.

Hypothesis: there will be a novel sequence present in at least one ant sample collected along the Forge River.

- Biodiversity is currently decreasing in the Forge River. This is due to the anthropogenic effects such as industrial farming of ducks has created a polluted, fresh water system. Industrial farming has resulted in an increase in heavy metal contamination and nitrates and phosphates (Swanson et al., 2010).
- A process called DNA barcoding identifies species by genetic sequence because phenotypic traits vary considerably among organisms. DNA barcoding is a system used for identifying an organism by analyzing and comparing specific genes. To barcode the ants, the mitochondrial gene Cytochrome Oxidase subunit 1 will be analyzed (Hebert et al., 2003).
- The CO1 gene is used primarily to inform species boundaries and relationships among closely related species and has limited reliability for informing deeper phylogenetic relationships (Andersen, A. N., Hoffmann, B. D., & Sparks, K. (2016).

Materials & Methods



Results

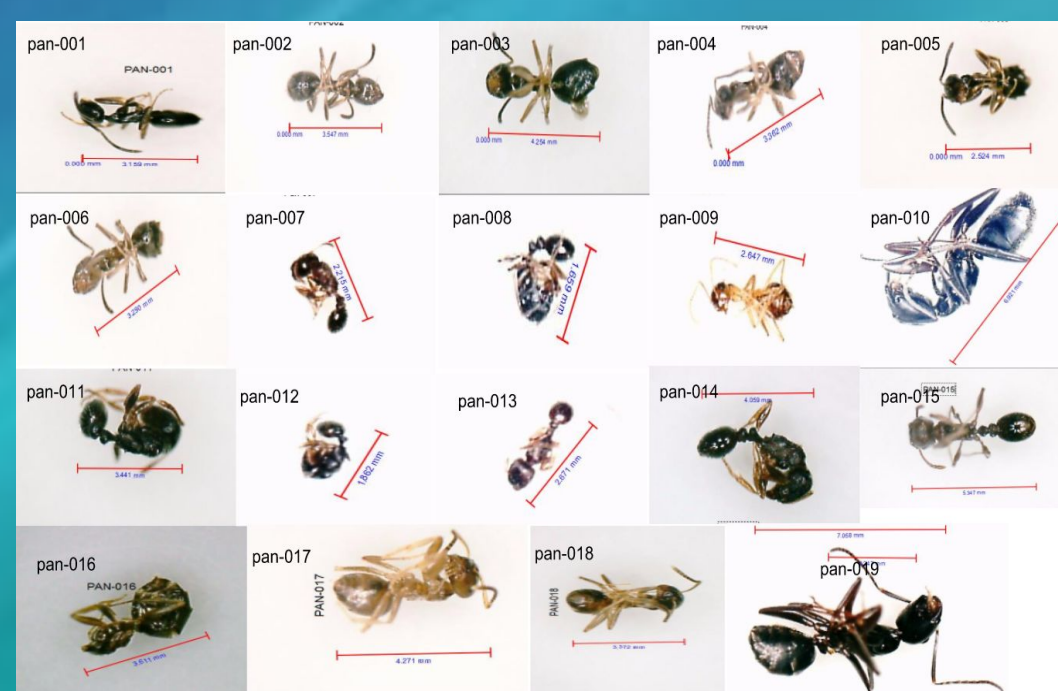


Figure 1: This figure demonstrates the phenotypes of ants along the forge river.



Figure 2: this figure demonstrates the concentration of phosphorus along the forge river.

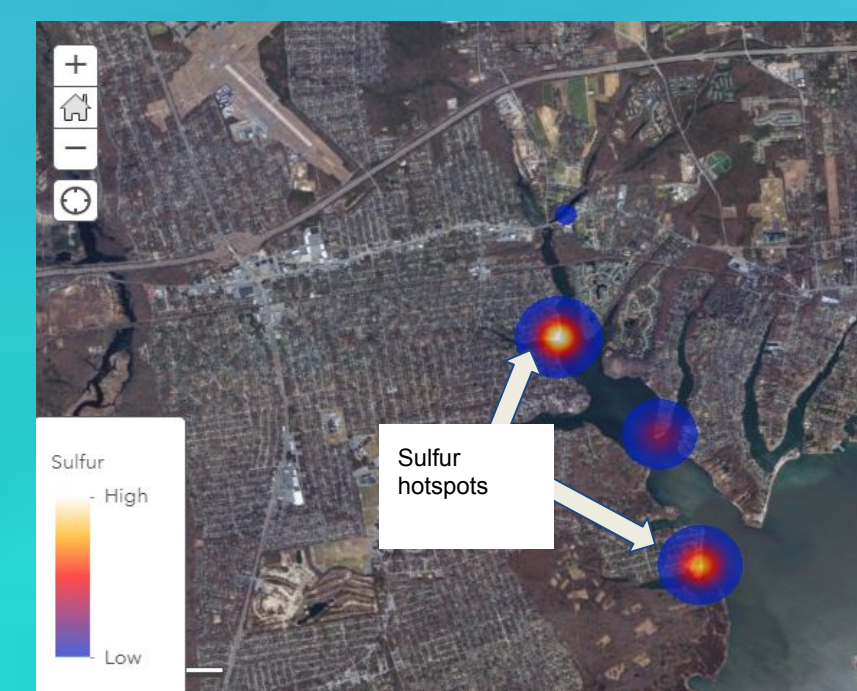


Figure 3: This figure demonstrates the concentration of sulfur along the forge river

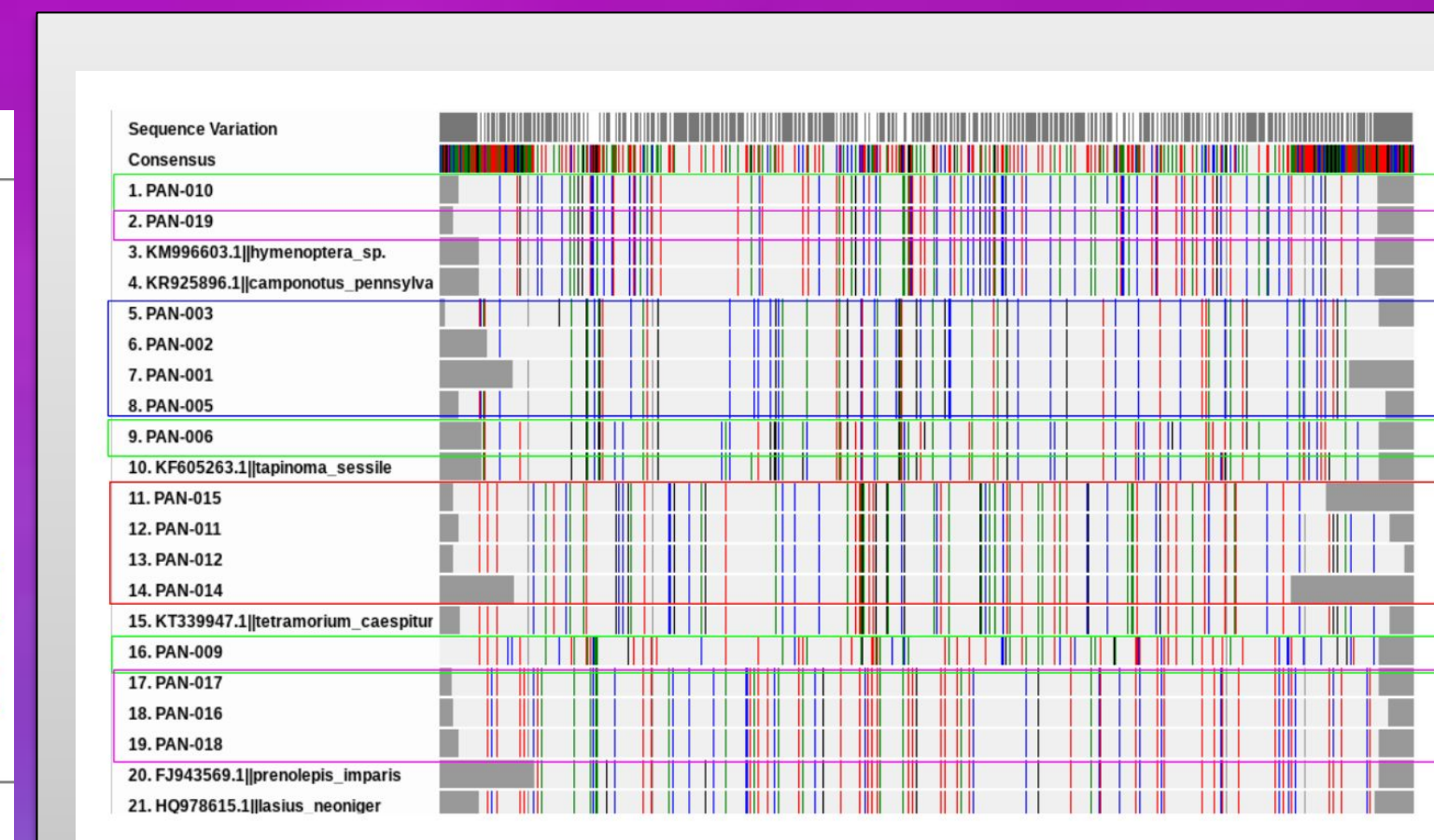
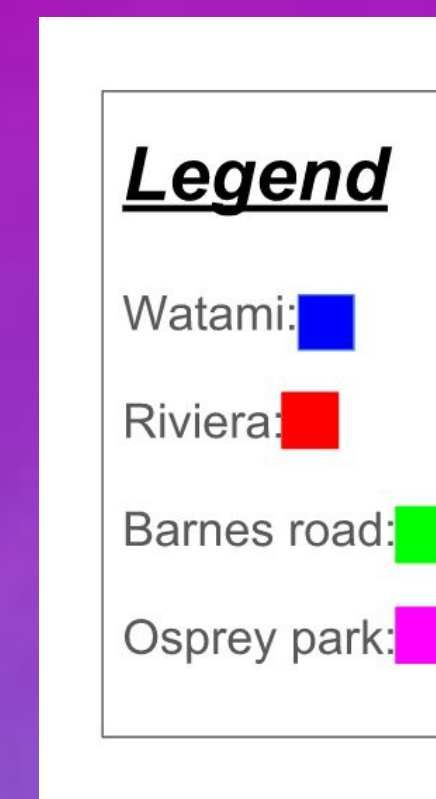


Figure 4: Demonstrates the barcode of ants collected along the Forge River. DNA barcoding is a method that uses a short genetic marker in an organism's dna to identify it as belonging to a particular species.

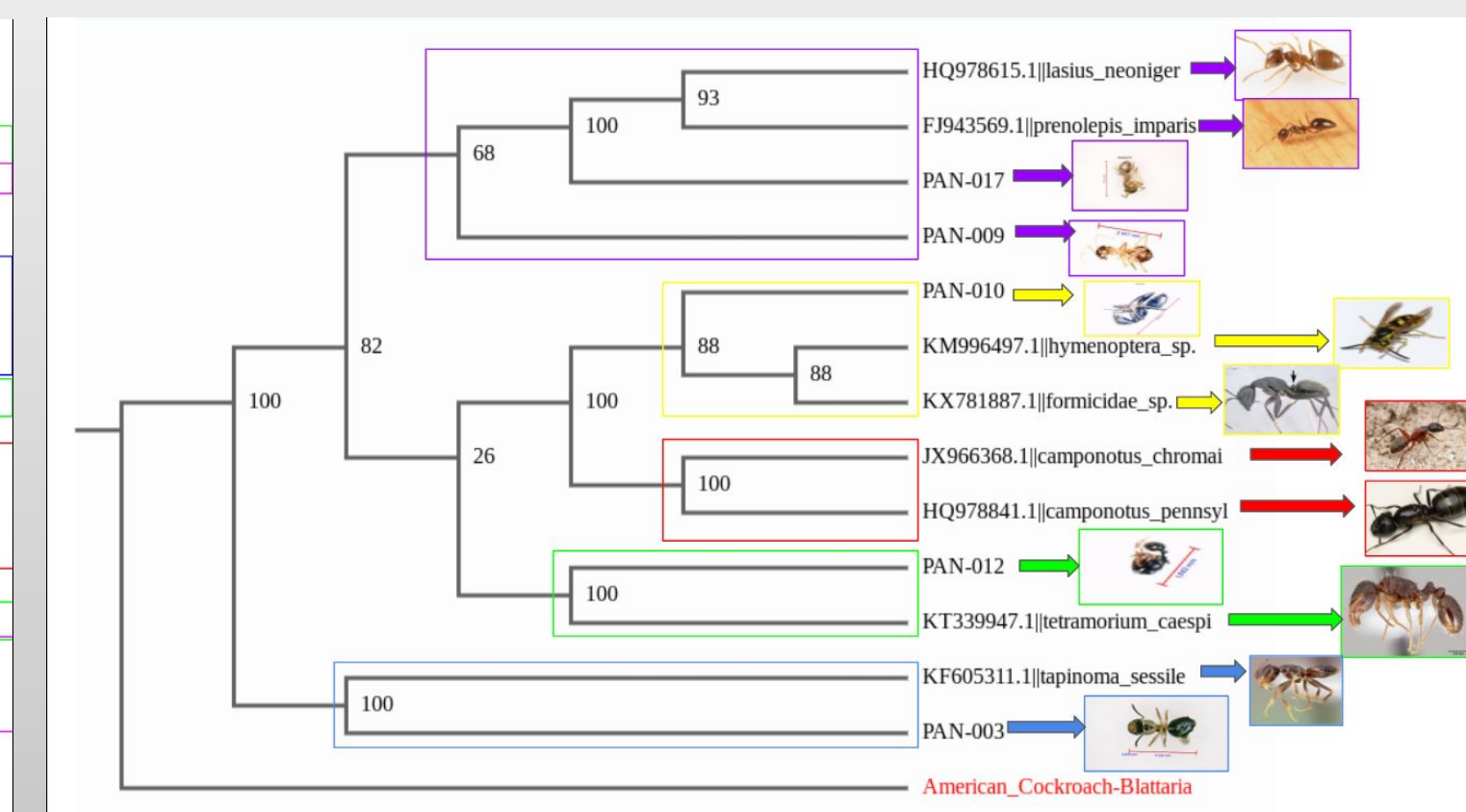


Figure 5: This cladogram demonstrates ancestral lineage of ants in relation to the reference organism. The higher the boot strap score the more related the samples are.

Discussion

The following research questions were posed: (1) *what is the overall trend in biodiversity along the forge river?* (2) *will there be a novel sequence present in ants collected from alongside the forge river?* while there were no novel sequences the following species were predominately found in each region of the Forge River:

Region	Species
Watami	Tapinoma sessile
Riviera	Tetramorium caespitum
Barnes road	Lasius neoniger
Osprey park	Camponotus pennsylvanicus, Tapinoma sessile, Prenolepis imparis.

Therefore there were regional trends in biodiversity and further research is being conducted to prove this is affected by pollution.

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References

- Vallelela, I., Wilson, J., Buchsbaum, R., Rietsma, C., Bryant, D., Foreman, K., & Teal, J. (1984). Importance of chemical composition of salt marsh litter on decay rates and feeding by detritivores. *Bulletin of Marine science*, 35(3), 261-269.
- Hunt, H. W., & Wall, D. H. (2002). Modelling the effects of loss of soil biodiversity on ecosystem function. *Global Change Biology*, 8(1), 33-50.
- Smith, M. A., Bertrand, C., Crosby, K., Eveleigh, E. S., Fernandez-Triana, J., Fisher, B. L., ... & Hroek, J. (2012). Wolbachia and DNA barcoding insects: patterns, potential, and problems. *PLoS one*, 7(5), e36514.