

Identifying Phylogenetic Relationships in Plants in Forest Park Using DNA Barcoding

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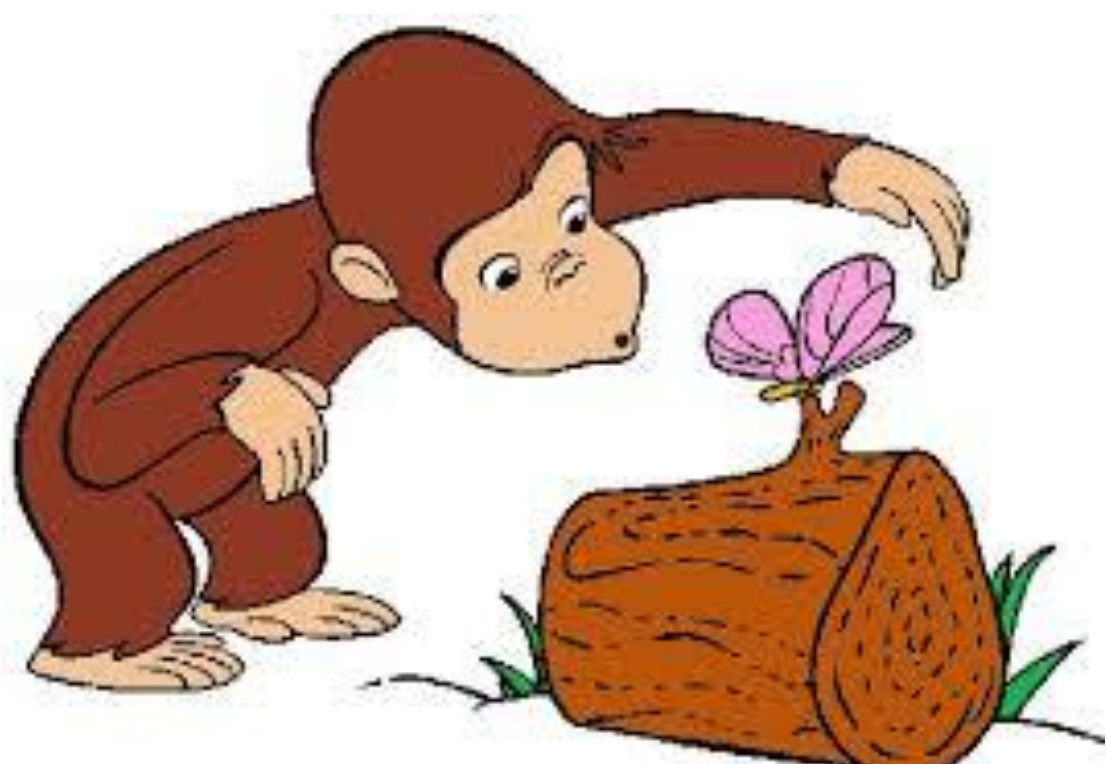
Forest Hills High School

Abstract

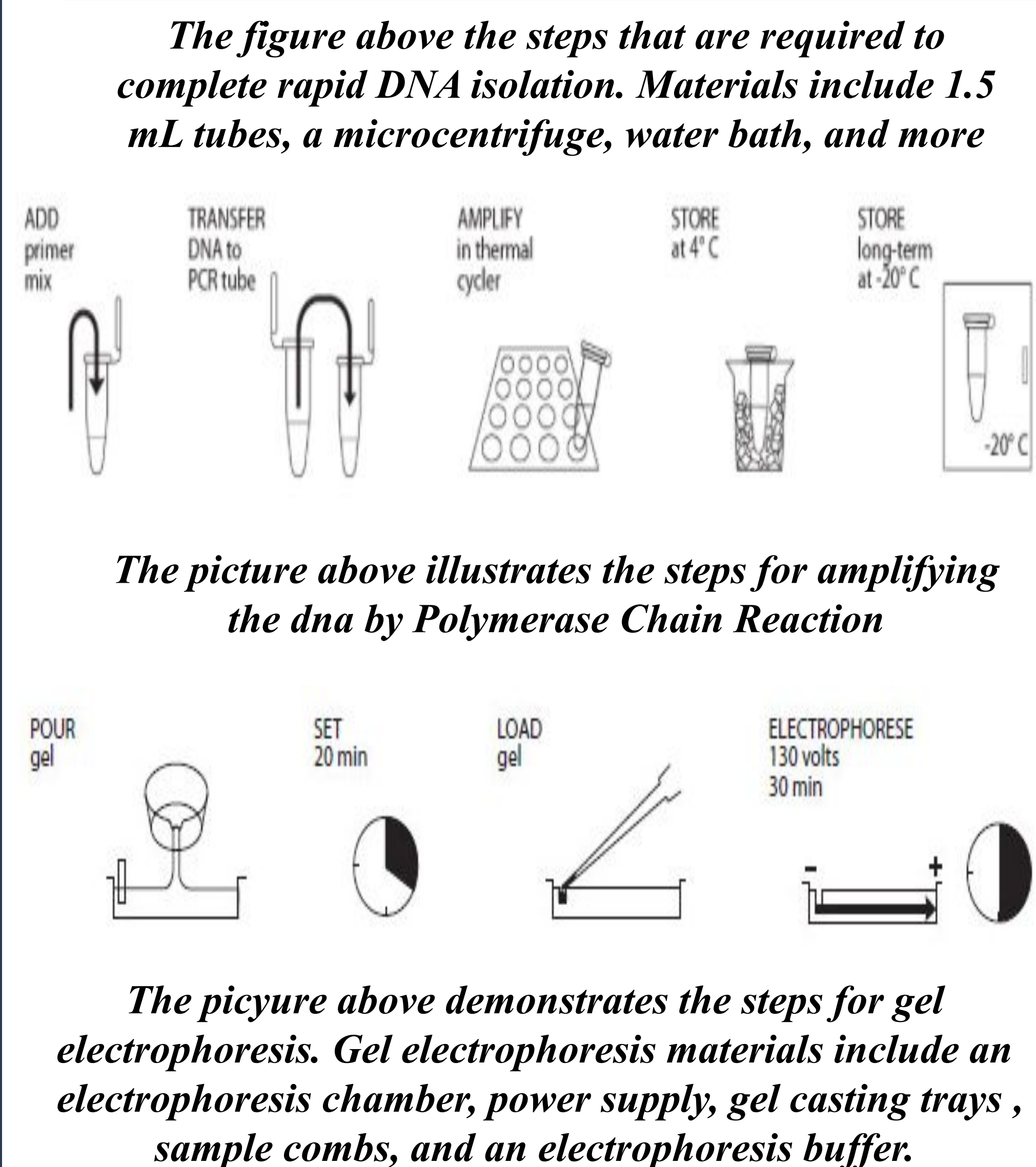
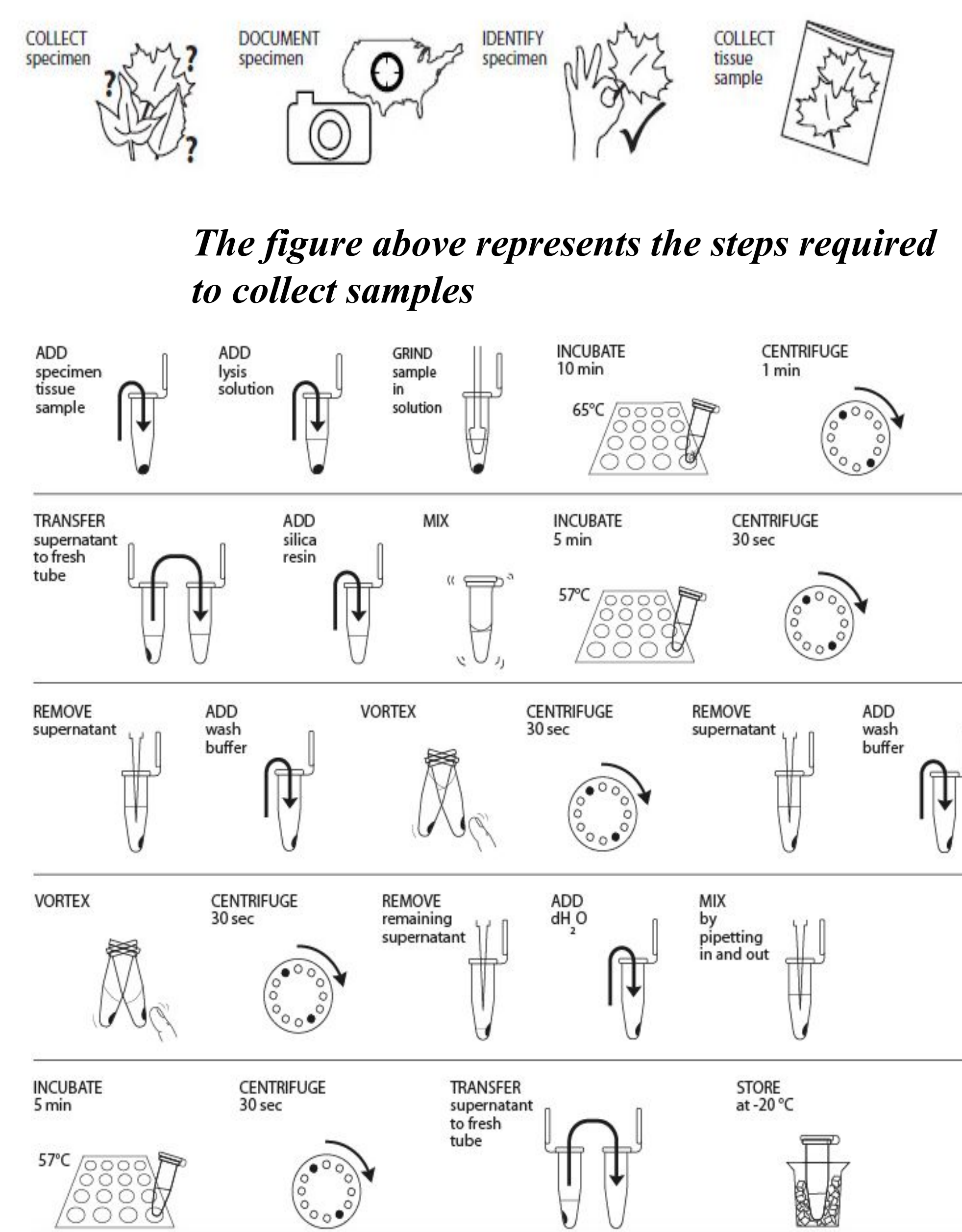
All living organisms store genetic information constructed from DNA. The genetic sequence in these molecules is fascinating evidence of the shared ancestry of organisms. DNA barcoding is a technique that aids in the breakdown of evolution in an ecosystem through the analysis of genetic variation in species. If DNA barcoding is used to identify phylogenetic relationships in an ecosystem, then it will aid in the understanding of the biodiversity in that ecosystem. The experimental method will include extracting DNA and locating a single gene to identify a species by comparing their nucleotide sequences to a barcode database. Finishing the experiment was not possible; results were going to be based on the identification of most, if not all, of the plants that were collected. However, the inferred results include that out of 10 plant samples, all of them would be similarly related. This inference was made based on the location of the samples. They were all located near each other. Even though quantitative data wasn't able to be analyzed, qualitative data suggest minimal biodiversity. A secondary project was carried out to mimic the methodology and whole purpose of the original experiment. Using ants as the test subjects, results will be drawn to assess biodiversity.

Introduction

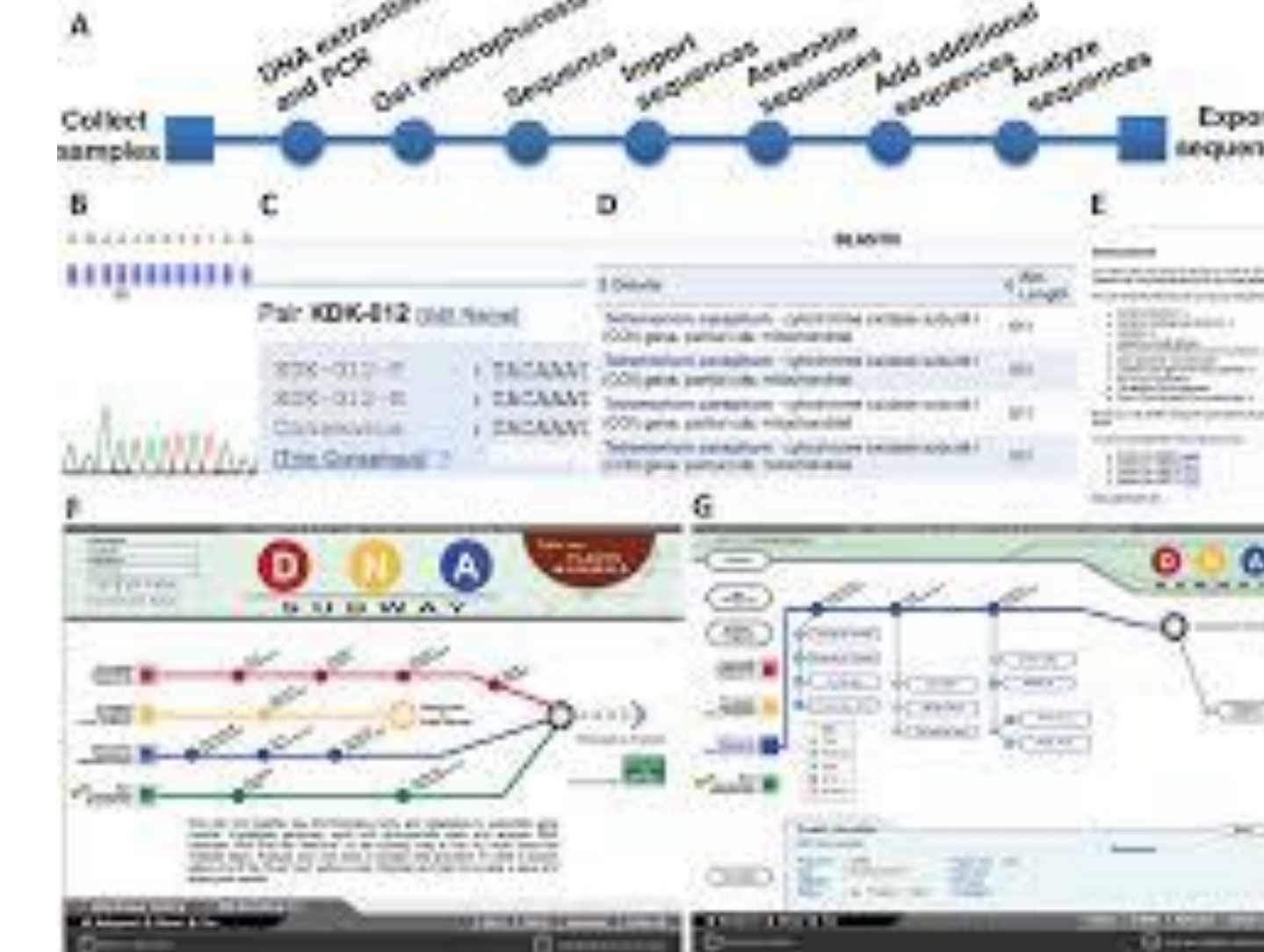
The question that will be tested is How can we use DNA barcoding to identify plant lineage and biodiversity in an ecosystem? Conducting DNA barcoding research, helps students create this relationship with nature as they are the main researchers and scientists during the whole procedure and doing this helps students become scientists who are identifying species biodiversity in NYC. This is a lesson of extreme value for urban students, like those in NYC, who are not concerned with realizing the interesting aspects attained from wildlife and the natural environment.



Methodology



Methodology (Cont.)



The figure to the left demonstrates the DNA Subway Blue Line which will search a local copy of a BLAST databases to check for published matches in GenBank. At the end of the BLAST results page, you can see the latest update to the DNA Subway BLAST database.

Results

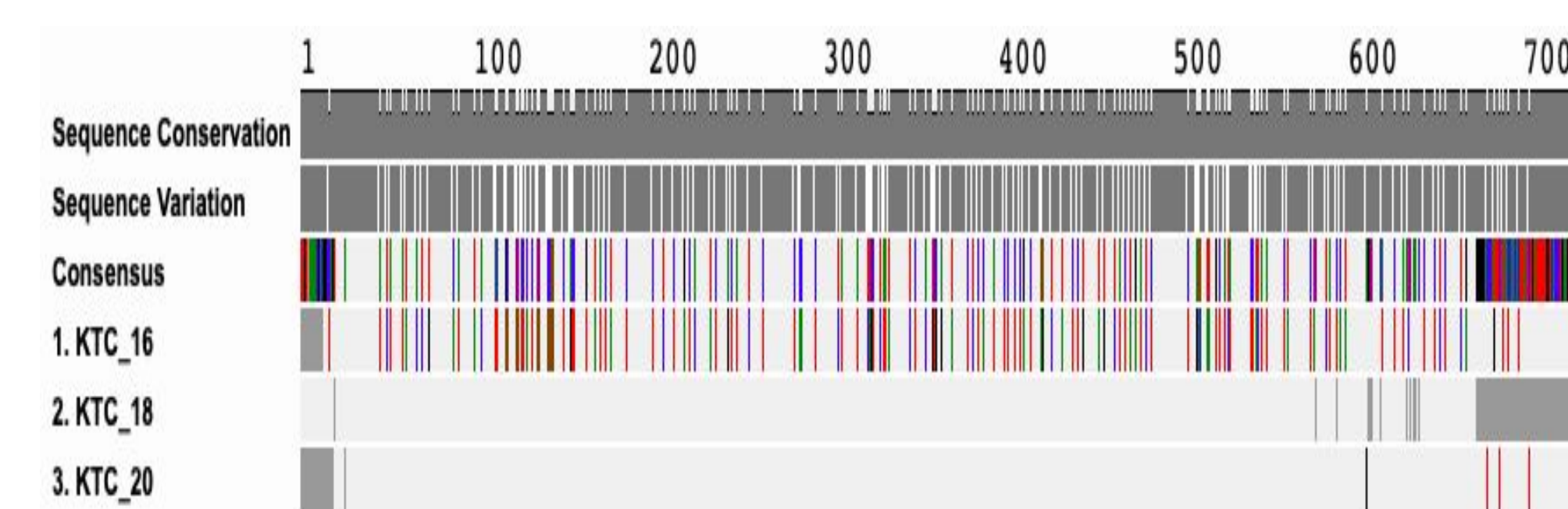
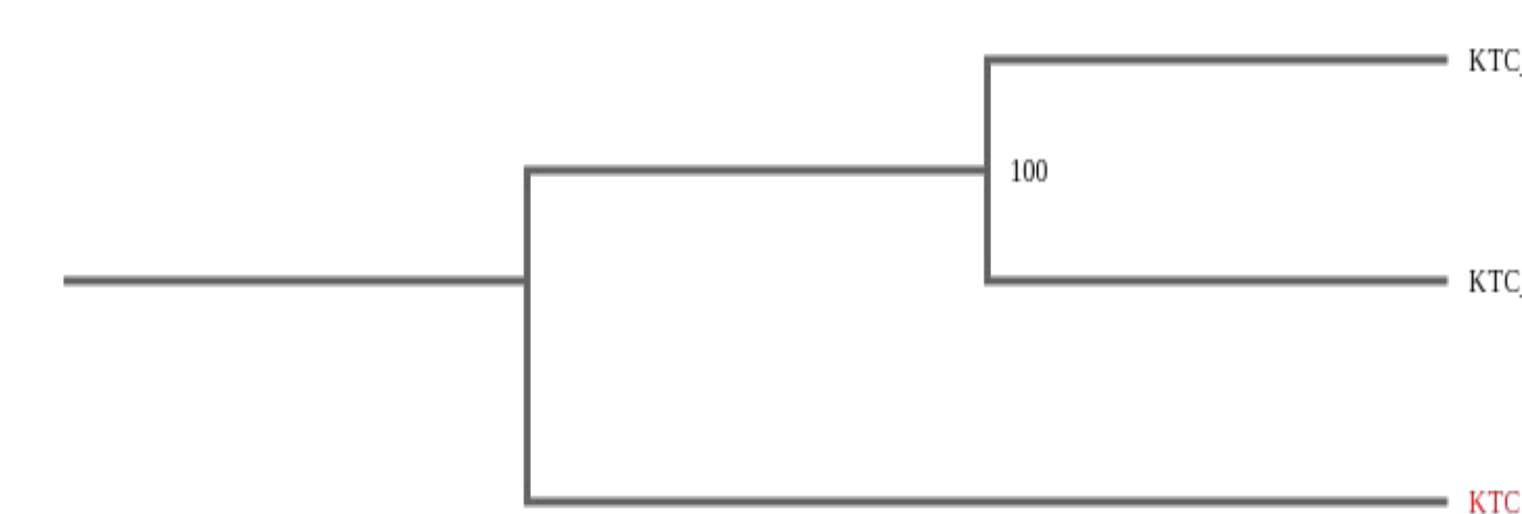


Figure above demonstrates the sample muscle alignment drawn from the DNA Blue subway based on the 3 samples that were sequenced successfully.



The phylogenetic tree above shows the relationship between the three DNA sequences.

Conclusion

Moreover, the inferred results include that out of 10 plant samples, all of them would be similarly related due to their location in which the samples were collected. The at home ant experiment only had 3 successful dna sequences which were put through DNA subway Blue Line and processed. Based on their DNA barcodes and the phylogenetic tree, the sequences proved to be related and somewhat similar in their DNA.

	C	1	2	3
C	-	80.25	98.21	99.30
1	80.25	-	77.24	79.53
2	98.21	77.24	-	97.86
3	99.30	79.53	97.86	-

The figure above demonstrates the percentage of the relationship between the three sequences.

KTC_20

Camponotus nearcticus - Camponotus nearcticus voucher
BIOUG01638-F04 cytochrome oxidase subunit 1 (COI) gene, partial cds 658

KTC_18

Camponotus nearcticus - Camponotus nearcticus voucher
BIOUG01638-F04 cytochrome oxidase subunit 1 (COI) gene, partial cds 627

KTC_16

Prenolepis imparis - Prenolepis imparis voucher
2017_SIENA_TA_001 cytochrome oxidase subunit 1 (COI) gene, partial cds 681

Acknowledgements

DNA learning Center Barcoding 101: Using DNA Barcodes to Identify and Classify Living Things. Retrieved from <https://dnabarcoding101.org/lab/>: Analyze PCR products by gel electrophoresis

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