Evaluating DNA Barcodes in Relation to Coquillettidia perturbans in Long Island, NY

Marvin Acosta, Gabriela Melgar, Diego Monroy & Carmen Sanchez
Mrs. Bettina Fantal, Mrs. Jessica Octaviano
Westbury High School/ Cold Spring Harbor Laboratory

Abstract

Coquillettidia perturbans, a common Long Island, New York, mosquito species, is a well-documented vector for numerous pathogens. An understanding of genetic structure within this species is paramount in designing effective vector control strategies. Herein, we report studies assessing the genetic diversity among Long Island C. perturbans populations using DNA barcoding techniques targeting the cytochrome c oxidase I (COI) gene as a tool for identifying potential genetic polymorphisms. The central hypothesis is that DNA barcoding of the COI gene in C. perturbans will reveal genetic polymorphisms consistent with findings of previous studies.

Introduction

Does COI gene variability reveal wide-ranging genetic polymorphisms among C. perturbans populations in New York State?, Coquillettidia perturbans is commonly found in Long Island, New York and is proven to be the causative agent of transmitting a wide range of pathogens. The aim of this study is to identify the level of genetic variation within and among regional populations and establish how well morphological identification reflects real genetic diversity.

Understanding the differences will help to create better control methods and reduce infections among the population. Identifying mosquito species by their appearance can be inaccurate because the mosquitos look morphologically similar. DNA barcoding has been proven to be a reliable method in identifying species and studying their genetic variety. Using this method, will allow for a better analysis of nucleotide sequences.

Materials & Methods

Mosquito samples of the species *Coquillettidia perturbans* were obtained from the Suffolk County Health Department for this study. A total of 20 mosquitoes were analyzed, of which 10 samples yielded sufficient DNA for further examination. Polymerase chain reaction (PCR) was used to amplify the mitochondrial cytochrome c oxidase I (COI) gene, commonly employed for species identification. Successful amplification was confirmed by gel electrophoresis.

Results

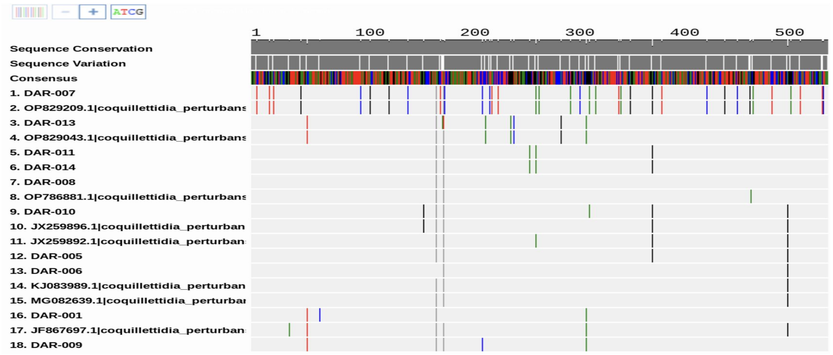

Figure 1. Shows the sequence alignment of the various *Coquillettidia perturbans*. Genetic similarities and differences are seen, displaying the sequence conservation, variation, and consensus sequences.

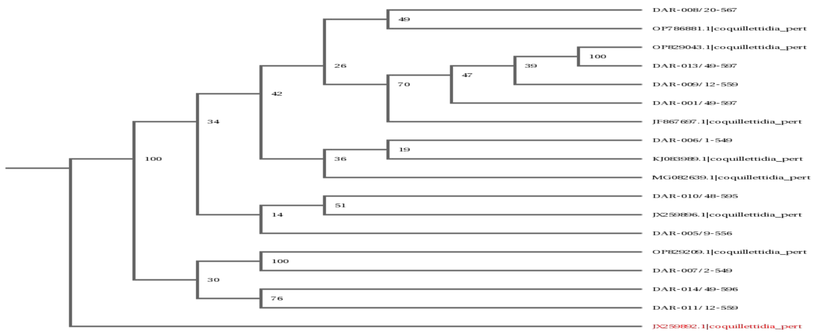

Figure 2. Shows the possibility of shared ancestry among the species of *Coquillettidia Perturbans* based on the similarities and differences within the COI gene.

	C	1	2	3	4	5	6	7	8	9	10	11	12
C	-	93.66	93.64	98.00	98.30	99.48	99.54	99.66	99.48	99.38	99.53	99.54	99.65
1	93.66	-	100.00	92.39	92.57	93.84	93.84	93.66	93.48	93.66	93.48	93.84	93.66
2	93.64	100.00	-	92.36	92.55	93.82	93.82	93.64	93.45	93.64	93.45	93.82	93.64
3	98.00	92.39	92.36	-	99.85	98.08	97.69	98.28	98.28	97.52	97.67	97.69	98.43
4	98.30	92.57	92.55	99.85	-	98.26	97.83	98.46	98.45	97.67	97.83	97.83	98.61
5	99.48	93.84	93.82	98.08	98.26	-	100.00	99.30	99.13	99.13	99.30	99.65	99.47
6	99.54	93.84	93.82	97.69	97.83	100.00	-	99.14	98.97	99.22	99.38	99.69	99.48
7	99.66	93.66	93.64	98.28	98.46	99.30	99.14	-	99.83	98.97	99.14	99.14	99.48
8	99.48	93.48	93.45	98.28	98.45	99.13	98.97	99.83	-	98.80	98.97	98.97	99.30
9	99.38	93.66	93.64	97.52	97.67	99.13	99.22	98.97	98.80	-	99.84	99.53	99.65
10	99.53	93.48	93.45	97.67	97.83	99.30	99.38	99.14	98.97	99.84	-	99.69	99.83
11	99.54	93.84	93.82	97.69	97.83	99.65	99.69	99.14	98.97	99.53	99.69	-	99.83
12	99.65	93.66	93.64	98.43	98.61	99.47	99.48	99.48	99.30	99.65	99.83	99.83	-

Figure 3. Sequence similarity for the COI gene of the different species analyzed from the *C. Pertubanns* genus. The higher the percentage, the more similarities within the genetic sequences of the COI gene..

According to the DNA subway pairwise website, all of the DAR isolates share high sequence similarity (≥97–99%) with one another and GenBank reference sequences (e.g., JX259896.1 and OP786881.1) and affirm that they are C. perturbans. However, a few of them (DAR-007, and DAR-013) are less sequence corresponding (~92–94%) with some others and show evidence of geographic variation, sequencing mistakes, or subspecies differences.

Discussion

The purpose of this research was to investigate the polymorphism within the DAR field-collected C. perturbans. The idea of polymorphism within these species would mean that there were essentially different species within the C. perturbans species itself. However, our results that we had retrieved from our experiment states something else. All of the DAR isolates share high sequence similarity (≥97–99%) with one another and GenBank reference sequences (e.g., JX259896.1 and OP786881.1) and affirm that they are C. perturbans. They are indeed all perturbans and have much genetic variation among them. In a situation, the species of C. perturbans may be susceptible to diseases and infections, but adapt throughout the years and becoming resistant to the diseases and infections . These differences are crucial for evolution, as they provide the raw material for natural selection and adaptation among a environment. In the future, it would help to collect newer samples and include more locations to better understand how these genetic differences match up with where the samples were collected. Our results may change due to the different sample size we collect, the age of these samples and how our experiment is conducted.

References

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