Secrets of the Buttermilk Channel

Species Richness of Macroinvertebrates in New York Harbor: Buttermilk Channel

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Abstract

The purpose of this research was to learn how to extract DNA from invertebrates, and to discover the species richness of the Buttermilk Channel. Another goal of this research project was to compare the effectiveness of the Folmer and Leroy primers. We found that Buttermilk Channel is not very diverse but with more and more awareness it may become so.

Hypothesis

We hypothesized that there would be little species richness because of the history of dredging and heavy boat traffic in the Buttermilk Channel.

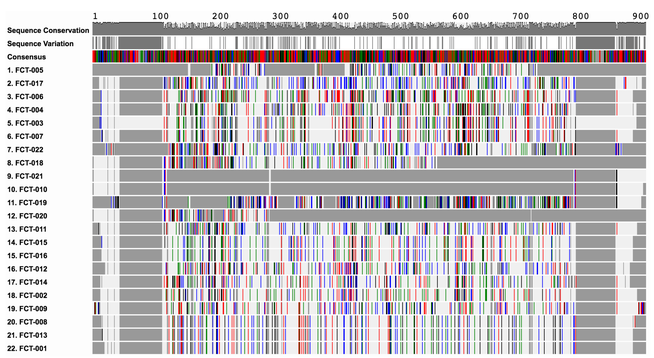
Introduction

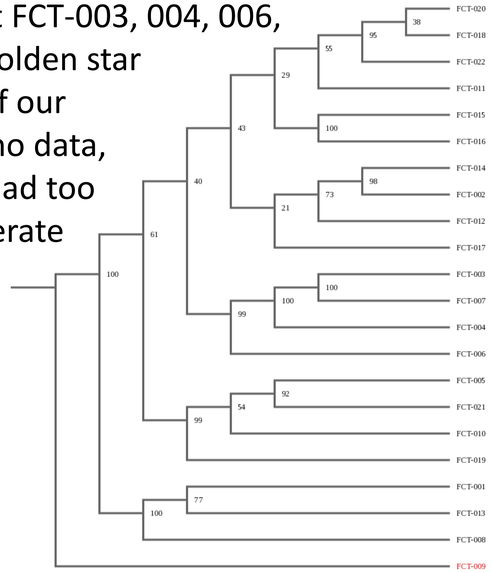
Invertebrates are one of the oldest and most diverse group of organisms (Alroy, Aberhan, and Bottjer, 2008). The biodiversity in the Hudson-Raritan estuary is a key factor in creating a healthy and sustainable ecosystem. The biodiversity index is an overarching topic that includes; biodiversity, species richness and species evenness.

Results

As you can see in the consensus chart, samples with similar base pair patterns were grouped together. We found that FCT-003, 004, 006, and 007 were most likely *Botryllus sohlosseri* (golden star tunicate) and closely related species. In many of our samples there are large chunks where there is no data, this is likely due to human error. If the sample had too many missing gaps, the program could not generate a possible species and was left blank, this was the case with FCT-010 and 021.

Anemabuddies Gel 1		Folmer et al Primer 700bp	Comments		Leroy Primer 400pb	Comments
FCT-001	Halichondria panicea	sponge		FCT-001	Halichondria panicea	
FCT-002	Urosalpinx cinerea	snail		FCT-002	Urosalpinx cinerea	
FCT-003	Botryllus schlosseri	golden start tunicate			no PCR product	
FCT-004	Botrylloides violaceus	colonial tunicate		FCT-004	Botrylloides violaceum	
FCT-005	Pione sp./Stephanauge nexilis (?)		many mismatches	FCT-005	Bonnevillia regia	
FCT-006	Molgula manhattensis	Sea Grape Tunicate/sea squirt		FCT-006	Hydra vulgaris	
FCT-007	Botryllus schlosseri	golden start tunicate		FCT-007	Botryllus schlosseri	
FCT-008	Halichondria panicea	breadcrumb sponge		FCT-008	Diadumene lineata	green sea anemone
FCT-009	Ectopleura crocea	In Hydrozoans genus		FCT-009	Botrylloides violaceum -	
FCT-010	No Match	match on GenBank: Cyanea sp. (jellyfish)/ questionable		FCT-010	Ampithoe valida	
FCT-011	Ampithoe valida			FCT-011	Lepidonotus squamatus	
FCT-012	Lepidonotus squamatus			FCT-012	Halichondria panicea	
FCT-013	Halichondria panicea	breadcrumb sponge		FCT-013	Crepidula fornicata	
FCT-014	Crepidula fornicata			FCT-014	Amphibalanus sp.	
FCT-015	Amphibalanus sp.	barnacle				
FCT-016	Amphibalanus sp.	barnacle		FCT-016	Amphibalanus sp.	
FCT-017	Parasabella microphthalma			FCT-017	Parasabella microphthalma	
FCT-018	Jassa marorata	amphipod		FCT-018	Jassa marorata	
FCT-019	Stenotrophomonas sp. / vibrio	bacteria- contamination/ often found in brackish saltwate		FCT-019	Halichondria panicea	
FCT-020	Lepidonotus squamatus			FCT-020	no seq available	
FCT-021	No Match	match on GenBank: match on GenBank: Cyanea sp. (jell		FCT-021	Zeuxis siquiorensis	sea snail
FCT-022	Monocorophium insidiosum	Amphipodalamphipod		FCT-022	Stenomoera rhwaca	amphipod





As for the Folmer and Leroy primers; the Leroy primer produced species names when the Folmer primer could not, however the same thing happened when the Leroy primer had no answer. We did not have the opportunity to accurately test whether these results were correct.

Methods

First we needed to isolate the DNA, add a series of wash buffers, add the primer, put it through a polymerase chain reaction machine, and send the copied DNA to a bioinformatics lab. After getting the sequences back we used a program called DNA Subway to analyze the results.

Discussion

The phylogenetic tree (fig. 1), shows the evolutionary relationships between all our samples and many of them are very closely related. In the consensus chart (fig. 2) the closer a species' sequence is to another, the more likely they are to be related. We had a fairly low rate of biodiversity, which supported our hypothesis, this is likely due to the extreme dredging in the 1900s. In regards to the different primers, the Leroy primer did come up with possible species names where the Folmer primer did not. However, on some samples we knew were amphipods the Leroy gave a result for a sponge (FCT-019). Overall I would recommend using the Leroy primer because it gives more results that appear to be accurate more of the time.

References

Advances in DNA metabarcoding for food and wildlife forensic species identification, 2016

A new versatile primer set targeting a short fragment of the mitochondrial COI region for metabarcoding metazoan diversity: application for characterizing coral reef fish gut contents, 2013