

Community Comparison of the Nutrient Cycling Abilities of Freshwater and Saltwater Bacterial Communities

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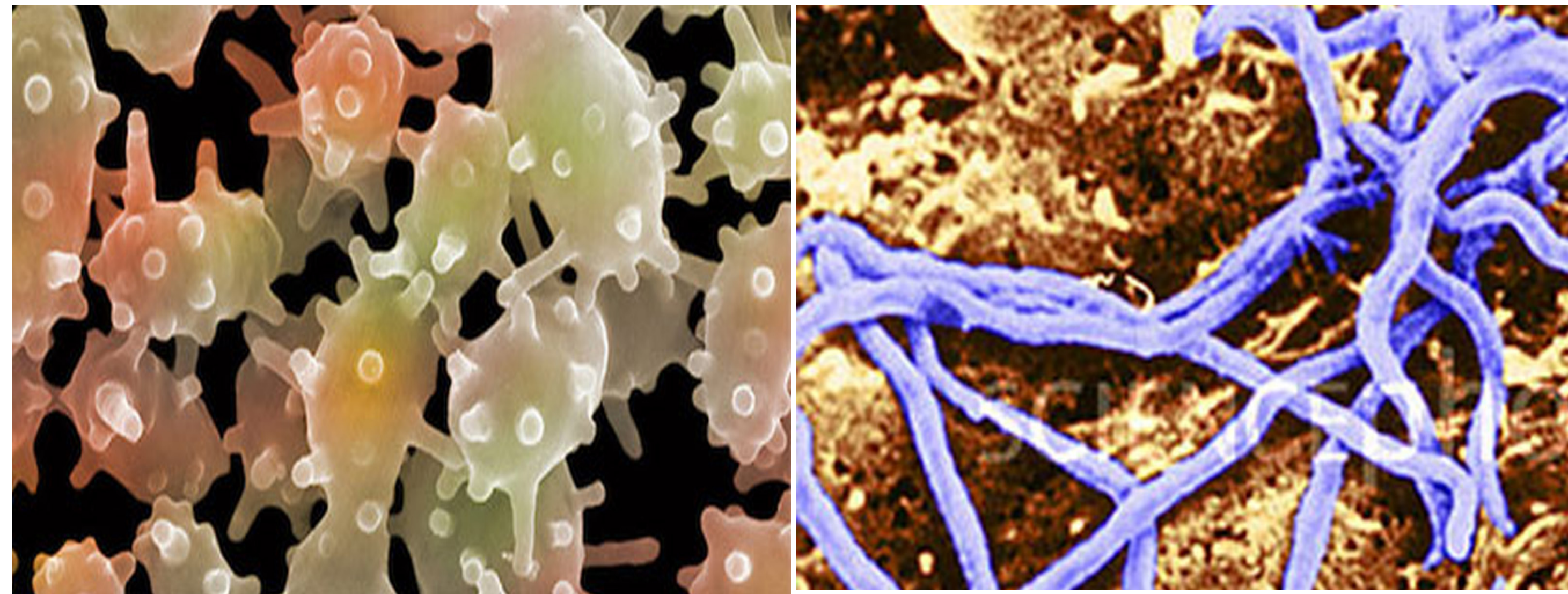


Fig. 1: Image of a Verrucomicrobia under an elec- Fig. 2: Image of Spirochaetes under an electron mi-
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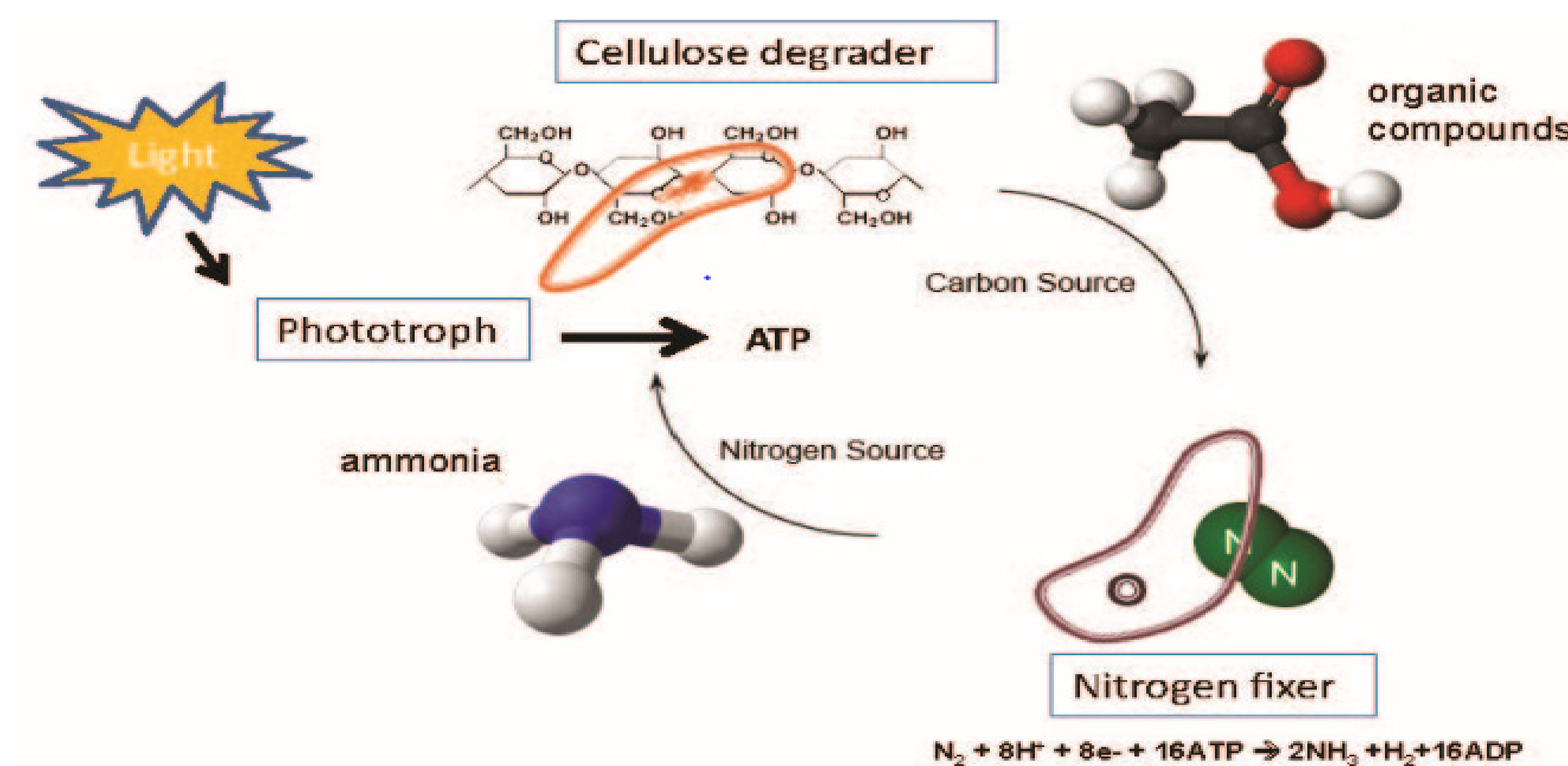


Fig. 3: Symbiotic relationships between microbes in a community for cellulose degradation and nitrogen fixation.

Introduction

Research into what bacterial communities metabolize can give insight into the environments they live in and how they coexist. We enriched a variety of stably growing marine and freshwater bacterial communities in order to extrapolate the cellulose digesting and nitrogen fixing potential of previously uncultured microbes. Cellulose degrading bacteria perform an important role in the carbon cycle by converting cellulose to glucose and other sugars with relative efficiency [1][2]. These cellulose digesting bacteria contain 3 different types of cellulase: exocellulases, endogluconases, and processive endogluconases [2]. We explored endogluconases within the previously unexplored communities in order to find which phyla are primarily responsible for the cellulose degradation process.

Similarly, nitrogen is important to the formation of nucleic acid and proteins for most organisms [3]. Nitrogenases break nitrogen into a usable form, so take part in the nitrogen cycle and nitrogen fixation, which are critical to the functioning of ecosystems. We researched the genetic composition of communities containing NifH (nitrogenase) genes in order to find their identity in hopes of determining the nitrogenase digesting ability of less researched phyla.

Previous groups have cultured bacteria from the Wellesley pond and Cape Cod, exposed them to different light wavelengths in order to sequence the metagenomes, and explored different trends using JGI IMG and BLAST. We primarily focused on the role of Spirochaetes and Verrucomicrobia because these phyla are present in our communities despite not being extensively studied in previous literature.

Community Composition

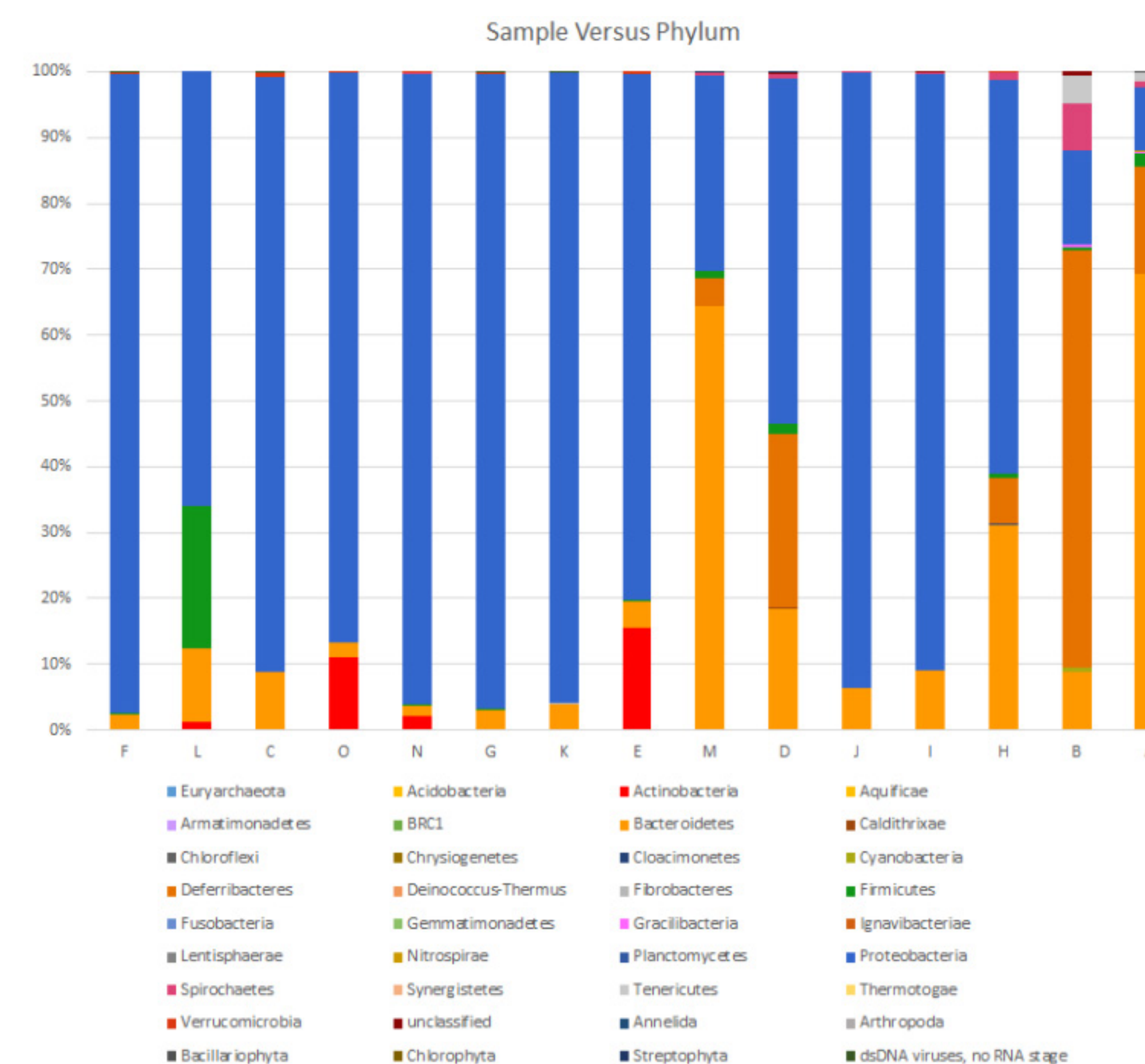


Fig. 4: Segmented bar chart of the phylum distributions for each sample. The first 8 samples are freshwater samples, while the last 7 are saltwater samples.

The largest phylum in these communities, especially those that are freshwater, is Proteobacteria. After the most prevalent phyla are removed from the graph, Verrucomicrobia are prominent in freshwater communities, while Spirochaetes are significant in saltwater.

Endogluconases

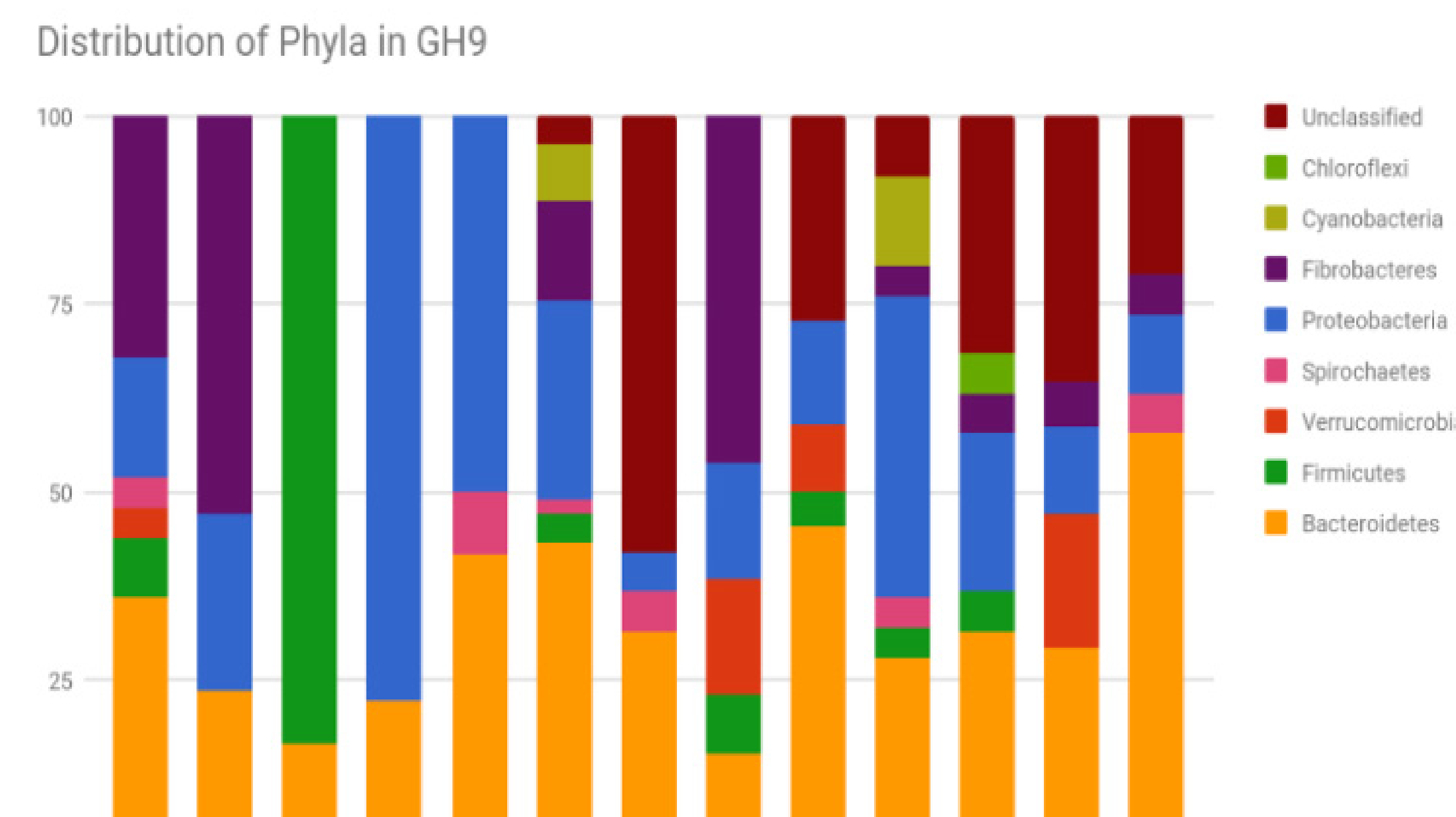


Fig. 5: Frequency of phyla in all of the GH9 scaffolds in each community

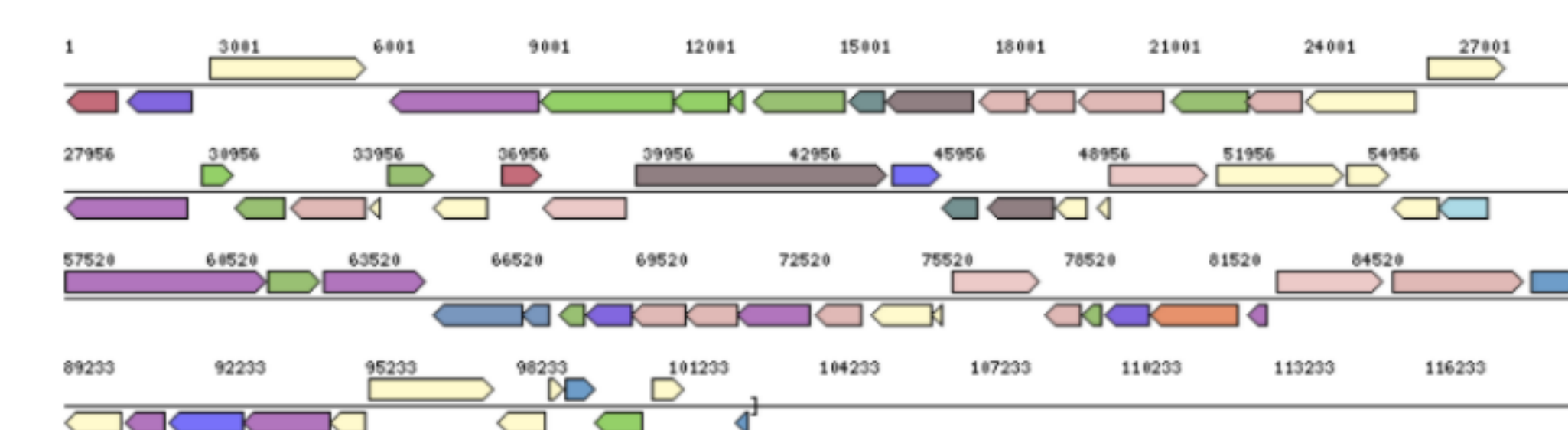


Fig. 6: Gene Neighborhood of Spirochaete GH9 scaffold in SCD17c

Bacteroidetes is the only phylum present in all of the GH9 communities. FCFF4, SCH14b, SCQ17a, FCR15b, SCR11c, and SCD17c all have Spirochaetes. We chose to focus on Spirochaetes because there is less literature surrounding their metabolism of cellulose. As you can see, we were able to find very complete sequences for Spirochaetes using BLAST.

Nitrogenases

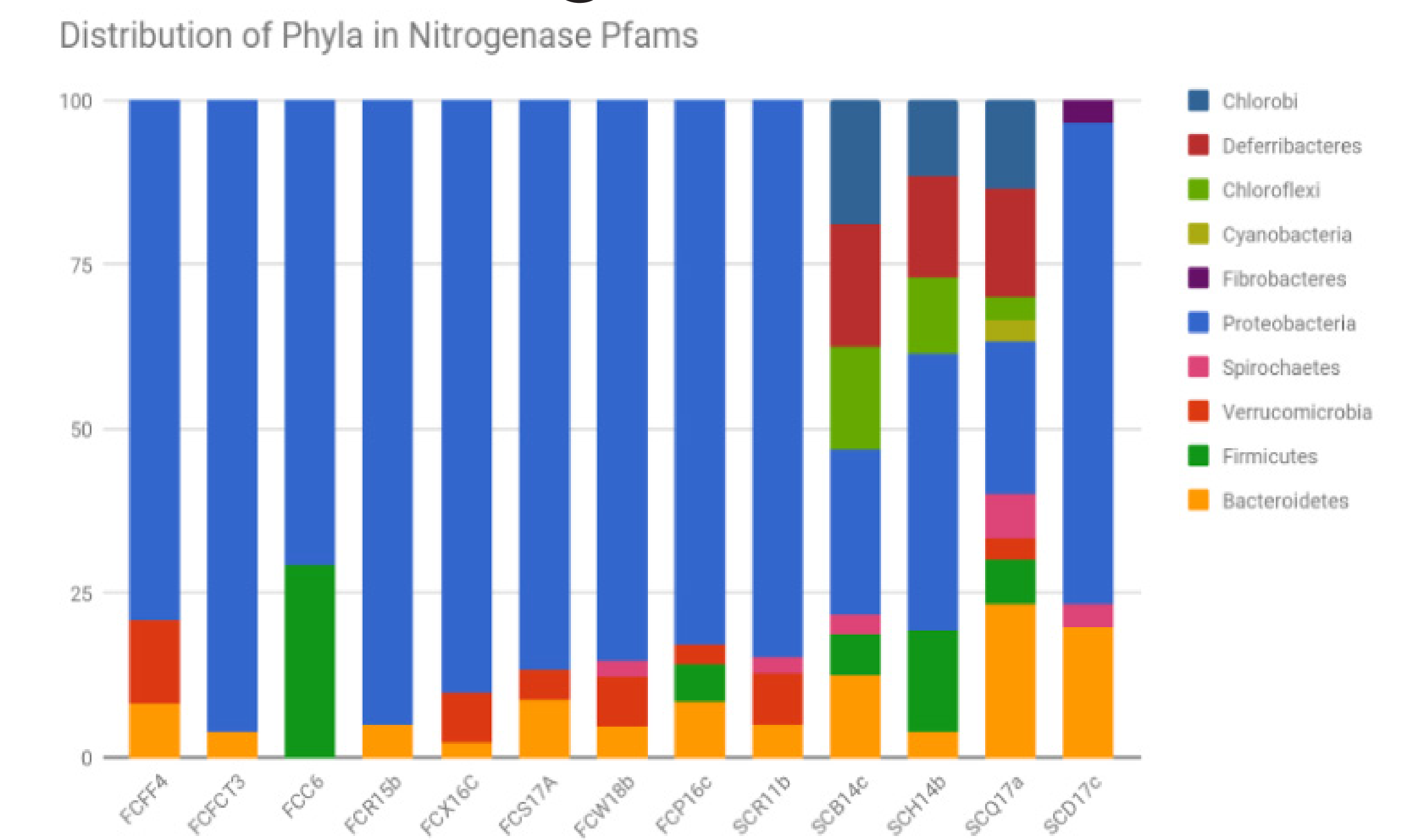


Fig. 6: Nitrogenase Pfams include Fer4_NifH (pfam 00142), Anf_vnfG (pfam 03139), and AnfO_nitro (pfam 09582)

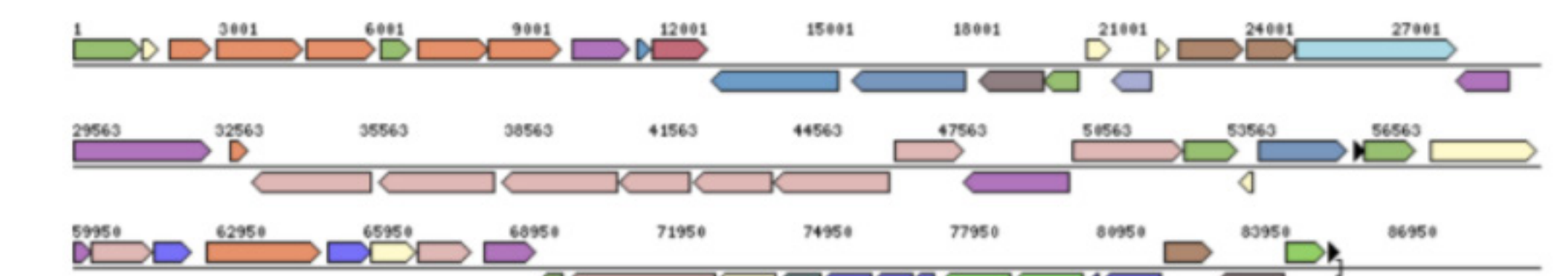


Fig. 7: Gene Neighborhood of Verrucomicrobia Opiuata NifH scaffold in FCS17 containing NifH and genes that flank NifH (NifV, NifB, NifE, and NifN).

The majority of these communities contain Proteobacteria. However, we chose to focus on the Verrucomicrobia containing nitrogenases because this was less well-studied. More than half (7/13) of these communities contain Verrucomicrobia (FCFF4, FCX16C, FCS17A, FCW18b, FCP16C, SCR11b, and SCQ17a). Above is a complete BLAST of a nitrogenase producing Verrucomicrobia.

Conclusion

From our research we were able to identify a few relevant trends involving phylum, environment, and metabolic ability. We found that Proteobacteria is the most common phylum in the communities by far, which accords with research that suggests this phylum is broad and diverse. We also discovered a relationship between Spirochaetes and cellulose degradation. Previous literature has shown that salt water Spirochaete bacteria contribute to cellulose degradation, but are not primary cellulose degraders. From the metagenome research we found that Spirochaetes harbor GH9 genes, which suggests that they can digest cellulose independent of other bacteria. We also found a relevant connection between Verrucomicrobia and nitrogen fixation. Previous research has shown that Verrucomicrobia are primarily found in freshwater environments, which our research supports. Some articles hint that Opiuataeae only fix nitrogen in extreme environments such as arctic and alpine biomes. Because our freshwater communities come from a Wellesley pond, we can conclude from our research that Verrucomicrobia also fix nitrogen in less severe environments. Our research therefore finds new relationships between bacteria, metabolic ability, and environment which suggest the presence of functional niches rather than environmental niches, indicating the importance of diversity within bacterial communities.

Cited Sources

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- [4] (Image source) <http://www.writersreserve.com/education/lexicon-of-life/kingdom-of-bacteria/>