The 16s rRNA Phylogeny of Moorea Bouillonii
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Marine Cyanobacterial secondary metabolites present important opportunities for pharmaceutical research. However, in order to effectively utilize these opportunities, taxonomic identification is necessary. Such identification is done through analysis of a ribosomal RNA unit known as 16s rRNA gene. This segment of the prokaryotic genome changes very little over time and thus allows for precise identification of very closely related organisms.

**Useful Compounds of M. Bouillonii**

The Gerwick chemistry lab isolated two compounds from the M. Bouillonii specimen; apratoxin A, which is known to be cytotoxic to pancreatic and lung cancer cells, and another previously unidentified amino glycol compound. This second compound was found to have cannabinoid receptor modulatory properties, indicating its potential medical use as an appetite regulator, as well as a chemotherapy relief and anti-cancer agent.

**Testing the DNA: Nanodrop and Gel Electrophoresis**

After DNA dilutions of 1:1, 1:1.5, 1:10, 1:50, and 1:100 were made, PCR proved to be successful for 1:10 and 1:50. This means that the correct segment of DNA was amplified, followed by cloning of the PCR products using the TOPO cloning (Invitrogen) method, hence, allowing the project to continue to transformation of the resulting plasmid into TOP 10 cells.

**Transformation of E.coli**

In order to mass-replicate the vector containing the gene of interest, the vectors were placed in chemically competent E.coli cells, which are capable of such mass replication. However, in order to effectively utilize these opportunities, taxonomic identification is necessary. Such identification is done through analysis of a ribosomal RNA unit known as 16s rRNA gene. This segment of the prokaryotic genome changes very little over time and thus allows for precise identification of very closely related organisms.

**Analyzing the Sequences**

The upper strand shows the 16s rRNA sequence for the Papua New Guinea unidentified cyanobacteria. The lower strand is the general 16s rRNA sequence for the Moorea Bouillonii species, as provided by the NCBI database. If the two strands were identical, we would expect no discordanse between the two sequences would be found. From this it can be concluded that the unidentified cyanobacteria is, in fact, a M. Bouillonii. This fact was already suspected as a result of the richness of its secondary metabolite production; a morphological identification at the time of collection. M. bouillonii is a tropical cyanobacterium that is filamentous and often form large, mat-like colonies. This finding is valuable to continued research on this useful organism.

**Comparing and Identifying**

This 1500 base pair sequence is used to identify the Cyanobacteria utilizing the very low rate of change from species to species. Only about 5 base pairs of this sequence are different than other closely related Cyanobacteria species. By identifying which base pairs are different, and the frequency of those alterations, a program can distinguish this organism from its relatives in a matter of seconds.

**References**


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