Position of HIP-1 (Highly Iterated Palindrome-1) in *Cyanobacteria* around DNA Methylase loci

Introduction

Highly Iterated Palindrome is a highly conserved DNA sequence, denoted as 5’-GCGATCGC-3’. This eight nucleotide sequence was thought originally to be only in Cyanobacteria, however, after further investigation it was shown that it is not as well conserved among all species of Cyanobacteria. HIP-1 has been associated with the enzyme Deoxyadenosine methylase whose core sequences is 5’-GATC-3’, which is present in HIP1. The question I pose is where is HIP1 located in certain Cyanobacteria and what is its relative position to DAM Methylase. With these results, I will develop a phylogenetic tree which will display the results of this project in an easy-to-view format of these bacteria’s relatedness with Highly Iterated Palindrome-1.

Methods

After further research, I determined my Cyanobactera samples to be *Thermosynechococcus elongatus BP-1, Cyanothece sp ATCC 51142, Anabaena variabilis ATCC 29413, Nostoc punctiforme PCC 73102, Synechococcus elongatus PCC 6301 and Synechococcus elongatus PCC 7942.* Using these organisms, whose genomes are provided within BioBike, I was able to obtain the Count-Of tool to determine the count of 5’-GCGATCGC-3’ within their genomes. After obtaining the count of HIP-1 sequences, I used the sequence-of function in order to examine the sequence first hand and determine if the HIP-1 sequences were indeed present where BioBike says. After confirming a majority of the HIP-1 sequences, I determined where the location of Deoxyadenine Methylase (DAM) gene is by using “(GENE-DESCRIBED-BY “Methylase” IN #$Thermosynechococcus-elongatus-BP-1)”. Using this tool, I was able to determine the start and stop coordinates for each of the DAM methylase genes. Once found, the genes can be looked at more closely to determine if where HIP-1 resides in relation to the gene. I looked before, after and within the DAM methylase genes to see if HIP-1 has any significance regarding its position to the genes.

Results

The results I found, showed that the Cyanobacteria I was looking at contained abundant amounts of Highly Iterated Palindrome-1. In Thermosynechococcus elongatus BP-1, I found the position of HIP1 to be around 1.254 nucleotides before the gene and 4, 845 nucleotides after the start of the gene. Within Cyanothece sp ATCC 51142, HIP1 occurs 1,540 nt after the DAM Methylase gene and 5,091 nucleotides before the gene.

Works Cited

Elhai, J. 2015 *Highly Iterated Palindromic Sequences (HIPS) and their relationship to DNA Methyltransferases.* Life (5): 921-948.

Delaye, L., and A. Moya. 2011 *Abundance and distribution of the highly iterated palindrome 1 (HIP1) among prokaryotes.* Mobile Genetic Elements 1(3): 159-168.