Bacterial Communication and Cognition Study of Cave Streptomyces Isolates ICC1 and ICC4

Directed Studies Proposal

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Abstract

From previous studies, two *Streptomyces* isolates (ICC1 and ICC4) from the Iron Curtain Cave in Chilliwack Canada were identified to shown antagonistic activities against multidrug resistant strains of *Escherichia coli*. The genomes of ICC1 and ICC4 were sequenced by Illumina MiSeq, assembled, and annotated. In these studies, the genes associated with secondary metabolite production were identified and annotated using the bioinformatics platforms antiSMASH and BAGEL. In this directed studies, the genomes of ICC1 and ICC4 will be analysed to see if they contain the GGDEF domain-containing protein gene (SRIM_RS22070) which is found to be involved in the formation of biofilms in *Streptomyces rimosus*. The DIVERGE 3.0 software will be used analyse the genomes of ICC1 and ICC4 to determine if the GGDEF domain-containing protein gene (SRIM_RS22070) is within their genome.

Introduction

In bacteria, chemical communication involves producing, releasing, detecting, and responding to small signal molecules which are called autoinducers (Waters 2005). The way bacteria communicate with one another using chemical signal molecules is similar to how higher or more complex organisms communicate (Federle 2003). The information supplied by these molecules is critical for synchronizing and organizing the activity of a large group of cells. An example of bacterial communication is a process called quorum sensing (Waters 2005). Quorum sensing involves the bacteria monitoring their cell-population density by measuring the concentration of secreted signal molecules. As the population of bacteria grows, the individual organisms produce and secrete the signal molecules into the extracellular environment. The bacteria are therefore able to determine the amount of other bacterial cells and alter specific gene expression accordingly. Other examples of bacterial communication include bioluminescence and biofilm formation.

Cyclic Diguaniosine Monophosphate (c-di-GMP) is a secondary messenger that represents a signaling system that regulates a variety of bacterial behaviors. It is crucial for driving the switch between motile individual cells and biofilm formation (Valentini 2016). c-di-GMP signals are integrated into the genetic differentiation network by the regulator BldD and sigma factor. C-di-GMP is synthesized from two GTP molecules by diguanylate cyclase which contains the GGDEF domain protein. A major sub group of proteins involved in the c-di-GMP signaling contain a GGDEF domain protein (Wei 2016). By analyzing the genomes of ICC1 and ICC4, it can be determined if they contain the GGDEF domain-containing protein gene (SRIM_RS22070) which is crucial for the formation of biofilms.

Objectives

The proposed research to be conducted will explore the bacterial genome of two *Streptomyces* isolates ICC1 and ICC4. The bacterial genomes of ICC1 and ICC4 have already been sequenced with Illumina MiSeq and some gene identification was done using a variety of bioinformatic tools such as BLAST, BAGEL, and antiSMASH. Therefore, the bacterial isolates will be analyzed for genes known to cause the formation of biofilms in *Streptomyces rimosus.*

Material and Methods

The bacterial genome sequences of ICC1 and ICC4 will be acquired in GFF format. The sequence of the GGDEF domain-containing protein gene (SRIM_RS22070) in *Streptomyces rimosus* will be determined. The genomic analysis will be conducted through the DIVERGE 3.0 software which allows the detection of functional divergence between genes.

Expected Results

This research project would be an introduction bacterial cognition and the concept cell communication is a critical factor in the diverse behaviors found in different bacteria. By identifying the genes that are involved and responsible for the formation of biofilms is a step towards better understanding the cognitive function of bacteria. In further research, identifying and labeling the genes that are responsible for different bacterial behaviors would allow us to learn more about the ecological function, adaptation, and evolution of bacteria.

Literature Cited

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