

Identification of genes involved in biosurfactant production from Antarctic soil bacteria

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Surface active metabolites known as biosurfactants are typically produced when bacteria are grown with water-immiscible substrates. Biosurfactant molecules can be derived from glycolipid, lipoprotein, phospholipid or high molecular weight polymers. Bacterial strains need to possess specific operons, enzymes and biochemical pathways to produce these biosurfactants and excrete them outside the cells. The roles of biosurfactants are not certain, however, many researchers have associated biosurfactants to hydrophobic substrate metabolism, cellular adhesion to surfaces, interaction with metals and antibiotic activity. Commercial and industrial demand for biosurfactants has been continuously growing as the cost for producing biosurfactants is competitive to synthetic surfactants while biosurfactants are environmentally friendly. From the environmental conservation aspect, biosurfactants can be applied as additives for microbially enhanced oil recovery (MEOR) technique for bioremediation.

The objective of this study is to identify genetic components involved in the production of biosurfactant in *Arthrobacter* sp. strain AQ5-05. This strain was isolated as a diesel degrading bacterium from soil samples obtained at King George Island, Antarctica. Complete genome of this strain was sequenced using Illumina MiSeq system and the whole genome sequencing data was published publicly (NCBI Taxon ID 2184581). Production of biosurfactant by strain AQ5-05 at various temperatures, pH and NaCl concentrations were studied. Based on the literature research, genes believed to be involved in biosurfactant production in this strain were identified using publicly available online bioinformatic tools. Experimental evidences are needed to confirm the functionality and validity of these findings.