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Alcanivorax borkumensis: A Hydrocarbon Feeder

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Abstract

Alcanivorax borkumensis is a hydrocarbon feeder bacterium. They are rod shaped bacteria living in marine environment where they feed on the hydrocarbons. They are born with the gene sets that produce specific proteins for the degradation of the hydrocarbons. They are used to clear and clean the oil spills from the oceans when there are disasters or any other leakages of oil in the ocean. A. borkumensis ability to degrade hydrocarbons and alkanes is a major point and an opportunity for the scientists to use these bacteria to clean up the environment and oceans. With the ongoing specter of oil spills from tankers, ocean-based drill rigs, and pipelines, the need for remediation strategies has never been greater.

Keywords: Alcanivorax • Hydrocarbon • Degradation • Bacteria

Introduction

Petroleum in water is highly dangerous for the lives of water animals. During shipping many disastrous accidents cause deaths of the water life just because of "Oil Spills". These oil spills cost big and long term damage to the ocean and the living organisms that live there. Oil (Petroleum) is a complex organic mixture of compounds. The oil spills results in the formation of oily layer at the coast of the oceans. There are many organisms with the ability to degrade hydrocarbons, but there is a bacteria that contains a unique and separate structure and function. These are *Alcanivorax borkumensis* we can say "Hydrocarbon Eaters" [1-3].

The susceptibility of these hydrocarbon eaters are ranked as; linear then branched then small aromatic and after all comes cyclic. *Alcanivorax* is a nonpathogenic hydrocarbon eater bacterium. *Alcanivorax borkumensis* is a rod bacterium. It produces some enzymes that work as degraders of hydrocarbons especially alkanes. 80% alkanes are degraded by *Alcanivorax borkumensis*. Alcanivorax contains special gene codes that make up these enzymes that degrade hydrocarbons and make them as "Hydrocarbon Eaters" [4-6].

Genomic Structure and Hydrocarbon Eating Ability

There are many other bacteria's and microorganisms that have the ability to degrade hydrocarbons but A borkumensis is of special interest as it is a marine bacterium and it is highly found in the

oil contaminated blooms, where it holds 80% of the bacterial community. The genomics of these bacteria tells us how this bacterium grows and feeds effectively on alkanes. A. borkumensis encodes exoplossacharide production of pili because hydrocarbons are poor water soluble as we know. Pili help borkumensis in attachment to the oil-water interface. The GC content in A. borkumensis is 54.7%, it contains a complete set of gene that are specially for the alkane degradation and the gene set is as follows: Alksb1gjh and there were more genes that were found encoding proteins that are involved in alkane degradation just like alkK, alkN and ankL these genes encodes proteins like alcohol dehydrogenase, oxidoreductases. alkane hydroxylases, rubredoxin, P450 cytochrome and rubredoxin reeducates [7].

The Marine Origin of A. borkumensis

The marine origin of Alcanivorax is proved as there were majority of the genes that encodes efficient scavenging programs just as high affinity for ABC transporters, to sequester nutrients that are essential for example; (Co, Zn, Fe, Mg, Mo and Mn). It flourishes in areas of heavy tides and can survive there. A. borkumensis live in salinities (range from 1%-12.5%) and they exist in temperature between 4 degree celsius-35 degree celsius. When borkumensis feeds on alkanes and pyruvate each cell produce a bio surfactant around the cell membrane. The substances that are present in that bio surfactant reduce the surface tension of H_2O and increase the efficacy of degradation of oil. They are emulsifiers too as they helps in creating oil-water emulsions, which makes oil soluble [8-12].

Metabolic and biotechnological potential: A. borkumensis has a limited range of substrates for it growth. A. borkumensis use simple

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hexoses carbohydrates for their nutrition and growth. *Alcanivorax* encode proteins which take a crucial and important part in metabolic reactions, including, 2 determinants, 8 hydrolases, 3 deacylases, 36 for cytochrome and 30 for oxido-reductases [13-15].

Discussion

Through analysis of *Alcanivorax borkumensis* genome we came to know about its high affinity for substrates of hydrocarbon and oligotrophic lifestyle, unusual metabolic capability, genomic response and environmental stresses. *A. borkumensis* adapts rapidly to the presence of alkanes and survive in most oceans by relying on streamlined. The ubiquity reflects its developed ability and wide nutrient uptake function, in other words for inorganic nitrogen and organic nitrogen.

Conclusion

Future functional studies e.g. spatiotemporal proteomics, transcriptional and metabolomics profiling will largely reveal our knowledge into marine hydro-carbon degradation processes of this bacteria. These studies will provide us a framework, which can be used to study the relation between hydrocarbon-degrading populations. This framework will undoubtedly help to develop new strategies for bioremediation of oil-contaminated marine environments.

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