

Biodegradation and transformation of comparative genomic analyses in mitochondria.

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Abstract

Polycyclic Aromatic Hydrocarbons (PAHs) are widespread environmental pollutants some of which have been shown to cause cancer in test subjects and are commonly regarded as a major contributor to the burden of cancer in humans. One microbe that has the ability to effectively break down petroleum hydrocarbons and PAHs is lutemaribacter. In the current investigation, we recovered three strains of the genus lutimaribacter for the first time from samples of saline lakes. These strains, designated exhibit reduced rRNA gene sequence similarities with legitimately published species of this genus.

Keywords: Evolution, Lamiinae, Mitochondrial genome.

Introduction

The type species is strains can develop at high NaCl concentrations and have an ideal growth temperature. The ability of the three isolates to break down varies. It is noteworthy that strain has a variety of PAHs-degradation capabilities. This paper offers a thorough evaluation of the new isolates of the genus from the salinity lake, including their strain isolation, polyphonic taxonomy, PAHs-biodegradation, and comparative genome analysis. The primary vector of *Xylophilus*, which causes pine wilt disease and results in significant economic and ecological losses, is the genus *Monochamus* within the subfamily lamiinae. There have only ever been three entire mitochondrial genomes of the genus *Monochamus* sequenced and there have never been any comparative mitochondrial genomic [1].

Here two *Monochamus* species, saltuarius had their mitochondrial genomes newly sequenced and annotated. The mitochondrial genomes of *Monochamus* species are preserved in terms of gene composition and arrangement. Except for trnS1, all transfer RNAs display the usual clover-leaf secondary structure. The mitochondrial genomes of Lamiinae show a bias like those of other longhorn beetles. Tandem repeat sequences are prevalent in the rich area and all protein-coding genes have undergone purifying selection. Congruent topologies were found among the trees derived from the five datasets by phylogenetic analyses, and Acanthocinini, Agapanthiini, Batocerini, Dorcaschematini, Pteropliini, and Saperdini's monophyly received strong support. The results of this work improve our knowledge of the evolution of the mitochondrial genome and will serve as a foundation for next population genetics and phylogenetic studies in this group [2].

Persistent Organic Pollutants (POPs), in particular are dangerous chemicals that are resistant to environmental deterioration and endanger a range of ecosystems, including human health. The representative organic pollutants, petroleum hydrocarbons and Polycyclic Aromatic Hydrocarbons (PAHs), are found in a variety of habitats, including the ocean, desert, saline lake, underground water, etc. These pollutants have drawn more attention because of their propensity to induce cancer and long-term persistence in the environment numerous studies have demonstrated that the main technique for eliminating PAHs from the environment is biodegradation. In particular, bioremediation of PAHs by functional microorganisms has become an ideal option for PAH removal due to its economic efficiency without cross-contamination. Numerous microorganisms that biodegrade petroleum hydrocarbons or PAHs, such as CycloHexyl Acetate (CHAA), Naphthalene, Phenanthrene [3].

However, previous studies have shown that petroleum hydrocarbons and PAHs are often co-metabolized by a group of bacteria or require the presence of an additional carbon source for complete mineralization Furthermore, bacteria with broad biodegradation activity for petroleum hydrocarbons and PAHs are also less well documented. In particular, bioremediation of PAHs by functional microorganisms has become an ideal option for PAH removal due to its economic efficiency without cross-contamination. Numerous microorganisms that biodegrade petroleum hydrocarbons or PAHs, such as CycloHexyl Acetate (CHAA), Naphthalene, Phenanthrene, or chrysene, have been identified from coastal habitats. However, previous studies have shown that petroleum hydrocarbons and PAHs are often co-metabolized by a group of bacteria or require the presence of an additional carbon source for

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complete mineralization. Furthermore, bacteria with broad biodegradation activity for petroleum hydrocarbons and PAHs are also less well documented. Aromatics are economic organic pollutants widely distributed in marine environments, and microorganisms of the genus demonstrate a high potential for bioremediation and degradation of aromatics [4,5].

Conclusion

Aromatics are one or more aromatic hydrocarbons, including monocyclic aromatic hydrocarbons (benzene, phenol, toluene, etc.) and polycyclic aromatic hydrocarbons (naphthalene, phenanthrene, pyrene, etc.) that are widely distributed in the marine environment. It is an economic organic compound containing an aromatic ring. Of course, aromatics are persistent and can accumulate in marine organisms and cause carcinogenic effects. Microbial bioremediation is an environmentally friendly and economical method of treating aromatic contamination. Studies have shown that *Bacillus*, *Mycobacterium*, *Sphingomonas*, *Pseudomonas*, and *Rhodococcus* can degrade aromatics with high efficiency. As a

model substrate for PAH metabolism, Phenanthrene has been extensively studied over his three decades and its bacterial degradation pathway has been extensively described.

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