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Publication Date
2005-06-24
Genetic Elucidation of Metabolic Diversity in *Dechloromonas aromatica* strain RCB

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The Dechloromonas aromatica genome has been finished. Dechloromonas aromatica is a key class permitting strain found ubiquitously in reductive environments. A facultative anaerobe, capable of aromatic hydrocarbon degradation, *D. aromatica* is a key bacterium in ensuring environmental bioremediation. The high-throughput sequencing of the genome has enabled the identification of a large number of protein coding sequences. Due to its metabolic versatility, strain RCB was selected for complete genome sequencing at the JGI Joint Genome Institute. The completed genome contains a single circular chromosomal DNA structure containing a total of 4.17 mega base pairs (Mb) with 93.5% of coding content. Each ORF annotation was conducted at Oak Ridge National Laboratory and the Virtual Institute for Microbial Stress and Metabolism (VIMS). The genome being sequenced can be found at the JGI website.

**Analysis of the Perchlorate Reduction Pathway**

Perchlorate, a previously unknown reductive contaminant found in the environment, has been shown to interfere with thyroid hormone synthesis by reductively converting iodide to hypoiodite (Hypo), an endocrine disruptor. This phenomenon has been associated with the perchlorate reduction pathway, which is a key process in perchlorate remediation. The perchlorate reduction pathway is a key process in perchlorate remediation, and it is catalyzed by the perchlorate reductase enzyme. The enzyme catalyzes the reduction of perchlorate to chloride, a process that is essential for the detoxification of perchlorate in the environment. The enzyme is encoded by the *pctA* gene, which is located on the *D. aromatica* chromosome. The enzyme is a member of the family of flavin-containing reductases, which are responsible for the reduction of a wide range of compounds, including chlorate and perchlorate.

**Signal Transduction: Interaction with the Environment**

- **Signal Transduction**
  - *D. aromatica* strain **RCB** encodes an unusually large number of proteins featuring the histidine kinase motif (1% of the genome). The presence of histidine kinases is crucial for the regulation of gene expression in response to environmental stimuli.
  - **D. aromatica** strain **RCB** encodes 71 histidine kinases, which are involved in various cellular processes, including cellular adaptation to environmental stressors. These proteins are found in a variety of functional modules, including signal transduction, metabolic regulation, and stress response.

**What’s Different about *Dechloromonas aromatica*?**

- A disproportionately high number of two-component sensors and phosphorelays (11% of the genome)
- A large number of two-component sensors, a phosphorelay, and a putative response regulator
- A putative response regulator (encoded by *pctA*) is highly conserved among bacteria
- The organisms also have a significant number of sensor kinase/two-component signal transduction genes

**Overview of Gene Function**

- **Aerobic and Anaerobic Aromatic Degradation**
  - **Benzene**
  - **Toluene**
  - **Ethylbenzene**
  - **Xylenes**
  - **D. aromatica** strain **RCB** is capable of degrading a wide range of aromatic compounds, including benzene, toluene, ethylbenzene, and the xylenes.

**Histidine Kinases in *D. aromatica* RCB: cytosolic and transmembrane proteins**

- **Histidine Kinases**
  - In general, the number of environmental stressors that pathways respond to is directly proportional to the number of histidine kinase-containing signal transduction genes present in the genome.

**Conclusions**

- We have finished the *Dechloromonas aromatica* genome, and we are currently annotating the resulting gene set.
- The TCA cycle has a large number of two-component signal transduction proteins (20% of the genome).
- The pathway analysis indicates that the *D. aromatica* strain **RCB** is capable of adapting to a variety of environmental conditions, including nutrient limitation and stress.
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**Diagram:**

- Diagram of *Dechloromonas aromatica* periplasmic reductase gene cluster
- Diagram of the perchlorate reduction pathway
- Diagram of histidine kinase proteins in *D. aromatica* RCB