What’s on the Menu: Identification of the Hydrocarbon Transport Systems as a First Step in Marine Oil-Degradation by Alcanivorax borkumensis

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Alcanivorax borkumensis has an important biotechnological application: these bacteria are able to degrade hydrocarbon contaminants during oil spills. To effectively use the bacteria, it is important to understand not only how the bacteria degrade hydrocarbons, but also how they transport water-insoluble oils into the hydrophilic interior of cells. No hydrocarbon transporter was revealed in A. borkumensis from its genome sequencing in 2006. The purpose of the current study was to employ both microbiological tools and bioinformatics to search for such transporters. Microbiological work involved the growth of A. borkumensis under different carbon sources that mimic oilfield hydrocarbons. Protein gel electrophoresis was performed to examine protein expression during growth. Various computational programs were then used to identify potential hydrocarbon transporters in A. borkumensis. The growth of A. borkumensis observed in the presence of chain-like, but not ring-like, hydrocarbons revealed its uptake selectivity. The differential protein expression profiles further demonstrated that the hydrocarbon-degradation pathway is different from the pyruvate-utilization pathway. The bioinformatics approach led to the significant discovery of both outer- (Abo_0193) and inner- (Abo_0687) membrane putative hydrocarbon transporters in A. borkumensis. The three dimensional models of Abo_0193 and Abo_0687 further supported their roles as potential chain-like hydrocarbon transporters. Taken together, this study revealed the presence of hydrocarbon transporters in A. borkumensis. Based on these findings, a model for the transport of hydrocarbons from the extracellular environment to the cytoplasm has been developed as a first step in marine oil-degradation by A. borkumensis.

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