Microaerophilic alkane degradation in Pseudomonas extremaustralis: a transcriptomic and physiological approach

Diesel fuel is one of the most important sources of hydrocarbon contamination worldwide. Its composition consists of a complex mixture of n-alkanes, branched alkanes and aromatic compounds. Hydrocarbon degradation in Pseudomonas species has been mostly studied under aerobic conditions; however, a dynamic spectrum of oxygen availability can be found in the environment. Pseudomonas extremaustralis, an Antarctic bacterium isolated from a pristine environment, is able to degrade diesel fuel and presents a wide microaerophilic metabolism. In this work RNA-deep sequencing experiments were analyzed comparing the expression profile in aerobic and microaerophilic cultures. Interestingly, genes involved in alkane degradation, including alkB, were over-expressed in micro-aerobiosis in absence of hydrocarbon compounds. In minimal media supplemented with diesel fuel, n-alkanes degradation (C13-C19) after 7 days was observed under low oxygen conditions but not in aerobiosis. In-silico analysis of the alkB promoter zone showed a putative binding sequence for the anaerobic global regulator, Anr. Our results indicate that some diesel fuel components can be utilized as sole carbon source under microaerophilic conditions for cell maintenance or slow growth in a Pseudomonas species and this metabolism could represent an adaptive advantage in polluted environments.