

Marine hydrocarbonoclastic bacteria and their capabilities to bioremediate marine oil spills: Functional Genomics, Physiology, Biochemistry

H. J. Heipieper

Department of Environmental Biotechnology, Helmholtz Centre for Environmental Research-UFZ, Permoserstrasse 15, 04318 Leipzig, Germany

Marine oil contaminations received public awareness due to the ongoing discussions of the environmental catastrophes of the Exxon Valdez tanker in Alaska in 1989, the Prestige tanker at the Spanish coast in 2002, and especially after the Deepwater Horizon oil spill in 2010 where about 700,000 tons of crude oil were released into the Gulf of Mexico. Here and in other marine environments polluted by crude oil, a special group of Gram-negative, gamma-proteobacteria named marine hydrocarbonoclastic bacteria were detected as key players in bioremediation [1]. These bacteria can only metabolize a few organic acids (acetate, pyruvate), and feed on a variety of aliphatic hydrocarbons instead. Several of these extraordinary marine bacteria such as *Cycloclasticus* sp., *Marinobacter* sp., *Thalassolituus* sp., *Neptunomonas* sp., *Oleiphilus* sp., *Oleispira* sp. and *Alcanivorax* sp. have been discovered in the sea all over the world always occurring in very small abundance. In case of an oil spill, however, they show a kind of bloom and can represent up to 80-90 % of the bacterial community [2].

Among the marine hydrocarbonoclastic bacteria, the mesophilic *Alcanivorax borkumensis* and the psychrophilic *Oleispira antarctica* are the best investigated species. The functional genomics of both bacteria were characterised [3,4]. In addition, detailed physiological studies regarding the adaptive strategies to their aliphatic substrates as well as to environmental stress conditions were carried out [4,5].

These investigations revealed the enormous adaptive potential of marine hydrocarbonoclastic bacteria regarding catabolic genes, cell surface modifications, incorporation of fatty acid intermediates into membranes and regulation of several stress response genes.

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References

- [1] Hazen et al. 2010. Deep-sea oil plume enriches indigenous oil-degrading bacteria. *Science* 330:204-208.
- [2] Yakimov et al. 2007. Obligate oil-degrading marine bacteria. *Curr. Opin. Biotechnol.* 18:257-266.
- [3] Schneiker et al. 2006. Genome sequence of the ubiquitous hydrocarbon-degrading marine bacterium *Alcanivorax borkumensis*. *Nature Biotechnol.* 24:997-1004.
- [4] Kube et al. 2013. Functional genome analysis of *Oleispira antarctica* RB-8, a key oil-degrading bacterium in cold and deep marine environments. *Nature Commun.* 4:2156.
- [5] Naether et al. 2013. Adaptation of hydrocarbonoclastic *Alcanivorax borkumensis* SK2 to alkanes and toxic organic compounds - a physiological and transcriptomic approach. *Appl. Environ. Microbiol.* 79:4282-4293.