Microbial piezophysiology: which role for high pressure in oil degradation?

Scoma Alberto[1], Ramiro Vilchez-Vargas[1], Marta Barbato[2], Francesca Mapelli[2], Sara Borin[2], Daniele Daffonchio[2] and Nico Boon[1]

[1] Laboratory of Microbial Ecology and Technology (LabMET), Ghent University
Coupure Links 653, B-9000, Gent, Belgium
E-mail: nico.boon@ugent.be

[2] Department of Food, Environmental and Nutritional Sciences (DeFENS), University of Milan
via Celoria 2, 20133, Milano, Italy

Most of the scientific research carried out so far in microbiology and biotechnology is focused on the understanding of biological kinetics at ambient pressure. This condition may characterize the large majority of microbes on dry land, while it does not apply to those living in the sea. Oceans are populated by a large variety of microorganisms that are able to survive in extremely harsh conditions (Kato *et al.*, 1998). Here, metabolic pathways are typically affected by high pressure (as well as by low temperatures) in a manner that is not completely clear. When oil spills occur, a relevant amount of hydrocarbons (HCs) is released into the environment (Adcroft *et al.*, 2010). In the case of marine accidents, such compounds will spread horizontally, eventually reaching the closest shores, and vertically, dropping downwards to the sea floor. Here, although HCs are present in nature, marine ecosystems may be able to degrade only a very minor fraction of such spills. Typically, one of the main reasons for HCs low biodegradability is their low solubility in water, preventing an efficient microbial uptake. It is known that high pressure increases oil solubility in water (Srivastan *et al.*, 1992), while also supporting an increase in the fluidity of cells' membrane (Bartlett, 2000), both easing microbial access to HCs. Microorganisms responsible for bioremediation are known to produce surfactants, which further enhance oil solubility, a condition known to feature the best degraders (Yakimov *et al.*, 1998). However, these factors are not sufficient to allow full remediation, and the majority of the spilled HCs persist for decades (Reddy *et al.*, 2002). In order to gain further insights on the role of hydrostatic pressure on the catabolic pathways triggered during HCs degradation, we tested four different HCs degraders (belonging to the genera *Alcanivorax* and *Marinobacter*, three of which are new isolates from surface water and sediment) at three different pressures (1, 55 and 105bars, correspondent to about 0, 550 and 1050m seawater-depth), using dodecane (C12) as a model HC. Evaluation of cells growth (as optical density) was coupled to a number of biochemical analyses, such as oxygen respiration, carbon dioxide production, hydrophobicity test (indirectly expressing the degree of access to HCs) and phospholipid fatty acids (PLFA) analysis. Further, transcriptomic analyses have been conducted to check the expression of the alkane monooxygenase gene (*alkB*) and the cytochrome P450 (*CYP153*), the most known genes responsible for HC degradation, and to unravel which other genes are triggered by high pressure in such conditions and are potentially involved in the degradation of HCs.

References

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