Microbial membrane lipid distribution shifts in Baltic Sea subsurface sediment enrichment cultures

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Sulfate-reducing, methanogenic, and sulfate/methane transition zones of marine coastal sediments are important locations of anoxic organic matter degradation. Recently, it has been found that the metabolic flexibility of microbial communities in these sediment zones is far greater than previously thought [1] [2]. Short chain fatty acids, such as propionate and butyrate, have been identified to be important intermediates in the anaerobic food chain [3]. However, little is known about the physiological cell membrane adaptations of in situ microbial populations. In order to observe how the microbial cell membranes respond to different nutrient substrates and metabolic strategies, sediment enrichment cultures were made from the sulfate, sulfate/methane transition, and methanogenic zones with different sulfate concentrations and either butyrate or propionate amendments as carbon substrates. The distribution of intact polar membrane lipids (IPLs) changed among the different sediment zones and available nutrient substrates, indicating shifts in membrane lipid responses to changing metabolic strategies. Hexose-lipids and phospholipids were more abundant in the butyrate amended sediments than propionate amended sediments of the sulfate/methane transition zone. Of particular interest was the presence of trimethylornithine (TMO) IPLs in multiple butyrate amended methanogenic zone enrichment cultures, due to the fact that TMOs have only previously been identified in low nutrient ombrotrophic methanogenic northern wetland subsurface planctomycete isolates and peats [4]. These results support growing evidence that microbial communities are flexible in their physiological response to different subsurface sediment zone metabolic regimes.

[1] Finke et al. (2007), *Env Microbiol* **9**, 1060-1071. [2] McInerney et al. (2008), *Ann N Y Acad Sci* **1125**, 58-72. [3] Müller et al. (2010), *Env Microbiol Rep* **2**, 489-499. [4] Moore et al. (2013), *Appl Env Microbiol* **79**, 6874-6884.