

Archaeal lipid biosynthesis in the Black Sea

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Archaea have an important role in global biogeochemical cycles and are key to understand the evolution of life. One of the traits that distinguish them from Bacteria and Eukarya is the structure of their membrane lipids. Membranes of Bacteria and Eukarya are composed of fatty acids linked to glycerol-3-phosphate (G3P) via ester bonds, while those of Archaea have isoprene-based chains linked by ether linkages to G1P. In order to predict the lipid composition of not-yet cultured archaea and the acquisition of their lipid biomarkers through evolution we can study the genetic capacity of a microorganism to synthesize a lipid compound of interest, which can be achieved by targeting their lipid biosynthetic pathways. In the last years, we have hypothesised that the enzyme involved in the first ether bond formation has a role in determining the relative abundance of the archaeal lipids synthesized [1], which was confirmed by the detection of key differences in this enzyme in 'shallow' and 'deep' Thaumarchaeota also coinciding with a change in the relative abundance of archaeal lipids with depth [2]. Recently, we also showed that members of the marine euryarchaeota group II (MGII) contain the archaeal lipid synthesis genes as well as those needed for bacterial-like fatty acid and ester-bond formation [3]. However, they lack the genetic potential to synthesize G1P backbone but rather G3P, which suggest that MGII harbour the potential to synthesize 'chimeric' archaeal membrane lipids. Here, I will overview these discoveries and present new insights in archaeal lipid biosynthetic pathways by analysing metagenomes obtained in the water column of the Black Sea.

[1] Villanueva *et al* (2014) *Nat. Rev. Microbiol.* **12**, 438-448.

[2] Villanueva *et al* (2015) *Environ. Microbiol.* **17**, 3527-

3539. [3] Villanueva *et al* (2017) *Environ. Microbiol.* **19**, 54-69.