Metabolic potentials of different lineages of the archaeal phylum Bathyarchaeota widespread in marine sediments

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Bathyarchaeota The archaeal phylum is cosmopolitan and abundant in the energy-deficient marine sub-surface sediments. There are at least 19 subgroups in the Bathyarchaeota phylum with high inter-group diversities, most likely also corresponding to a high metabolic diversity. Recent genomic and enzymatic evidences indicate that members of Bathyarchaeaota have variable metabolisms such as methane metabolism and acetogenesis^[1,2,3].We conducted metagenome analysis of deep-sea subsurface sediments, recovered 27 bathyarchaeotal genomic bins. These bathyarchaeotal genomes could be assigned to at least seven lineages which provided us a chance to reveal and compare the metabolic potentials of different lineages of the phylum.

Majority of the recovered bathyarchaeotal genomic bins contain most of genes for inorganic carbon fixation via the reductive acetyl-CoA (Wood-Ljungdahl) pathway. All the seven Bathy-groups investigated here contain the acetyl-CoA synthetase (ADP-forming, Acd) commonly used in Archaea for acetate metabolism, while only two groups have the Phosphate acetyltransferase(Pta) and acetate kinase(Ack) which are mostly used for acetate production/assimilation in bacteria. Besides, different lineages of Bathyarchaeota were shown to contain specific set of genes targeting a variety of organic substrates. Our analysis further demonstrated that this ubiquitous and abundant subsurface archaeal group has adopted a versatile life strategy to make a living under energy-limiting conditions, and different lineages of Bathyarchaeota have evolved specific physiological properties and adapted to distinct ecological niches.

Ref:

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