

Shared patterns and temperature-related characteristics in functions and structures across the methanogenic pangenome

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Methanogenesis is thought to be one of the most ancient metabolisms on Earth and plays a crucial role in the global carbon cycle. Today methanogens inhabit a wide variety of environments and are phylogenetically distributed across multiple archaeal clades. Given their phylogenetic and environmental diversity, one might wonder: What exactly makes a microorganism a methanogen? And: Which traits allow methanogens to adapt to the wide variety of environments they can be found in today?

In this study, we focus on genome resolvable differences between methanogens based on (1) the substrate they use for methane production (CO₂, acetate, and/or methylamines) and (2) the temperatures at which they grow. We first establish the methanogenic core genome (that is, the functional groups shared by all methanogens) before diving deeper into pangenome functional attributes.

A total of 225 gene groups comprise the core shared by all organisms in our analysis. The majority of these gene groups are functionally related to biosynthesis, while genes unique to specific organisms are largely related to cell wall biosynthesis, the cytoskeleton, and cell motility functions. The unique fraction of genes shows temperature and also protein domain content variability, hinting at an evolvable portion of the methanogen phenotype. Thermotolerant methanogens have a smaller proteome compared to their psychrotolerant counterparts. We explore temperature related trends in amino acid utilization, and protein-structure variation across temperature groups. Finally, we explore the phylogenies of core genes and the leaf-to-leaf phylogenetic distances across temperature groups.