

Comparative genome analyses of *Methanoculleus* species from various habitats

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Currently, total six *Methanoculleus* species genomes were available, including *M. taiwanensis* [1], *M. sediminis* [2], *M. marisnigri* [3], *M. bourgensis* [4], *M. thermophilus* [5] and *Methanoculleus* strain MH98A [6], which were isolated from various habitats, including sediments at Deformation Front region, submarine mud volcano, Black Sea, sewage sludge, marine sediment under nuclear power plant and gas hydrate associated sediment at Krishna Godavari Basin (India), respectively. Through comparative genomic analyses using Integrated Microbial Genomes (IMG) system at DOE's Joint Genome Institute (JGI) website, the results showed *M. taiwanensis* contains significantly high abundance of Cluster of Orthologous Groups (COGs) in the category of 'signal transduction mechanisms', which indicates this species may have more sensing modules to monitor environmental changes. In addition, the genome of *M. bourgensis* harbors highly abundant transposase genes, which may be disseminated from microbial communities in its habitat, the sewage treatment plant, where is a breeding ground for antibiotic resistant bacteria. All *Methanoculleus* genomes contain three coding genes for trehalose synthases, which convert ADP-glucose to trehalose. In addition, structural genes adjacent to trehalose synthase genes, which comprise signaling module of PAS domain containing proteins, heat shock protein Hsp20 family proteins, arabinose efflux permeases and multiple surface proteins with FAS repeat, may indicate that trehalose synthases gene clusters in *Methanoculleus* strains play roles involved stress response and regulation through accumulation of compatible solutes and modification of surface proteins. Through comparative genomic analyses, we could gain more insight in understanding the life under the deep sea, especially for the methane based ecosystems.

[1] Weng *et al.* (2015) *Int J Syst Evol Microbiol* **65**, 1044-49. [2] Chen *et al.* (2015) *Int J Syst Evol Microbiol* **65**, 2141-47. [3] Anderson *et al.* (2009) *Stand Genomic Sci* **1**, 189-196. [4] Maus *et al.* (2012) *J Bacteriol* **194**, 5487-8. [5] Rivard & Smith (1982) *Int J Syst Evol Microbiol* **32**, 430-36. [6] Dabir *et al.* (2014) *Mar Genomics* **18PB**, 139-140.