

Methanoarchaea Isolated from Deep Sea Mud Volcanoes

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Mud volcanoes are the most important pathways for methane emission from deep marine sediments into atmosphere. They are related to the occurrence of hydrocarbons and fluid discharge (methane and CO₂), an important component of global carbon cycles. The submarine mud volcanoes, gas seeps and mud diapirs were observed at the upper slope domain of eastern part of accretionary wedge at offshore southwestern Taiwan [1]. Two methanogens, strain S3Fa^T and CYW5 were isolated from sediment collected by Ocean Researcher I cruise ORI-934 in 2010 nearby the submarine mud volcanoes MV4 and MV5, respectively, located at the upper slope of southwest Taiwan. Both strains are irregular cocci and use formate or hydrogen plus carbon dioxide as only catabolic substrates. Surprisingly, the cannulae like structure as *Pyrodictum abyssi* growing as networks of cells was observed in strain CYW5. Both strains grew optimally at 37°C, but the range of temperature growth for strain S3Fa^T and CYW5 was 20-50 °C and 20-42 °C, respectively. And strain S3Fa^T could tolerate higher salt concentration (1 M NaCl) than strain CYW5 (0.51 M). Phylogenetic analysis revealed that strain S3Fa^T was most closely related to *Methanoculleus marisnigri* JR1^T (99.3% 16S rRNA gene sequence similarity). Whereas, genome relatedness between strain S3Fa^T and JR1^T computed by Genome-to-Genome Distance Analysis (GGDA) and Average Nucleotide Identity (ANI) with values of 46.3-55.5% and 93.08%, respectively, which both strongly supported strain S3Fa^T belonging to a new species of *Methanoculleus* and name as *Methanoculleus sediminis* [2]. The strain CYW5 was related to the member of family Methanomicrobiaceae with 95 % identity. It was suggested that strain CYW5 may be a candidate for new genus. Through these novel methanogens, we could gain insight into the communities of methanogenic archaea in the marine mud volcano habitat.

[1] Chen et al. (2014) J. Asian Earth Sci. 92:201-214.

[2] Chen et al. (2015) Int. J. Syst. Evol. Microbiol. 65:2141-47.