Genomic analysis of methanogenic archaea reveals a shift towards energy conservation -
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Background: The metabolism of archaeal methanogens drives methane release into the environment and is critical to understanding global carbon cycling. Methanogenesis operates at a very low reducing potential compared to other forms of respiration and is therefore critical to many anaerobic environments. Harnessing or altering methanogen metabolism has the potential to mitigate global warming and even be utilized for energy applications.

Results: Here, we report draft genome sequences for the isolated methanogens Methanobacterium bryantii, Methanosarcina spelaei, Methanosphaera cuniculi, and Methanocorpusculum parvum. These anaerobic, methane-producing archaea represent a diverse set of isolates, capable of methylotrophic, acetoclastic, and hydrogenotrophic methanogenesis. Assembly and analysis of the genomes allowed for simple and rapid reconstruction of metabolism in the four methanogens. Comparison of the distribution of Clusters of Orthologous Groups (COG) proteins to a sample of genomes from the RefSeq database revealed a trend towards energy conservation in genome composition of all methanogens sequenced. Further analysis of the predicted membrane proteins and transporters distinguished differing energy conservation methods utilized during methanogenesis, such as chemiosmotic coupling in Msar. spelaei and electron bifurcation linked to chemiosmotic coupling in Mbac. bryantii and Msph. cuniculi.

Conclusions: Methanogens occupy a unique ecological niche, acting as the terminal electron acceptors in anaerobic environments, and their genomes display a significant shift towards energy conservation. The genome-enabled reconstructed metabolisms reported here have significance to diverse anaerobic communities and have led to proposed substrate utilization not previously reported in isolation, such as formate and methanol metabolism in Mbac. bryantii and CO2 metabolism in Msph. cuniculi. The newly proposed substrates establish an important foundation with which to decipher how methanogens behave in native communities, as CO2 and formate are common electron carriers in microbial communities.

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