Gene Ontology Terms Describe Biological Production of Methane

Endang Purwantini[1*] (epurwant@vbi.vt.edu), Trudy Torto-Alalibo[1], Joao C. Setubal[1,2], Brett M. Tyler[1,3] and **Biswarup Mukhopadhyay**[1]

[1]Virginia Bioinformatics Institute, Virginia Tech, Blacksburg, VA. 24061 USA

[2]Department of Biochemistry, Institute of Chemistry University of São Paulo, Brazil

[3]Center for Genome Research and Biocomputing, Oregon State University, Corvallis, OR. 97331 USA

http://mengo.vbi.vt.edu

Project Goals: The MENGO consortium in collaboration with the community of microbiologists engaged in bioenergy research and the Gene Ontology (GO) consortium aims to develop a comprehensive set of Gene Ontology terms that will describe bioenergy related biological processes and to annotate relevant microbial genomes with appropriate GO terms. The MENGO project is a community-oriented multi-institutional collaborative effort that aims to develop new Gene Ontology (GO) terms to describe microbial processes of interest to bio-energy production. Such terms will aid in the comprehensive annotation of relevant genes in diverse microbial genomes. Among the 200 terms developed so far are a comprehensive set that describes processes involved in the biological production of methane/methanogenesis.

Biologically, methane is generated by methanogenic archaea from H_2 + CO_2, secondary alcohol + CO_2, formate, carbon monoxide, acetate, methanol, methylamines, and methanethiols. Pathways for methanogenesis from these substrates use unusual coenzymes such as coenzyme F_{420}, methanofuran, tetrahydromethanopterin, coenzyme M, cofactor F_{430}, and coenzyme B. Methanogenesis allows efficient mineralization of biological polymers in anaerobic niches of nature and thereby plays an important role in carbon cycle. This integrated process is leveraged for the production of methane from renewable resources and for waste treatment. The MENGO team has created some terms that are useful for describing the biological processes allowing methanogenesis from carbohydrates, including the biosynthesis of relevant coenzymes. Additionally, methanogenesis related gene products of certain methanogenic archaea such as *Methanocaldococcus jannaschii, Methanosarcina barkeri, Methanosarcina thermophilla, Methanosaeta concilii, Methanopyrus kandleri,* and *Methanothermobacter marburgenensis* have been manually annotated with GO terms.

Funding for the MENGO project is provided by the Department of Energy as part of the Systems Biology Knowledgebase program - grant# DE-SC000501.