

Methanotrophs- Role in Environmental Engineering Specific to Reversal of Global Warming

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Abstract- Methanotrophs are members of Archaeobacteria that play an important role in mitigation of climate change by reducing methane emissions from landfills and geothermal power stations. Two types of methanotrophs are existent in nature – high capacity methanotrophs and low capacity methanotrophs. Methane monooxygenase enzyme produced by these organisms plays a major role in utilization of methane as a sole source of carbon and energy. Two types of monooxygenases have been isolated from methanotrophs -soluble methane monooxygenase (sMMO) and particulate methane monooxygenase (pMMO). Cells with pMMO expressed high affinity for methane than sMMO producing cells. Methane gas is harmful to environment as it a potential greenhouse gas and is produced due to several anthropogenic activities. Methane is 72 times more potent than carbon dioxide in trapping heat in a period of 20 years. Hence formulation of new strategies is essential in environmental engineering by exploiting methanotrophs for reversal of global warming.

Index Items - Methane, methanotrophs, globalwarming, pMMO, sMMO.

I. INTRODUCTION

Methane levels have more than doubled over the last 150 years especially after the Industrial Revolution. This change is brought about by human activities and intensive farming increasing the methane levels in the atmosphere. Industrial Revolution resulted in the increased addition of methane due to anthropogenic sources. Fossil fuel utilization and intensive livestock farming have caused the current increased methane levels that account to 60% of all human methane emissions [1]. Other sources include landfills and waste disposal (16%), biomass burning (11%), rice agriculture (9%) and biofuels (4%). Microbiological mediated bioremediation of methane emission sites has been a subject of much research over the past decade. Aerobic-mediated bioremediation examines the utilization of gram negative methanotrophs, microorganisms that consume methane as their sole source of carbon and energy. These microorganisms play an important role in degradation of methane owing to the diverse environments in which methanotrophs are found,

the range of substrates they can degrade and ease of stimulation in the presence of methane and oxygen. Different groups of bacteria are known to exhibit the capability to degrade methane like Γ -Proteobacteria, α -Proteobacteria, Verrucomicrobia, Euryarchaeota phylum of the Archaea.

II. SOURCES OF METHANE EMISSIONS:

There are two ways in which methane is emitted into the environment- one is by natural organic matter decomposition and second is from anthropogenic activities resulting in more methane emissions. The main natural sources include wetlands, termite hills and oceans [1]. 36% of methane is emitted from natural sources and the rest of the majority 64% is due to human sources like landfills and livestock farming. The most important source of methane generation is production, transportation and use of fossil fuels.

III. NATURAL SOURCES OF METHANE

EMISSION:

Paddy fields for rice production are man-made wetlands with high moisture content, depleted oxygen concentration and have ample organic material. This environment supports the methane producing microbes that release methane by decomposing the organic matter. The swamp-like environment of rice fields results in 9% of human methane emissions. Growing of paddy generates 31 million tonnes of methane per annum.

Termites are a significant natural source of methane. Methane is produced during normal digestion process of termites. Termites consume cellulose but rely on micro-organisms in their gut to digest it. These micro-organisms produce methane during the process. This creates 12% of natural methane emissions [6].

Another significant natural source of methane comes from the oceans. Methane producing microbes living in the ocean are responsible for these emissions. This accounts to 10% of natural methane emissions [7]. Globally, oceans create 19 million tonnes of methane per year [8].

IV. HUMAN SOURCES OF METHANE

EMISSIONS:

A large part of methane emission is contributed by leakages from natural gas industry as methane is the main component of the natural gas. The activities that lead to the release of methane include the extraction, processing and transportation of natural gas. Incomplete combustion of fossil fuels also results in methane emissions [1].

Another important source of methane emissions is gut of farm animals where enteric fermentation of organic substances takes place. Normal digestion process in farm animal's accounts to 27% of human methane emissions as farm animals like cows, sheep and goats are reared by human beings [1]. It is projected that livestock farming for meat creates 90 million tons of methane per year [4]. Landfills and dumping of solid waste also releases methane into the environment. This occurs due to the decomposition of solid waste in landfills and waste dumps. Animal and human waste further adds more methane into the environment. These sources account for 16% of human methane emissions. Landfills and waste generate 55 million tonnes of methane per annum. Incomplete burning of Biomass leads to large amount of methane emissions accounting to 11% of human methane emissions. Large open fires to destroy crop waste and clearing of land for agriculture or other purposes is another reason for methane release. Natural wildfires also contribute to methane emissions. Biomass burning creates 38 million tonnes of methane per year.

Biofuels produce 12 million tonnes of methane per annum. Incomplete biofuel combustion leads to the production of methane accounting to 4% of human methane emissions. Half of the world's populations, about 2.7 billion people, use solid biofuels to cook and heat their homes on a daily basis adding more and more methane to the environment. [5].

V. MICROORGANISMS CONSUMING METHANE:

Though some of methane produced gets absorbed by methane-consuming microorganisms most of it gets released into the atmosphere. The methanotrophs are aerobic bacteria that utilise methane as a sole source of carbon and energy. One important enzyme produced by these microorganisms i.e., methane monooxygenase (MMO) plays major role in utilisation of methane. Methanotrophs are ubiquitous and can co-metabolize many aliphatic and aromatic compounds. Bio-stimulation of methanotrophic bacteria is accomplished through the addition of methane and other gaseous nutrients resulting in an increase in contaminant biodegradation and biotransformation [9, 10].

Methanotrophic bacteria have been isolated from a wide variety of environments including soils [11], sediments, landfills [12], ground water [13], seawater [14,15], peat bogs [16], hot springs [17], plant rhizosphere [18], salt reservoirs [19] and the Antarctica [20].

Methanotrophs were grouped according to their morphology, type of resting stage, intra-cytoplasmic membrane structures and physiological characteristics [11]. Eight genera of methanotrophs are characterized - *Methylococcus*, *Methylomonas*, *Methylomicrobium*, *Methylobacter*, *Methylocaldum*, *Methylosphaera*, *Methylocystis* and *Methylosinus*. These genera are divided into two distinct physiological groups.

Type I Methanotrophs (*Methylomonas*, *Methylomicrobium*, *Methylobacter*, *Methylocaldum*, *Methylosphaera*) assimilate formaldehyde produced from the oxidation of methane (via methanol) using the ribulose monophosphate pathway. They have cell membranes that are composed of predominantly 16-carbon fatty acids and possess bundles of intracytoplasmic membranes.

Type II methanotrophs (*Methylocystis* and *Methylosinus*) utilize the serine pathway for formaldehyde assimilation. They have intracytoplasmic membranes arranged around the periphery of the cell and contain predominantly 18-carbon fatty acids [21]. Membranes of the genus *Methylococcus* possess a combination of characteristics of both type I and type II methanotrophs.

VI. ROLE OF METHANOTROPHS IN CLEAN UP OF ENVIRONMENT:

In recent years there has been an increased interest in the utilization of microorganisms for restoration of environment. The usefulness of microorganisms with a diversity of metabolic activities in wide ranging applications coupled with advances in the technology have led to successful demonstrations in the ever-expanding bioremediation in specific to restoration of environment.

The application of environmental biotechnology as a successful remediation tool depends on the ability to stimulate or enhance specific activity of indigenous or inoculated microorganisms. The challenge has been to enhance the activity of these microorganisms and develop means to bring the contaminant into direct contact with the organisms to achieve optimal bioremediation [22].

To oxidise methane, methanotrophs use an enzyme called methane monooxygenase whose essential cofactor is usually copper but some microbes use iron as a cofactor. Understanding how methanotrophs handle copper is therefore of great importance for all potential applications of these organisms [23].

Methanotrophs oxidize methane by first initiating reduction of an oxygen atom to H₂O₂ and then transformation of methane to methanol using the enzymes methane monooxygenases (MMOs). There are two types of MMOs isolated from methanotrophs: soluble methane monooxygenase (sMMO) and particulate methane monooxygenase (pMMO). Cells containing pMMO have demonstrated higher growth capabilities and higher affinity for methane than sMMO containing cells. It is proposed that copper ions may play a key role in both pMMO regulation and the enzyme catalysis, thus limiting pMMO cells to more copper-rich environments than pMMO producing cells [2].

The discovery and characterization of Csp1 protein from a methanotrophs helped in elucidating the mechanism involved in binding to large quantities of copper aiding in methane oxidation.

VII. Future Prospects:

New insight into methanotrophs, bacteria oxidizing methane, helps in development of an array of biotechnological applications that remove methane and protect environment from this potent greenhouse gas.

REFERENCES

- [1] Bousquet, P., S. C. Tyler, P. Peylin, G. R. Van Der Werf, C. Prigent, D. A. Hauglustaine, E. J. Dlugokencky, J. B. Miller, P. Ciais, J. White, L. P. Steele, M. Schmidt, M. Ramonet, F. Papa, J. Lathière, R. L. Langenfelds, C. Carouge, and E.-G. Brunke. "Contribution of anthropogenic and natural sources to atmospheric methane variability." *Nature* 443, no. 7110 (2006): 439-443.
- [2] Lieberman, R. L.; Rosenzweig, A. C. (2004). "Biological Methane Oxidation: Regulation, Biochemistry, and Active Site Structure of Particulate Methane Monooxygenase". *Critical Reviews in Biochemistry and Molecular Biology*. 39 (3): 147–164.
- [3] Dlugokencky, E. J., E. G. Nisbet, R. Fisher, and D. Lowry. "Global atmospheric methane: budget, changes and dangers." *Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences* 369, no. 1943 (2011): 2058-2072.
- [4] Thornton, P. K.. "Livestock Production: Recent Trends, Future Prospects." *Philosophical Transactions of the Royal Society B: Biological Sciences* 365, no. 1554 (2010): 2853-2867.
- [5] Dlugokencky, E. J., E. G. Nisbet, R. Fisher, and D. Lowry. "Global atmospheric methane: budget, changes and dangers." *Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences* 369, no. 1943 (2011): 2058-2072.
- [6] Christian, T. J., R. J. Yokelson, B. Cárdenas, L. T. Molina, G. Engling, and S.-C. Hsu. "Trace gas and particle emissions from domestic and industrial biofuel use and garbage burning in central Mexico." *Atmospheric Chemistry and Physics* 10, no. 2 (2010): 565-584.
- [7] Hanson, R. S.; Hanson, T. E. (1996). "Methanotrophic bacteria". *Microbiological reviews*. 60 (2): 439–471.
- [8] Household air pollution and health." World Health Organization: Media Centre. <http://www.who.int/mediacentre/factsheets/fs292/> (accessed August 7, 2014)
- [9] Loulergue, Laetitia, Thomas F. Stocker, Dominique Raynaud, Jean-Marc Barnola, Bénédicte Lemieux, Thomas Blunier, Valérie Masson-Delmotte, Renato Spahni, Adrian Schilt, and Jérôme Chappellaz. "Orbital And Millennial-scale Features Of Atmospheric CH₄ Over The Past 800,000 years." *Nature* 453, no. 7193 (2008): 383-386.
- [10] Holmes, AJ; Roslev, P; McDonald, IR; Iversen, N; Henriksen, K; Murrell, JC (1999). "Characterization of methanotrophic bacterial populations in soils showing atmospheric methane uptake". *Applied and Environmental Microbiology*. 65 (8): 3312–8.
- [11] Whittenbury, R., Phillips. K. C. and Wilkinson, J. G. Enrichment, isolation and some properties of methane utilizing bacteria. *J. Gen. Microbiol.* 61, 205-218. (1970).

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- [12] Smith, K.S., Costello, A. M. and Lidstrom. M. E. (1997). Methane and trichloroethylene oxidation by an estuarine methanotroph. *Methylobacter* sp. Strain BB5.1. *Appl. Environ. Microbiol.* 63:4617-4620.
- [13] Fliermans, C.B., T.J. Phelps, D. Ringelberg, A.T. Mikell, and D.C. White. Mineralization of trichloroethylene by heterotrophic enrichment cultures. *Applied and Environmental Microbiology* 54:1709-1714 (1988).
- [14] Holmes, A.J., Owens, N. and Murrell, J. C. Detection of novel marine methanotrophs using phylogenetic and functional gene probes after methane enrichment. *Microbiology* 141:1947-1955 (1995).
- [15] Murrell, J. C. and Holmes, A. J. Molecular ecology of marine methanotrophs. In: *Molecular Ecology of Aquatic Microbes*. NATO ASI Series. Vol. G 38, (Joint. I. Ed.). pp. 366-390. Springer-Verlag. Berlin. (1995).
- [16] Dedysh, S. N., Panikov, N. S. and Tiedje, J. M. Acidophilic methanotrophic communities from Sphagnum peat bogs. *Appl. Environ. Microbiol.* 64, 922-929. (1998).
- [17] Bodroosy, L., Holmes, E. M., Holmes, A. J., Kovacs, K.L. and Murrell, J. C. Analysis of 16S rRNA and methane monooxygenase gene sequences reveals a novel group of thermotolerant methanotrophs. *Methylocaldum* gen. Nov., *Arch. Microbiol.* 168:493-503. (1997).
- [18] Gilbert, B., Amus, B., Hartmann, A. and Frenzel, P. In situ localization of two methanotrophic strains in the rhizosphere of rice plants. *FEMS Microbiol. Ecol.* 25:117-128 (1998).
- [19] Khelmelenia, V.N., N.G. Starostina, M.G. Tsvetkova, A.P. Sokolv, N.E. Suzina, and Y. A. Trotenko. Methanotrophic bacteria in saline reservoirs of Ukraine and Tuva *Microbiol.* 65: 686-703 (1996).
- [20] Bowman, J.P., L. Jimenez, I. Rosario, T.C. Hazen and G.S. Sayler. Characterization of the Methanotrophic Bacterial Community Present in a Trichloroethylene-Contaminated Subsurface Groundwater Site. *Appl. Environ. Microbiol.* 59:2380-2387 (1993).
- [21] Hanson, R. S. and Hanson. T. E. Methanotrophic bacteria. *Microbiol. Rev.* 60: 439-471 (1996).
- [22] Murrell, J. C. Molecular genetics of methane oxidation. *Biodegradation* 5:145-149:(1994).
- [23] Murrell, J. C., McDonald, J.R. and Bourne, D. G. Molecular methods for the study of methanotroph ecology *FEMS Microbiol. Ecol.* 27:103-114 (1998).
- [24] Cardy, D.N.L., V. Laidler, G.P.C. Salmond and J.C. Murrell. Molecular analysis of the methane monooxygenase (MMO) gene cluster of *Methylosinus trichosporium* OB3b. *Mol. Microbiol.* 5:1261-1264. (1991).