

一酸化炭素酸化菌の分子生物学的研究
Molecular biology of carboxydotrophs

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研究成果概要

Prokaryotes called carbon monoxide (CO) oxidizers use CO as carbon or energy sources with CO dehydrogenases (CODHs), which are divided into nickel-containing CODH (Ni-CODH) sensitive to O₂ and aerotolerant molybdenum-containing CODH (Mo-CODH). For CO oxidizers, redox state of surrounding environments may be a limiting factor to utilize CO because known CO oxidizers have either Ni- or Mo-CODH. However, genome and phylogenetic analyses of our new thermophilic bacterial isolate, strain G301, revealed that it is *Parageobacillus* sp. that has genes for both Ni-CODH and Mo-CODH. By comparison of the G301 genome with its close relatives, G301 was appeared to be the only isolate possessing both Ni-CODH and Mo-CODH genes while its close relatives have either or none of them. Reconstruction of the respiratory machinery indicated that CO oxidation by Ni-CODH was coupled with H₂ production, and CO oxidation by Mo-CODH was coupled with reduction of O₂ and nitrate. Our genome comparison revealed no significant differences in genome structures and cellular functions between the CO oxidizers and the non-CO oxidizers of *Parageobacillus*, suggesting that genes encoding CODHs would be retained exclusively for anaerobic and aerobic CO metabolisms and their related respirations in this genus.

To expand diversity of CO oxidizers, we cultured sediment of Jiunji-onsen of Shizuoka with CO and conducted metagenome analyses. We obtained Metagenomic Assembled Genomes (MAGs) of *Thermolithobacter ferrireducens* as a newly hydrogenogenic CO oxidizers. Further we successfully isolated the hydrogenogenic CO oxidizers from some aquatic environments and sequenced their genomes.

Anaerobic CO oxidizers bearing Ni-CODH gain carbon and energy from CO with metabolic pathways such as Wood-Ljungdahl pathway (WLP). WLP consists of two branches: methyl branch that uptakes CO₂ and H₂ by formate dehydrogenase (Fdh) and carbonyl branch that uptakes CO or CO₂ by Ni-CODH/acetyl CoA synthase. To gain insight into microbial contributions to CO metabolisms in the human gut, we analyzed prokaryotic MAGs in a gut microbiome dataset. We identified 1,302 potential CO oxidizers (4.3%) out of 30,609 MAGs. Majority of them belong to orders Oscillospirales (31.6%), Lachnospirales (29.1%), and Veillonellales (26.3%) of phylum Bacillota. MASs of Oscillospirales and Lachnospirales possessed incomplete WLP pathway. These MAGs lacked genes related to utilization of CO₂ +

H₂ for formate synthesis but possessed genes for utilization of formate derived from glycolysis. Veillonella MAGs possessed gene clusters possibly related to CO oxidization coupled with oxaloacetate production and/or nitrate respiration.

CO is also occurred in the ocean. Aerobic CO oxidizers are predicted to consume over 80% of oceanic CO. Although aerobic CO oxidizers are presumably to be ubiquitous in the ocean, global distribution and diversity of them remain unknown. Thus, we investigated 52,325 marine MAGs to identify aerobic CO oxidizers bearing Mo-CODH and biogeographic distribution of them. As a result, 1,792 MAGs belonging to 274 species in nine phyla were identified as aerobic CO oxidizers. Depth, temperature, dissolved oxygen (DO), and salinity of environments where MAGs of CO oxidizers and non-CO oxidizers distributed were not significantly different ($p>0.05$), thus niche partitioning was not suggested.

発表論文(謝辞あり)

• Isolation and genomic and physiological characterization of Parageobacillus sp. G301, the isolate capable of both hydrogenogenic and aerobic carbon monoxide oxidation (2023)

bioRxiv, DOI: 10.1101/2023.01.17.524042

学会発表(謝辞あり)

日本微生物生態学会 第35回大会

- 海洋表層の炭素、エネルギー循環を駆動する好気的一酸化炭素酸化菌の探索
- 琵琶湖第二湖盆底泥における潜在的 CO 酸化活性を持つ微生物の探索
- 淡水底質環境からの水素(H₂)生成型一酸化炭素(CO)酸化菌の分離及び性状解析
- 水圏環境中に潜在する水素生成型一酸化炭素酸化菌の探索とゲノム特性の解明

The International Human Microbiome Consortium Congress 2022

- Comprehensive genomic analysis uncovered CO-utilizing pathways in human gut microbiome