

Integrative genome-scale metabolic modeling reveals versatile metabolic strategies for methane utilization in *Methylobacterium album* BG8

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The Manuscript Microscope Sentence Audit is a research paper introspection system that parses the text of your manuscript into minimal sentence components for faster, more accurate, enhanced proofreading.

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Manuscript Source: <https://www.biorxiv.org/content/10.1101/2021.03.21.436352v1>

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- Depending on the source of the input text, the Sentence Audit may contain occasional html artefacts that are parsed as sentences (E.g. "Download figure. Open in new tab").
- Always consult the original research paper as the true reference source for the text.

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All queries, feedback or suggestions are also very welcome.

Research Paper Sections:

The sections of the research paper input text parsed in this audit.

[illegible]

Title **Integrative genome-scale metabolic modeling reveals versatile metabolic strategies for methane utilization in *Methylobacterium album* BG8**

S0 [001] Abstract

Abstract

S0 [002] **Methylobacterium album BG8 is an aerobic methanotrophic bacterium that can mitigate environmental methane emission, and is a promising microbial cell factory for the conversion of methane to value-added chemicals.**

Methylobacterium album BG8 is an aerobic methanotrophic bacterium ...
... that can mitigate environmental methane emission, ...
... and is a promising microbial cell factory ...
... for the conversion ...
... of methane ...
... to value-added chemicals.

S0 [003] **However, the lack of a genome-scale metabolic model (GEM) of *M. album* BG8 has hindered the development of systems biology and metabolic engineering of this methanotroph.**

However, ...
... the lack ...
... of a genome-scale metabolic model ...
... (GEM) ...
... of *M. album* BG8 has hindered the development ...
... of systems biology ...
... and metabolic engineering ...
... of this methanotroph.

S0 [004] **To fill this gap, a high-quality GEM was constructed to facilitate a system-level understanding on the biochemistry of *M. album* BG8.**

To fill this gap, ...
... a high-quality GEM was constructed ...
... to facilitate a system-level understanding ...
... on the biochemistry ...
... of *M. album* BG8.

S0 [005] **Next, experimental time-series growth and exometabolomics data were integrated into the model to generate context-specific GEMs.**

Next, ...
... experimental time-series growth ...
... and exometabolomics data were integrated ...
... into the model ...
... to generate context-specific GEMs.

S0 [006] Flux balance analysis (FBA) constrained with experimental data derived from varying levels of methane, oxygen, and biomass were used to model the metabolism of *M. album* BG8 and investigate the metabolic states that promote the production of biomass and the excretion of carbon dioxide, formate, and acetate.

Flux balance analysis ...
... (FBA) ...
... constrained ...
... with experimental data derived ...
... from varying levels ...
... of methane, ...
... oxygen, ...
... and biomass were used ...
... to model the metabolism ...
... of *M. album* BG8 ...
... and investigate the metabolic states ...
... that promote the production ...
... of biomass ...
... and the excretion ...
... of carbon dioxide, ...
... formate, ...
... and acetate.

S0 [007] The experimental and modeling results indicated that the system-level metabolic functions of *M. album* BG8 require a ratio > 1:1 between the oxygen and methane specific uptake rates for optimal growth.

The experimental ...
... and modeling results indicated ...
... that the system-level metabolic functions ...
... of *M. album* BG8 require a ratio > 1:1 ...
... between the oxygen ...
... and methane specific uptake rates ...
... for optimal growth.

S0 [008] Integrative modeling revealed that at a high ratio of oxygen-to-methane uptake flux, carbon dioxide and formate were the preferred excreted compounds; at lower ratios, however, acetate accounted for a larger fraction of the total excreted flux.

Integrative modeling revealed ...
... that at a high ratio ...
... of oxygen-to-methane uptake flux, ...
... carbon dioxide ...
... and formate were the preferred excreted compounds; ...
... at lower ratios, ...
... however, ...
... acetate accounted ...
... for a larger fraction ...
... of the total excreted flux.

S0 [009] The results of this study reveal a trade-off between biomass production and organic compound excretion and provide evidence that this trade-off is linked to the ratio between the oxygen and methane specific uptake rates.

The results ...
... of this study reveal a trade-off ...
... between biomass production ...
... and organic compound excretion ...
... and provide evidence ...
... that this trade-off is linked ...
... to the ratio ...
... between the oxygen ...
... and methane specific uptake rates.

S0 [010] Anthropogenic activities have led to significant increases in atmospheric methane¹, which contributes to climate change and perturbs the global carbon cycle ².

Anthropogenic activities have led ...
... to significant increases ...
... in atmospheric methane¹, ...
... which contributes ...
... to climate change ...
... and perturbs the global carbon cycle ².

S0 [011] However, methane derived from renewable sources is an attractive substrate in the production of value-added products ^{3–5}, and methane-conversion processes represent a promising trend in bioindustry ^{6,7}.

However, ...
... methane derived ...
... from renewable sources is an attractive substrate ...
... in the production ...
... of value-added products ^{3–5}, ...
... and methane-conversion processes represent a promising trend ...
... in bioindustry ^{6,7}.

S0 [012] Methanotrophic bacteria utilize methane as their source of carbon and energy, and these microorganisms have become increasingly important in the biomanufacturing of valuable chemical compounds ^{4,8–10}.

Methanotrophic bacteria utilize methane ...
... as their source ...
... of carbon ...
... and energy, ...
... and these microorganisms have become increasingly important ...
... in the biomanufacturing ...
... of valuable chemical compounds ^{4,8–10}.

S0 [013] Although methanotrophic species are metabolically active under both aerobic and anaerobic conditions ^{11–14}, considerations of cost, sustainability, and environmental impact have led to a preference for aerobic methane-oxidizing bacteria in large-scale biorefining applications ^{15,16}.

Although methanotrophic species are metabolically active ...
... under both aerobic ...
... and anaerobic conditions ^{11–14}, ...
... considerations ...
... of cost, ...

... sustainability, ...
... and environmental impact have led ...
... to a preference ...
... for aerobic methane-oxidizing bacteria ...
... in large-scale biorefining applications 15,16.

S0 [014] *Methylomicrobium album* BG8 (formerly known as *Methylobacter albus*, *Methylomonas albus*, or *Methylomonas alba*) is an obligate aerobic, gram-negative, gammaproteobacterial methanotroph that uses methane or methanol as its sole source of carbon and energy 17.

Methylomicrobium album BG8 ...
... (formerly known ...
... as *Methylobacter albus*, ...
... *Methylomonas albus*, ...
... or *Methylomonas alba*) ...
... is an obligate aerobic, ...
... gram-negative, ...
... gammaproteobacterial methanotroph ...
... that uses methane ...
... or methanol ...
... as its sole source ...
... of carbon ...
... and energy 17.

S0 [015] A DNA-DNA hybridization study revealed high levels of similarity between its genome and those of *Methylomicrobium agile* ATCC 35068 (99.16%), *Methylovivimicrobium alcaliphilum* 20Z (75.69%), and *Methylovivimicrobium buryatense* 5G (76.64%) 18.

A DNA-DNA hybridization study revealed high levels ...
... of similarity ...
... between its genome ...
... and those ...
... of *Methylomicrobium agile* ATCC 35068 ...
... (99.16%), ...
... *Methylovivimicrobium alcaliphilum* 20Z ...
... (75.69%), ...
... and *Methylovivimicrobium buryatense* 5G ...
... (76.64%) ...
... 18.

S0 [016] Recent phylogenomic analyses based on the average amino acid identity and average nucleotide identity have shown that *M. album* BG8 is also closely related to *Methylomicrobium* (formerly *Methylosarcina*) *lacus* LW14 19.

Recent phylogenomic analyses based ...
... on the average amino acid identity ...
... and average nucleotide identity have shown ...
... that *M. album* BG8 is also closely related ...
... to *Methylomicrobium* ...
... (formerly *Methylosarcina*) ...
... *lacus* LW14 19.

End of Sample Audit

This is a truncated Manuscript Microscope Sample Audit.

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