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Methanotrophic consortium isolated from the unique Chernevaya taiga soil and its feasibility in agrosoil

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INTRODUCTION & AIM

Aerobic soils serve as significant sinks for atmospheric methane, with their effectiveness influenced by the diversity and activity of soil methanotrophs. Land-use changes, particularly the conversion of natural ecosystems to agriculture, can substantially alter these microbial communities. A promising strategy to restore methane oxidation capacity is the introduction of active, ambient methane-oxidizing bacteria.

Forest soils are an important methane sink, and this natural process plays a crucial role in regulating the amount of methane in the atmosphere A varied and active community of microorganisms, particularly methane oxidizing bacteria (methanotrophs), is responsible for this capacity. Chernevaya taiga is a unique forest ecosystem in West Siberia, Russia, known for intense microbial activity related to the nitrogen and carbon cycles. However, studies focusing on methane cycling and the isolation of methanotrophs within these forests have not been conducted.

We hypothesized that active methanotrophs might be present in these soils with specialized adaptations to harsh environmental conditions. Our aim was to isolate a stable, active, highly enriched methanotrophic consortium from chernevaya soil and evaluate whether an isolated consortium can sustain its survival and methane-oxidizing activity when incorporated into agro-soil in a different area.

METHOD

- Isolation of Methane-Oxidizing Consortium from Chernevaya Taiga Soil, Tomsk region, West Siberia, Russia
- Characterization of Taxonomic Composition of Isolated Consortium T1
- Inoculation of Soddy-Podzolic Agrosoil with T1 Consortium
- Sample Source, Determination of Soil Methanotrophic and Respiration Activity
- DNA Extraction, Quantitative PCR and Illumina 16S rRNA Sequencing
- Bioinformatics Analysis and Statistical Analysis

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RESULTS & DISCUSSION

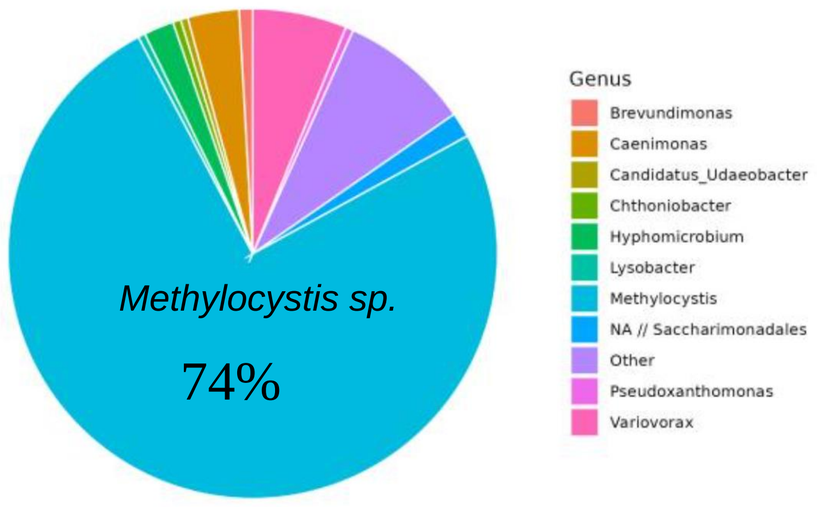

Fig.1. Composition of T1 methanotrophic consortium.

We isolated methanotrophic consortium T1 exhibited exceptionally high methane oxidation rates from the dark gray soil of the Chernevaya taiga, Tomsk region. 16S rRNA gene profiling revealed the absolute predominance (74%) of *Methylocystis* sp. (Fig.1).

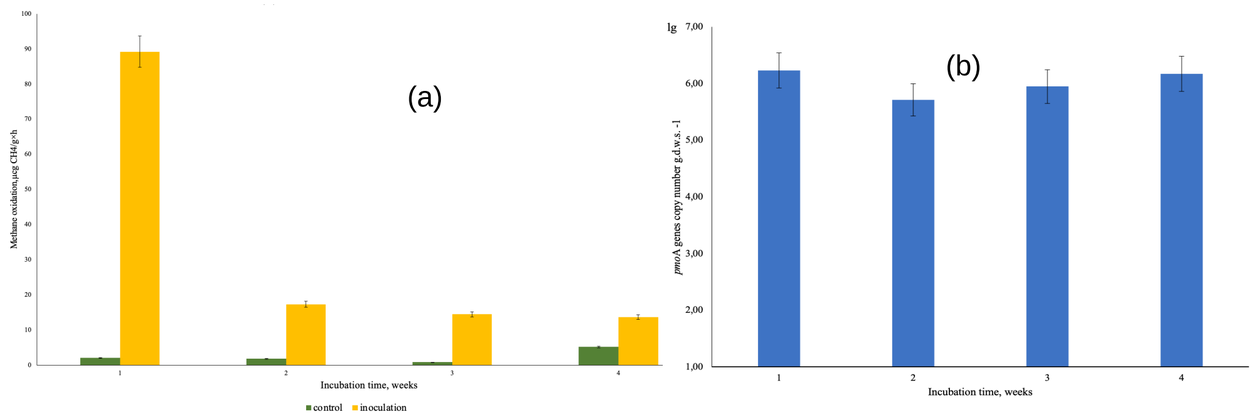

Fig.2. (a)The dynamic of methane oxidation: (b)The number of copies of *pmo*A genes per gram of soil in inoculation experiment.

The effects of inoculating this consortium were evaluated in a four-week laboratory incubation experiment using microcosms of soddy-podzolic agro-soil. Inoculated soils exhibited significantly higher methane oxidation potentials compared to non-inoculated soils (Fig.2a). Furthermore, *pmo*A gene copy numbers in the inoculated soils were significantly higher, compared with the non-inoculated microcosms (5×10^3 copies g^{-1}) and remained at a relatively high level of $8.81 \times 10^5 – 1.47 \times 10^6$copies g^{-1}, which indicates the significant presence of methanotrophs within the agrosoil microbial community (Fig 2b).

CONCLUSION

The methanotrophic consortium T1, isolated from the soil of the Chernevaya Taiga, was successfully inoculated into agro-soil to restore its methanotrophic activity in laboratory microcosm experiments. Inoculating soil with methanotrophs presents a promising strategy for mitigating methane emissions from agricultural activities and contaminated sites.

FUTURE WORK / REFERENCES

Further research is essential to validate these findings in natural systems and to understand the broader ecological implications of introducing methanotrophs on methane cycling and soil health.