

Re-inoculation of a soil-borne methanotrophic mixed culture: Testing the CH₄ mitigation potential in different soil types

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Background

- Soil-borne methane oxidizing microorganisms act as a terrestrial methane (CH₄) sink and are potentially useful in decreasing global CH₄ emissions.
- Understanding the ecophysiology of methanotrophs is crucial for a thorough description of global carbon cycling and for the successful application of methanotrophic microorganisms in CH₄ mitigation strategies.
- The aims of the study were (a) to test different soil sites for CH₄ oxidation performance at field and laboratory scales, (b) to isolate an effective methanotrophic mixed culture (MMC), (c) to describe the influence of different carbon sources on this MMC and (d) to evaluate if the MMC once re-inoculated to the soils can alter the CH₄ balance of soils.

Material and Methods

Here, we report the *in situ* balance of soils from abandoned landfills (L), meadows (M) and wetlands (W) (all located in Tyrol/Austria), their capacities to produce and oxidize CH₄ at laboratory-scale and the isolation of a soil-borne methanotrophic-heterotrophic mixed culture (MMC) that was used for carbon (C₁ and C₂) feeding experiments and re-inoculation trials. CH₄ flux rates were determined employing a static chamber technique (Hofmann *et al.* 2016). For potential methane oxidation (PMO) analysis, soil was weighed into flasks that were closed, gassed with 1% (v/v) CH₄ and 2.5% (v/v) CO₂ and incubated at 25°C for 24 h. For isolation of a MMC, soil samples were inoculated to liquid dilute nitrate mineral salts (DNMS) medium (Dedysh and Dunfield 2017). Growth and PMO of the MMC in response to different carbon sources (C₁ and C₂) were studied. MMC was also re-inoculated into all soils and success was evaluated by PMO measurements. DNA from cultures and soil samples was extracted by using the NucleoSpin Soil Kit (Macherey-Nagel, Germany). Microbial abundances (total bacteria, type I and type II MOB) were quantified by droplet-digital PCR (ddPCR), following the protocol provided in Praeg *et al.* (2021), and 16S amplicon sequencing was performed to characterize the methanotrophic and accompanying microorganisms.

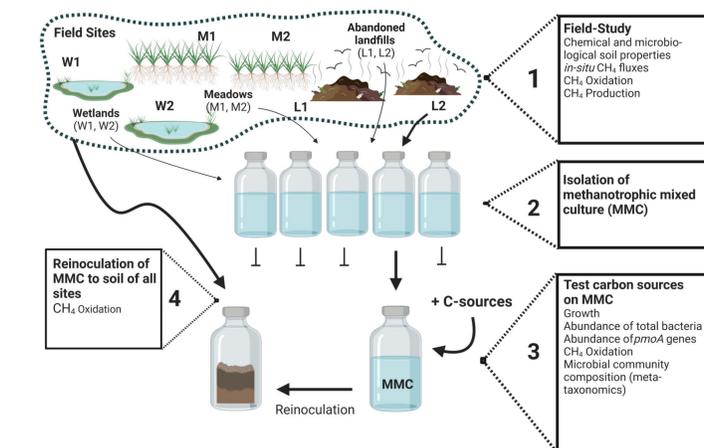


Fig. 1: Schematic representation of the experimental set-up: field-related investigations (1), the isolation procedure for gaining a methanotrophic-heterotrophic mixed culture (MMC) (2), testing of different carbon sources (3) and re-inoculation of the MMC to all soils (4).

Results & Discussion

❖ *In-situ* gas measurements showed net CH₄ balances of +/- 0 in the meadows and landfills, whereas the **wetlands** had clearly positive CH₄ balances, ranging from +5.0 to +100 μmol CH₄ m⁻² h⁻¹.

❖ MMCs were isolated from the soils (**Fig.2B**) (from all sites) - one derived from a **landfill** led to the **strongest and most stable mixed culture** and was used for all further experiments.



Fig. 2: (A) Determination of the potential methane oxidation capacity (PMO) of the soils and (B) cultivation of a stable methanotrophic (mixed) culture.

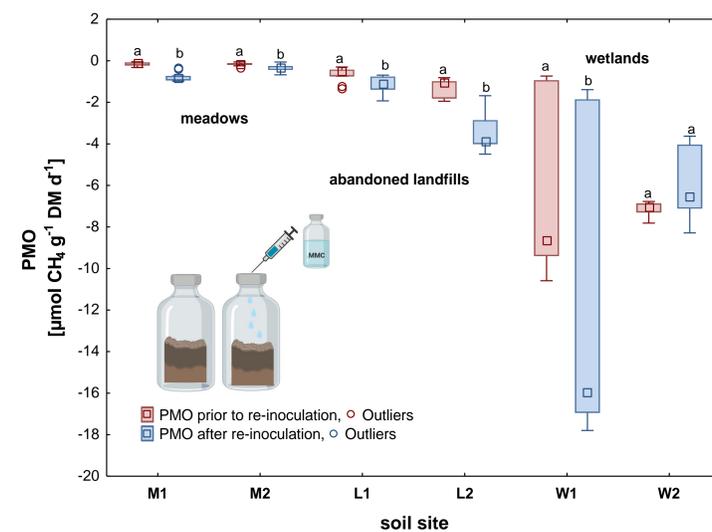


Fig. 3: Comparison of potential CH₄ oxidation (PMO) capacity (μmol g⁻¹ DM d⁻¹) after 24 h, before and after re-inoculation with a methanotrophic mixed culture (MMC) (n=9). The letters given refer to significant differences before (prior to) and after re-inoculation per site (p<0.05, independent t-test). M1, M2, meadows; L1, L2, abandoned landfills; W1, W2, wetlands. DM, dry matter.

❖ Inoculation of soils with the MMC distinctly and soil-specifically enforced the PMO, except for the wetland W2 (**Fig.3**).

❖ The relative **increase** in PMO was **most pronounced** in **landfill L2** and reached a 3-times higher CH₄ oxidation capacity (**Fig.3**).

Conclusion & Outlook

- Working toward natural and soil-borne methanotrophic mixed consortia provides promising grounds for future mitigation of CH₄ emissions from soils.
- The success of re-inoculating the mixed-methanotrophic culture (MMC) to soils varied depending on soil type. However, our results showed that a stable MMC has the potential to positively influence the CH₄ balance of soils.
- The re-inoculation stood its test under laboratory conditions and was a first step toward field trials. Further investigations will be necessary to prove its suitability and efficiency *in situ* and for long-term application.

❖ Besides the methanotrophic community, consisting of methanotrophs of **type I and II**, also a diverse **heterotrophic community** was present within the MMC (**Fig.4**).

❖ Applied **carbon sources** significantly influenced both heterotrophic and methanotrophic members of the MMC and distinctly **changed the community composition** and the abundance of MOB (**Fig.4** and **5**).

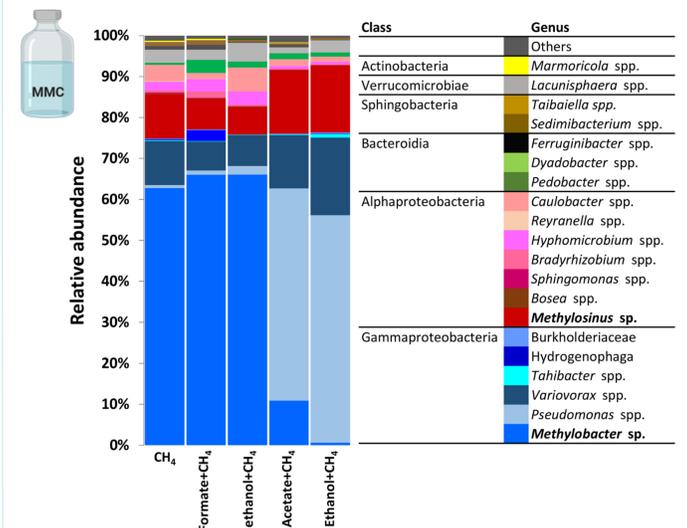


Fig. 4: Effects of different C sources in addition to CH₄ on the microbial community composition (relative abundances of microbial taxa) presented at the highest resolvable tax level. Taxa with a relative abundance <2% are summarized as 'Others'. Bars represent means (n=3).

❖ All substrate additions caused increases of total bacteria compared to the controls (CH₄ supply only), with significant increases in the case of methanol and ethanol amendments (**Fig.5**).

❖ While formate and methanol (**C₁ supply**) led to significant increases in MOB type I, the **C₂ sources** (acetate and ethanol) significantly decreased the abundance of type I. In contrast, type II methanotrophs were increased by the addition of C₂ sources (**Fig.4** and **5**).

❖ Studying mixed cultures carries the risk of working with an undifferentiated culture but offers the advantage of promoting near-natural conditions compared with pure cultures and allows feedbacks between heterotrophic and methanotrophic microorganisms.

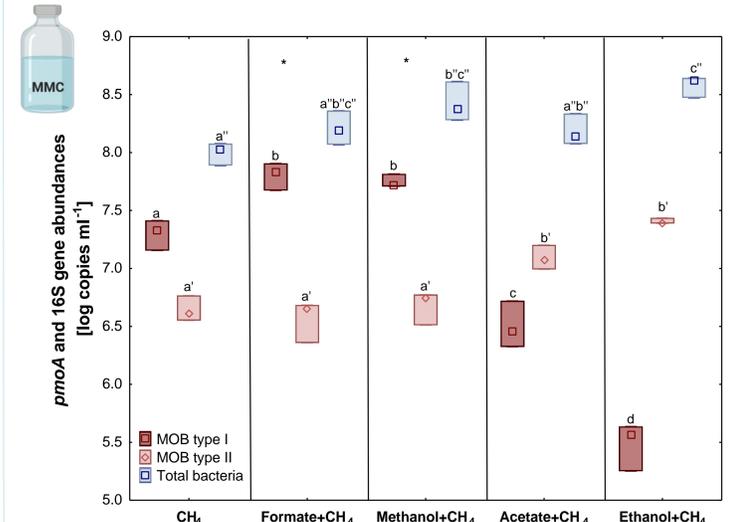


Fig. 5: Effects of different C sources in addition to CH₄ on abundances of methane oxidizing bacteria (MOB) and total bacteria (all n=3). Data are shown in log copies ml⁻¹ culture suspension, small squares show median values, and boxes indicate 25-75%. Small letters (e.g.: a, a', a'') indicate significant differences between MOB type I, MOB type II, and total bacteria, respectively (p<0.05, Bonferroni post-hoc test), and asterisks (*) show differences between the sum of MOB compared to the control (CH₄) approach (p<0.05, independent t-test).

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