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Kinetics of methane oxidation and structure of the methanotrophic microbial community in tropical upland soil under different land use

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Three upland soils from Thailand; a natural forest (SK soil), a 16-year old reforested site (AC soil), and an agricultural field (CF soil) were studied with regard to methane uptake and the community composition of methanotrophic bacteria (MB). Methane uptake rates were similar to rates published for respective forest and farmland soils of the temperate zone. Rates were lower in the agricultural soil than in the native forest or the reforested sites. SK and AC soils showed a clear vertical zonation for active methane oxidation between 15 cm and 40 cm, while in CF soil no clear active layer was observed. In SK and AC soils, high concentration of inorganic nitrogen compounds was detected in the top 15-cm soil while there was no clear distribution trend found in CF soil. Kinetic coefficients revealed that soil at SK site had a high affinity for methane (Km of 50 ppmv), whereas soil at AC and CF sites, on the other hand, showed low affinity for methane (Km of 700 - 2000 ppmv). These results indicate that land use type significantly affects rates, depth distribution and kinetics of methane oxidation in tropical soils. Sites also differed in the community composition of MB, which was characterized by denaturing gradient gel electrophoresis (DGGE) of pmoA gene fragments (encoding for a subunit of particulate methane monooxygenase) that were PCR-amplified from total soil DNA extracts. Cluster analysis based on the DGGE banding patterns indicated that the communities of MB in the forested and reforested sites were similar to each other but different from the community of the farmland site. Sequence analysis of excised DGGE bands indicated that Methylobacter spp. and Methylocystis spp. were present at the sampling sites. Sequences of

the "forest soil cluster" or "upland soil cluster alpha" (USC-alpha), which is postulated to represent organisms involved in atmospheric methane consumption in diverse soils, were detected only in samples from the SK and AC sites, as were sequences that formed a separate branch related to USC-alpha. Further sequences were detected that may represent uncultivated groups of MB in the Gamma-Proteobacteria. Finally, an unknown sequence cluster may represent either pmoA or amoA (coding for a subunit of the ammonia monooxygenase of ammonia oxidizing bacteria). In conclusion, our results indicate that land use of tropical forests affects activity and structure of the methane-oxidizing microbial community.