Living on the edge: Planctomycetes at the oxic / anoxic interface in northern wetlands

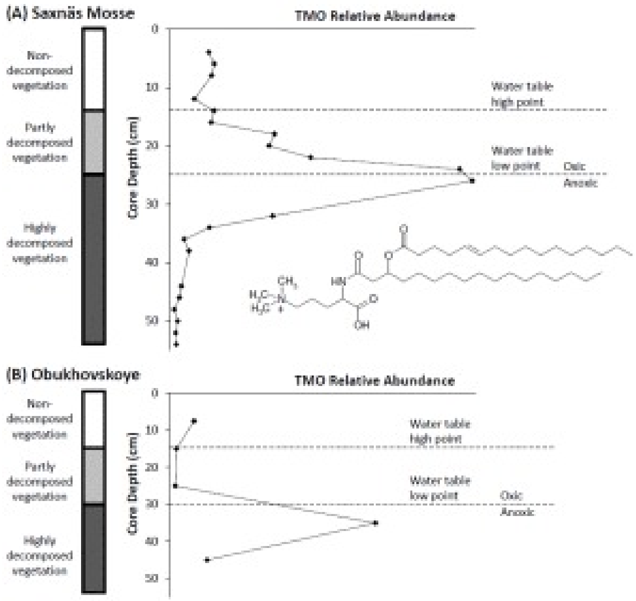

Fig. 1. Relative abundance of trimethylornithine (TMO) membrane lipid in (A) Saxnäs Mosse soil and; (B) Obukhovskoye soil. TMO molecular structure inset.

Peat - accumulating northern wetlands make up approximately one-third of the global soil organic carbon pool. Nutrient - poor and acidic conditions, as well as low temperatures and decay - resistant Sphagnum moss-dominated vegetation, result in low rates of microbial decomposition of plant debris and net carbon sequestration in these ecosystems. Recent studies have revealed that planctomycetes appear to be involved in degradation of Sphagnum moss debris. Novel trimethylornithine (TMO) membrane lipids have recently been characterized as abundant lipids in various Sphagnum wetland planctomycete isolates, but the occurrence of these TMO lipids in the environment has not yet been confirmed. We applied a combined membrane lipid and genetic analysis of peat samples collected from two northern wetlands (Saxnäs Mosse Bog, Sweden; and Obukhovskoye Bog, Russia) in order to investigate the preferred niche and abundance of TMOproducing planctomycetes.

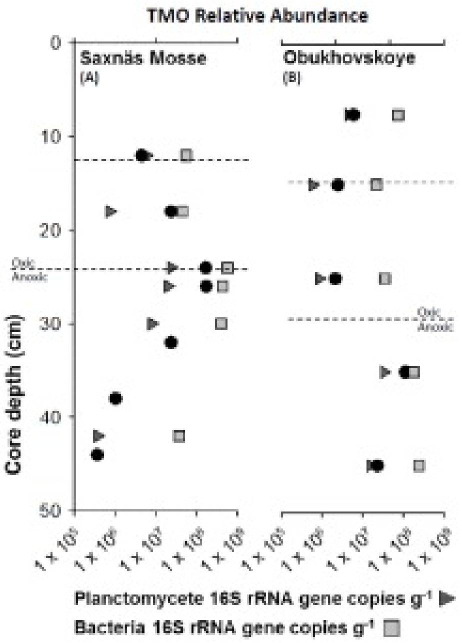

Fig. 2. Comparison of planctomycete and total bacterial 16S rRNA gene copy numbers per gram of sediment in comparison with relative trimethylornithine (TMO) membrane lipid abundance down core in the (A) Saxnäs Mosse, and the (B) Obukhovskoye peat bogs. Dotted lines indicate water table high and low points.

TMOs were present throughout the depth profiles of both Sphagnum bogs, but their concentration peaked at the oxic/anoxic interface, which coincided with a maximum abundance of planctomycete-specific 16S rRNA gene sequences. The sequences detected at the oxic/anoxic interface were affiliated with the Isosphaera group, while sequences present in the anoxic peat layers were related to an uncultured planctomycete group. Genetic analysis identified Planctomycetes as the major bacterial group at the oxic/anoxic interface at the Obukhovskoye peat (54% of total 16S rRNA gene sequence reads), followed by Acidobacteria (19% reads), while in the Saxnäs Mosse peat, Acidobacteria were dominant (46%), and Planctomycetes contributed to 6% of the total reads. The detection of abundant TMO lipids in planctomycetes isolated from peat bogs and the lack of TMO production by cultures of acidobacteria and other bacterial groups suggest that planctomycetes are the producers of TMOs in peat bogs. Culture experiments showed that the Isosphaera-like planctomycete strain PX4 produced a larger fractional abundance of TMO lipids compared to other membrane lipids when grown at micro-oxic conditions. The higher accumulation of TMOs at the oxic/anoxic interface and the change in the planctomycete community with depth suggest that these IPLs could be synthesized as a response to changing oxygen levels at the oxic/anoxic interface.

Publication

Abundant Trimethylornithine Lipids and Specific Gene Sequences Are Indicative of Planctomycete Importance at the Oxic/Anoxic Interface in Sphagnum-Dominated Northern Wetlands.
Moore EK, Villanueva L, Hopmans EC, Rijpstra WI, Mets A, Dedysh SN, Sinninghe Damsté JS
Appl Environ Microbiol. 2015 Sep