

Microbial Methane Cycling in Mackenzie Delta Lakes: Comparing Microbial Community Diversity and Activity with Environmental Parameters

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• **Background:** Methane, a potent greenhouse gas, is also a substantial source of carbon and energy for ecosystems within Arctic lakes. Complex communities of microbes in the water column and sediment of these lakes play a vital role in the production and consumption of methane, and ultimately influence the net amount of methane that's released to the atmosphere or cycled through local food webs. Canada's Western Arctic contains many large and complex lake systems, but research on methane dynamics and microbial communities in the region has been limited. The Mackenzie River Delta floodplain is extremely productive relative to the surrounding tundra landscape, and makes substantial contributions to the global methane budget, especially in the spring when rapid ice break-up causes methane, accumulated under the ice throughout the winter in the Delta's ~45,000+ lakes, to suddenly escape to the atmosphere (see Figure 1, inset). This project characterizes the structure and activity of methane- and carbon-cycling microbial communities in Mackenzie Delta lakes. This was done by:

1. Analyzing microbial community structure via sequencing of the 16S rRNA gene from lake water DNA samples collected from multiple lakes across the ice cover to ice free season
2. Incubation experiments of lake water with stimulants and inhibitors of methane cycling processes

• **Initial results** show that seasonal shifts in lake biogeochemistry – such as dissolved methane and oxygen concentrations, trace metals, temperature, pH, and carbon quality – correspond to shifts in overall microbial community structure (Figure 2); that the dominant methane- and methyl-cycling microbial groups shift as a function of season, independent of lake origin (Figure 3); that lake waters have microbial communities capable of methane oxidation and production under bulk oxic conditions but are net methanotrophic in the summer (Figure 4); and that the microbial community structure does not change appreciably when exposed to methane-cycling stimulants or inhibitors over a period of 48 hours (Figure 5).

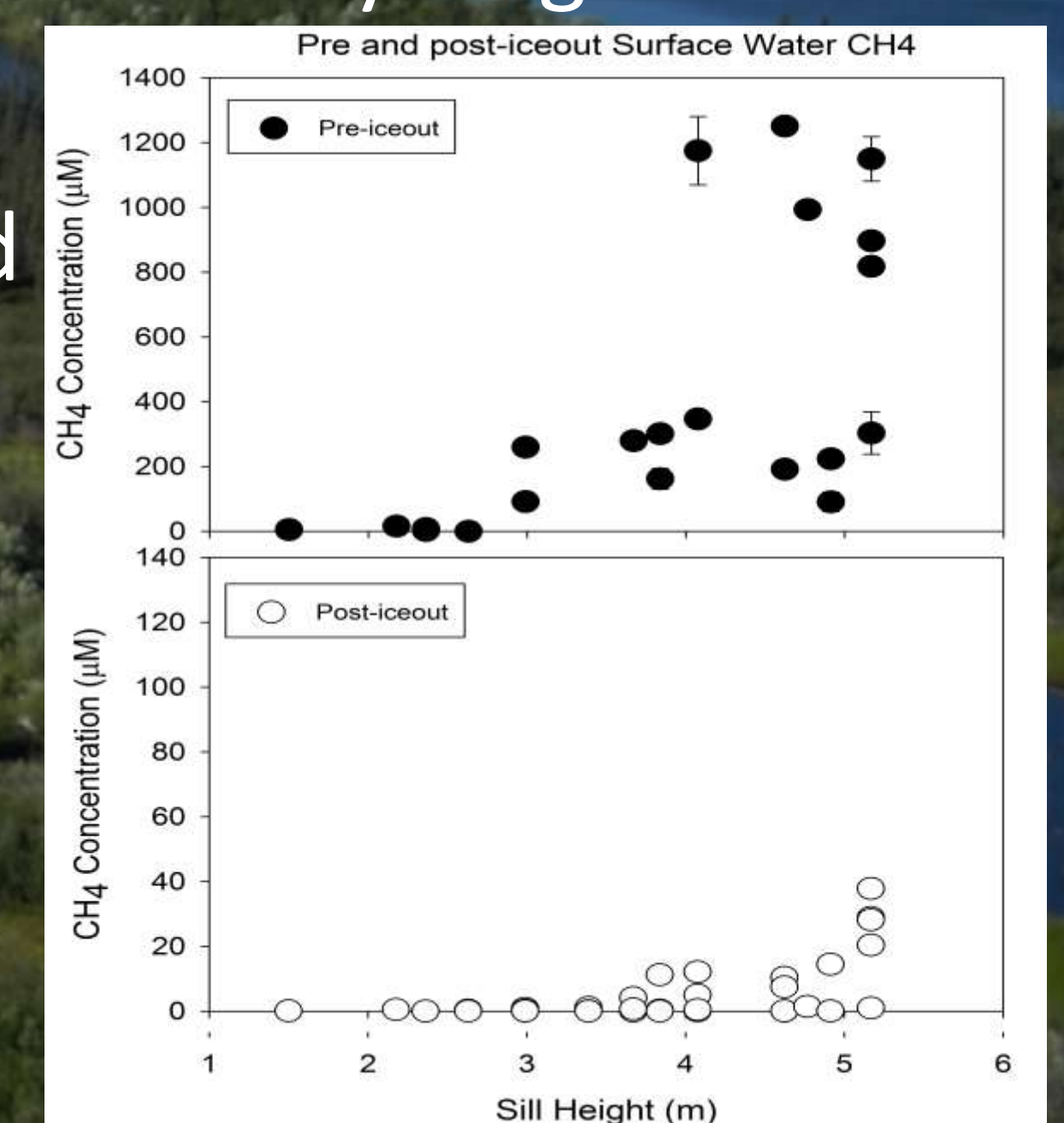


Figure 1 – Pre- and Post-ice-out methane concentration from 43-lake survey of Delta lakes. Sill height represents the elevation of the lakes relative to the Mackenzie River, and thus their degree of isolation from Spring flooding events. Higher sill elevations = shorter river-to-lake connection times. Source: McIntosh et al., in preparation.

Study System and Project Design

Satellite imagery of Mackenzie Delta East Channel near Inuvik, NT, and the 43-lake and 6-lake (highlighted) study area.

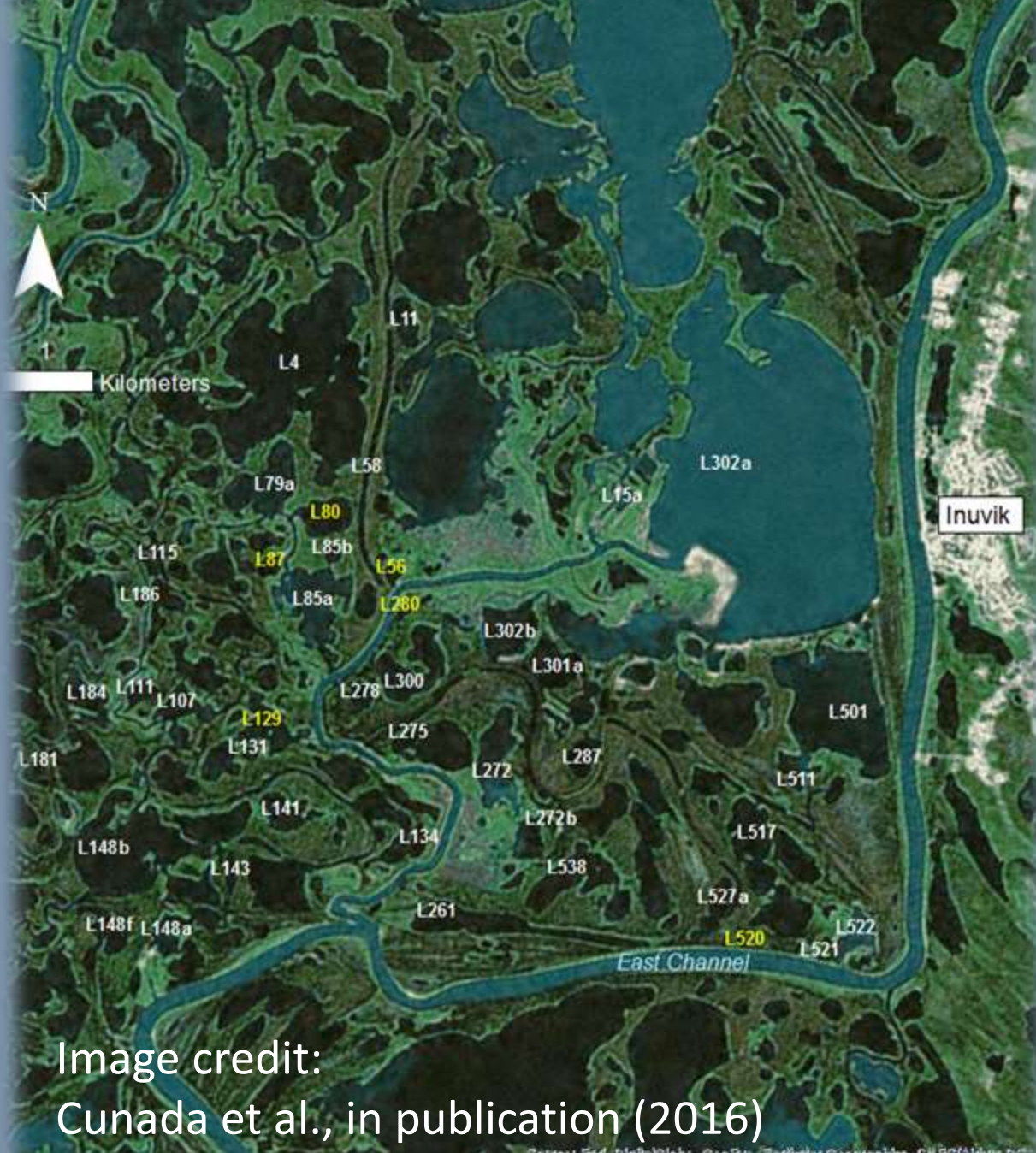


Image credit: Cunada et al., in publication (2016)

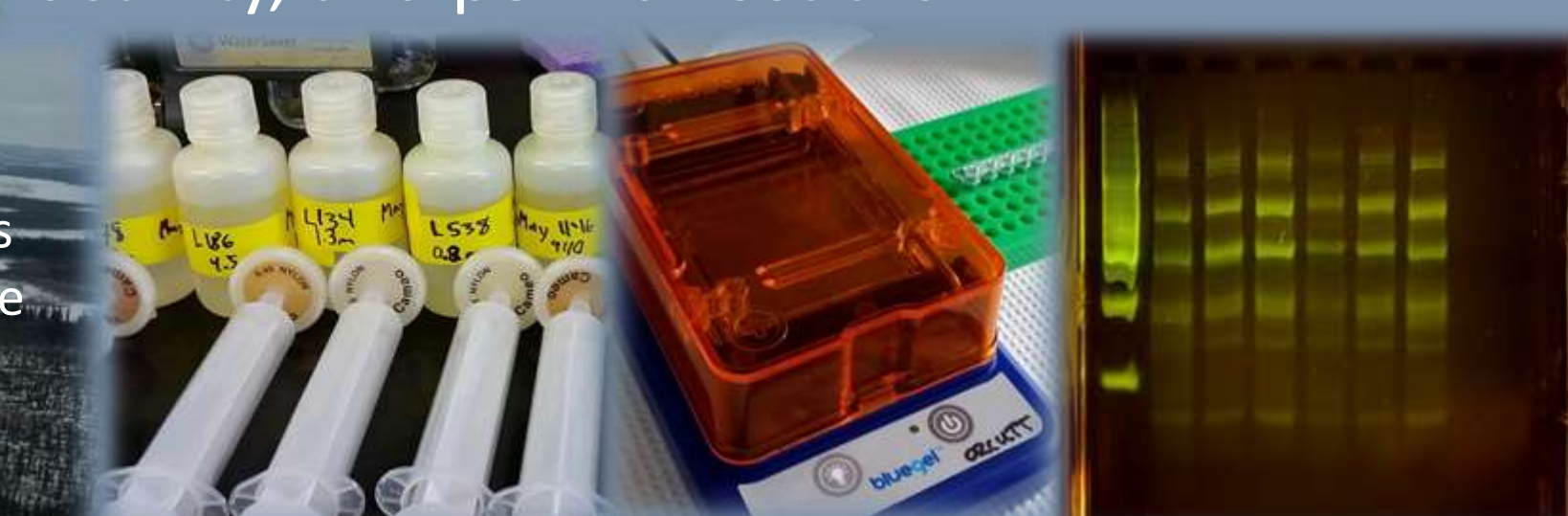


Mackenzie River East Channel near Inuvik, NT, May 9, 2016. As water levels rise and snow starts to melt, water starts to flow along the sides of the river, on top of the ice.



A side-channel of the Mackenzie River East Channel near Inuvik, NT, May 11, 2016. Rising temperatures and spring flooding cause rapid ice breakup and sudden methane release to the atmosphere.

The Mackenzie River Delta in Canada's Northwest Territories, hereafter referred to as The Delta, is the largest river system in Canada, and the second largest floodplain delta in the circumpolar Arctic region. The Delta floodplain contains over 45,000 lakes, mostly small and shallow, which are incredibly productive compared to the surrounding tundra areas. These lakes have varied biogeochemistry and bio-availability of carbon driven by variation in their annual river-to-lake connection times with the Mackenzie River which in turn influences the magnitude and duration of annual Spring flooding events, aquatic photosynthetic activity, and permafrost thaw¹.



Flooding regimes, aquatic plant density, and thermokarst activity (permafrost thaw along the lake margins) all influence the carbon quality and subsequent bacterial activity, productivity¹, and methane dynamics of the lakes.

Water samples were taken at the end of winter and throughout the summer of 2016 from a broad set of 43-lakes and a sub-set of 6 lakes that represent the varying lake types found throughout the Delta (satellite image, top-left). Water was filtered and DNA extracted for 16S-rRNA-gene sequencing analysis, a gene that is highly conserved microbes and used to characterize microbial populations. Gene sequencing data was coupled with biogeochemical measurements to determine the correlation between lake chemistry and microbial community structure (See Figure 2).

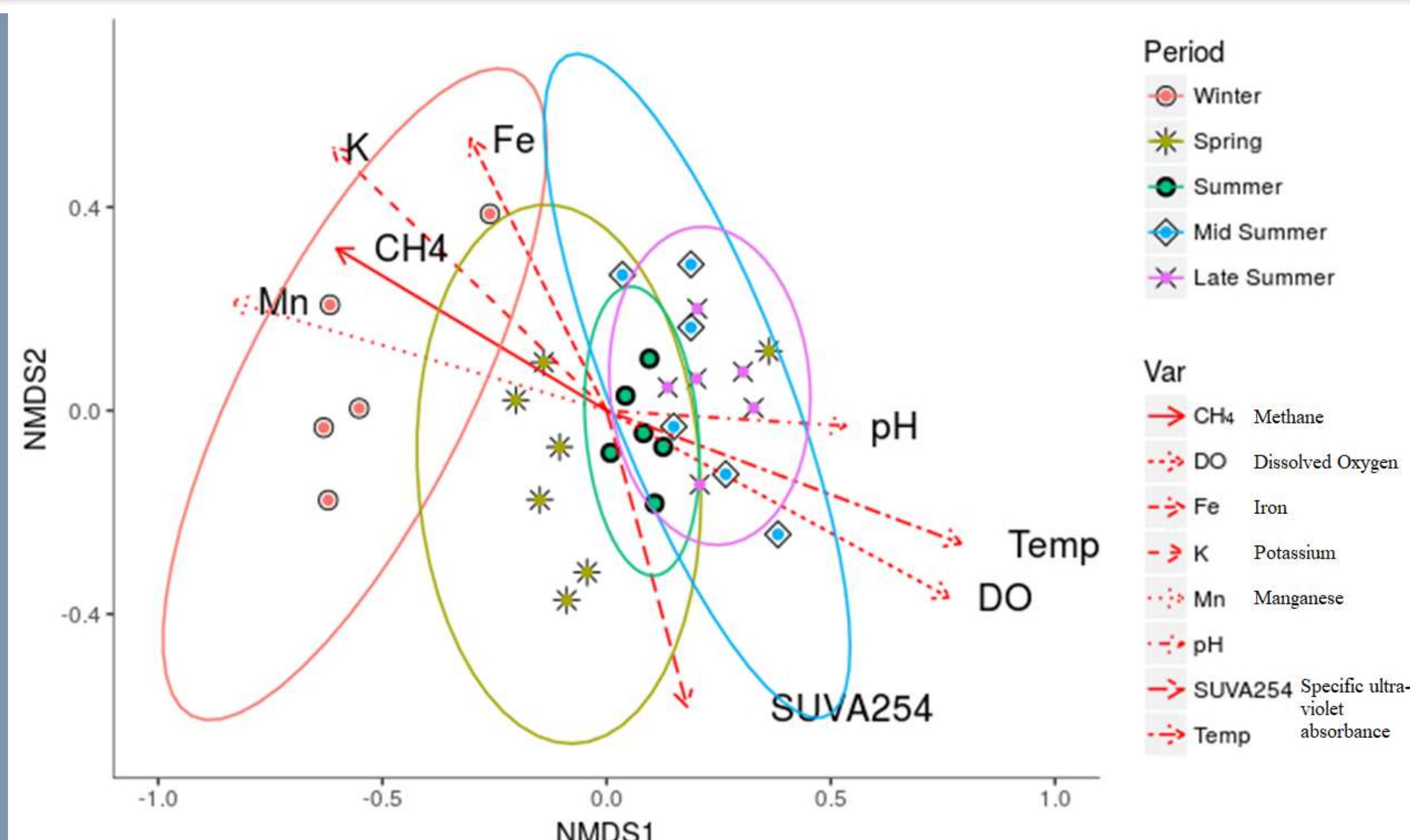


Figure 2 – NMDS (non-metric multi-dimensional scaling) of 6-lake samples separated into seasonal periods (ellipses) based on the Bray Curtis dissimilarity among samples calculated from 16S rRNA-gene sequencing data. Gene sequences were clustered into groups that share 97% sequence similarity, known as operational taxonomic units or OTU's. The relative distance between points indicates the similarity among samples based on shared OTU's. The red arrows represent the correlation between environmental variables and microbial community structure as calculated by NMDS ordination of the Bray Curtis dissimilarity matrix, with the direction and magnitude of the arrow indicating the significance of the correlation.

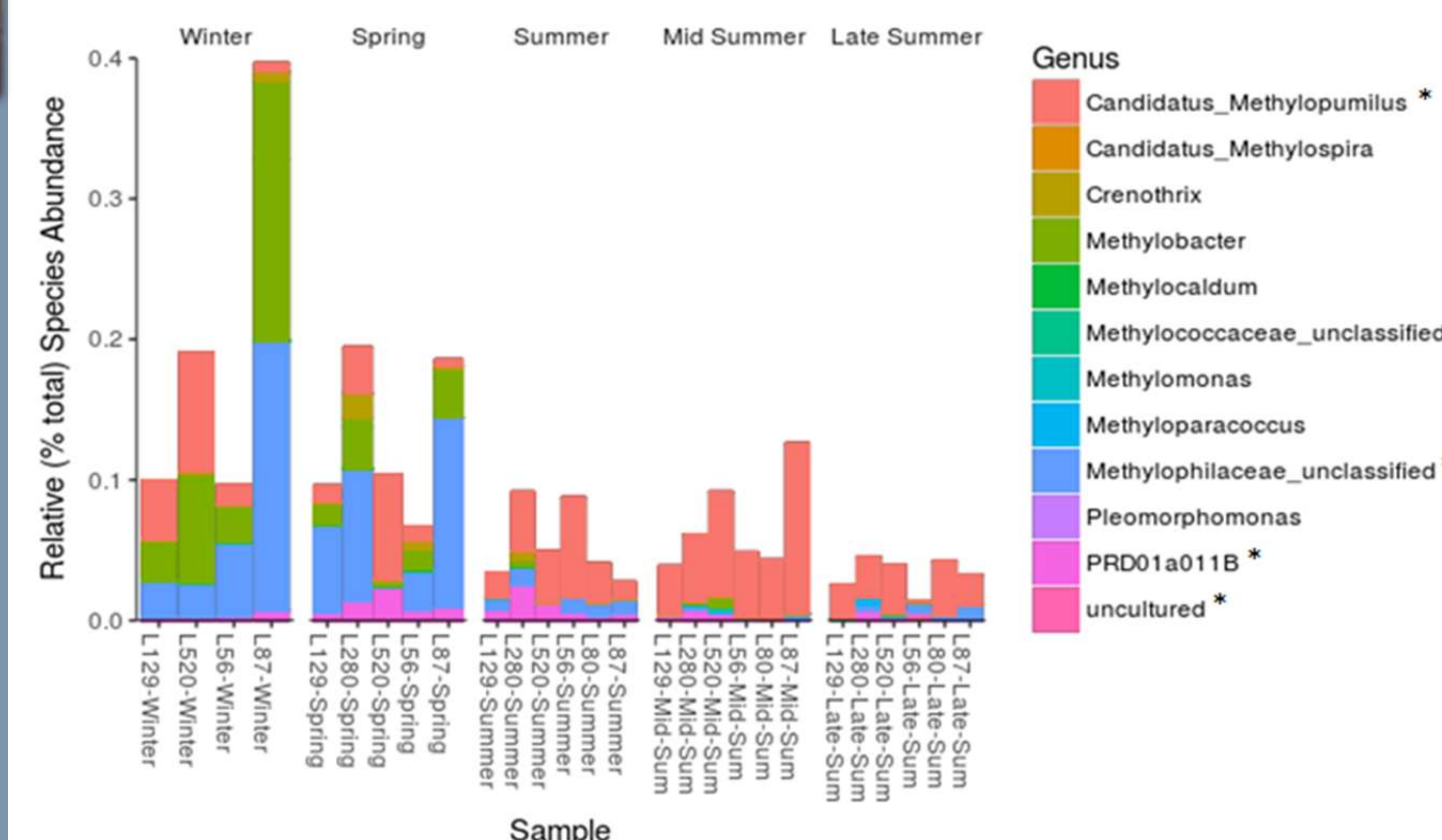


Figure 3: Bar-plot of the relative abundance (% of total abundance) of methano- and methylotroph genus from the 6-Lake set, organized by season. Relative abundance of methanotrophs is between 10-40% in Winter and 8-20% in Spring, corresponding with elevated methane concentrations in the lakes during this time period. * = methylotroph groups, or organisms that feed primarily on methanol.

Experimental Enrichment of Nutrients and Methanogenesis Inhibition

Incubation experiments were performed on water from three lakes with differing river-to-lake connection times, biogeochemical properties and carbon quality end-points. Incubations with various treatments (methanogenesis inhibitor bromo-ethanosulfane (BES), nutrient spike, and combination) were applied to determine methane oxidation (MOX) rates under varying conditions, and isolate the individual effects of methane oxidation and methanogenesis in the water column.

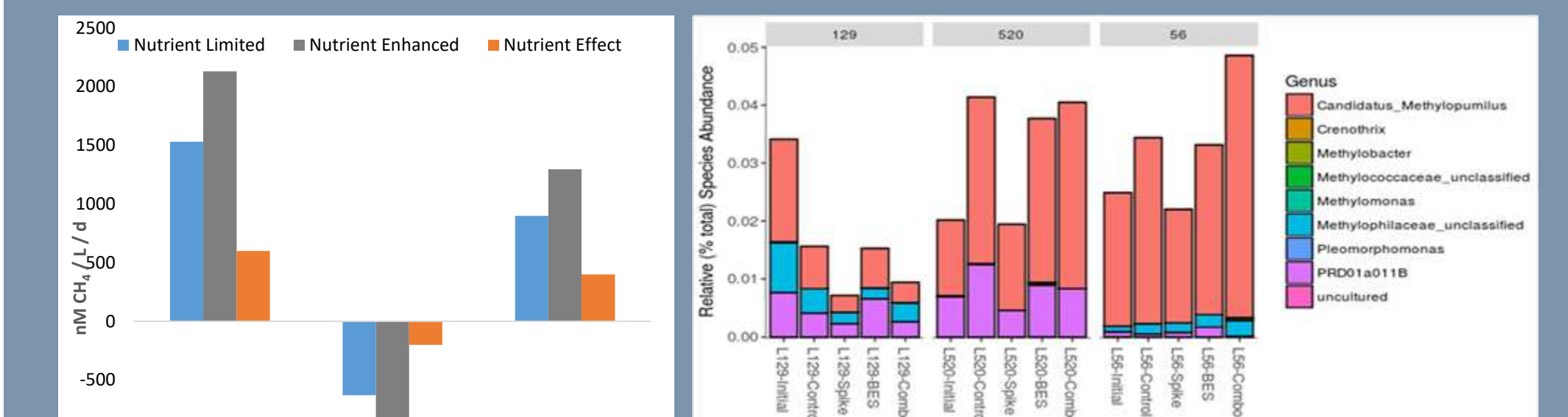


Figure 4 – Summary of rates of methane oxidation (MOX), methanogenesis (MEG), and the net effect of MOX - MEG for lake 520 (pictured below, a thermokarst lake with a very short river-to-lake connection time) under nutrient limited and nutrient enhanced conditions.

Discussion: Microbial communities are strongly influenced by season and the associated changes in lake biogeochemistry that occur. Methane and trace metals have the strongest influence on microbial community structure in Winter, a time when methane concentration and the relative abundance of methane-linked groups is highest. Carbon quality - as indicated by measurements of SUVA₂₅₄ - has stronger influence in Spring, when methane concentration and the relative abundance of methane-linked groups starts to decline. Temperature, DO and pH (higher values correspond with high rates of macrophyte photosynthesis) drive diversity in the summer. Relative abundance of methane-associated bacteria decline over summer. Early results from the enrichment experiment will be further developed to discern the relationship between methane cycling and the specific activity of methane-related functional groups.

Lake 520, a.k.a. Dock Lake, a spatially isolated and thermokarst-affected lake (notice the slumping trees!). Photo Credit: Danny Swainson Photography, June 25, 2016. FB/Instagram: @danny.swainson



This project wouldn't have been possible without the passion, shared knowledge, expertise, and experience of our research team and partnerships with various Arctic organizations and research institutions. Thanks to all the people and organizations that helped make this project a success! Photo Credit: Beth Orcutt