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# Being flushed into the Kolyma river in Northeast Siberia

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In June and August 2019, we sampled the Kolyma River which is the sixth largest Arctic river and the only one with a watershed completely underlain with continuous permafrost. Under climate change scenarios, it is predicted that increasing amounts of organic-rich deposits will drain each year during the freshet period into the streams and main stems of Arctic rivers. This organic carbon is mineralized through photochemical and microbial processes into $CH_4$ and $CO_2$. In this study, we used metagenomic and 16S-amplicon approaches to determine the riverine microbial community structure and function along a 120 km transect in the main stem and tributaries of Kolyma River. In parallel, we measured additional water biogeochemical parameters and highly resolved spatial measurements of $pCH_4$ in June. Our results showed that at the end of the flood period in June, $pCH_4$ was seven times higher in tributary waters than in the main stem. The microbial communities in the main stem were spatially distinct. In addition, both water sources exhibited successional turnover from freshet to base flow conditions in August. The microbial consortia in the river were influenced by the distance from tributary inputs rather than by geographical distance. We identified higher abundances of methanoges within the orders *Methanosarcinales* and *Methanobacteriales* during the freshet and in the tributary waters. However, the elevated $CH_4$ concentrations are mostly of allochthonous origin at the time of sampling because the contribution of methanogens to the total community was < 0.03 %. Methanotrophic *Methylophilaceae* outnumbered methanogens by three orders of magnitude, and unlike the methanogens did not exhibit an apparent spatial trend. Outgassing of $CH_4$ occurs locally and close to the potential source in June limiting its transport with the streamflow to other areas of the river and to the Arctic Ocean. Our results give insight in the spatial and temporal surface concentrations of riverine $CH_4$ and the distribution of the microbial $CH_4$-cycling communities in an Arctic river under permafrost thaw influence.