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## Methane producing and reducing microorganisms display a high resilience to the effects of short term drought in a Swedish hemi boreal fen.

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The effect of anthropogenic climate change on peatland ecosystems is of major concern since they act as a significant global carbon sinks. One of the largest climatic threats to peatlands are droughts. Combined warming and reduced precipitation result in lower water table depths, which alters methane production, increases soil respiration, and consequently shifts peatlands to carbon sources. Droughts in peatlands facilitate aeration of previously anoxic layers allowing aerobic microbes to populate and consume previously unavailable carbon substrates. Despite clear environmental pressures, the responses from functional groups, such as methanogenic archaea, to short term droughts on community abundance, diversity and composition of functional genes is still poorly understood. To investigate this, we applied the molecular technique “captured metagenomics”, to identify the variability in functional diversity of microorganisms involved in the metabolism of methane during the 2018 summer drought. In addition, we measured methane fluxes, water table depths, and soil and air temperatures. We observed that the drought significantly reduced methane fluxes in plots dominated by *R. alba* and *C. vulgaris*, but the same was not observed in sites dominated by *E. vaginatum*. The proportion of methanogens to methanotrophs reduced by 12% in favour of methanotrophs during the drought. Interestingly, both methanogens and methanotrophs declined in relative abundance during the drought – expect for one genera, the type II methanotroph *Methylocella*, which increased in relative abundance. During the non-drought year, the highest  $\beta$ -diversity was observed in *E. vaginatum* plots, but during the drought the highest  $\beta$ -diversity changed to *R. alba* plots. Significant differences were observed between the abundance of captured genes when tested via PERMANOVA between the drought and non-drought year ( $p \geq 0.01$ ). However, the PERMANOVA revealed that only 15% of the variance in abundances can be explained by year. Interestingly, genes including *cutL*, *hdr*, *coxS*, *mvhA*, *metF*, *fdhA*, *frmB*, *cutM* and *cooS* were significantly more abundant during the drought when compared to the non-drought year. We conclude that only small shifts occurred in the structure and function of the microbial community, indicating that methanogens and methanotrophs hold a strong resilience to relatively short-term drought events.