Effects of experimental warming and clipping on metabolic change of microbial community in a US Great Plains tallgrass prairie soil

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Abstract

While more and more studies are being conducted on the effects of global warming, little is known regarding the response of metabolic change of whole soil microbial communities to this phenomenon. In this study, functional gene changes at the mRNA level were analyzed by our new developed GeoChip 3.0. Soil samples were taken from a long-term climate warming experiment site, which has been conducted for ~8 years at the Kessler Farm Field Laboratory, a 137.6-ha farm located in the Central Redbed Plains, in McClain County, Oklahoma. The experiment uses a paired factorial design with warming as the primary factor nested with clipping as a secondary factor. An infrared heater was used to simulate global warming, and clipping was used to mimic mowing hay. Twelve 2m × 2m plots were divided into six pairs of warmed and control plots. The heater generates a constant output of ~100 Watts m\textsuperscript{-2} to approximately 2 °C increase in soil temperature above the ambient plots, which is at the low range of the projected climate warming by IPCC. Soil whole microbial communities’ mRNA was extracted, amplified, labeled and hybridized with our GeoChip 3.0, a functional gene array covering genes involved in N, C, P, and S cycling, metal resistance and contaminant degradation, to examine expressed genes. The results showed that a greater number and higher diversity of genes were expressed under warmed plots compared to control. Detrended correspondence analysis (DCA) of all detected genes showed that the soil microbial communities were clearly altered by warming, with or without clipping. The dissimilarity of the communities based on functional genes was tested and results showed that warming and control communities were significantly different (P<0.05), with or without clipping. Most genes involved in C, N, P and S cycling were expressed at higher levels in warming samples compared to control samples. All of the results demonstrated that the whole microbial communities increase functional gene expression under warming with or without clipping in order to adapt the changed out environment. More detail analysis is underway.