



Effects of land-use management on soil microbes to degrade organic matter through captured metagenomics and metatranscriptomics

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The role of microbial communities in different soil ecosystem processes has been hard to determine in the past due to their vast diversity both in terms of taxonomy and functions. Molecular methods such as high-throughput sequencing of environmental communities have made it easier to delve into these diverse ecosystems and understand their functions. Trait-based approaches through quantification of functional genes and their expression have shown to be much more meaningful in explaining ecosystem functioning than the taxonomy based approaches. One such approach is the “captured metagenomics” technique where only the genetic regions of functional enzymes involved in a particular ecosystem process such as carbon metabolism is targeted from the genetic pool and sequenced. This allows focused investigations of ecosystem processes through functional genes in complex environments such as soils.

In our study, we have implemented this method to look into the effects of land-use management on the functional genetic diversity of microbial communities to degrade soil organic matter (SOM). Soils from different agricultural and grassland fields in southern Sweden were chosen in this study. Oligonucleotide probes were generated based on the genetic sequences of enzymes involved in organic matter degradation from public databases. On the DNA level, there was a significant shift in the functional genetic diversity of microbes to degrade SOM due to land-use management. Grasslands had a higher abundance and diversity of genes coding for enzymes involved in SOM degradation than agricultural soils. The amount of nitrogen was the main factor that affected the functional diversity of the microbes that degrade SOM in these soils. Interestingly, there was no correlation between the functional diversity of microbes to their taxonomic diversity measured through traditional ribosomal sequencing.

In addition, for the first time the capture method was used in large scale, targeting many genes coding for SOM degrading enzymes coupled with RNA/cDNA from the soils to quantify their expressions. For this, the soils from different land-use managements were treated with straw, while the microbial growth rates in these soils were also monitored for a month. RNA was extracted from at three different time points from both treated and untreated soils from different land-use managements. Agricultural soils with straw addition had higher relative microbial growth rates and higher abundance of gene sequences captured compared to the control and grassland soils. Land-use management seems to be the most significant factor in affecting the expression of SOM degrading genes in these soils. Additional analyses of the generated data are expected to provide valuable insights on how land-use management affects the microbial responses during addition of organic matter in soils.