

Exploring the activity of microorganisms in the forest soil using metatranscriptomics

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Understanding the ecology of forest soils is very important because they belong to the largest carbon sinks globally. Metatranscriptomics seems to be perfectly suitable for the exploration of microbial involvement in soil processes but until recently it was technically difficult to use it successfully for these highly complex environments. Here we used metatranscriptomics combined with microbial community analysis to describe the roles of individual microbial taxa in the coniferous forest soil in two contrasting seasons. Both the microbial community composition and the pool of microbial transcripts were found to be highly diverse and characterised by the high abundance and activity of fungi. The differences in seasonal functioning of the ecosystem consisted of a combination of moderate changes in microbial community composition and profound

changes in taxon-specific microbial transcription profiles. These differences were more significant in soil than in litter. Most importantly, fungal contribution to total microbial transcription in soil decreased from 33% in summer to 16% in winter. In particular, the activity of the ectomycorrhizal fungi that quantitatively dominate this environment was reduced in winter. The results indicate that plant photosynthetic production was likely the major driver of changes in the functioning of microbial communities in the studied ecosystem across seasons. Technically, the annotation of functions and taxonomic affiliations is relatively precise for bacteria but less reliable for the fungi and archaea, due to the lower number of fully sequenced and annotated genomes. These limitations will hopefully decrease in the future along with the advances in microbial genomics.