



Depth-dependent abundance and distribution of microorganisms in forest soil

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Soil microorganisms involved in carbon cycling face different habitat conditions in topsoil and subsoil environments. While the habitat conditions and mechanisms influencing the abundance of soil microorganisms and development of soil microbial communities in topsoil are well investigated, these dynamics have been largely unexplored in deeper soil horizons. Limited information is available on the effects of different environmental factors such as water content, pH and available organic carbon (OC) on soil microorganisms in subsoil. More research is needed about both the abundance and composition of microbial communities and, by extension, the microbial decomposition of soil organic matter in deeper soil horizons. We investigated both the abundance of microorganisms and the composition of the microbial communities in soil samples of a podzolic Cambisol from a European beech (*Fagus sylvatica* L.) forest stand in Lower Saxony, Germany. The samples were taken along three transects in a grid sampling pattern. Each transect consisted of 64 sampling points, eight vertical, from a depth of 10 cm to a depth of 185 cm, by eight horizontal, starting at the root zone of an individual beech tree, from zero to 315 cm. Environmental measurements included pH, soil water content, OC and root-associated carbon. Microbial biomass was determined using the chloroform fumigation extraction (CFE) method. Abundances of bacteria, fungi, archaea and seven of the most important taxa specific groups of bacteria in the soil samples were evaluated with quantitative PCR. In agreement with previous studies, soil microorganisms were most abundant in topsoil and decreased with depth. The composition of the total microbial community shifted significantly with increasing depth. While bacteria were detectable in all horizons, fungi exhibited patchy distribution below 60 cm and archaea were not detectable in samples below a sampling depth of 60 – 80 cm. Within the bacterial community, both taxa-specific declines and changes in distributions were observed. We investigated the contributions of pH, OC, soil water content, and root density on microbial community composition within the different soil layers, as well as shifts in the strength of these influences with increasing depth. This study provides a deeper understanding of the complexity of subsoils and associated microbial communities.