



## **Time series of enzyme activities during microbial growth in contrasting soils under beech**

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The competition of microbial cells for nutrients (e. g. N or P) and carbon (C) infers the survival of the fittest principle favored by natural selection, depending on soil properties and nutrient availability. Therefore, the functional properties of dominating population, i.e. growth rate, carbon use efficiency, enzymes production and maintenance requirements are dependent on both soil nutrition potential and on the quantity and quality of the substrate input, implying different responses in microbial growth strategies. Up to now it is uncertain, how soil enzyme systems respond during the growth and the retardation of microorganisms in soils of contrasting nutritional status.

We determined microbial growth by kinetic approach in high resolution, via substrate-induced respiratory response of microorganisms, enabling the estimation of total and growing biomass of the microbial community. Glucose and a combination of glucose and yeast were used as easily available substrates. Time series of potential hydrolytic extracellular enzyme activities were determined in order to elucidate enzyme production strategies of microorganisms at various stages of microbial growth. We expected faster growth and greater proportion of actively growing microbial biomass in soil amended with yeast extract + glucose versus sole glucose amendment, because a broader community including auxotrophic microorganisms gets activated by specific growth factors and metabolites from microbial necromass (yeast extract).

In face of a smaller proportion of actively growing microbial biomass up to 32% faster specific growth rate of microorganisms was found in nutrient poor than in nutrient rich soil when the substrate combination was added. The proportion of growing microbial biomass was only 8% higher in nutrient-rich than in nutrient-poor soil with the addition of glucose. Substrate specific responses of enzyme activities indicated contrasting substrate utilization strategies during microbial growth.

For the combined substrate amendment, the cross correlation of acid phosphatase between the two sites was highly significant, indicating harmonized time constraints of acid phosphatase during the phase of unlimited microbial growth. Similar relation was found for  $\beta$ -glucosidase during exponential growth, reflecting similar enzymatic substrate utilization irrespective of soil nutritional status. We conclude that the fast growing microbial community members activated by yeast amendment contribute significantly to an increased enzyme activity during the phase of exponential growth and thus strongly increase the SOM decomposition and nutrient mining from SOM.