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Umwelteinflüsse auf Funktion und Diversität von Bodenorganismen

Autoren

S. Loeppmann¹, M. Semenov², Y. Kuzyakov¹, E. Blagodatskaya¹

¹Georg-August-Universität, Ökopedologie der gem. Zonen, Göttingen; ²Dokuchaev Soil Science Institute, Moscow

Titel

Towards to physiological status of soil microorganisms determined by RNA:dsDNA ratio

Abstract

Despite soil microorganisms spend most of their lifetime in a state of dormancy, they are quickly activated by substrate input and easily switch to growth. As both the dsDNA- and RNA- contents increase during microbial growth, the RNA:dsDNA ratio reflects a promising predictor, whether the response of a microbial community to environmental changes is due to an increase in population (by dsDNA) or due to an increase in activity (by RNA). This prediction of the RNA:dsDNA ratio can be accomplished by the comparison of microbial incubation approaches with and without addition of easily available substrates. We exhibited the RNA:dsDNA ratios for four contrasting soil types during substrate-induced growth. Overall, after glucose addition, a strong increase of dsDNA and RNA contents were determined in most of the soil types during 72 h of incubation. Furthermore, we identified distinct temporal soil-specific RNA:dsDNA patterns. The dsDNA- and RNA-contents yielded 26–174 and 0.3–30 $\mu\text{g g}^{-1}$ soil, respectively. The soil texture was strongly associated with the reduction of RNA recovery, by means of an exponential decrease of RNA-content with increasing clay content. The lower RNA recovery in virgin and arable Chernozem (>30%) compared to soil types with lower clay contents (<17% for Retisol, Luvisol and Calcisol) suggests, that the undercount of RNA yields in clayey soils biased the RNA:dsDNA ratio, and subsequently the physiological state of the microbial community is not adequately represented in soils with clay contents exceeding 30%.