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## Proteomics as a tool to combine the *nir* genepool and the activity of Denitrifying microbes

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The characterization of microbial functions is essential to understand turnover processes in soil ecosystems. To measure the *potential* of a soil for a particular process the diversity and number of the corresponding genes is a good indicator. To characterize the *actual activity* of the microbial community however mRNA and protein based studies are necessary. We investigated the influence of different farming management techniques over one vegetation period on the denitrification activity in the rhizosphere of wheat. We used the nirK and nirS as marker genes. We followed dynamics of the gene-, transcript- and enzyme pool quantitatively and qualitatively. It could be clearly shown that independent from the time of sampling and the management technique applied, the diversity of the gene pool was always much higher compared to the diversity of transcripts and enzymes. Transcript pool and enzyme pool however were closely related. Over the vegetation period a significant dynamic in all three pools very visible. High numbers of genes, transcripts and enzymes were detected mainly after the application of N-fertilizer, low numbers in all three pools were found mainly in autumn. The number of transcripts and enzymes was depending on the amount of fertilizer applied. The data from the expression studies (transcript and enzyme pool) were in good correlation to the measured N<sub>2</sub>O production rates at the corresponding time points