

Impact of catch crop mixtures and soils on microbial diversity and nitrogen cycling communities in agroecosystems

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In light of the projected world's population growth, food supplies will necessarily have to increase. Soils are an essential component for achieving this expansion and its quality and fertility are crucial for bio-economic productivity. Catch crops can be an option to preserve or even improve soil productivity because of their effect on soil fertility and health. A long-term field experiment of the CATCHY project (Catch-cropping as an agrarian tool for continuing soil health and yield-increase) with two contrasting crop rotations was established in two different locations in Northern and Southern Germany. Single catch crops (white mustard, Egyptian clover, phacelia and bristle oat), catch crop mixtures (a mixture of the above and a commercial mixture) and main crops (wheat and maize) have been grown.

To investigate how catch crops can affect the microbial diversity and particularly the microbial nitrogen cycling communities, we are studying first the short-term effect of different catch crop mixtures on the microbiomes associated with soils and roots. We compared these microbiomes with wheat plants, representing the microbial community before a catch crop treatment. Roots, rhizosphere and bulk soils were collected from representative samples of wheat plants from one field. The same compartments were also sampled from one fallow treatment and three catch crops variants from three fields each. The variants consisted of white mustard and the two catch crop mixtures. All fields were sampled by triplicate.

Quantitative analyses were carried out by qPCR based on key functional marker genes for mineralization (ureC), nitrification (amoA), dissimilatory nitrate and nitrite reduction to ammonium –DNRA- (nrfA), denitrification (nirK, nirS, nosZ), and nitrogen fixation (nifH). These genes were targeted at the DNA and RNA level for the characterization of the microbial population and the actual transcription activity, respectively. We detected the presence and activity of microbial populations capable of performing all the main processes of the N-cycle except DNRA. In bulk soils the expression levels of genes for nitrification and denitrification were significantly higher in Northern than in Southern Germany. In contrast, the expression level of amoA genes in the rhizosphere were significantly higher in Southern than in Northern Germany, suggesting that amoA genes may be controlled by the plant and that this control is dependent on location as well. The microbial population structure was studied using rRNA and nifH amplicon sequencing of DNA extracts obtained from root, rhizosphere and bulk soils of wheat plants and catch crops. DNAs were sequenced using the Illumina platform (MiSeq platform). The OTU-based analysis showed that microbiomes from the three compartments studied were distinct in both locations. Additionally, the taxonomic-based analysis revealed also how plant roots selected for particular bacteria and excluded others. For example, wheat selected for β -Proteobacteria making up 35% of the bacterial community in roots but only 10% in bulk soil.

These preliminary results indicate that location and catch crop treatments may have large effects on composition and activity of microbial communities and may be suitable to identify microbial functions which help to maintain or improve soil fertility and plant yield.