In situ evaluation of microbial contribution to nitrogen cycling in soil

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There is increasing concern about the sustainability of agro-ecosystems, especially for the degraded arable soil. The only way to sustain soil quality is balancing the loss of soil organic matter (SOM) by returning crop residues, which is transformed and become SOM eventually. In addition, the immobilization of residue fertilizer nitrogen (N) is very important for reducing the environmental risk of fertilizer N loss. However, how different soil microorganisms contribute the transformation of both plant residue and fertilizer N and how the substrate-derived SOM is stabilized is not clear. The linkage of long term microbial function in extraneous N transformation and stabilization might merely be explicit by probing into the time-integrated response and acclimation of soil microorganisms to substrate supply. Differentiating between the newly synthesized and the inherent portions of microbial residue biomarker such as amino sugars, by ^{15}N tracing techniques, can provide an integrated view of long-term microbial dynamics, as opposed to live biomass. Hence, the response of different microbial populations to C and N supply was investigated based on the dynamics of glucosamine (GluN) and muramic acid (MurN). Here, we firstly undertook laboratory incubation with a silt loam soil amended with C and N isotope labeled substrates. A multi-year field experiment was then conducted in a temperate agro-ecosystem using crossly ^{15}N-labeled fertilizer and maize stalk. The ^{13}C and ^{15}N enrichments in the target amino sugar were identified by gas chromatography/mass spectrometry and those in soil was measured by elemental analyzer-isotope ratio mass spectrometer. In the incubation microcosms, the dynamic transformations of extraneous C and N into amino sugars were compound-specific, indicating different contributions of heterogeneous microbial residues over time. The extraneous N was preferentially utilized by bacteria firstly stimulated by available C but then dominantly converted by fungus population and stabilized in fungal products in succession. In the field experiment, the microbial transformation of fertilizer N depends on carbon availability, especially for the initially formation of bacterial residue, while the immobilization of maize stalk N was dominantly attributed to fungus-functioned decomposition of recalcitrant components with less extent passing through mineralization. The carbon-controlled substrate utilization induced a shift from a bacterial to fungal dominant community and the similar succession dynamics of fertilizer and maize stalk N related microbial populations.

There was no preferential utilization of inorganic N over stalk N into amino sugars during both the incubation course and the field tracing experiment. On the contrary, the microbial utilization efficiency of maize stalk N was remarkably higher than fertilizer in the field except for the first-year decomposition. The effective maintenance of maize stalk N in soil may be an important mechanism for soil N accumulation and replenishment in conservation tillage systems.