Microbial colonization of legume crop residues during decomposition in a cold temperate climate

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Introduction

The rotational benefits of pulse crops include N contribution to nonlegume crops. The N is released from crop residues during microbial decomposition. The objective of this study was quantify microbial colonization of legume crop residues and relate it to N release from the residues.

Materials and Methods

We quantified soil microbial biomass C (MBC) and bacterial functional diversity (Shannon index, H') on decomposing residues of two pea varieties (Camry, a semi-leafless variety, and 4010, a normal-leafed silage pea variety), faba bean grown for seed, faba bean green manure (GM) and chickling vetch GM. Nitrogen released from the residues was concurrently quantified.

Results and Discussion

- During 12 months of decomposition, the order of MBC on residues was faba bean $GM \ge vetch \ GM \ge faba bean \ grown \ for seed \ge Camry \ pea \ge 4010 \ pea, \ and \ H' \ on \ Camry \ pea \ residues \ was \ less \ than \ that \ on \ the \ other \ residues.$
- The pattern of colonization with time was a rapid increase of MBC in the first four weeks after residue placement at legume crop harvest in summer or fall, followed by a slight decrease during winter, then a gradual increase from spring to fall of the following season (Fig. 1). The pattern for H' was similar, except that the decrease during winter was accelerated between spring and summer of the following season, and started increasing again between summer and fall (Fig. 2).
- The pattern of N release from the crop residues also followed a similar trend to that of MBC on the residues, except that N release continued to increase slowly during winter (Fig. 3).
- There was positive correlation (r = 0.413*) between MBC on the residues and N released from the residues during the 12-month period. Bacterial diversity (H') was not related to N released, presumably because H' decreased between spring and summer when N release continued to increase. H' was negatively correlated with the residue C/N rations during the 12 months of decomposition (r = -0.367*).
- When only the first month of decomposition and N release were considered, both MBC and H' were negatively correlated with %N remaining in residues (r = -0.535* and -0.592*, respectively, n = 15).

Conclusion

Legume GM residues were heavily colonized by soil microorganisms, resulting in rapid initial N release from these residues relative to residues of legumes grown for seed (except faba bean). Therefore, microbial colonization of crop residues can be a good indicator of N release from the residues.



Figure 1. Microbial biomass C (MBC) on legume crop residues during decomposition.



Figure 2. Functional diversity (Shannon index, H') of bacteria on legume crop residues during decomposition.



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