Monocrop culture long term straw return impact on soil structure, abundance and microbiota catabolic activity: consequences on soil functions

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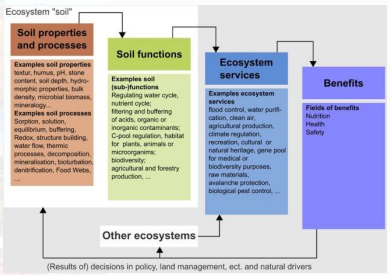
Abstract:

Returning straw to soil is an effective way to sustain or improve soil quality and crop yields. However, a robust understanding of the impact of straw return on the composition of the soil microbial communities under field conditions has remained elusive. The objective of this study was to investigate how straw-incorporating practices affect bacterial communities and carbon source utilization capacity. Therefor, we characterized the effects of wheat straw return on soil bacterial and fungal communities in a wheat–soybean rotation system over a 2-year period. Soil microbiota structure and abundance assessment was done using PLFA technique. Microbiota catabolic activity was performed with EcoPlate approach. Our results has shown that wheat straw return affected the soil bacterial community especially gram positive bacteria, gram negative bacteria, and actinobacteria , but not fungal community. The carbon utilization ability of soil microorganisms in first year treatment was significantly higher than that of the second-year treatment ($P < 0.05$). The utilization ability of carboxylic acids, polymers, and other mixtures of carbon sources in the first year of treatment was higher than those from the second year. These findings suggest that long-term straw incorporation affects the abundance and carbon utilization ability of soil microorganisms within 0–20 cm soil depths, among which, gram positive bacteria, gram negative bacteria, and actinobacteria may play crucial roles in bacterial communities and carbon source utilization capacity.

Introduction:

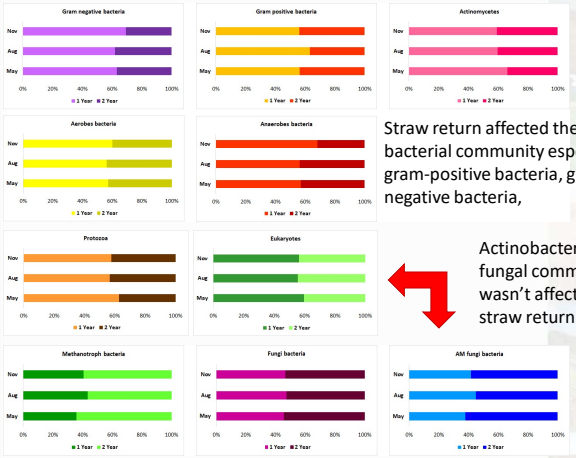


Soil microbial biomass is based on a unifying driver or set of environmental drivers that need to be adequately understood.

Crop **straw** is widely used to manage soil organic carbon (SOC) sequestration as an environmentally friendly practice

Excessive **straw return** always brings **challenges** for crop production and soil quality

Results and discussions:



Straw return affected the soil bacterial community especially gram-positive bacteria, gram negative bacteria,

Actinobacteria and fungal community wasn't affected by straw return.

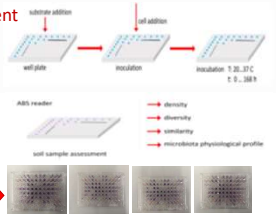
Analytical approach:

Soil microbiota phenotypic structure and abundance assessment was performed using PLFA approach with GC-FID.

Microorganisms	PLFA biomarkers
Gram positive bacteria	i14:0; a14:0; i15:0; a15:0; i16:0; a16:0; i17:0; a17:0; (Branched PLFA)
Gram negative bacteria	i15:0-3OH; i15:1; 2OH-16:1; i16:1; 16:1ω5c; 16:1ω7c; 16:1ω9c; i17:1; 17:1ω8c; 18:1ω5c; 18:1ω7c; 18:1ω9c; cy17:0; 18:0; cy19:0;
Aerobe	18:1ω10; 18:1ω9; 18:1ω7; 16:1ω7c;
Anaerobes	cy17:0, cy19:0;
Methanotrophs	16:1ω8c; 16:1ω5c;
Nitrate reducing bacteria	18:2ω6c; 18:3ω3
Sulfate reducing bacteria	17:1 ω7c; 10Me16:0; 17:1ω6; 15:1; i17:1ω7c; cy18:0ω7,8; i15:1ω7c; i19:1ω7c;
Actinomycetes	10Me16:0; 10Me18:0; 10Me17:0;
Fungi	18:2ω9; 18:1ω9; 18:3ω6; 18:3ω3
Arbuscular mycorrhizal fungi	16:1ω5
Saprotrophic fungi	18:2ω6c
Ectomycorrhizal fungi	18:2ω9c

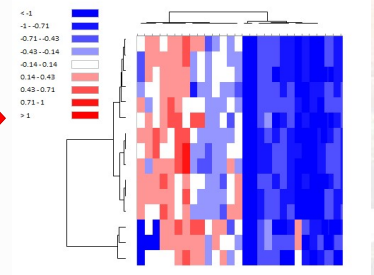
Phospholipids derived fatty acid methyl esters used for microbiota phenotypic structure identification.

Microbiota catabolic assessment using PLFA approach.

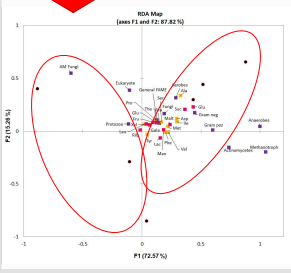


Microbiota catabolic potential: sole C, C x N, and C x P sources

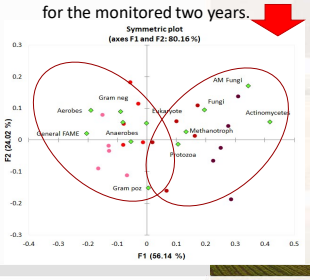
The carbon utilization ability of soil microorganisms in first year treatment was significantly higher than that of the second-year treatment ($P < 0.05$).



RDA analysis differential straw return impact on amino acids consumption by microbiota.



Symetric plot of microbiota catabolic activity for the monitored two years.



Conclusions:

- The utilization ability of carboxylic acids, polymers, and other mixtures of carbon sources in the first year of treatment was higher than those from the second year.
- These findings suggest that **long-term straw incorporation affects the abundance and carbon utilization ability of soil microorganisms within soil depths**, among which, gram positive bacteria, gram negative bacteria, and actinobacteria may play crucial roles in bacterial communities and carbon source utilization capacity.

References:

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