

The effects of transgenic soybeans with sulfur-rich amino acids on soil microbial community structure

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Abstract

This study was conducted to evaluate the effects of quality-improved transgenic soybeans on the structure of microbial communities in rhizosphere soil under agricultural field conditions based on the phospholipid fatty acid (PLFA) method. Two different groups of transgenic soybeans with sulfur-rich amino acids were used. The results showed that in comparison to the non-transgenic soybeans, the soil microbial communities in the rhizosphere associated with the transgenic lines changed significantly. In both group A and B, the PLFA contents changed significantly and 14 specific PLFAs were identified in Group A, and 13 in Group B. Correlation analysis found that the microbial characterization of Group A and the total concentration of PLFA's of the transgenic line OE-8 were significantly higher than those of the non-transgenic line, as well as the lines 17-4 and 57 in Group B. The dominant PLFA mown plots were 16:0, 10Me18:0 and 18:1 ω 7c in Group A, and 15:0, 16:0 and 14Me16:0 in Group B. The results suggested that the microbial community structure changed after planting transgenic soybeans.

Key words:

Transgenic soybean;
Soil microorganism community;
PLFA;
Sulfur-rich amino acids

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Site description

The experiment was performed at Pukou, Nanjing, eastern China. The field area is about 5m×10m. The soil was mixed before planting.

All the experiments according to transgenic lines were performed based on local laws

Table 1 Soybean Materials

	Recipient	Transgenic lines		
Transgenic group A (Name)	Nannong 88-1 (CK1)	OE-8	OE-7	RNAi-3
Transgenic group B (Name)	N2899 (CK2)	17-4	21-8	57

Soil sampling

Soil samples were collected at the seedling, squaring, flower and mature stages of soybean development. For each sampling, rhizosphere soil was collected in 10cm deep around the root.

According to the different function, the soil samples were stored at 4°C and room temperature until analysis.

PLFA analyses

Lipid extraction and PLFA analyses were performed using the modified Bligh and Dyer-method (Bligh and Dyer 1959, Can J

Biochem Phys 37, 911-917; Peacock et al. 2001, Soil Biol Biochem 33, 1011-1019)

Table 2 PLFA (phospholipid fatty acid) for calculating soil microbial biomass

Microbial group	PLFA signatures
Bacteria in general	15:0、i15:0、a15:0、16:0、i16:0、16:1ω5、16:1ω9、16:1ω7t、17:0、i17:0、a17:0、cy17:0、18:1ω5、18:1ω7、18:1ω7t、i19:0、a19:0、cy19:0
Gram-positive bacteria	10Me16:0、10Me17:0、10Me18:0、i15:0、a15:0、i16:0、i17:0、a17:0
Gram-passive bacteria	16:1ω5、16:1ω7t、16:1ω9、cy17:0、18:1ω5、18:1ω7、cy19:0
Anctinomycete	10Me16:0、10Me17:0、10Me18:0
Fungi	18:1ω9、18:2ω6、18:3ω6、18:3ω3
Anaerobic bacteria	cy17:0、cy19:0
Aerobic bacteria	16:1ω7、16:1ω7t、18:1ω7t、i15:0、a15:0、15:0、i16:0、16:1ω9、i17:0、a17:0、17:0
Methanotrophs	16:1ω8c、16:1ω8t、16:1ω5c、18:1ω8c、18:1t、18:1ω6c

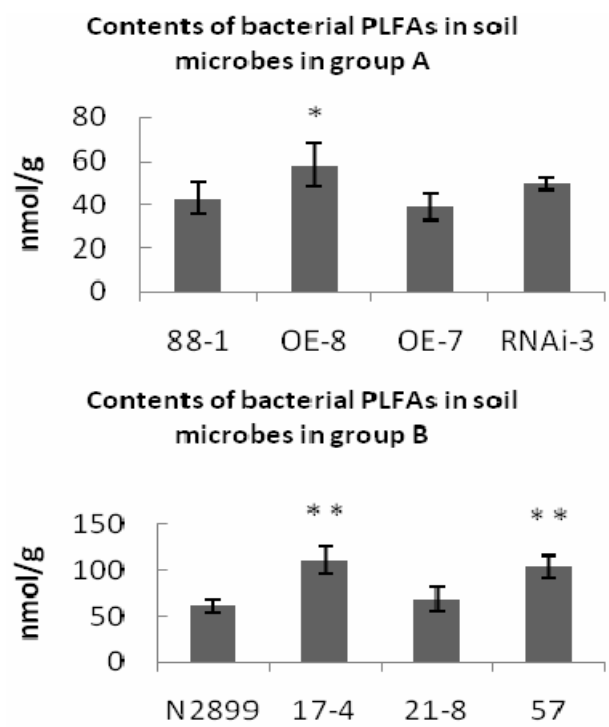
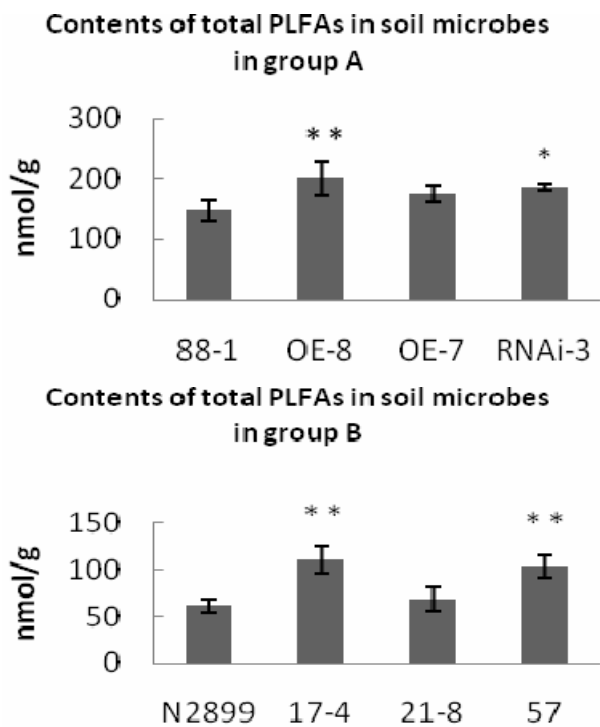


Fig. 1 Total PLFAs in soil microbes in Group A and B. Total PLFA of transgenic lines OE-8 and RNAi-3 in Group A, and 17-4 and 57 in Group B were significantly higher than the respective non-transgenic line.

Fig. 2 Total PLFAs in soil bacterium in Group A and B. Total PLFA of transgenic lines OE-8 in Group A, and 17-4 and 57 in Group B were significantly higher than the respective non-transgenic line.

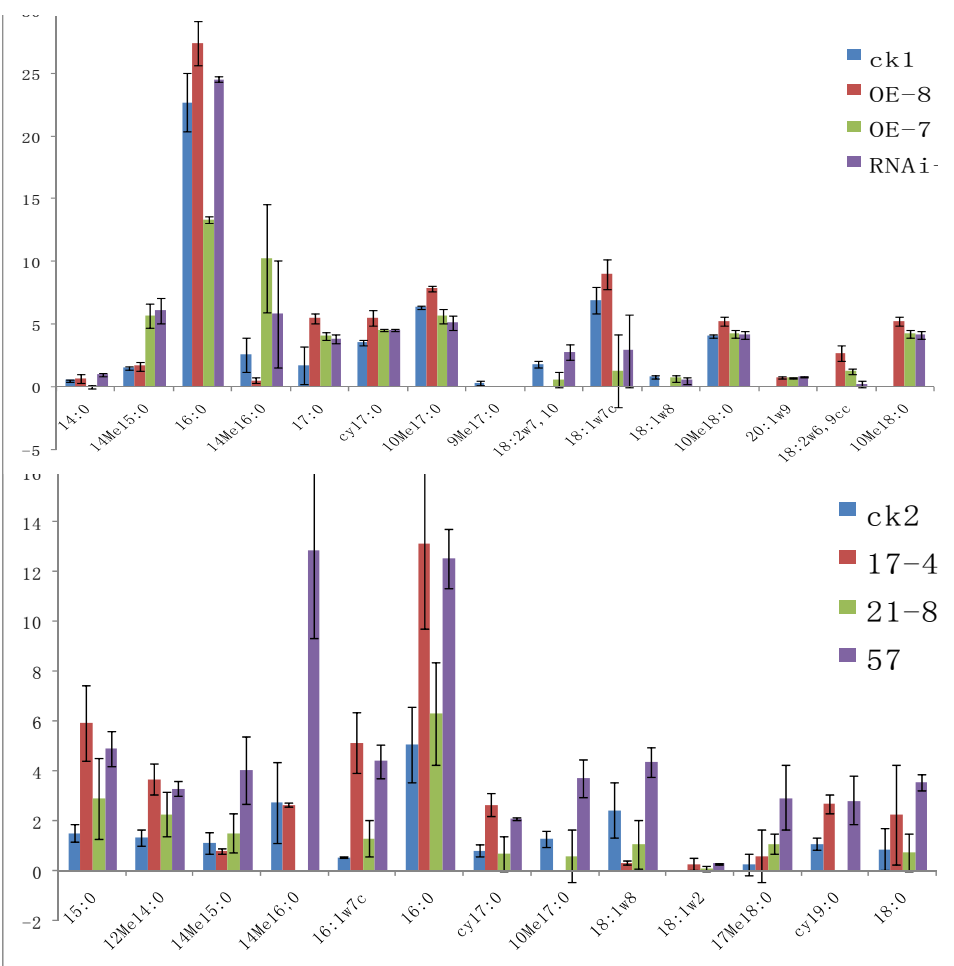


Fig. 3 Single PLFA content of two soybean groups in soil microbes. There were 15 difference PLFAs in group A and 13 in group B. PLFA (phospholipid fatty acid) for calculating soil microbial biomass is listed in Table 2.

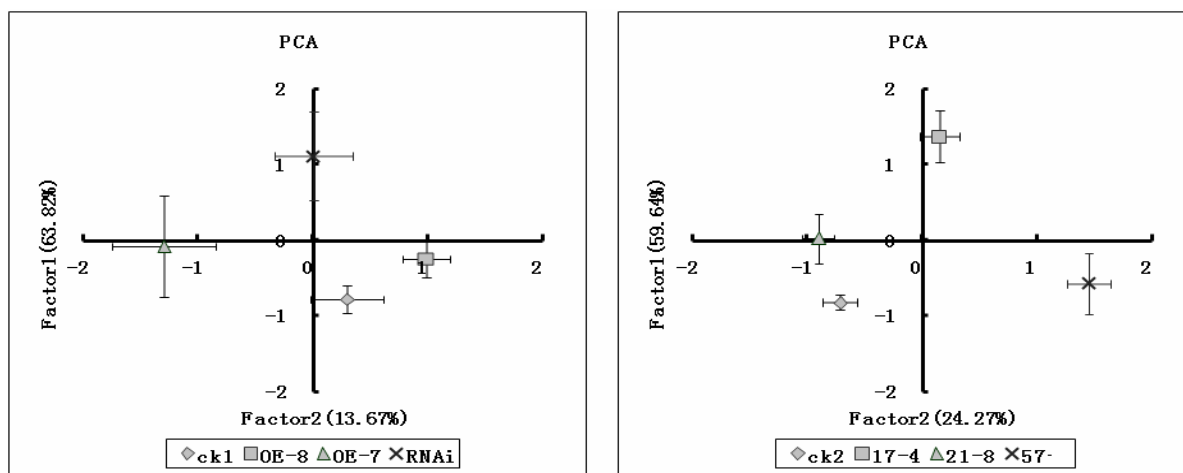


Fig. 4 Principal component analysis based on PLFA data to determine whether the soil microbial community structure change after planting the transgenic soybean. In group A, transgenic line OE-8 was significantly different from CK1 in factor 1 (Left), and in group B, transgenic line 57 was significantly different from CK2 in factor 1 (Right).

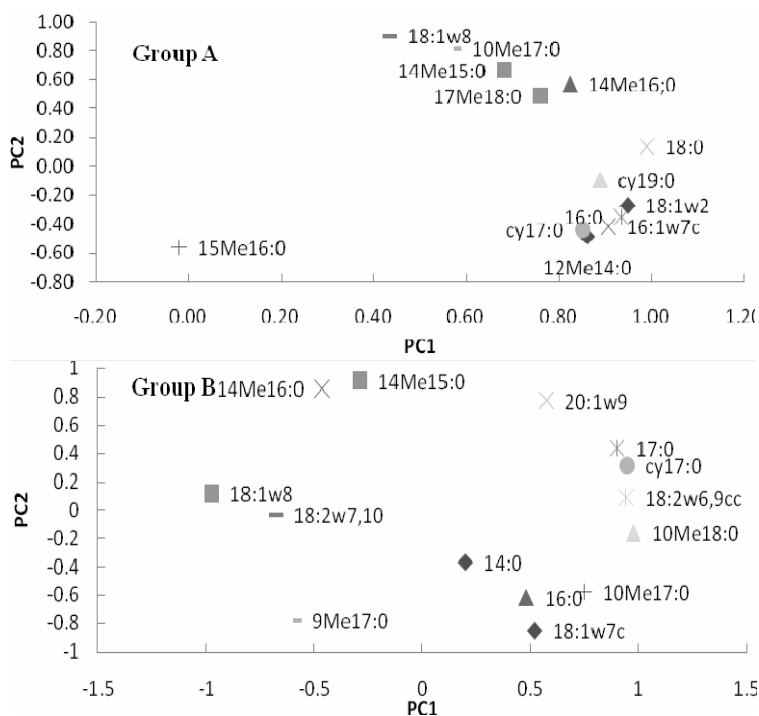


Fig. 5 Eigenvector loadings of PLFA contributing to soil microbial communities in Group A and B. Both Group A or Group B, the typical bacterial fatty acids (17:0,18:0, cy19:0, etc.) have a higher contribution to the value in the principal component 1. The representative fatty acids 10Me17:0 and 10Me18:0 for actinomycetes have a higher contribution value both in the principal component 1 and 2.

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