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转基因棉花不同生物量对土壤微生物群落结构的影响

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Effects of Transgenic Bt Cotton Biomass on Soil Microbial Community Structure, Based on Phospholipid Fatty Acid Analysis

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摘要 用磷脂脂肪酸图谱分析方法评价了3个转基因棉花品种(晋棉26、晋棉44、中棉所41)和它们相应的近等位非转基因棉花品种(晋棉7、冀合492、中棉所23)不同生物量对土壤微生物群落结构的影响。每个品种生物量为0 g, 2 g, 4 g, 6 g, 8 g粉碎棉株与200 g土混匀, 在28 °C培养箱中培养45 d后进行分析。结果表明, 随着棉花生物量的增加, 土壤微生物总量显著增加, 而且土壤微生物群落结构发生明显变化, 细菌和放线菌所占比例明显减少, 真菌比例显著增加。转基因棉花与非转基因棉花的差异因品种和还田量而表现不同。

关键词: 生物量 土壤微生物 磷脂脂肪酸图谱分析 群落结构 转基因棉花

Abstract: We evaluated the effects of transgenic Bt cotton biomass on soil microbial communities using soil incubation and phospholipid fatty acid(PFLA) analysis. We used three transgenic Bt cotton lines(Jinmian 26, Jinmian 44, and CCRI 41) and their isogenic non-Bt cotton lines (Jinmian 7, Jihe 492, and CCRI 23). Different plant biomasses (0, 2, 4, 6, and 8 g) were mixed with 200 g of soil for each line, and incubated at 28 °C for 45 days. The total concentration of PLFAs significantly increased with increasing cotton biomass, and the microbial community was characterized by a predominance of fungi in the soil amended with cotton biomass in comparison with the control(soil without cotton biomass). In contrast, the microbial community was characterized by a predominance of bacteria and actinomycetes in the control soil. Differences between Bt-cotton and non-Bt soils depended on cotton lines and cotton biomass in the soil.

Keywords: community structure soil microbes Bt cotton phospholipid fatty acid analysis cotton biomass

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