

研究论文

大豆连作对土体和根际微生物群落功能的影响

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摘要 试验采用Biolog方法在大田试验条件下研究了不同连作年限大豆在结荚期和收获期根际和土体微生物群落功能多样性的变化。试验结果表明, 在结荚期和收获期根际微生物群落功能多样性、均匀度指数和AWCD均显著高于土体。在结荚期迎茬和连作8a的土体微生物多样性、AWCD均高于正茬和连作4a土体; 在收获期正茬和迎茬处理的土体微生物多样性、AWCD高于连作4a和8a。结荚期迎茬、连作4a和8a处理的根际微生物群落AWCD均显著高于收获期, 说明在大豆植株生长旺盛的结荚期微生物群落的根际效应比收获期更明显。在这两个生长期降解氨基酸, 糖类和羧酸类碳源的微生物可能是连作影响的主要土体微生物类群。

关键词 [大豆](#); [土壤](#); [微生物群落](#); [连作障碍](#); [Biolog](#)

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Effect of soybean continuous cropping on bulk and rhizosphere soil microbial community function

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Abstract Soybean is a main crop in northeast China, but a reduction in crop production occurred widely as a result of continuous soybean cropping on the same soil. This phenomenon is called continuous cropping obstacles. When soybean is cropped continuously in the same field for years, the yield would be reduced by 10%~30% or even more. The area with continuous cropping problem is about 700 000 hm² in parts of northeast China alone. Much work on the problem has been done, however, the origin of replant disease remains unexplained.

Some researchers considered the problem as a disturbance of soil fertility due to the facts that soil enzyme activities and pH decreased and soil structure degraded after continuous soybean cropping. Another hypothesis for the soil problem concerns the phytotoxic or allelopathic effects of shoot or root residues. The latest hypothesis for the decline in soil health focuses on the shift of soil microbial community in continuous cropping system, but it is not yet proved. Therefore, this study aimed to determine the effects of soybean replant disease in the field on rhizosphere and bulk soil microbial community functions. The bacterial community function was characterized for 4 cropping systems, namely, normal rotation with corn (corn-corn-corn-soybean, CCCS), alternation of soybean with other crops (soybean-corn-soybean, SCS), continuous soybean for 4 years (CS4) and continuous soybean for 8 years (CS8) at podding and harvest stages using Biolog method. Our results showed that functional diversity, evenness indices and AWCD from rhizosphere microbial community were significantly higher than those from bulk soil microbial community at both growth stages. Functional diversity and AWCD of bulk microbial community from SCS and CS8 were higher than those from CCCS and CS4 treatments at podding stage; At harvest stage functional diversity and AWCD from CCCS and SCS were higher than those from CS4 and CS8. AWCD o

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f rhizosphere microbial community from the treatments of SCS, CS4 and CS8 at podding was higher than that at harvest stage, suggesting that soybean root might excrete larger amounts of organic carbon at first stage than at latter stage. The microbes degrading amino acid, carbohydrate and carboxylic acid were mainly affected by soybean continuous cropping in bulk soil.

Key words [soybean](#) _ [soil](#) _ [microbial](#) [community](#) _ [continuous](#) [cropping](#) _ [Biolog](#)

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