不同施肥处理对农田土壤微生物区系和 功能的影响

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摘要:本研究采用 DGGE 和 Biolog 两种方法,研究了五种不同施肥处理对土壤微生物区系组成和功能的影响。采用 UPGMA 对 DGGE 试验结果进行聚类分析得出,小麦季中不施肥对照(T1)和常规氮磷钾肥(T2)聚为一类,相似性为41%,常规氮磷钾肥+秸秆还田(T4)和常规氮磷钾肥+秸秆还田+秸秆腐熟剂(T5)聚为一类,相似性为52%,而70%常规氮磷钾肥+有机肥(T3)单独聚为一类;玉米季也得到类似的结果,只是T1和T2的相似性为68%,T4和T5相似性达78%,而T3依然归为一类,这说明不同施肥处理间土壤微生物区系存在相似性。经过切胶测序及BLAST比对发现大多为不可培养细菌,可培养细菌中多为芽孢杆菌属和类芽孢杆菌属。Biolog 试验采用主成份分析得出,T1和T2土壤微生物功能类似,T4和T5土壤微生物也具有相似的功能,而T3则单独分为一类。其中,T5和T4的土壤细菌群落对底物碳源的代谢活性最强,T3处理次之,T2和T1最低。通过这两种不同试验方法的分析可以看出不同施肥处理对土壤微生物区系和功能的影响存在关联性。

关键词: 施肥; 微生物区系; DGGE; Biolog

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Effects of different fertilization on structure and function of soil bacterial community

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Abstract: In this paper, we used DGGE and Biolog to study the composition and function of soil microbial flora. Based on the UPGMA analysis, the results of the DGGE indicate that T1 (CK) and T2 (single inorganic fertilizer treatment) have a similarity of 41% in wheat season, T4 (conventional NPK + straw) and T5 (conventional NPK + straw + straw decomposing inoculants) have a similarity of 52%, and T3 (70% conventional NPK + organic fertilizer) is clustered into one group alone. In corn season, the similarity between T1 and T2 is 68%, which is grouped into the first category, the similarity between T4 and T5 is 78%, which is grouped into the second category, and T3 as the third category. These results show that there are similarities between different fertilizer treatments. Through a series of experiments of gel cutting, sequencing and BLAST comparison, we find that most of bacteria in the tested soils is uncultured and the main cultured bacteria belong to Bacillus and Paenibacillus. Using principal component analysis, the results of Biolog show that T1 and T2 have similar microbial functions, and T4

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