

用SRAP标记研究根际土壤微生物的遗传多样性

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Genetic diversity in rhizosphere soil microbes detected with SRAP markers

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摘要

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摘要 将近年来新建立的分子标记技术——相关序列扩增多态性(sequence-related amplified polymorphism, SRAP)应用于土壤微生物遗传多样性研究。采用22对引物组合对20种植物根际土壤微生物进行了分析,共获得237个扩增位点,其中多态性位点221个,占93.2%。平均每对引物组合的多态位点比例(PPL)、多态信息含量(PIC)、等位基因单体型(Ah)和遗传杂合度(He)分别为93.78%、0.94、18.05和0.92,说明SRAP对根际土壤微生物具有较强的鉴别能力,也反映了本研究中20种不同植物的根际土壤微生物具有丰富的遗传多样性。水稻的2个不同种植地和4个不同发育时期期间的根际土壤微生物遗传距离差异极显著,但2个不同水稻品种间的差异不显著。Shannon多样性指数揭示,水稻根际土壤微生物的遗传多样性最低,莴苣的最高。按照非加权类平均法(UPGMA)聚类,在遗传距离0.454的水平上,可将20种植物根际土壤微生物分为三类:第一类是水稻根际土壤微生物,第二类是种植于大棚温室的芹菜根际土壤微生物,第三类为其余18种旱作植物根际土壤微生物。本研究结果证明SRAP是分析土壤微生物遗传多样性的有效手段。

关键词: 根际土壤微生物 SRAP 遗传多样性 遗传距离 聚类分析

Abstract: We have attempted to use the SRAP (sequence-related amplified polymorphism) markers, a new molecular technology, to study genetic diversity in soil microbes. We sampled rhizosphere soil microbes from 20 plant species and employed 22 SRAP primer combinations. A total of 237 scorable fragments were identified, of which 221 (93.2%) were polymorphic loci. The average percentage of polymorphic loci (PPL), polymorphism information content (PIC), allele haplotype (Ah), and expected heterozygosity (He) for each primer combination were 93.78%, 0.94, 18.05 and 0.92, respectively. Our results revealed rich genetic diversity in rhizosphere soil microbes and the high ability of SRAP to resolve samples based on their genetic basis. Differences in genetic distance for rice rhizosphere microbes between two locations, and that among four different developmental stages were both significant at 0.01 level, but the difference was not significant between two varieties. Shannon diversity indices indicated that the genetic diversity of rhizosphere soil microbes was lowest in rice and highest in lettuce. The rhizosphere soil microbes from 20 plant species could be clustered into three groups at the 0.454 (GD) level based on UPGMA, in which the first group was from rice, while the second group was from celery planted in plastic green house, and the third group was from 18 other plant species cultivated in dry lands. Our results suggest that SRAP is an efficient method for analyzing the genetic diversity in rhizosphere soil microbes.

Keywords: rhizosphere soil microbe SRAP genetic diversity genetic distance cluster analysis

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