

研究论文

大气CO₂ 倍增对植物根内AMF群落的影响

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摘要 采用环境控制生长室控制CO₂浓度的方法, 研究了CO₂浓度(350~400μmol mol⁻¹和680~750μmol mol⁻¹)对植物根内丛枝菌根真菌(arbuscular mycorrhizal fungi, AMF)群落的影响。12种宿主植物于CO₂浓度不同的生长室栽培180d后收获取样, 通过CTAB法提取共生菌根内丛枝菌根真菌的DNA, 由特异引物U1/U2扩增编码核糖体28S大亚基的rDNA部分序列, 并进行DGGE电泳分析。结果表明, 12种植物根内的AMF存在特异的AMF类群(unique species group, US)和共有类群(common species group, CS), 而且CO₂浓度倍增使US减少而CS增加。与350μmol mol⁻¹对照相比, 700μmol mol⁻¹处理的玉米、刺苋、大豆、陆稻、无芒稗、黑麦草6种植物的AMF群落多样性下降, 下降幅度分别达27.12%、16.84%、10.12%、8.62%、8.58%和2.67%; 白车轴、牛筋草、早熟禾、鼠曲草、野燕麦、北美车前6种植物的AMF群落多样性上升, 分别达76.26%、28.50%、17.60%、15.08%、1.46%和0.96%。CO₂倍增处理后12种植物的AMF多样性平均指数略呈上升趋势。研究指出未来环境变化(如CO₂增加)将影响AMF群落结构从而影响菌根共生体的形成。

关键词 大气CO₂倍增; 丛枝菌根真菌; 物种多样性; PCR-DGGE

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The effects of elevated atmospheric CO₂ on AMF community colonized in roots of various plant species

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Abstract The effects of elevated CO₂ on the species diversity of arbuscular mycorrhizal fungi (AMF) in roots of various species of host plant were studied under pot culture condition in greenhouse. Twelve common cover plants in subtropical orchards were selected as host plants of AMF colonization in this research. These twelve host species were grown at ambient (350μmol mol⁻¹) and elevated CO₂ (ambient + 350μmol mol⁻¹) concentrations in growth chamber, respectively. The plants were sampled at 180th day after seedling and DNA of AMF in plant roots was extracted by CTAB method. The partial rDNA sequence encoding ribosomal 28S big unit was amplified with special primers U1/U2 for fungi, and PCR products were analyzed with denaturing gradient gel electrophoresis (DGGE). Species diversity was presented by using Shanno-Weiner diversity index. AMF colonized in roots of 12 host plant species were divided into two different groups, unique species (US) group and common species (CS) group. Results showed elevated CO₂ could enhance species numbers of AMF in US group but reduced that in CS group. Under elevated CO₂ condition species diversity of AMF community colonized in Zea mays, Amarat

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hus spinosus, Glycine max, Oryza sativa, Echinochloa crusgalli var mitis and Lolium perenne decreased by the corresponding percentage of 27.12%, 16.84%, 10.12%, 8.62%, 8.58% and 2.67%, while that in Trifolium repens, Eleusine indica, Poa annua, Gnaphalium affine, Avena fatua and Plantago virginica tended to increase by 76.26%, 28.50%, 17.60%, 15.08%, 1.46% and 0.96%, respectively. The average biodiversity index of AMF colonized in the roots of all 12 plants tended to increase when CO₂ concentration increased from 350 μmol mol⁻¹ to 700 μmol mol⁻¹. These results also indicated that the response of species diversity of AMF community to atmospheric CO₂ enrichment largely depended on characteristics of host plant. Biennial plants, including Avena fatua, Plantago virginica, Poa annua, Trifolium repens and Gnaphalium affine increased AMF diversity (with the exception of Lolium perenne), while annual plants Zea mays, Amaranthus spinosus, Oryza sativa, Glycine max and Echinochloa crusgalli var. mitis decreased it. (except Eleusine indica).

Key words elevated atmospheric CO₂ arbuscular mycorrhizal fungi (AMF) species diversity PCR-DGGE

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