

综合评述

土壤宏基因组学技术及其应用

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摘要 传统的基于培养的研究方法只能反映土壤中少数(0.1%~10%)微生物的信息,而大部分微生物目前还不能培养,因而这部分微生物资源尚难以被有效地开发利用.宏基因组学是分子生物学技术应用于环境微生物生态学研究而形成的一个新概念,主要技术包括土壤DNA的提取、文库的构建和目标基因克隆的筛选.它可为揭示微生物生态功能及其分子基础提供更全面的遗传信息,并已在微生物新功能基因筛选、活性物质开发和微生物多样性研究等方面取得了显著成果.本文对土壤宏基因组学技术的方法和应用作了详细介绍.

关键词 [宏基因组学](#) [土壤DNA提取](#) [文库构建](#) [文库筛选](#) [应用](#)

分类号

Methodology and application of soil metagenomics

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Abstract

Culturable microorganisms provide very limited information on soil microbial diversity, because only 0.1%-10% of soil microorganisms can be cultured under conventional laboratory conditions. A novel culture-independent approach, *i. e.*, metagenomic methodology, has been developed as an effective tool for the discovery of new natural products and microbial functions. Soil metagenomic methods, comprising isolation of soil DNA and construction and screening of clone libraries, enable to peep at more complete scenario of soil microbial communities, and thus, to better understand their interactions. This methodology is of great potential for use in the studies of soil microbial communities and their functional genes, and in the discovery of new biocatalysts for industry and pharmacy. This review summarized some advances of soil metagenomic study.

Key words [metagenomics](#) [isolation of soil DNA](#) [library construction](#) [library screening](#) [application](#)

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