专论与综述

油藏微生物群落研究的方法学

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摘要 油藏微生物群落的解析和认知是开发和应用微生物采油技术的基础。利用各种提高油藏微生物可培养 性的方法和非培养技术解析不同油藏微生物的群落结构、功能和多样性,对定向调控油藏微生物群落、开发和 应用有效微生物驱油技术具有重要的指导意义。通过调查新近发展的提高微生物可培养性的方法和措施以及不 依赖于培养的分子微生物生态学技术,总结了油藏微生物群落研究方法学的最新进展。提高微生物可培养性的 方法和措施主要通过模拟微生物的生存环境,减少富营养的毒害作用、添加信号分子维持微生物细胞间的作用 和提供新型电子供体和受体等手段采用稀释法、高通量培养法等方法得以实现;不依赖于培养的分子微生物生 态学技术主要包括荧光原位杂交、末端限制性片断长度多态性分析、变性梯度凝胶电泳和构建克隆文库等技 术。这些方法学的进展为更有效的获得各种油藏微生物资源、调控油藏微生物群落以提高石油采收率提供理论 指导。

关键词 微生物群落; 非培养技术; 微生物采油; 提高微生物可培养性

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Progress in methodological research of microbial commu nity in oil fields

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Abstract

Understanding microbial community in oil reservoirs is crucial to application of microbial enhance d oil recovery (MEOR) technology. Much effort has been directed toward more insights into th e microbial community in oil field, resulting in the development of culture dependent and independ ent techniques. Culture-dependent methods for enhancement of microbial culturability and cultur e-independent methods for analyzing microbial communities are reviewed in an attempt to better u nderstand the recent progress in methodological researches on the oil field microbial communitie

Microbial community is analyzed conventionally by culture-dependent approaches which cultivat e, enrich and isolate microbial cells, identify and count them, then figure out the microbial structur e from the data of the cultivated microbial cells. However, the cultivating nutrients and condition s afforded in laboratory are too simplified and somehow far different from those in the environmen ts where microorganisms live. Consequently, majority of microorganisms can not grow and be cul 本文作者相关文章 turable. In addition, microorganisms grow at different speeds on the same media and under the sa me conditions, leading to different enrichment and increase of the microbial population. The relativ e amounts of the cultivated microorganisms are therefore different from the real ratio of the micro organisms in the environments. As a consequence, the pattern of microbial community structure o btained by the conventional culture-dependent methods is not true and not helpful for directing th

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e development and application of MEOR.

Two strategies, the increasing microbial culturability and culture-independent methods, are therefo re developed and applied for getting more culturable microbial isolates and more insights into the r eal microbial community structure and functions. Increasing microbial culturability is to cultivate mi croorganisms with novel methods and under novel conditions. These novel cultivating conditions i nclude: "oligotrophic" media instead of "rich" nutrients, adding signal molecules, novel electronic d onating and accepting chemicals to media, etc.. The novel cultivating methods include dilution cult ure, high-through culturing, diffusion-growth chamber, cell encapsulation, sequence-guiding isolati on techniques, etc. which can mimic environmental conditions and lead to more microorganisms c ultivated. Although the novel cultivating techniques and conditions can make much more microorg anisms culturable, they can not figure out the overall pattern of microbial community structure, th e culture-independent approaches are therefore absolutely necessary for analyzing oil reservoir mi crobial community. Culture-independent approaches are based on the analyses of the functional g enes, such as mcrA gene, and 16S rRNA and its gene (16S rDNA). The analyzing techniques co ntain FISH, T-RFLP, DGGE, clone library and sequencing etc.. Many researches with the cultur e-independent methods have showed the power of these methods and got many new ideas on th e structure and functions of the microbial community in oil reservoirs. Moreover, it is a trend to ap ply both culture-dependent and culture-independent approaches to understand the functions of mi croorganisms for MEOR and structure of microbial community. With the microbial strains obtaine d from oil reservoirs and the knowledge of oil reservoir microbial community, MEOR can be dev eloped and applied feasibly and reliably by manipulating the microbial community in the oil reserv oirs.

 Key words
 microbial
 community
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 d
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