中国农业科技导报 2009, 11(1) 73-79 DOI: ISSN: 1008-0864 CN: CN 11-3900/S

863课题进展

3种DNA提取方法对养殖池塘不同生境菌群PCR-DGGE分析的影响

何夙旭1,周志刚1,姚斌1,白东清2

(1.中国农业科学院饲料研究所农业部饲料生物技术重点实验室, 北京 100081|
2.天津农学院水产科学系天津市水产生态及养殖重点实验室, 天津 300384)

摘要：

比较3种DNA提取方法(溶菌酶法、CTAB法及珠磨法)对养殖池塘几种生境(底泥、饲料、草鱼肠道内容物及肠道壁)菌群PCR-DGGE分析的影响。结果表明,以3种提取方法获得的DNA为模板均能进行16S rDNA V3区特异性片段扩增；但不同DNA提取方法对池塘不同生境菌群DGGE指纹图谱存在显著影响。DGGE指纹图谱显示草鱼肠道内容物菌群(溶菌酶法)与肠道壁菌群(溶菌酶法)存在较高一致性,底泥菌群(CTAB法)及饲料菌群(溶菌酶法)与鱼体肠道菌群(包括内容物菌群和肠道壁菌群)则存在明显差异,但肠道菌群与底泥菌群的相似度相对更高。研究提示采用微生物分子生态学工具对养殖池塘不同生境进行菌群结构分析时,需提前优化DNA提取方法；在以投饲为主的养殖鱼塘中,草鱼肠道菌群更多源自于池塘底泥。

关键词： 养殖池塘；菌群； PCR-DGGE

Effects of Three Different DNA Extraction Methods on the Analysis of Bacteria Community from Different Micro-ecological Environments in a Farming Pond by PCR-DGGE

HE Su-xu1, ZHOU Zhi-gang1, YAO Bin1, BAI Dong-qing2

(1. Key Laboratory for Feed Biotechnology, Ministry of Agriculture, Feed Research Institute, Chinese Academy of
Agricultural Sciences, Beijing 100081|
2. Tianjin Key Laboratory of Aqua-ecology and Aquaculture,
Fisheries Science Department, Tianjin Agricultural University, Tianjin 300384, China)

Abstract:

This study compareed the effects of three different DNA extraction methods (lysozyme digestion, CTAB method and bead mill) on analyzing bacteria from different micro-ecological environments in an farming pond (pond sludge, feed, intestinal content and intestinal wall of grass carp) by PCR-DGGE. The results showed that 16S rDNA V3 fragments were successfully amplified from samples extracted by three DNA extraction methods in all micro-ecological environments; but different DNA extraction methods had remarkable influence on DGGE fingerprints of bacteria under different micro-ecological environments. The cluster analysis of DGGE fingerprints showed that the bacterial community of intestinal content (lysozyme digestion) was almost identical to that of intestinal wall (lysozyme digestion) in grass carp, while the bacterial community of pond sludge (CTAB method) or feed (lysozyme digestion) showed obvious difference to the intestinal bacterial community of grass carp. However, the bacterial community of pond sludge was more similar to intestinal bacterial community compared to that of feed. This study indicated that DNA extraction method should be optimized before analyzing the structure of bacterial community under different micro-ecological environments in an farming pond, and most of the intestinal microbiota in grass carp were derived from the pond sludge in the feed-fed farm pond.

Keywords: aquaculture pond bacterial community PCR-DGGE

收稿日期 2008-10-21 修回日期 2008-11-17 网络版发布日期

DOI:

基金项目:

国家863计划项目(2007AA100605)；天津市农业科技合作项目（0704090）资助。

通讯作者: 周志刚,副研究员,博士,硕士生导师,从事水产微生物工程及水产动物营养与饲料研究。Tel:010-

82106073；E-mail:zhou_zg@msn.com
作者简介: 何夙旭,硕士研究生,主要从事水产动物消化道分子生态学研究。
作者Email:

参考文献：

本刊中的类似文章

文章评论

反馈人		邮箱地址	
反馈标题		验证码	2093