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研究报告

南海底层鱼突额鹦嘴鱼Scarus ovifrons Temminck et Schlegel | 1846肠道产酶微生物研究 黄光祥[1,2] 周志刚[2] 何夙旭[2] 邵娜[2] 石鹏君[2] 刘玉春[2] 姚斌[2]

[1]华中农业大学水产学院,武汉430074 [2]中国农业科学院饲料研究所,北京100081 摘要:

通过不同培养基对南海底层鱼突额鹦嘴鱼ScantsovifrousTemmincketSchlegel, 1846肠道微生物进行分离与 16S、18SrDNA鉴定,并构建系统发育树,然后结合选择性培养基进行产蛋白酶、甘露聚糖酶、木聚糖酶、纤维素酶、淀粉酶等微生物的筛选。结果表明,从突额鹦嘴鱼肠道分离纯化出23株微生物,其中14株产酶,以产蛋白酶与淀粉酶为主,部分产纤维素酶、甘露聚糖酶、木聚糖酶;产酶微生物主要为Bacillussp.;分离出3株菌(H-16、J-13与Y-13G)其16S、18SrDNA序列与模式种相似度低于97%,为潜在的新种。研究表明,南海底层鱼突额鹦嘴鱼肠道含有大量产酶微生物。

关键词: 突额鹦嘴鱼Scarus ovifrons Temminck et Schlegel 1846 肠道 产酶微生物

Studies on the Intestinal Enzyme-Producing Microflora in |Typical Marine Finfish Scarus ovifrons Temminck et |Schlegel, 1846 at Sublayer of the South China Sea

 $\label{thm:huang-sum} \mbox{HUANG } \mbox{|Guang-xiang| ZHOU Zhi-gang, HE Su-xu, SHAO Na, |SHI Peng-jun, LIU Yu-ehun| YAO Bin$

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Abstract:

The intestinal microflora in Scants ovifrons Temminck et Schlegel, 1846 at suhlayer of the South China Sea were isolated and identified by 16S, 18S rDNA sequences as well as the neighbour-joining phylogenetic trees. And the enzyme-producing microflora such as protein enzyme, mannanase, xylanase, cellulose enzyme, and amylase were screened by selective culture medium. The results showed that 23 isolates of intestinal microflora were identified, in which 14 isolates were the enzyme-producing microflora and mainly excreted protein enzyme and partly excreted cellulose enzyme, mannanase and xylanase; theenzyme-producing microflora were mainly Bacillus sp.; the isolate of H-16, J-13 or Y-13G from the intestine of Scarus ovifrons Temminck et Schlegel, 1846 might represent new microflora due to the less than 97% similarity after the blast of its 16S or 18S rDNA sequence. The results indicated that rich enzyme-producing microflora existed in the intestine of the marine finfish Scarus ovifrons Temminck et Schlegel, 1846 at sublayer of the South China Sea.

Keywords: Scarus ovifrons Temminck et Schlegel, 1846 intestine enzyme-producing microflora 收稿日期 2007-08-29 修回日期 2007-09-12 网络版发布日期

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