

# 利用肠道菌群的分布和16S DNA序列研究鲤科肠道菌系统演化关系 Phylogenetic Analysis of Intestinal Bacterium Using the Distribution of Intestinal Bacterium in Cyprinidate Fishes and 16S DNA Sequence Data Set

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**摘要** 肠道微生物与寄主具有复杂的、多方面的相互依存效应,这种依存效应所产生的共生关系或协同进化关系既可反映寄主间的系统演化关系,也可显示肠道微生物间的系统演化关系,共生关系或协同进化关系是由于寄主与肠道微生物两者之间存在着相互自然选择作用所形成的,在长期的进化历程中逐步发生的共生关系信息很可能被记录在DNA序列中。本文通过检测鲤鱼科8种鱼中9种肠道菌群的分布含量对这9种菌群进行分析,且利用从GenBank调取这9种肠道细菌菌属的43个种或亚种的16S DNA序列的构建NJ树和MP树,将这6个科9个属43个种或亚种分为革兰氏阴性和革兰氏阳性两大类群(一级分枝)。在这两大类群中,又以科为单位分为6个亚类群(二级分枝),而肠杆菌科中则以属为单位分为4个小类群(三级分枝),此外球状菌与杆状菌也能截然分开。将16S DNA的NJ树隐去所有的种,以属为单位所得到的以分枝形式的无根树在拓扑结构上与菌群分布含量(寄主范围)所构建的无根树相近,但芽孢杆菌在两种无根树的位置中有较大的差异。如果提高检测水平,扩大所检测的寄主对象,这种差异有可能消除。

**Abstract:** There is a complex- and multi-effect for interdependent survival between intestinal-microorganisms and hosts. The symbiosis or coevolution that results from this effect for interdependent survival is used to reveal the phylogenies of hosts as well as intestinal microorganisms. The symbiosis or coevolution between intestinal microorganisms and hosts has been generated by interactive natural selection occurred between them. The symbiosis information that has been formed by interactive natural selection during a long evolutionary process must be recorded in DNA sequences. According to this point of view, we analyzed the phylogeny of 9 intestinal bacteria genera using their contents in intestines of 8 Cyprinidate species. At the same time, we fetched the 16S rRNA gene DNA sequences of 43 intestinal bacteria species being included in these nine genera of six intestinal families from GeneBank and constructed phylogenetic trees by NJ and MP methods. The NJ tree and MP tree have the same topologic configuration and are identical with the classical phylogenetic tree. Both the trees of 16S rRNA gene separated 43 bacteria species into gram-negative bacteria group and the gram-positive bacteria group, which are the first branches. Each of the first branches (groups) made again 6 subbranches (subgroups) where each subbranch is a family. Especially, the subbranch (subgroup) of enterobacteriaceae made again four small branches as genus taxon. This tree also shows that bacilliform bacterium is distinct from each other in the NJ and MP trees. After all species on the tree are merged, the topological configuration of the unrooted tree of 16S gene is closed to that of the host range unrooted tree. However, the position of bacillus is greatly changed on both the unrooted trees. The difference can be found if we increase the examination level and extend the hosts examed.

**关键词** [肠道细菌](#) [16S DNA序列](#) [系统演化](#) **Key words** [intestinal bacteria](#) [16S DNA sequence](#) [phylogeny](#)

分类号

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## Abstract

## Key words

