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Microbial communities in the intestinal tracts of coastal fish

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It is found by the plate count method that the intestinal tracts of marine fish are dominantly colonized by members of genus *Vibrio*. However, Sugita et al. (2005) reported that the direct counts of intestinal contents from coastal fish ranged from 10^9 to 10^{10} cells/g, regardless of fish specimens and food habitat, while the viable counts ranged from 10^3 to 10^9 CFU/g. This finding demonstrated that the culturability of intestinal bacteria is different among fish specimens. This study therefore examined the microbial communities of the intestinal tracts of coastal fish using the clone library method.

Coastal fish were collected using conventional line fishing gears at the Tanoura Inlet in Shimoda, Shizuoka, Japan. The DNA was extracted from each intestinal sample of fish and 16S rDNAs were amplified by PCR to construct clone libraries. The 16S rDNA sequence of each clone was analyzed by a model ABI 3130*xl* Genetic Analyzer. The similarity in 16S rDNA sequences between a given isolate and other organisms was compared with all sequence data in the DDBJ/EMBL/GenBank databases using the BLAST algorithm and identification to species was confirmed by phylogenetic analysis using Clustal W software package. Direct counts were determined by the epifluorescent staining method after fixation with Lugol iodine solutions.

Direct counts of the intestinal contents from the file fish *Stephanolepis cirrhifer* and black rockfish *Sebastes inermis* were 2.2×10^9 and 2.7×10^9 cells/g, respectively. A total of 59 and 58 clones constructed from the file fish and black rockfish, respectively, were mainly composed of genera *Pseudomonas*, *Propionibacterium*, *Sphingomonas*, *Methylobacterium*, *Haemophilus* and *Moraxella*, which have not yet been isolated from coastal fish by the plate count method. Members of Vibrionaceae were not detected in both clone libraries. Microbial communities in the intestinal tracts of other coastal fish are in progress.