Supplementary Methods and Materials

Coral 18S rRNA gene cloning, sequencing and phylogeny analysis

Briefly, the 18S rRNA gene was PCR amplified with the primers 18S1 (5'-AACCTGGTTGATCCTGCCA-3') and 18S2 (5'-TGCAGGTTCACCTACAGAA-3'), as described by Borchiellini et al. (1). The PCR products (~ 1.8k bp) were then purified and ligated into a pCR2.1 TOPO vector (Invitrogen, USA) according to the manufacturer's protocol. Sequences for both directions of the insert were obtained using an ABI sequencing machine (ABI3730). Multi-alignment between the sequences and references was conducted with the ClustalW program, and a bootstrap phylogenetic tree (Fig. S1) was then generated with the MEGA software using the neighbor-joining method (2). The 18S rRNA sequences were deposited into GenBank with the accession number HM067604-HM067613.

TRFLP analysis of the microbial communities

The primers 26F (5'-AGAGTTTGATCCTGGCTCAG-3') and 1055R (5'-CACGAGCTGACGACAGCCAT-3'), corresponding to *Escherichia coli* 16S rRNA gene positions 26-45 and 1055-1074, respectively, were used for the PCR amplification. Amplification was conducted with a Bio-Rad thermal cycler using the following cycling conditions: initial denaturation at 94°C for 5 min; 26 cycles of 94°C

for 45 sec, 55°C for 45 sec, and 72°C for 1 min; and final extension for 6 min at 72°C. About 500 ng of PCR products were digested with 10 U of the restriction enzyme *Msp* I at 37°C for 6 h, ethanol was precipitated and re-dissolved in 10 µl of double distilled water (ddH_2O). Ten microliters of purified products were mixed with 0.5 µl of an internal size standard (ET-550R; Amersham Biosciences, NJ, USA), denatured at 95°C for 2 min, snap cooled on ice, and subjected to a MegaBACE genetic analyzer (Amersham Biosciences, NJ, USA) operating in the genotyping mode to generate the chromatography. After electrophoresis, the sizes of the fluorescently labeled terminal restriction fragments (TRFs) were determined by comparison with the size standard using a Genetic Profiler (Amersham Biosciences, NJ, USA). TRFs that were greater than 35 and less than 900 bp were excluded from the statistical analysis to screen out background noise and inaccurate size determination.

References

1. **Borchiellini C, Manuel M, Alivon E, Boury-Esnault N, Vacelet V, Le Parco Y**. 2001. Sponge paraphyly and the origin of Metazoa. J. Evol. Biol. **14(1)**:171-179.
2. **Kumar S, Dudley J, Nei M, Tamura K.** 2008. MEGA: a biologist-centric software for evolutionary analysis of DNA and protein sequences. Briefings in Bioinformatics **9**:299-306.