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The AHL-producing bacteria in the intestinal tracts of ayu *Plecoglossus altivelis*

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Quorum sensing is known to be a mechanism for controlling gene expression of many pathogenic factors in response to an expanding bacterial population. In many Gram-negative bacteria, the diffusible quorum sensing signal molecule is a member of the *N*-acylhomoserine lactone (AHL) family. Therefore, the present study was carried out to examine the distribution of AHL-producing bacteria in the intestinal tracts of ayu *Plecoglossus altivelis* for the better understanding of ecology of the fish intestinal bacteria.

The intestinal contents of cultured specimens of ayu were serially diluted and plated onto TS, MacConkey, GAM and FM agar media. The TS and MacConkey agars were incubated under aerobic conditions and the GAM and FM agars were incubated under anaerobic conditions, both at 20°C for five days. About 20 colonies were isolated from each agar plate and examined for the production of AHL using *Chromobacterium violaceum* CV026. Moreover, the isolated bacteria were subjected to the identification to species based on the 16S rDNA nucleotide sequences, which were 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 the identification to species was confirmed by phylogenetic analysis using the Clustal W software package.

Total viable counts were 5.9×10^5-1.3×10^9 CFU/g in the ayu intestines, 4.2×10^4 CFU/mL in the rearing water and 8.9×10^4 CFU/g in the pelleted diets. The density of AHL-producers were 7.2×10^2-2.8×10^8 CFU/g in the ayu intestines, 1.3×10^4 CFU/mL in the rearing water and $<4.5\times10^3$ CFU/g in the pelleted diets. Major AHL-producers derived from ayu were identified as *Aeromonas hydrophila*. In addition, the genera *Plesiomonas*, *Citrobacter*, *Vibrio*, *Shewanella* and *Cetobacterium* were isolated from the ayu intestines as major components.