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# GENOME SEQUENCING AND MAPPING OF SEX-DETERMINING LOCUS IN AYU *PLECOGLOSSUS ALTIVELIS*

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## Abstract

The ayu/sweetfish *Plecoglossus altivelis*, belonging to the family Plecoglossidae, has a 1-year lifespan and an XX/XY sex-determination system. The ayu is economically important for the food industry and recreational fishing in Japan. However, few genomic resources of the ayu are available. In this study, we produced the draft genome sequence of ayu by using a whole genome shotgun method based on next-generation sequencing and identified sex-associated loci by genotyping-by-sequencing of a wild population. Genomic DNA was extracted from tissue of a male ayu reared at Tokyo University of Marine Science and Technology. Short-read DNA sequencing was carried out on the Illumina HiSeq2000 platform with 300 bp, 3 kb, 8 kb, 20 kb, and 40 kb libraries. Genomic DNA was also sequenced on a PacBio RSII for long-read sequencing. Short reads were assembled *de novo* using Platanus Genome Assembler. PacBio long reads were used for gap filling and to upgrade short-read assembly using the PBJelly pipeline. To identify sex-associated loci, 46 individuals (23 males and 23 females) from a wild population were genotyped by genotyping-by-sequencing. Approximately 250× coverage for short reads and 15× coverage for long reads (estimated genome size of ayu: 450 Mb) were obtained by shotgun sequencing. Assembly of Illumina and PacBio sequencing reads yielded 1,202 scaffolds longer than 5,000 bp. The longest scaffold was 12 Mb, and the assembly had an N50 value of 2.9 Mb. The total size of assembly was 460 Mb, which coincides well with the estimated genome size of ayu. An association analysis revealed that male-associated single nucleotide polymorphisms were located in four scaffolds that may represent the putative sex-determining locus. Our draft genome sequence is expected to accelerate the establishment of economically valued strains of ayu through genomic breeding.

*Key words: sex-determining locus, sex determination, whole genome sequencing, ayu,*

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