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## Genome-wide association study using single marker analysis and Bayesian methods for the gonadosomatic index in the large yellow croaker

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### Abstract

The gonadosomatic index (GSI) is an economically important trait in the large yellow croaker (*Larimichthys crocea*), a mariculture fish species with high commercial value in Southeast China. However, progress in the genetic research on this species is relatively lacking. To identify the relevant genes and chromosome regions associated with the GSI, we performed a genome-wide association study (GWAS) on a population of 500 individuals (237 males and 263 females), using single marker analysis and Bayesian methods. The genotyping-by-sequencing method was used to construct the libraries, and 29,748 SNPs were subsequently found in the genome of *Larimichthys crocea*. A total of six different SNPs, located on LG3, LG6, LG8, and LG16, were determined to be significantly associated with the GSI. Among them, only two SNPs were found by both GWAS methods. By integrating the results of two GWAS methods with the biological functions of the genes, six candidate genes (viz., *FZD3*, *DDX4*, *EDC3*, *CITED3*, *SOX9-b*, and *LOC106602108*) were revealed to be associated with the GSI in the large yellow croaker. These functional genes are involved in gonadal development or gonadogenesis, providing the basis for further study on genetic mechanisms and marker-assisted selection in this fish species. In this study, we found that the combination of single marker analysis and Bayesian methods could identify more SNP loci associated with the phenotypes. Thus, we suggest performing these two methods simultaneously in GWAS.

**Keywords:** Large yellow croaker, Genotyping-By-Sequencing, Genome-wide association study, Single marker analysis, Bayesian method

### 1. Introduction

The large yellow croaker (*Larimichthys crocea*) is one of the most important marine fish species with high commercial value in Southeast China and East Asia (Liu, et al., 2008). Nevertheless, an enormous loss

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