

# GENOME-WIDE ASSOCIATION STUDY (GWAS) FOR DETECTING GENETIC VARIANTS ASSOCIATED WITH GROWTH TRAITS IN OLIVE FLOUNDER (*Paralichthys olivaceus*)

Julan Kim\*, Jong-Won Park, Minhwan Jeong, Dain Lee, Hyejin Kim, Chaehyeon Lim and Hyun-Chul Kim  
Genetics and Breeding Research Center, National Institute of Fisheries Science, Geoje 53334, Republic of Korea

## Abstract

The olive flounder (*Paralichthys olivaceus*) is a commercially important fish species in East Asian countries, with most productions coming from South Korea. Selective breeding has been applied for about 20 years to improve growth performance of olive flounder, which is one of the most important traits in aquaculture breeding programs and productivity. This study aimed to detect genetic factors associated with growth traits (body weight and total length) through Genome-Wide Association Study (GWAS), incorporating mixed linear models, Bayesian model and simple regression model.

National Institute of Fisheries Science in Korea initiated family-based breeding programs to enhance growth traits of olive flounder, and selection has been conducted for 8 generations since then. Growth traits (body weight and total length) were measured at 18 months in the 8th generation, consisting of 217 families, and the phenotypic distribution of growth at 18 months were analyzed.

To detect single nucleotide polymorphisms (SNPs) associated with growth traits, the individual genotypes of 3,223 fish measured for body weight and total length at 18 months were analyzed using a 120K SNP chip specific to olive flounder, which is a customized Affymetrix Axiom Genotyping Array. As a result, 69 SNPs associated with body weight and 85 SNPs associated with total length were identified using mixed linear model, and the detected SNPs using Bayesian model were shown. The lambda values were found to be 0.947 and 0.964 in the mixed linear model. For both body weight and total length traits, due to overestimation, the simple regression model was shown to be inappropriate for identifying genetic variants associated with growth traits of olive flounder. Our results suggest that genetic variants associated with growth traits can be discussed in the context of their potential role in underpinning genetic variation in growth traits, and these detected SNPs may contribute to promoting genomic selection in breeding programs of olive flounder.

## Results

### Family-based selective breeding

- F1 2005
- F2 2007
- F3 2009
- F4 2011
- F5 2012
- F6 2015
- F7 2017
- F8 2019
- F9 2021
- F9 2024

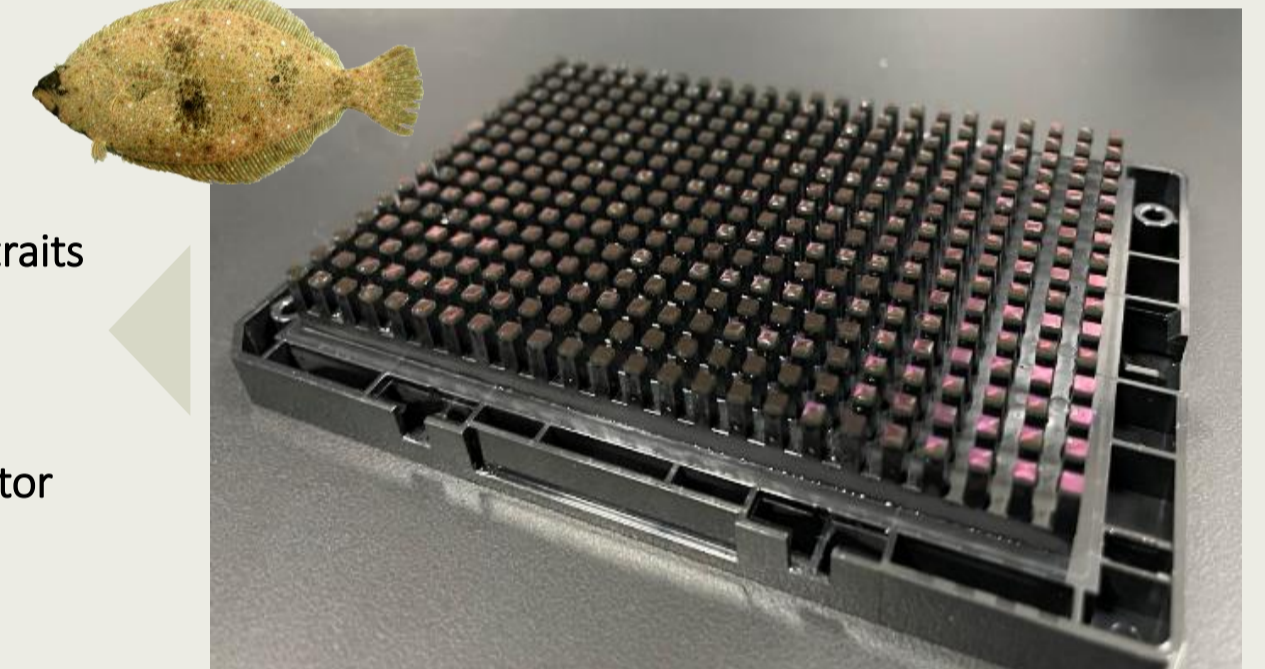


### Reference population for GS

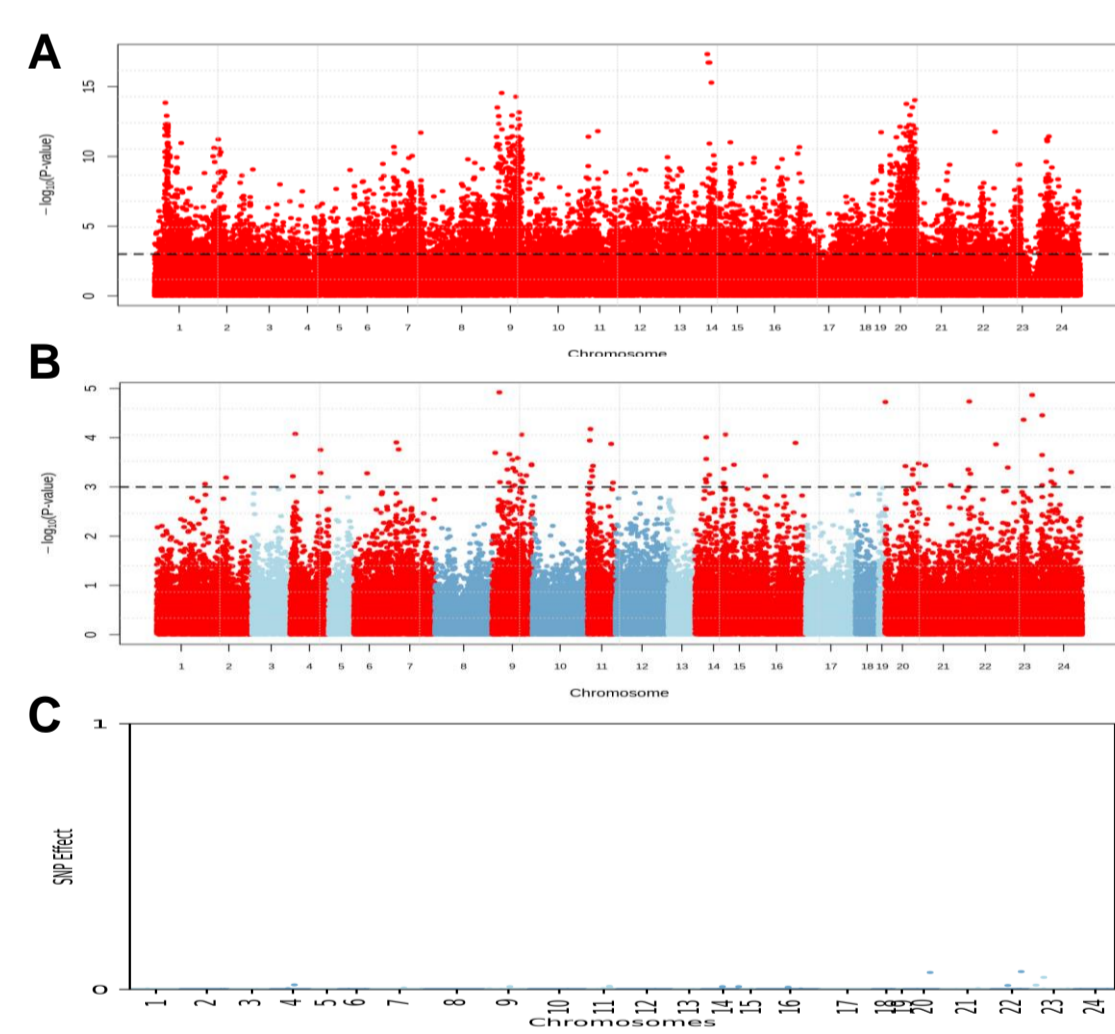


- Pedigree
- Phenotype (Fast-growing traits at 18 months)
  - Body weight
  - Total length
  - Condition factor
- Genotype

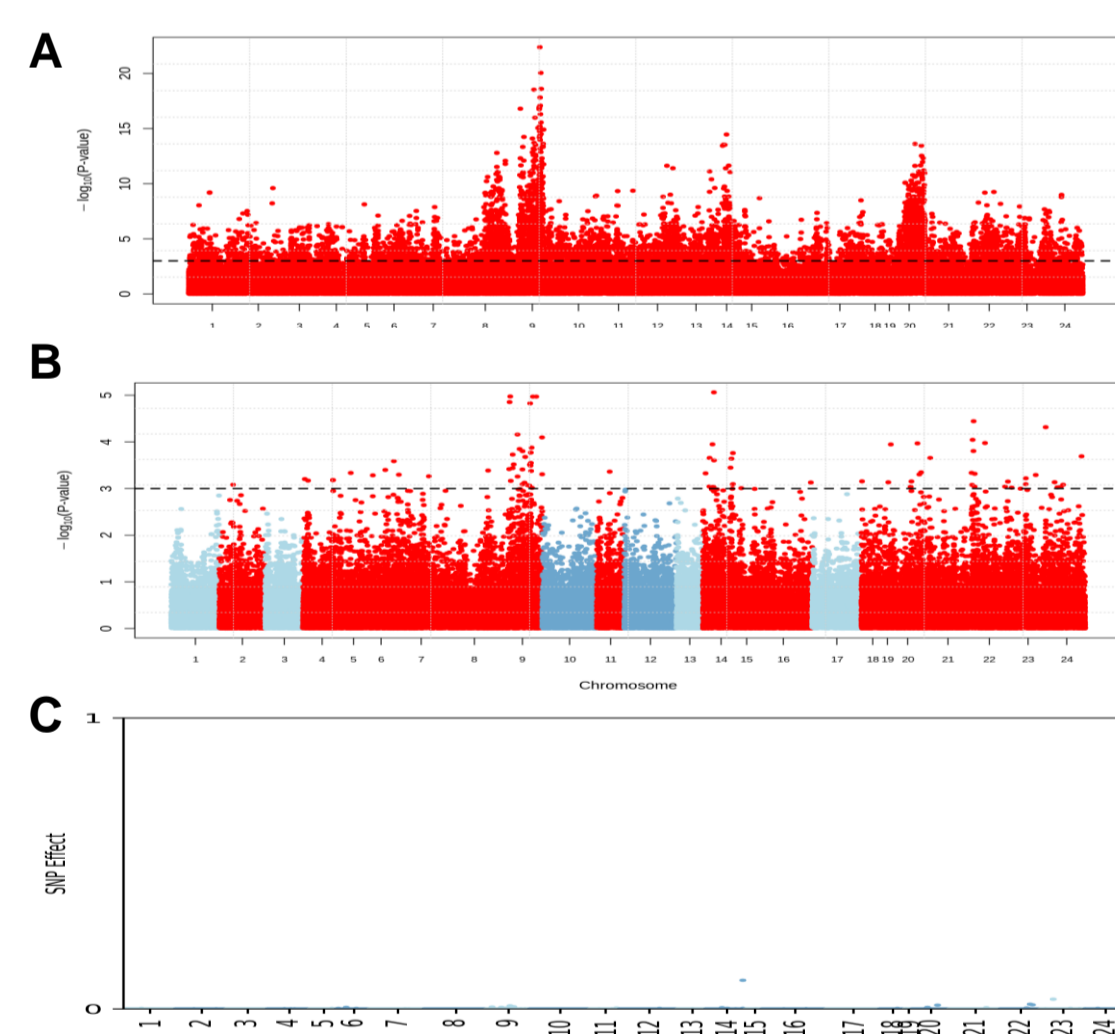
### High-density 120K SNP chip



## Genome-wide association study(GWAS) for detecting SNPs associated with fast-growing traits



◀GWAS of fast-growing trait (body weight at 18 months) of olive flounder. A, simple regression model. B, mixed linear model. The threshold for p-value was set at 0.001. C, Bayesian model. Body weight were assessed at 18 months and genotype data was analyzed using 120K SNP chip. Quality control of genotype data was conducted using plink 1.9 software, wherein SNPs with minor allele frequency (MAF) less than 1%, Hardy-Weinberg equilibrium (HWE) less than  $10^{-4}$ , and call rate less than 90 were filtered out.



◀GWAS of fast-growing trait (total length at 18 months) of olive flounder. A, simple regression model. B, mixed linear model. The threshold for p-value was set at 0.001. C, Bayesian model. Total length were assessed at 18 months and genotype data was analyzed using 120K SNP chip. Quality control of genotype data was conducted using plink 1.9 software, wherein SNPs with minor allele frequency (MAF) less than 1%, Hardy-Weinberg equilibrium (HWE) less than  $10^{-4}$ , and call rate less than 90 were filtered out.

## Conclusions & Future work

- We established reference population among 8<sup>th</sup> generation of olive flounder for fast-growing traits for GS(genomic selection).
- Genotype data was analyzed using customized 120K SNP chip of olive flounder.
- GWAS was performed to detect genetic variants associated with fast-growing traits (body weight and total length at 18 months).
- SNPs associated with fast-growing traits might serve as promising markers for genomic selection for improving fast-growing traits.
- Multiple-traits selective breeding of olive flounder will be performed with genomic selection by establishing disease-resistant reference population as well as fast-growing reference population.

## ◆ Acknowledgement ◆

This work was supported by the National Institute of Fisheries Science, Ministry of Oceans and Fisheries, Korea (R2024032).



Ministry of Oceans and Fisheries  
National Institute of Fisheries Science  
Genetics and Breeding Research Center

