

Optimization of an Asian seabass genetic improvement program: Genomic selection for growth performance and harvest traits

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ABSTRACT:

Asian seabass, also known as barramundi (*Lates calcarifer*), is widely distributed throughout the tropical regions of the western Pacific and Indian oceans. In Thailand, Asian seabass is a significant fishery commodity, contributing 43% of 107,800 tons of total production among Southeast Asian countries (FAO, 2021). Because it is a large sized fish with a long growing period (10 to 15 months) and a generation interval of 3 to 4 years, genomic selection provides an efficient strategy to improve growth performance and to accelerate the rate of genetic progress. However, the high cost of genotyping animals using high-density SNP arrays may prevent its application in small-sized seabass breeding programs. In this study, we evaluated the utility of low-density SNPs for genomic prediction of weight and fillet yields. A total of 1,047 fish were genotyped for 29,521 single nucleotide polymorphisms. Genome-wide association studies (GWAS) using the weighted genomic best linear unbiased prediction (wGBLUP) procedure revealed polygenic nature of harvest traits. GBLUP and BayesB were implemented using five sets of informative SNPs specific to each trait and five sets of evenly-spaced markers at the same density. Prediction accuracies were evaluated via five-fold cross-validation with five iterations. Using trait-specific panels with the largest effects of 500 to 2,000 SNPs under GBLUP, the prediction accuracies increased substantially for all traits relative to those from using full SNPs, i.e., by ~70% for body weight (BW), by ~100% for standard length (SL), by ~97% for fillet weight (FW) and by ~660% for fillet yield (FY). A similar trend in prediction accuracy was observed from BayesB. Improvement in accuracy was marginal for evenly-spaced markers compared to full SNPs, i.e., by ~25% for BW, SL, FW and by ~30% for FY. Close relationship between training and validation fish appeared to be a major contributing factor to the favorable performance of prediction models for the within-family selection scheme in our seabass genetic improvement program.

KEYWORDS:

Fillet yield; GBLUP; GWAS; prediction accuracy