

Past, present and future stories in genetic improvement of commercially important penaeid shrimp in Thailand: From population genetics to genomic studies

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ABSTRACT:

Progress in genetic improvement of penaeid shrimp has been slow because knowledge on mechanisms controlling their traits relative to production parameters is lacking. Selection for increased juvenile growth rates and disease resistance is feasible in shrimp. Breeding stocks with high disease-resistance and relatively high growth rates are of particular interest to the shrimp industry. Here, genetic improvement of black tiger shrimp *Penaeus monodon*, Pacific white shrimp *Litopenaeus vannamei* and banana shrimp *Fenneropenaeus merguensis* is discussed. Genetic diversity and population differentiation of these species were performed and applied for selection of appropriate stocks for the establishment of their breeding programs. Single nucleotide polymorphisms (SNPs) were used for analysis of association between SNP genotypes and growth parameters of *P. monodon*. Several growth-associated SNPs were identified and can be used for selection of fast growing shrimp. Molecular breeding offers more accurate selection than traditional (phenotype-based) breeding. Marker-assisted selection (MAS) can be used for identification of quantitative trait loci (QTL) with large effects on interesting phenotypes. In addition, genome-wide association studies (GWAS) for association analysis, and genomic selection (GS) for estimation of genome-wide molecular breeding values are applied to study complex traits such as growth and disease resistance in *L. vannamei* and *F. merguensis*. Our on-going breeding program of *L. vannamei* aims to generate ammonia-tolerant shrimp that also show high growth. The stocks obtained will be tested for disease resistance to major pathogens (e.g., WSSV and/or EHP) in the future. In addition, GWAS and GS will also be applied for genetic selection of *F. merguensis*. Families showing high and low estimated breeding values (EBVs) from conventional selection will be analyzed using genotyping by sequencing (GBS), GWAS and QTL mapping, genomic EBVs will be applied for selection of high growth with improved WSSV resistance of *F. merguensis*.