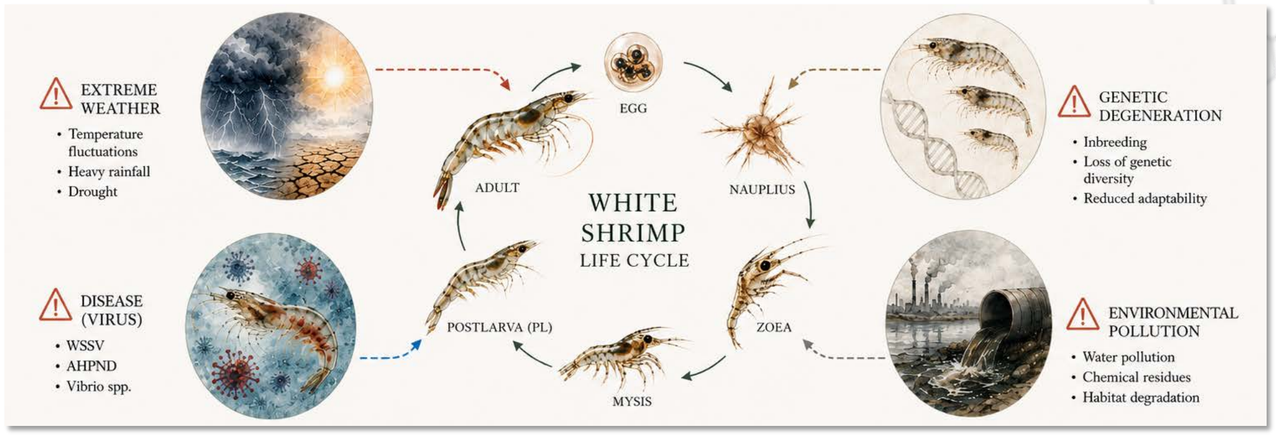
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GENOMIC IDENTIFICATION OF GROWTH AND IMMUNITY-RELATED SNP MARKERS IN WHITE SHRIMP MUSCLE TISSUE FOR MARKER-ASSISTED BREEDING

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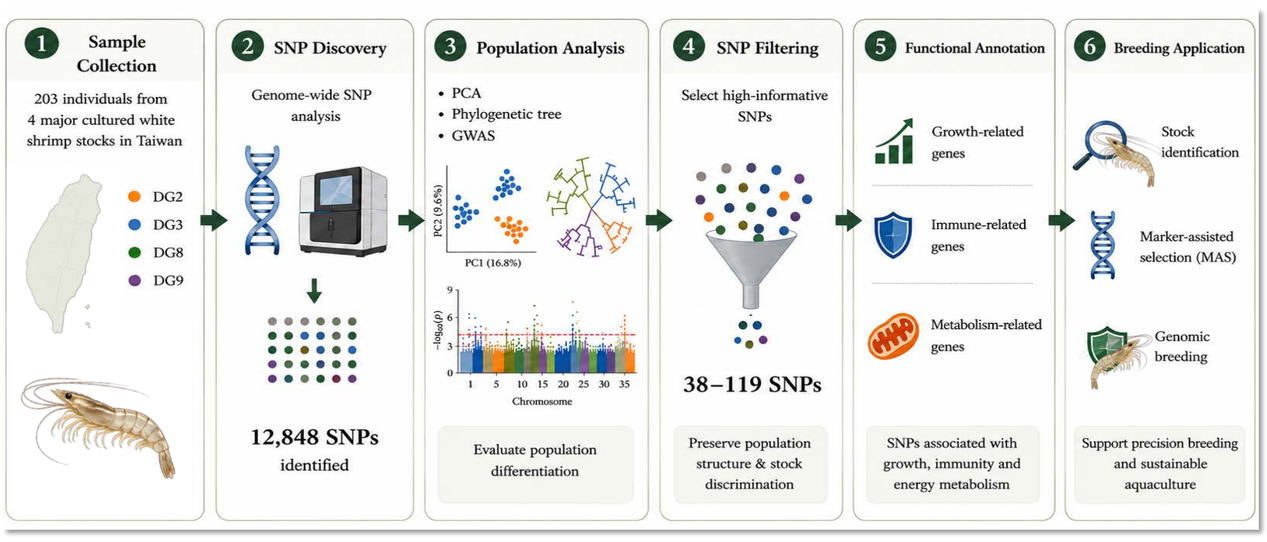
Background



Abstract

- White shrimp (*Litopenaeus vannamei*) is one of the most important aquaculture species worldwide.
- This study investigated genomic differences among four major cultured white shrimp stocks in Taiwan.
- SNP analysis, PCA, and GWAS were conducted to identify high-informative SNP markers.
- A reduced panel of 38–119 SNPs successfully preserved population structure and stock discrimination.
- These SNPs were associated with growth, immune response, and energy metabolism.
- The developed SNP marker system shows strong potential for stock identification and marker-assisted selection (MAS).

Experimental workflow



Result

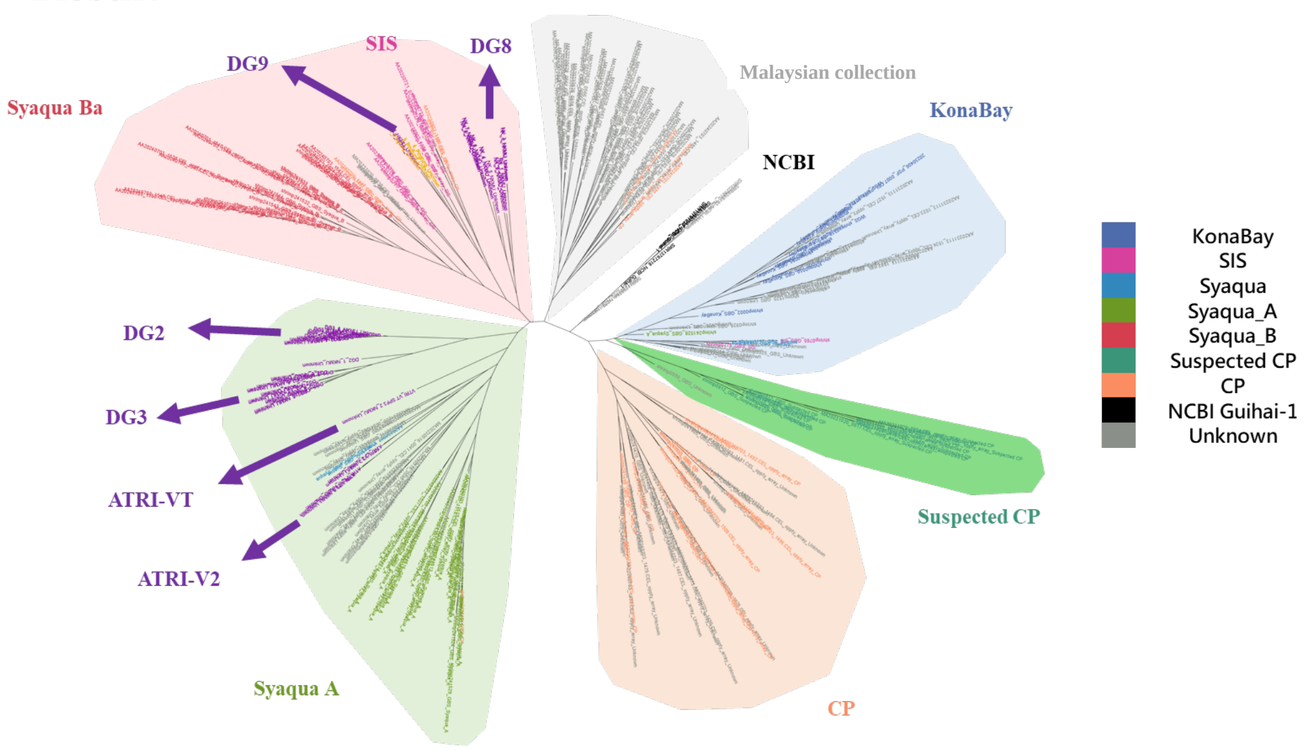


Figure 1. Phylogenetic identification of Taiwanese white shrimp populations.
Phylogenetic analysis identified six major genetic clusters among Taiwanese cultured white shrimp populations. DG8 and DG9 were associated with Syaqua_B, whereas DG2 and DG3 clustered with Syaqua_A, indicating diverse broodstock origins.

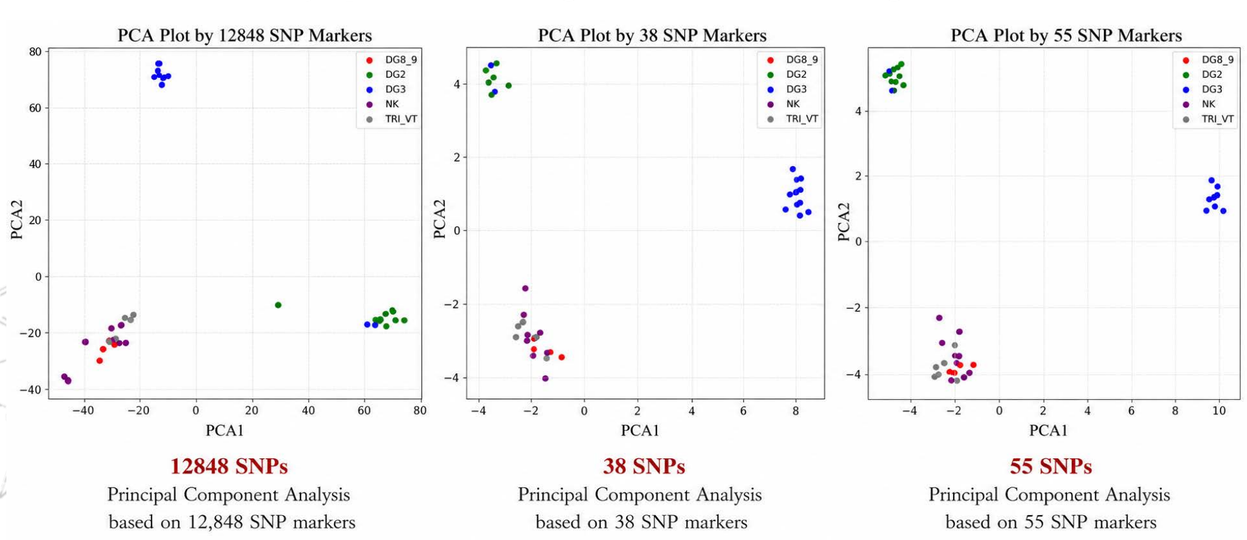


Figure 2. PCA analysis based on different SNP marker sets.
PCA analysis using 12,848 genome-wide SNPs and reduced SNP panels (38 and 55 SNPs) showed that population structure and genetic differentiation among cultured white shrimp populations were clearly preserved. The selected high-informative SNP markers effectively maintained clustering patterns comparable to those obtained using the full genome-wide SNP dataset.

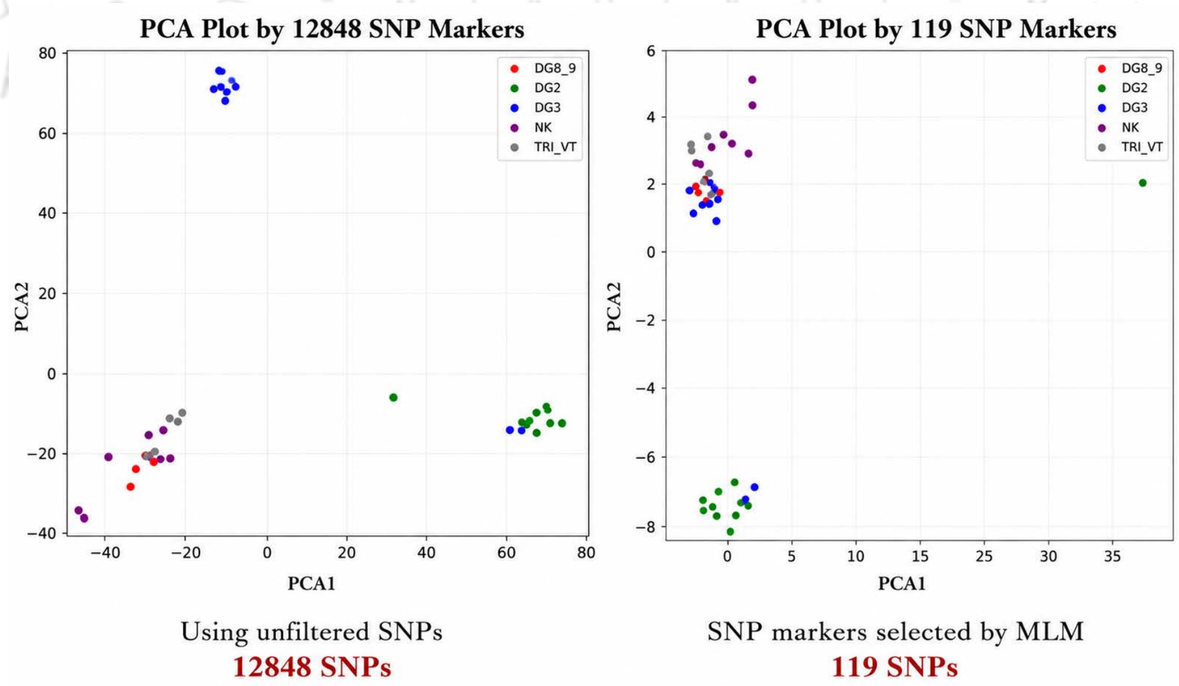


Figure 3. PCA analysis using genome-wide and reduced SNP marker sets.
PCA analysis using 12,848 genome-wide SNPs and a reduced panel of 119 SNP markers showed that the major population structure and genetic differentiation among cultured white shrimp groups were clearly preserved.

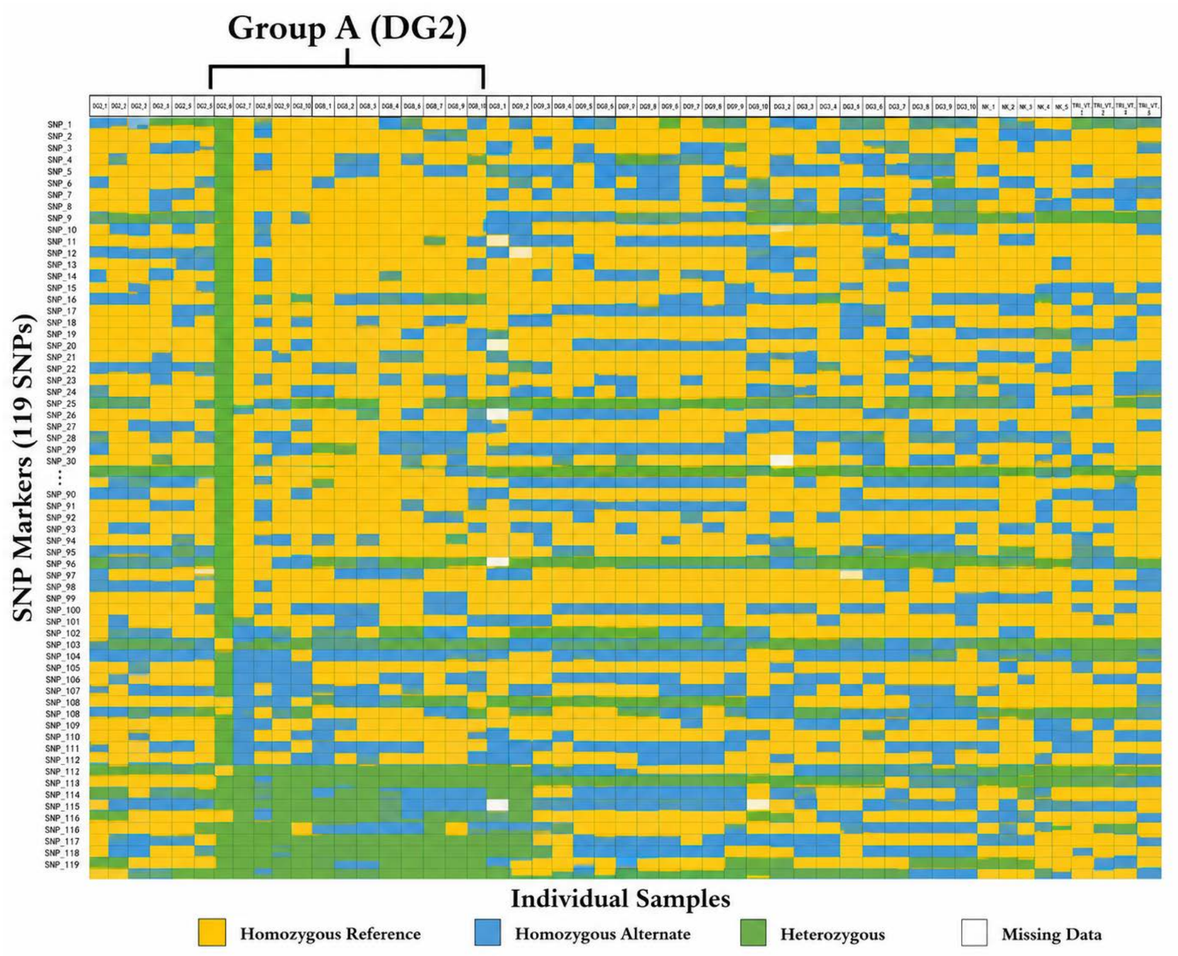


Figure 4. Heatmap analysis of 119 informative SNP markers in cultured white shrimp populations.
Heatmap analysis of 119 informative SNP markers revealed distinct genotype patterns among cultured white shrimp populations, demonstrating clear genetic differentiation and population-specific SNP distributions.

Table 1. Functional pathways of SNP-associated candidate genes

Functional category	Representative genes	Biological significance
Growth regulation	IGF-binding protein, BMP receptor	Growth and developmental regulation
Immune response	EP4 receptor, lymphotoxin inhibitor	Immune activation and disease resistance
Energy metabolism	NAD(P) oxidase, monocarboxylate transporter	Oxidative metabolism and stress adaptation
Neural signaling	glutamate receptor-related genes	Signal transduction and stress response
Cellular regulation	G-protein regulator, Hook homolog 3-like	Intracellular transport and cellular communication

Conclusions

- Genome-wide SNP analysis revealed clear genetic differentiation among cultured white shrimp populations in Taiwan.
- Reduced SNP panels (38–119 SNPs) successfully preserved population structure and stock discrimination.
- Candidate SNP-associated genes were mainly related to growth, immune response, and energy metabolism.
- The developed informative SNP marker system shows strong potential for stock identification and marker-assisted selection (MAS) in white shrimp breeding.