METABOLITE SIGNATURES LINKED TO GROWTH TRAITS IN *Penaeus vannamei*: TOWARD METABOLOMICS-GUIDED SELECTIVE BREEDING

Ya-Li Shiu*, Yu-Shen Wu, Fan-Hua Nan, Chun-Hung Liu
Corresponding Author: Chun-Hung Liu (chliu@mail.npust.edu.tw)
National Pingtung University of Science and Technology, Taiwan
National Taiwan Ocean University , Taiwan

Aquaculture

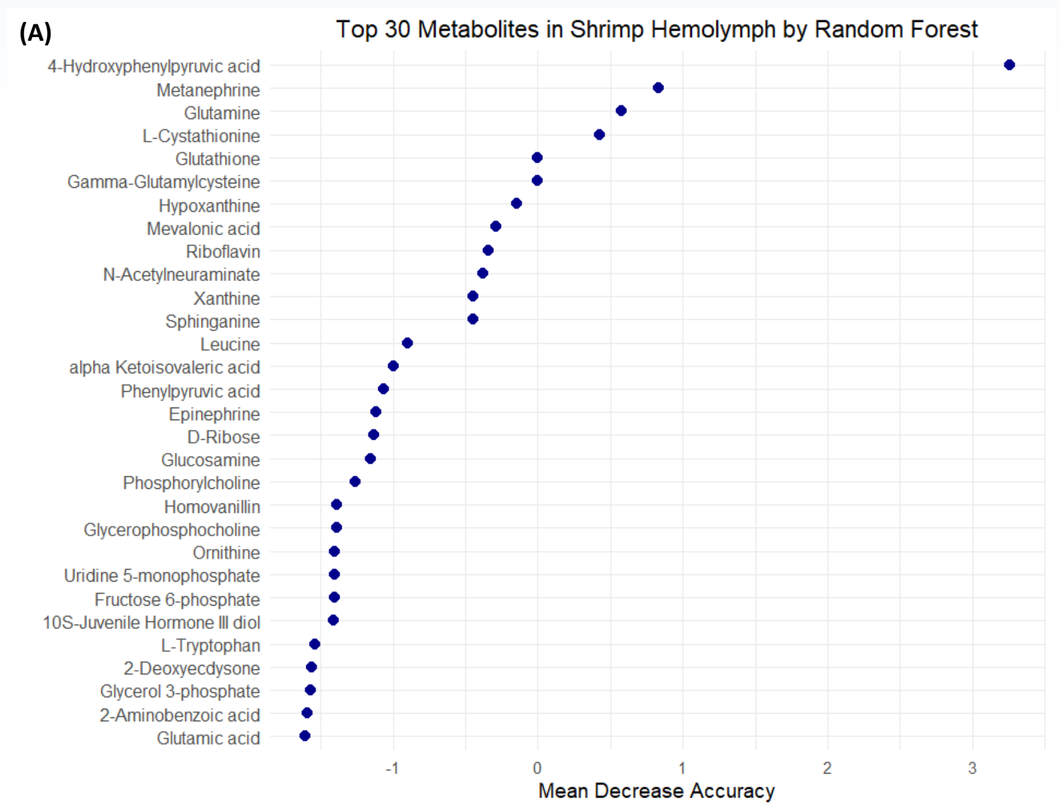
Abstract

This study applied an LC–MS/MS-based metabolomics approach to investigate hemolymph metabolic variation among four strains of white shrimp and to discover potential indicators associated with growth performance. Comparative metabolite profiling of DG2, DG3, DG8, and DG9 revealed strain-dependent metabolic differences, with 11/27, 16/28, 30/73, and 96/11 significantly altered metabolites detected under positive and negative ionization modes, respectively. OPLS-DA analysis demonstrated clear discrimination between fast- and slow-growing individuals, suggesting distinct metabolic phenotypes linked to growth capacity. Functional enrichment based on KEGG pathways indicated significant involvement of amino acid biosynthesis, energy metabolism, purine pathways, and pantothenate and CoA biosynthesis, highlighting changes in nucleotide turnover and cellular energetic status. In addition, growth-related pathways, including arachidonic acid metabolism and insect hormone biosynthesis, were markedly modulated. By integrating machine learning with Random Forest and ROC/AUC evaluation, two metabolites—juvenile hormone III acid and phosphorylcholine—were identified as reliable growth-associated biomarkers in hemolymph. These findings provide novel insights into the metabolic regulation of shrimp growth and support the feasibility of incorporating metabolomics into breeding strategies to enhance aquaculture productivity.

Results

Table 1. Statistics of differential metabolites in hemolymph (fast-growing shrimp vs slow-growing shrimp)

Strains	Positive ion mode			Negative ion mode		
	Up	Down	Total	Up	Down	Total
DG2	10	1	11	0	27	27
DG3	13	3	16	27	1	28
DG8	5	25	30	10	63	73
DG9	58	38	96	5	6	11



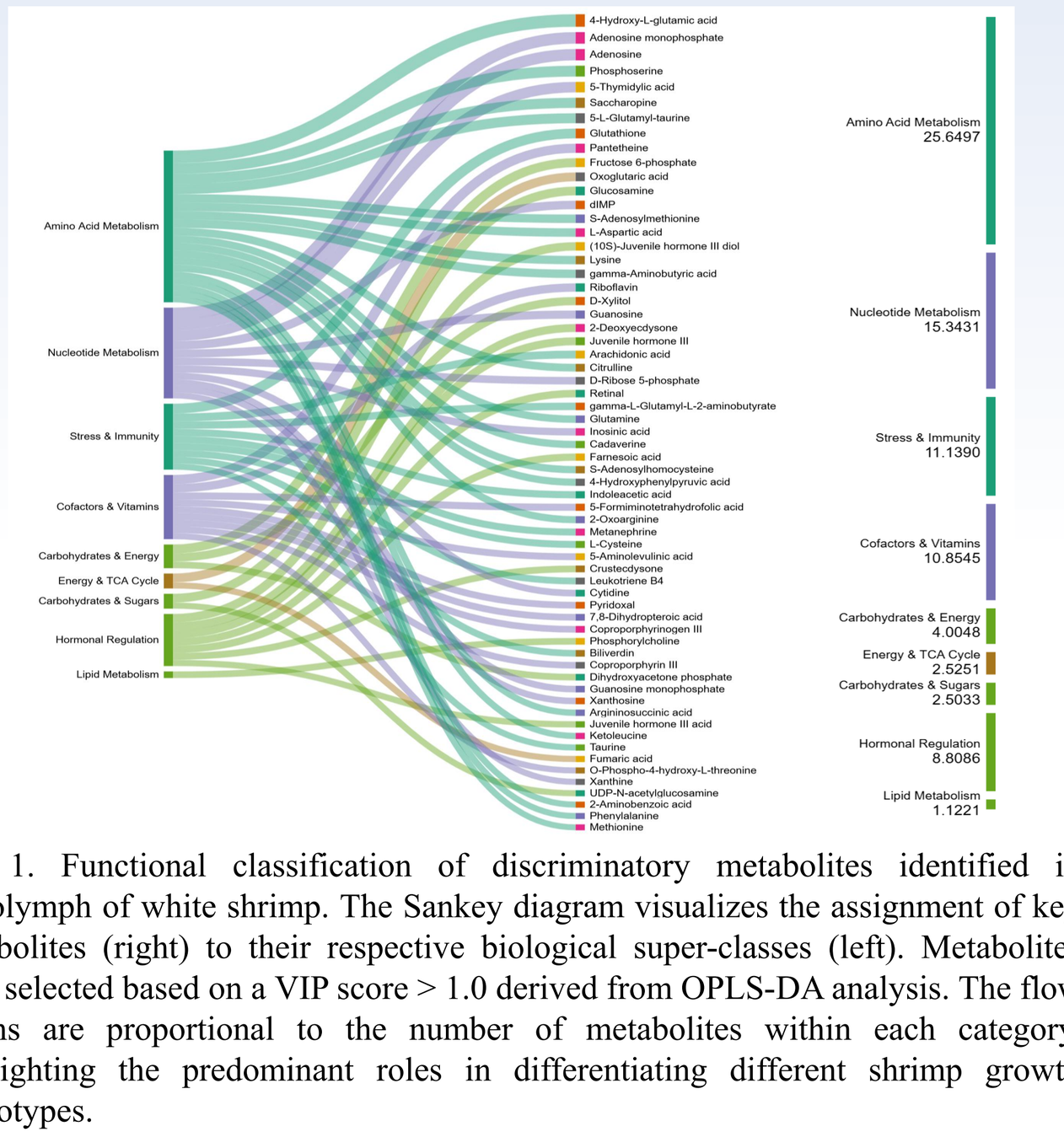
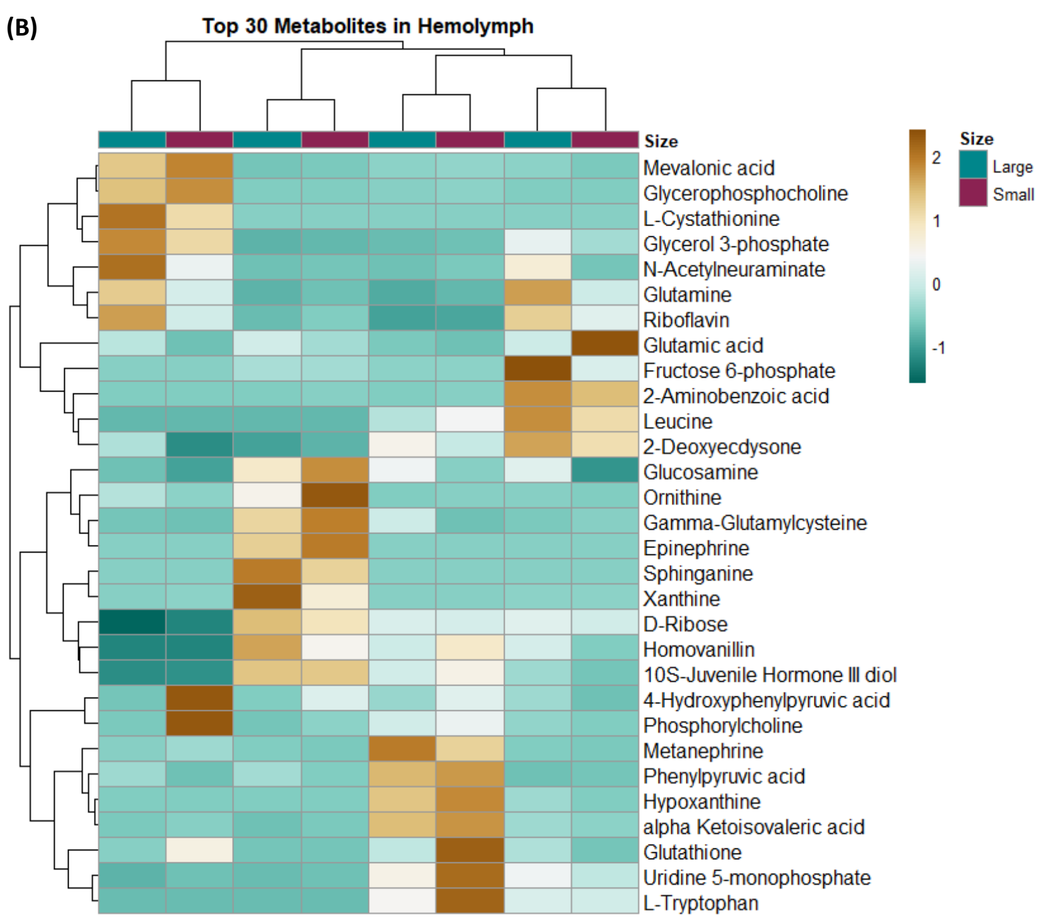
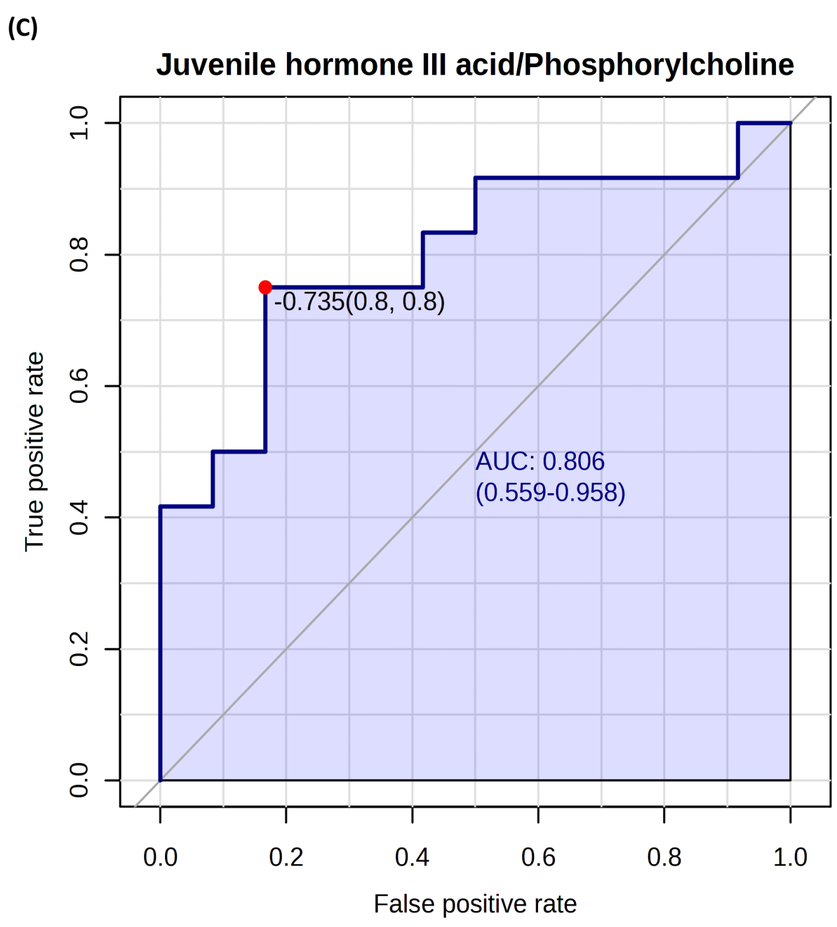


Fig. 1. Functional classification of discriminatory metabolites identified in hemolymph of white shrimp. The Sankey diagram visualizes the assignment of key metabolites (right) to their respective biological super-classes (left). Metabolites were selected based on a VIP score > 1.0 derived from OPLS-DA analysis. The flow widths are proportional to the number of metabolites within each category, highlighting the predominant roles in differentiating different shrimp growth phenotypes.





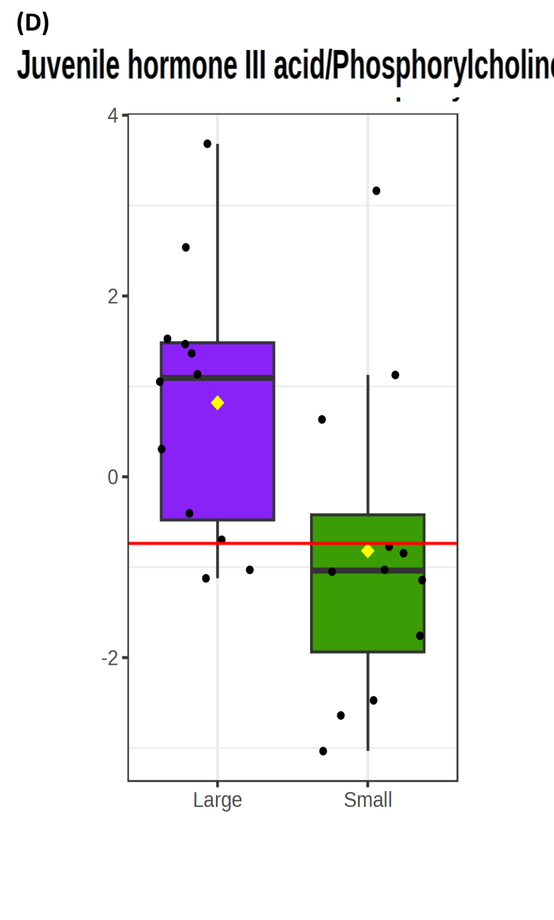


Fig. 2. Integrated metabolomic analysis of hemolymph in different growth phenotypes of four shrimp strains. (A) Random Forest variable importance plot of the top 30 metabolites. (B) Hierarchical clustering heatmap of the top 30 metabolites. (C) ROC curve of Juvenile hormone III acid / Phosphorylcholine ratio. (D) Relative abundance of Juvenile hormone III acid / Phosphorylcholine ratio.

Conclusion

This study demonstrates that hemolymph metabolomic profiling can effectively distinguish growth performance among four white shrimp strains. Distinct metabolic signatures were associated with fast- and slow-growing individuals, highlighting the importance of amino acid metabolism, energy production, and nucleotide turnover in growth regulation. Integrative analysis identified juvenile hormone III acid and phosphorylcholine as robust biomarkers for growth performance, supported by machine learning and ROC validation. These results suggest that metabolomics-based biomarkers have strong potential for application in shrimp selective breeding and productivity improvement in aquaculture systems.