Genome resource-based multi-omics approach in non-model aquatic animals for environmental health assessment

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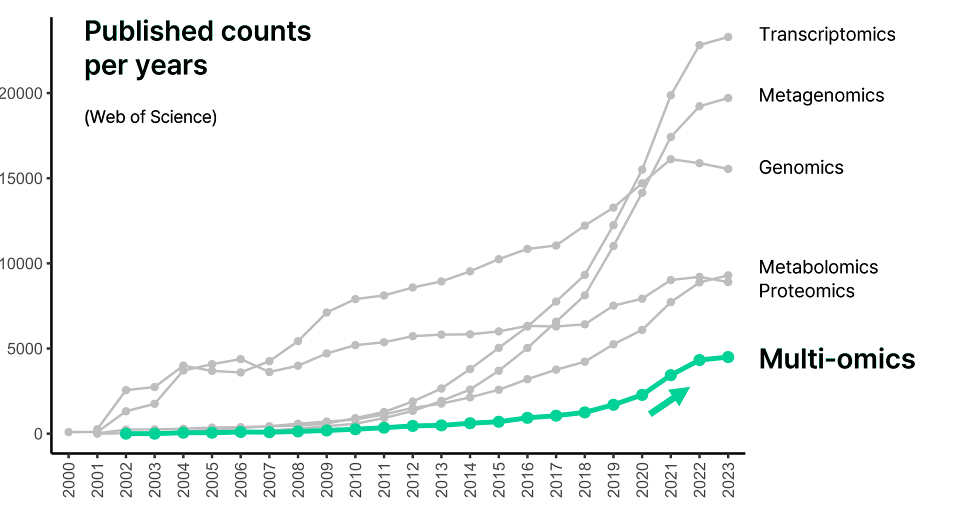
Abstract

In the field of aquatic ecotoxicology, toxicity assessment at molecular level through multi-omics approaches has been primarily conducted in model organisms such as zebrafish and water fleas in laboratory rather than on native species in real-world environments. In this study, we aimed to use a multi-omics platform with non-model domestic species for health assessment by analyzing molecular and biochemical responses. To facilitate omics applications, we established genome database for the swamp shrimp *Neocaridina denticulata* and the pale chub *Zacco platypus*. For the toxicity assessment of triclosan (TCS) as an aquatic pollutant, *N. denticulata* and *Z. platypus* were exposed to TCS for acute toxicity evaluation. A range of TCS concentrations below LC50 values was determined to reduce mortality effects. We analyzed molecular and biochemical responses at the transcriptomic, proteomic, and metabolomic levels in response to TCS exposure. Finally, we integrated the three omics dataset such as transcriptome, proteome, and metabolome, obtained from the two species exposed to TCS. We found that glutathione metabolism was commonly changed in both species in response to higher concentrations of TCS. Furthermore, *N. denticulata* exhibited differential expression in carbohydrate metabolism such as glycolysis or starch metabolism, whereas *Z. platypus* showed significant changes in oxidative phosphorylation. Through the integration of multi-omics datasets, we identified several biomarkers with potential applications in health assessment and further validated their applicability in actual field environments.

Introduction

- **Background**



- **Objectives**

Choosing the appropriate organisms in domestic field

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Construction of genome-based multi-omics platform

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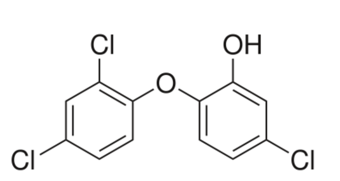
Biomarker discovery for health assessments about aquatic pollutant

M&M

- **Exprimental organisms**

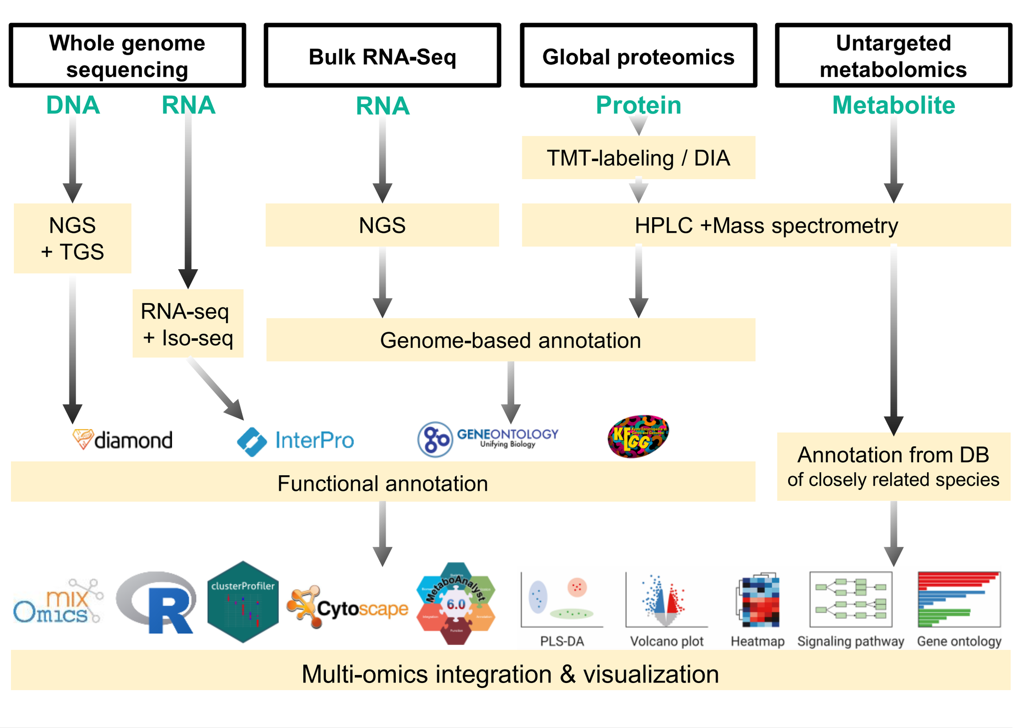
Neocaridina denticulata *Zacco platypus*

- **Chemical**



Triclosan
Antimicrobial agent
Since 1960s, pesticide, mouthwash, and sanitizer ...
Endocrine disruptor effect

- **Multi-omics platform**



Result 1. *Neocaridina denticulata*

Figure 1. sPLS-DA analysis

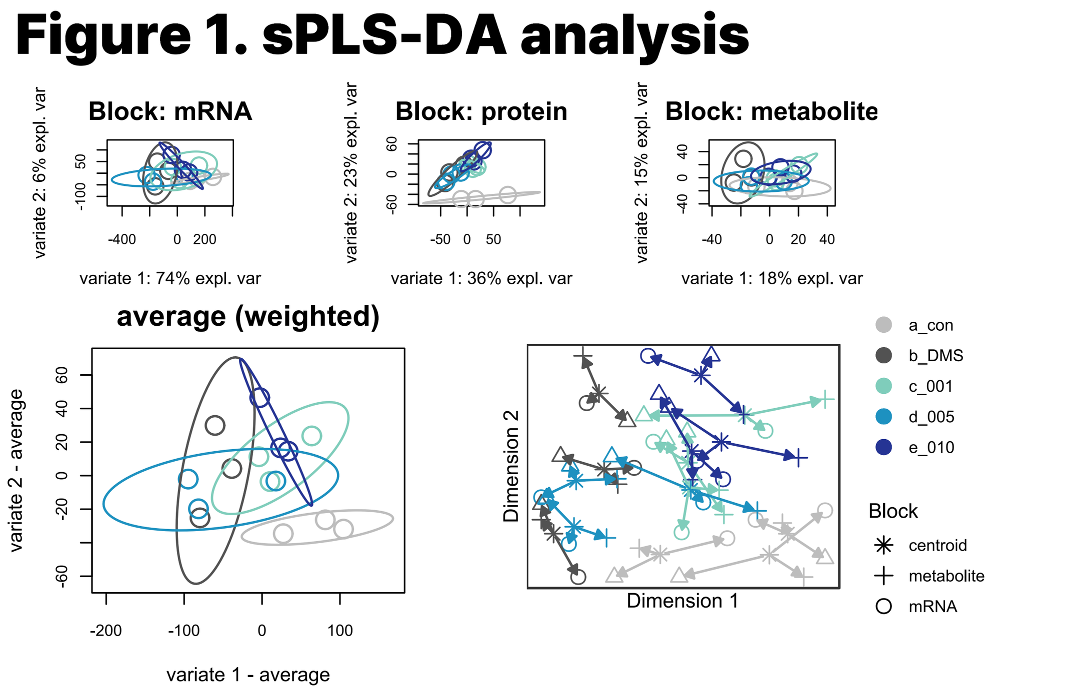


Figure 2. Differential expression

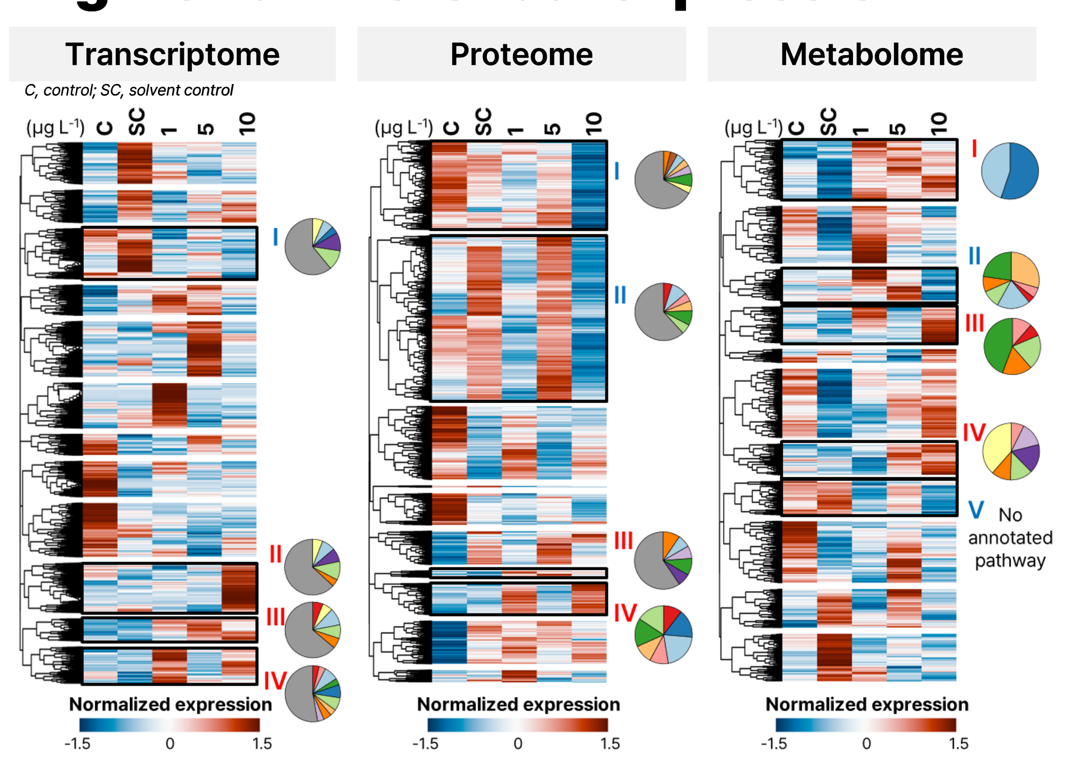


Figure 3. KEGG enrichment

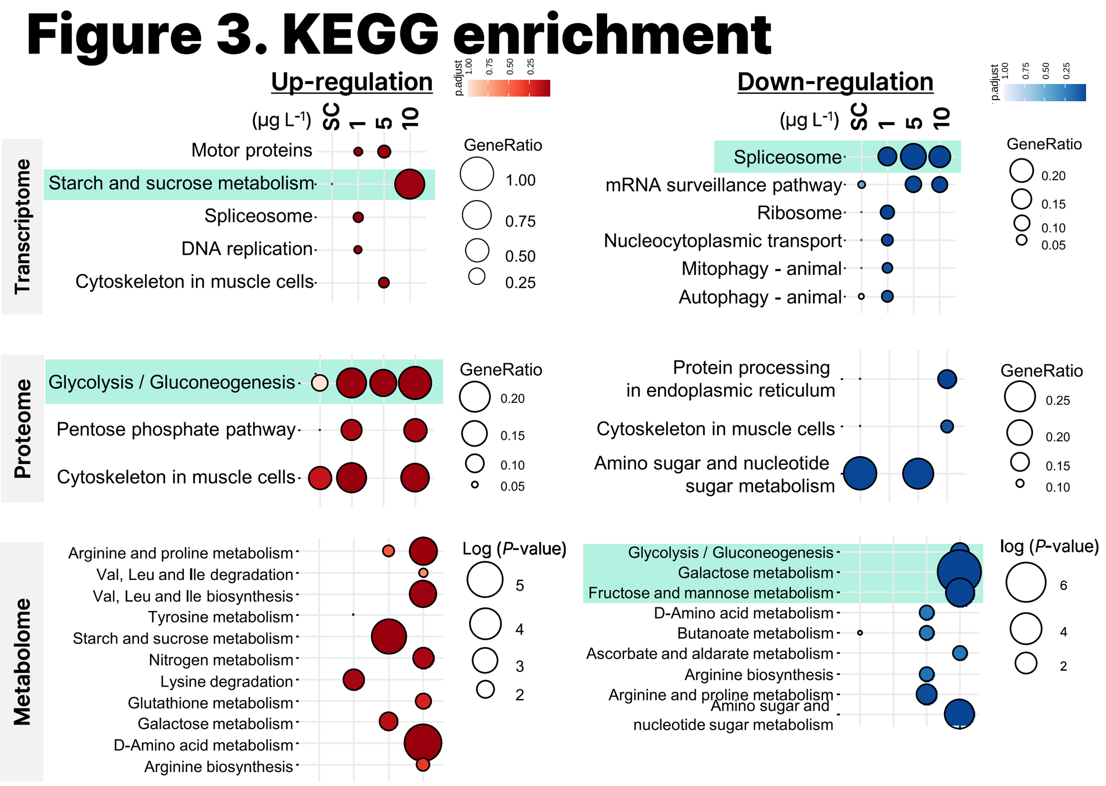
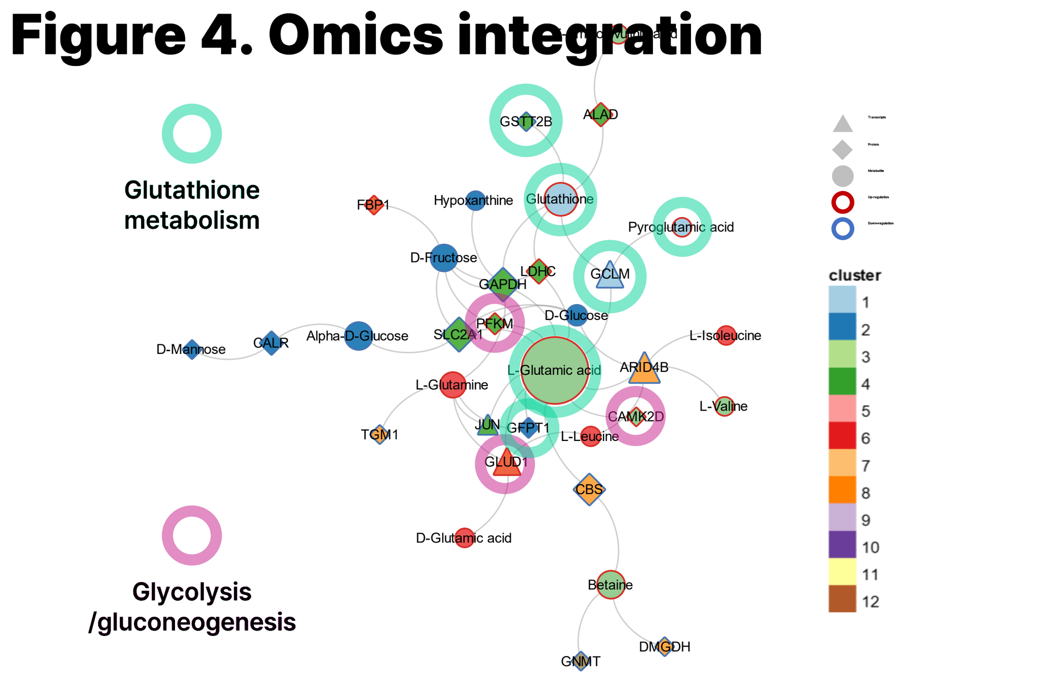


Figure 4. Omics integration



Result 2. *Zacco platypus*

Figure 1. sPLS-DA analysis

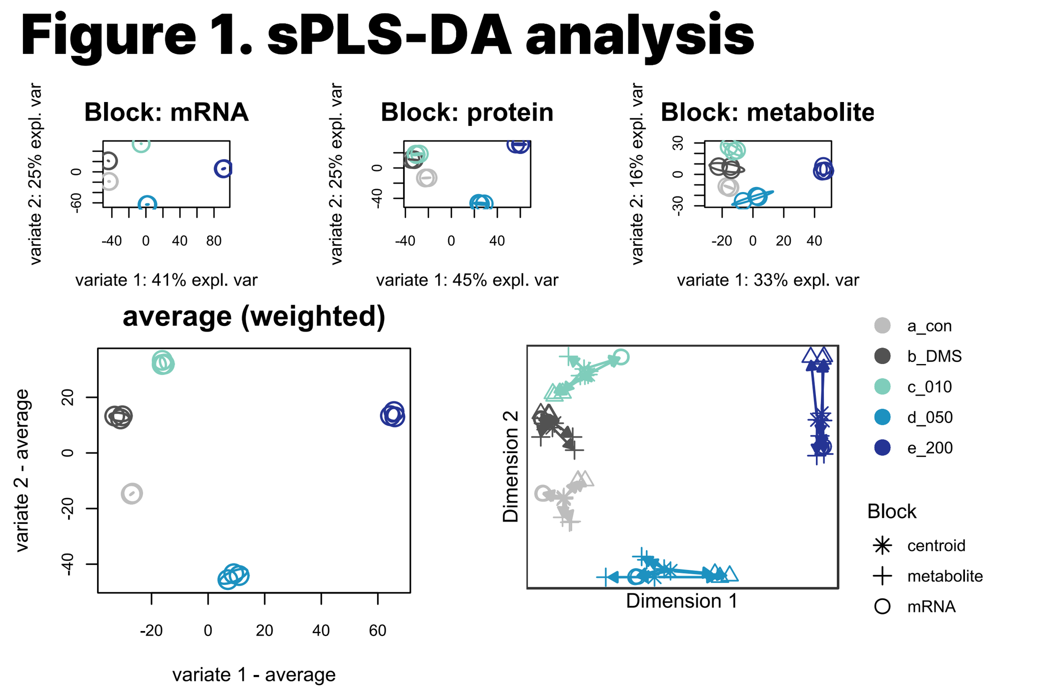


Figure 2. Differential expression

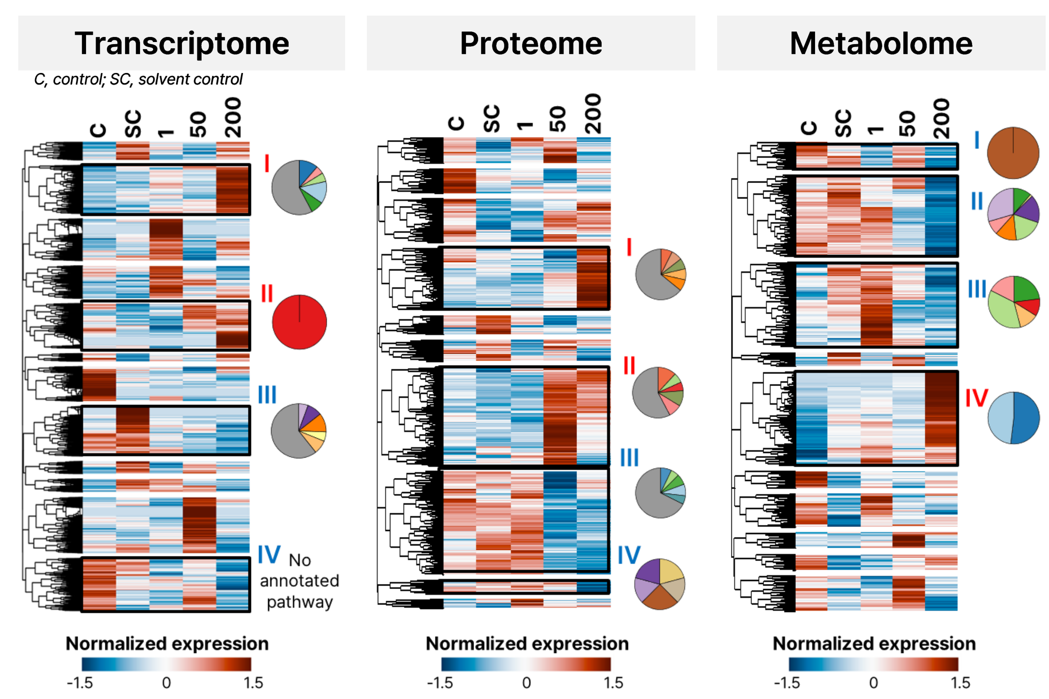
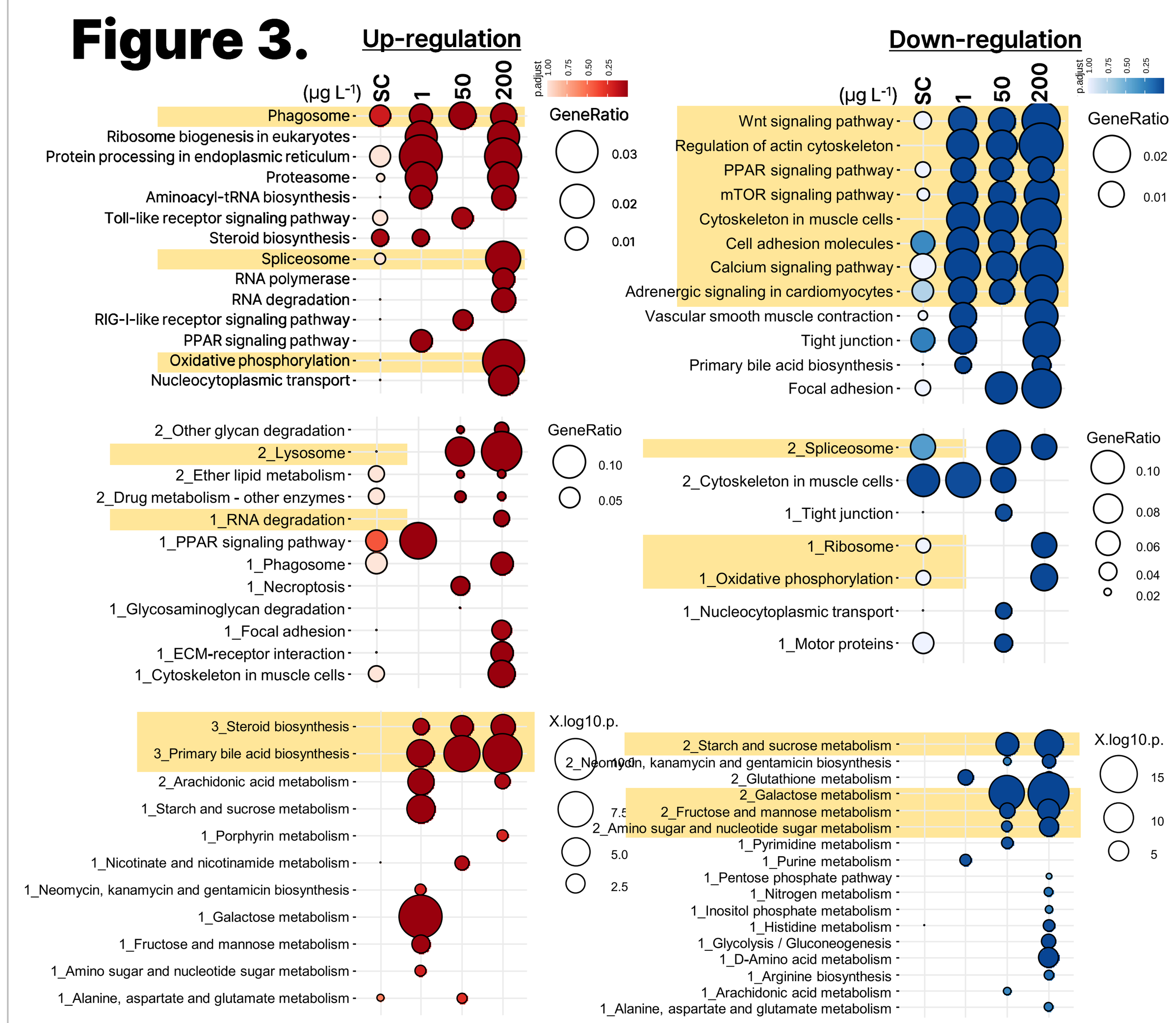


Figure 3.



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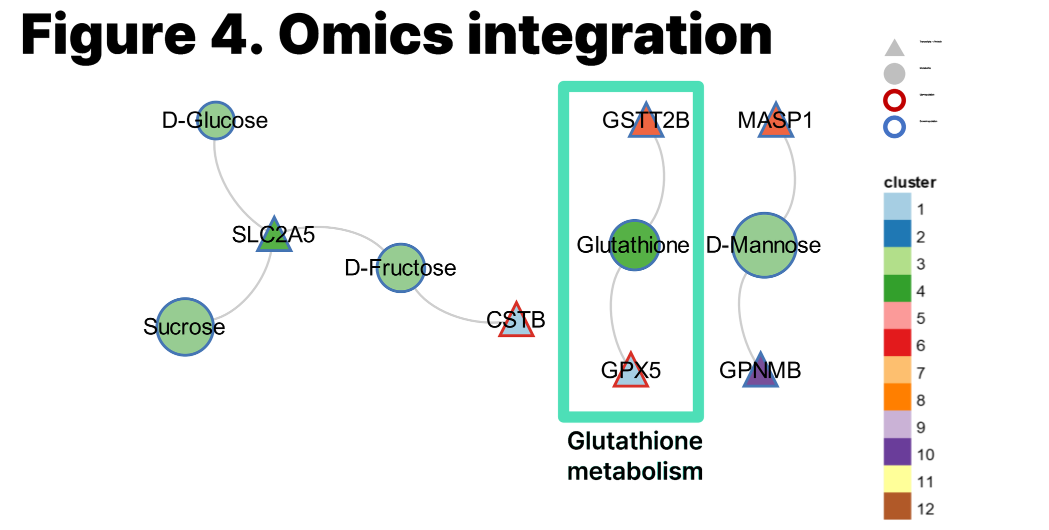

Conclusion

Triclosan → Genomics + Proteomics, Transcriptomics, Metabolomics →

- Starch and Sucrose metabolism
- Glycolysis/Gluconeogenesis
- Glutathione metabolism

- Oxidative phosphorylation
- Glutathione metabolism
- mTOR, PPAR Signaling
- Steroid biosynthesis

⇨ **Application**
Performing biomarker-based gene expression analysis on field samples for health assessment (4 major rivers in South Korea)