The Effect of Cu^{2+} Stress on the Expressions of Genes Related to Immune Response and Oxidative Stressin the Kidney of *Gymnocypris eckloni*

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1 Introduction

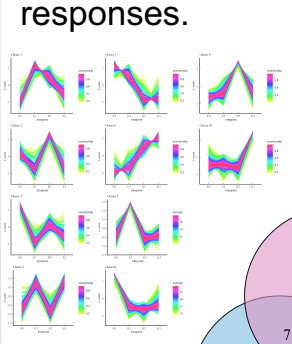
This study will provide an important theoretical basis for an in-depth analysis of the molecular response mechanism of *G.eckloni* under heavy-metal stress, and also provide valuable references for protecting *G.eckloni* and other aquatic organisms from the harm of heavy-metal pollution.

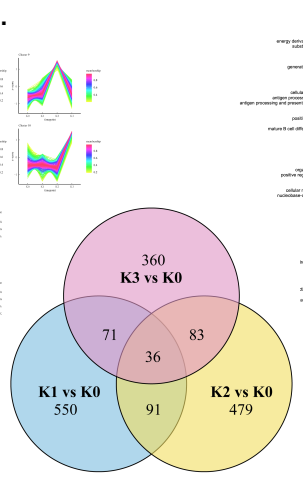
2 Method

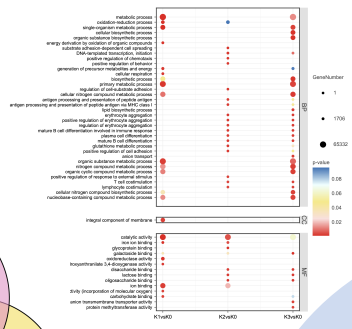
A toxicity test was conducted under Cu^{2+} stress: *G.eckloni* were divided into three experimental groups and one blank control group. After exposure to 0.01 mg/L Cu^{2+} for 0, 6, 36, and 72 hours, the fish were dissected to collect kidney tissues for transcriptome sequencing and data analysis.

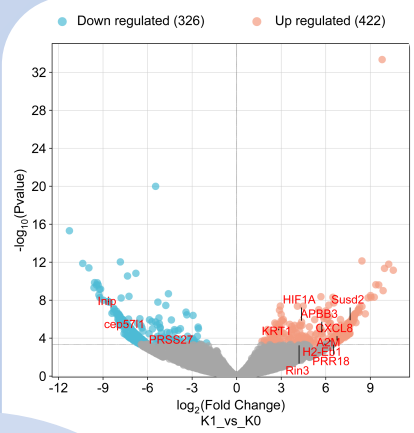
3 Result

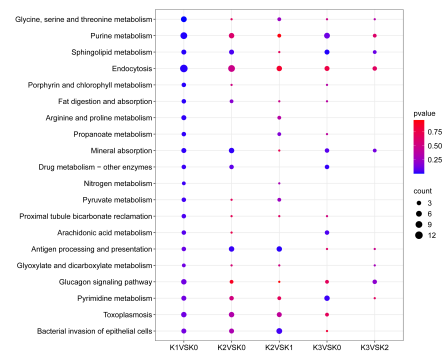
A total of 36 common differentially expressed genes (DEGs) were identified across different stages of Cu^{2+} stress. The top 50 GO terms were predominantly associated with metabolic processes and immune responses.





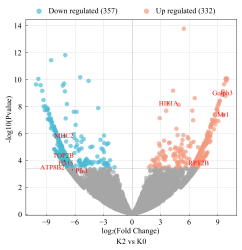


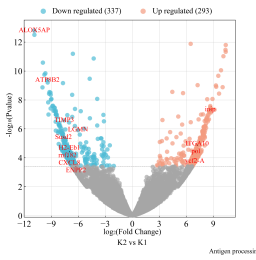




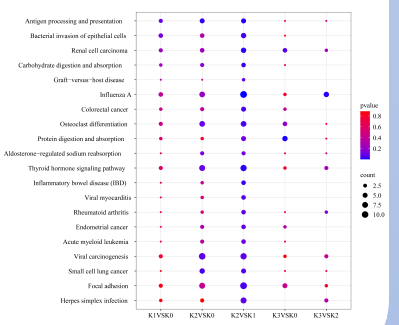
After 6 hours post Cu^{2+} exposure, the significantly enriched KEGG pathways were primarily associated with metabolism, signal transduction, and cellular defense.

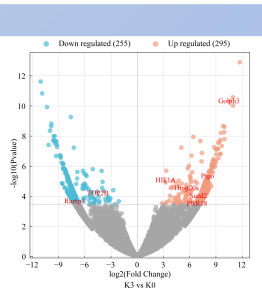
Result

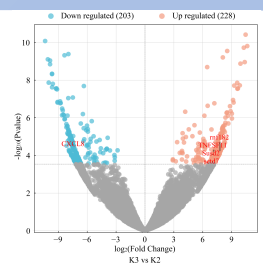




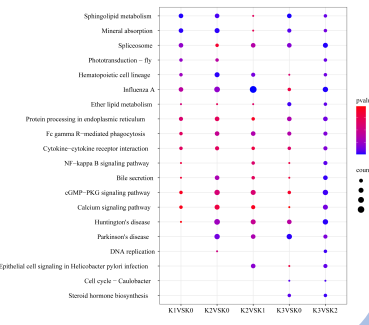
After 36 hours under Cu^{2+} stress, the focus of the cellular response evolved from metabolic adjustment towards pathological processes and immune reactions.







After 72 hours of Cu^{2+} stress, the focus of the cellular response evolved further from immune and metabolic regulation to pathological alterations, signal transduction, and the processing of genetic information.



4 Conclusion

The renal response of *G.eckloni* to Cu^{2+} stress was time-dependent, with a primary activation of metabolic pathways at 6 h, a significant shift to pathological and immune responses at 36 h, and a predominant involvement of genetic information processing and signal transduction pathways at 72 h.