

# OMICs- based biomarker selection for difenoconazole and metalaxyl toxicity in zebrafish embryos.

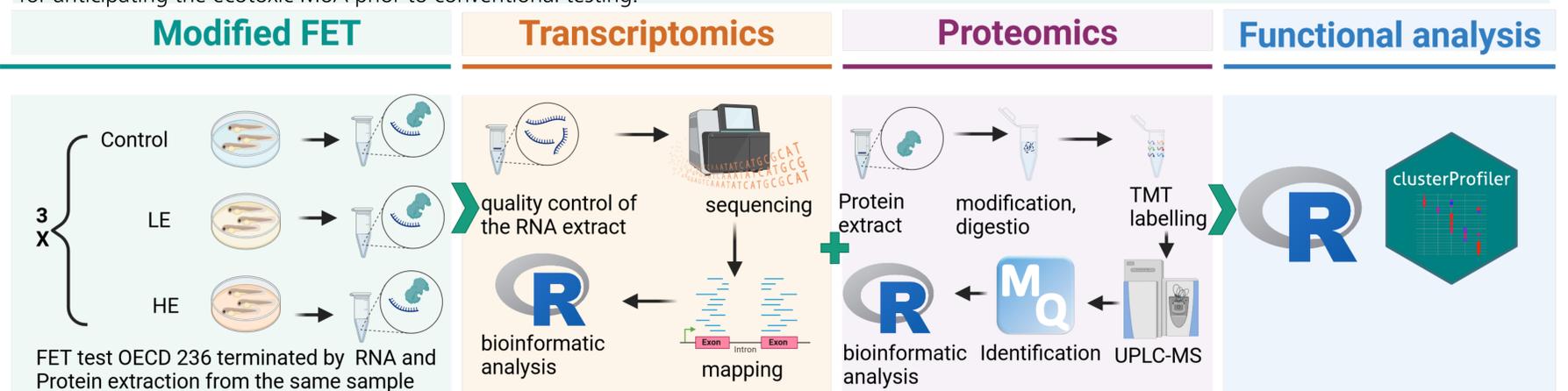
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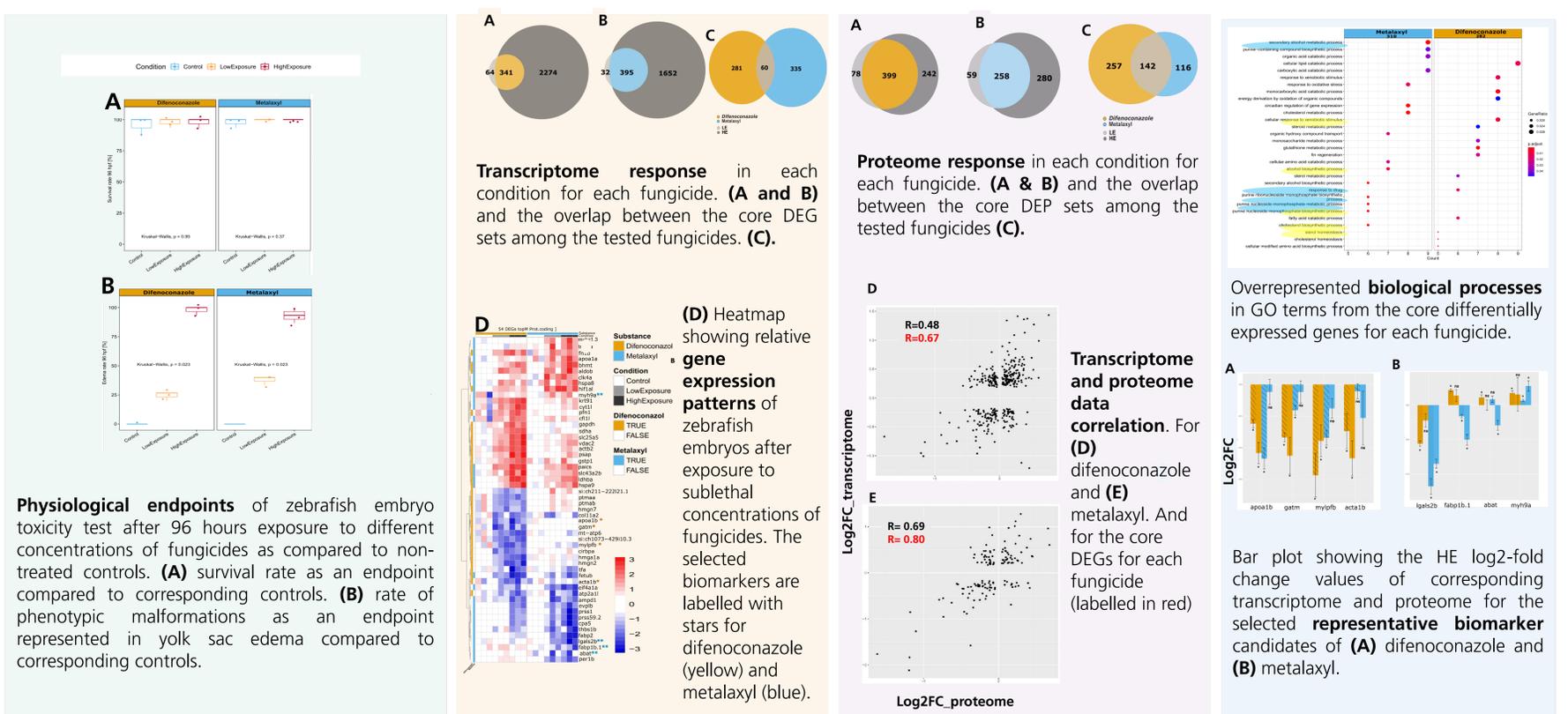
## Background

A number of previous studies have examined the adverse effects of fungicides on non-target organisms inhabiting the ecosystem, and the findings of these studies highlighted the potential of fungicides to interfere with biological processes of organisms beyond fungi. The conventional testing strategies for evaluating ecotoxicity of chemical substances is increasingly time-consuming and costly. Moreover, conventional hazard assessment strategies offer limited insights into molecular and biological mechanisms underlying ecotoxicity. The integration of OMICs techniques in ecotoxicology can enhance our understanding of key events (KE) and key event relationships in an Adverse Outcome Pathways (AOPs). Our present study focuses on investigating early molecular responses in zebrafish embryos to the fungicides difenoconazole (sterol biosynthesis inhibitor) and metalaxyl (nucleic acid metabolism inhibitor), with the goal of identifying mode of action (MoA)-specific biomarker candidates, Which will potentially lead to the development of a predictive approach for anticipating the ecotoxic MoA prior to conventional testing.

## Methodology



## Results



## Conclusion

The most significant outcomes of this study were as follows: (1) molecular responses indicated concentration-dependent responses for both fungicides at both transcriptome and proteome levels. (2) ORA pointed out a number of biological processes influenced by the overrepresented gene sets, and some of the indicated biological processes were biologically related to the FRAC MoA of the corresponding tested fungicide. (3) Some DEG sets showed substance-specific expression patterns, from which potentially substance-specific biomarker candidates were selected for difenoconazole (apoa1b, gatm, mylpfb and acta1b) as well as metalaxyl (lgals2b, abat, fabp1b.1 and myh9a). (4) The biological functions of the selected biomarker candidates were also related to the FRAC MoA of the corresponding fungicide. (5) A correlation between the detected transcriptome and proteome was recorded.