

Differentially Expressed Genes in Grapevine associated with Epigenetic Changes Identified under Combined Stress

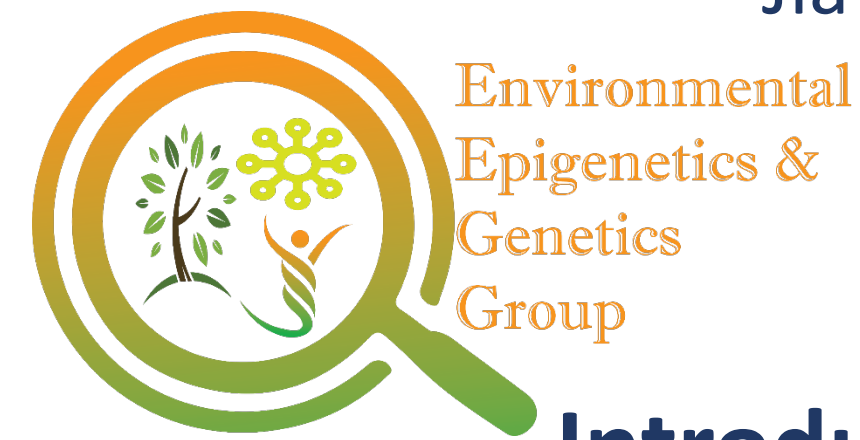
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Introduction

Studies have shown that extensive agricultural losses worldwide are attributed to heat, often in combination with drought. The effects of heat and drought stress will become more severe as the expected changes in environmental conditions continue to unfold. It is predicted that up to 81% of the current grape growing acreage in the US could be lost by 2040. Limited amount of physiological and molecular studies for grapevine have focused on the effects of combined stress. The few that targeted combined stress focused mainly on physiological response. This study aimed to compare changes at the global gene expression levels of grapevine under drought, heat, and combined stress, to identify the general stress response and the possible differences in the mechanisms employed to form such response.

Material and Methods

- 94 Cabernet Sauvignon plants under control, drought, heat and combined drought and heat conditions.
- Samples were collected at 6 sampling times (ST1=1st day of plant acclimation; ST2 = 1st day of drought treatment; ST3=11th day of drought and 1st day of heat treatment; ST4= 12th day of drought and 2nd day of heat treatment; ST5= Day of stress removal; ST6= Physiological recovery), and sequenced
- Differential expression analysis using RNA-Seq data
- Gene ontology and network analysis.
- KEGG pathway analysis

Results

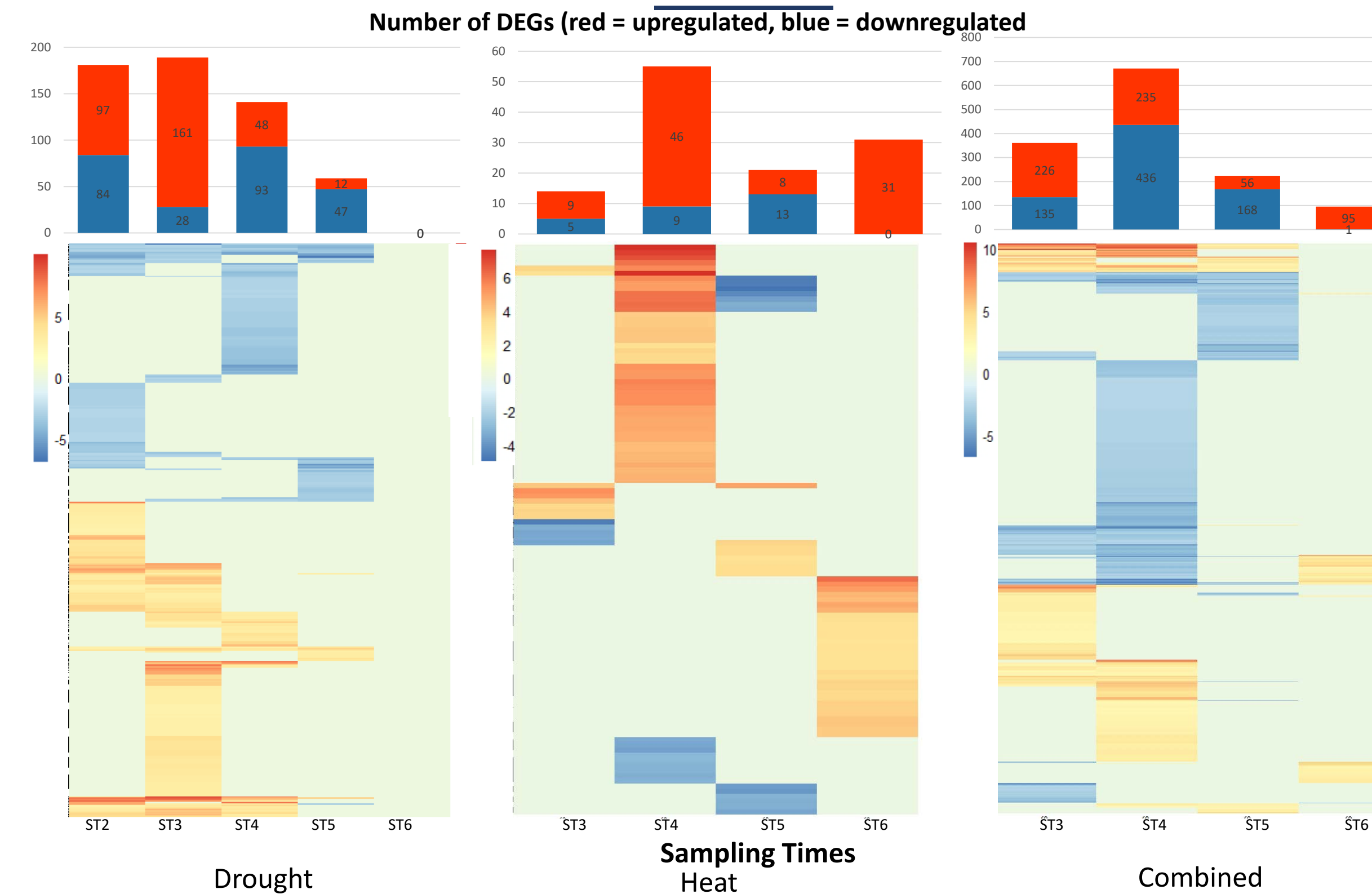


Figure 1. Number of differentially expressed genes (DEGs) identified under drought, heat, and combined treatments.

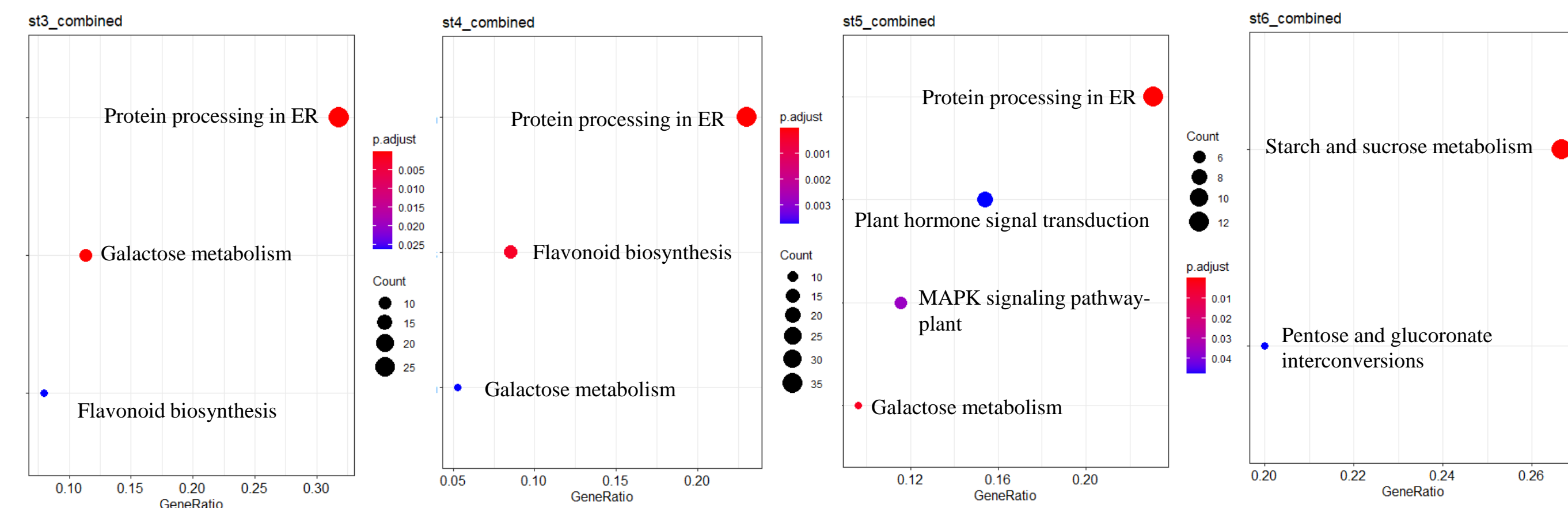


Figure 2. Top KEGG functional enriched pathways of DEGs under combined stress at different sampling time points. P-adj < 0.05

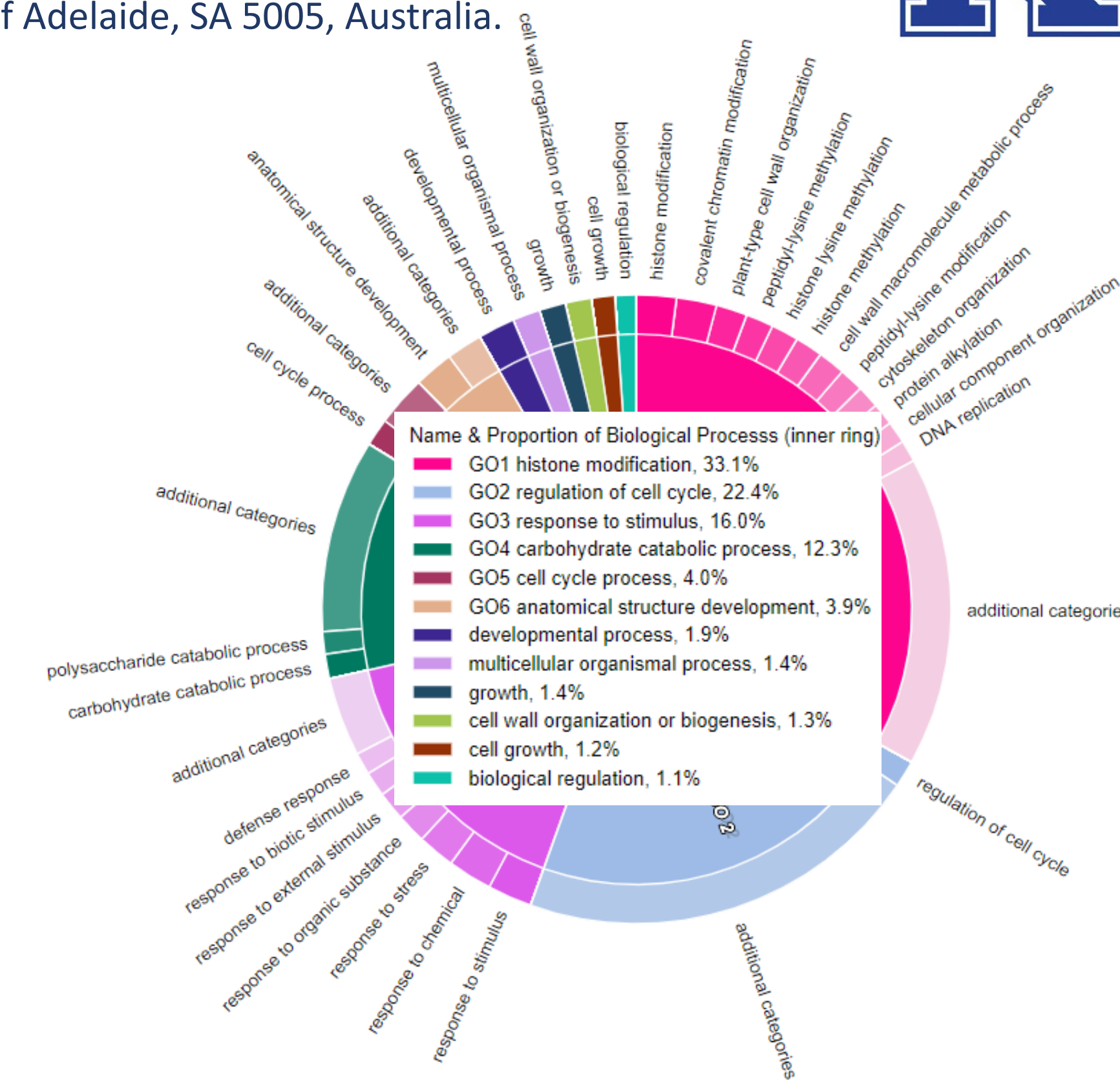


Figure 3. The top 30 GO terms associated with DEGs identified under combined stress.

Conclusions

- Combined stress induced more differentially expressed genes compared to individual stress (Figure 1).
- Key pathways under combined stress are protein processing in ER, Galactose metabolism, flavonoid biosynthesis, and MAPK signaling pathway. Different pathways at physiological recovery (ST6) were enriched (Figure 2) compared to other time points.
- GO terms associated with epigenetic changes (histone modification) identified under combined stress (Figure 3).