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Transcriptomic and morphological responses to salt stress in Wolffia australiana

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In the face of climate change and the demand for more sustainable alternatives to industrial operations, duckweed plants are utilized across a diverse set of applications – from wastewater treatment, to feedstock production, to bioenergy and bioproduct generation. The *Wolffia* genus is the smallest and fastest-growing known angiosperm, making it of particular interest for duckweed research, as well as plant biology more broadly. With these plants becoming more relevant under an increasingly volatile climate, it is crucial to understand stress susceptibility of these plants. Here we examine early salt stress response in *Wolffia australiana* plants over time and under different degrees of salt stress. We examined the phenotypic effects of different salt concentrations (0mM, 50mM, 100mM, 150mM) on growth rate and chlorophyll content. All concentrations of salt stress resulted in decreased growth rate compared to the 0mM control, as well as a persistent increase in chlorophyll content. Given that 100mM produced the clearest stress phenotype without being lethal to the plants, we assessed transcriptomic response at this concentration via bulk RNA-sequencing over a 48-hour timecourse, which identified specific genes, gene families, and functional pathways involved in response to salt stress. Genes upregulated under stress tended to be enriched in metabolic processes and stress response, whereas downregulated genes were enriched in reproductive and biosynthetic processes. This study will provide important insights into the mechanisms of salt stress response in *Wolffia*, and how they differ from other plants.

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References

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