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Transcriptomic and Epigenetic Insights into Flowering and Sexual Reproduction in *L. aequinoctialis*

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Duckweeds are aquatic monocotyledons including the smallest and fastest-growing angiosperms. They predominantly propagate clonally, making sexual reproduction and floral development poorly explored. The most fertile duckweed species belong to the section *Alatae*, which includes *Lemna aequinoctialis*, *Lemna perpusilla* and recently described interspecific hybrids including *L. x aoukikusa* (Stepanenko et al., 2025). To investigate the molecular basis of duckweed sexual reproduction, we generated transcriptomic profiles of reproductive tissues from the highly fertile hybrid accession *L. aequinoctialis* 8011. As a relatively recent hybridization event, *la8011* constitutes an excellent model for studying flowering because of its highly synchronized floral development and the ability to evaluate the contribution of each subgenome.

Duckweed evolution has been associated with gene loss linked to clonal propagation, including components of the RNA-directed DNA methylation (RdDM) pathway (Ernst et al., 2025). This is reflected in the absence of the canonical 24-nt small RNA peak (Ernst et al., 2025; Dombey et al., 2025). Our transcriptomic data reveal activation of genes involved in 24-nt small RNA biogenesis during flowering, consistent with preliminary small RNA-seq findings where these elements are restored. Additionally, we observed a slight increase in CHH methylation in anthers, seeds, embryos and endosperms, supporting activation of the RdDM pathway.

These findings suggest that reproductive development is accompanied by finely tuned, cell-specific epigenetic reprogramming that resets epigenetic marks accumulated during clonal propagation. Together, our results provide new insight into the genomic, and epigenetic dynamics underlying natural hybridization and flowering, establishing a molecular framework for future duckweed breeding.

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References

Ernst E, Abramson B, Acosta K, et al. Duckweed genomes and epigenomes underlie triploid hybridization and clonal reproduction. *Curr Biol.* 2025;35(8):1828-1847.e9. doi:10.1016/j.cub.2025.03.013
Stepanenko A, Braglia L, Fuchs J, et al. Genome diversity and evolution of the duckweed section *Alatae* comprising diploids, polyploids, and interspecific hybrids. *Plant J.* 2025;122(2):e70158. doi:10.1111/tpj.70158

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