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Small meets smaller: rewiring small RNA silencing in duckweeds

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Small RNA pathways play important regulatory and genome defense roles in plants, 21-to-24-nt short interfering (si)RNAs and micro (mi)RNAs guide the silencing of transposable elements (TEs), viruses and endogenous genes, acting both at the transcriptional gene silencing level (TGS), through RNA-directed DNA methylation (RdDM), and post-transcriptionally (PTGS). Duckweeds unique reduced morphology and reproduction, and a wide gradient of genome size and TE content from the TE-poor *Spirodela polyrhiza* (~138 Mb, ~20% TEs) to the TE-rich *Wolffia* (~850 Mb, ~75% TEs), makes them a powerful comparative system to ask how a simplified body plan, a clonal lifestyle and contrasting genome organization shape plant RNA and epigenetic silencing.

Several studies have shown that duckweeds run a streamlined silencing machinery with uneven losses. The RdDM and transcriptional-silencing arm is simplified while the antiviral/PTGS arm lacks as well several key silencing factors. In *Spirodela* and *Wolffia*, this reduced toolkit still resolves TEs sharply: silencing and DNA methylation concentrate on young, intact elements, and the contrasting TE loads of the two species reorganize their small RNA and methylation landscapes accordingly. Across these analyses siRNAs of all size classes are frequently produced from the same loci, indicating that the pathways might be wired differently from the canonical pathways established in *Arabidopsis* rather than simply reduced.

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