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Investigating siRNA-mediated silencing in duckweeds, a potential model for translational repression in plants

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In eukaryotes, post-transcriptional gene silencing (PTGS) involves the production of small interfering RNAs (siRNAs) and their incorporation into ARGONAUTE (AGO) proteins. The resulting siRNA-AGO complex mediates mRNA cleavage and/or translational repression, leading to degradation via RNA decay pathways and ultimately resulting in reduced protein expression. In plants, mRNA cleavage is believed to be the main mode of action of siRNA-AGO complexes, and although translational repression has been shown, it is not yet well understood. Interestingly, in duckweeds, a group of small aquatic flowering plants, siRNA-mediated transgene silencing causes strong loss of protein synthesis, while mRNA levels remain largely unchanged. On the contrary, loss of siRNA results in restoration of protein levels. This observation suggests that translational repression, rather than mRNA degradation, may be a predominant mechanism of gene regulation in this group of plants. To investigate this hypothesis, we are exploiting transgene silencing in duckweeds to analyze the fate and turnover of mRNAs, targeted or not by siRNAs, using a combination of polysome profiling, SLAM-seq, and ribosome footprinting. Understanding silencing mechanisms in duckweeds will expand the knowledge of silencing mechanisms, mostly investigated in a handful of plant models, and potentially provide further insights into their translational repression mechanisms.

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References

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