Salt & Splice: DGCR14L, A new player in mRNA splicing

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How is a cell fine-tuned for viability under different circumstances? Cells can generate protein diversity, which allows a broader range of responses, through alternative splicing (AS). AS modulates the active and non-active form of proteins under abiotic stresses such as salt stress. Overexpression of splicing factors regulates AS and provides salt stress tolerance to plants (Cui et al., 2014; Gu et al., 2018). Arabidopsis *DIGEORGE-SYNDROME CRITICAL REGION 14-like* (*DGCR14L*) plays a role in pre-mRNA splicing similar to its human orthologs (Kanno et al., 2020). In humans, DGCR14 interacts with the proteins of the spliceosome complex (Takada et al., 2018). However, in plants, the underlying mechanism of DGCR14L and its role in salt stress is largely unexplored.

In this issue of *Plant Physiology*, Xie et al. (2023) explored the involvement of AtDGCR14L and pre-mRNA splicing in salt stress tolerance. The authors examined insertion null mutant and overexpression (OE) lines of AtDGCR14L and showed that photosynthesis is compromised in the loss-of-function mutant but OE lines were not affected. Similarly, the loss-of-function mutants, but not OE lines, showed enhanced sensitivity to salt stress. Furthermore, *AtDGCR14L* expression levels are elevated after salt treatment, suggesting it plays a role in salt tolerance.

Previously, by using an introduced GFP construct, Kanno et al. (2020) had shown that *atdgcr14l* mutants have splicing defects. To identify the role of AtDGCR14L in splicing more globally, Xie et al. performed transcriptome analysis of DGCR14L mutant and OE lines. These results showed accumulated aberrant spliced variants in mutants but no splicing deficiencies in the OE line, demonstrating conclusively the role of AtDGCR14L in pre-mRNA splicing.

To investigate the mechanism of how AtDGCR14L contributes to pre-mRNA splicing, the authors performed interaction studies and found that AtDGCR14L interacts with a protein of the early spliceosome complex, U1-70k. They further conducted substitution analysis in the conserved motif (TWG) of AtDGCR14L that disrupted the interaction between mutated AtDGCR14L and U1-70k. Overexpression of mutated AtDGCR14L in *atdgcr14l* mutants failed to recover normal growth under salt stress, indicating that the TWG motif is essential for the biological functions of AtDGCR14L.

Additionally, the authors identified an RNA that in *atdgcr14l* mutants showed a significant increase in an alternatively spliced form, which leads to a deletion of the C-terminal leucine zipper domain. This mRNA encodes a core subunit of the chromatin remodeling complex, SWITCH/SUCROSE NONFERMENTING (SWI3A). To understand the role of SWI3A in AtDGCR14L-mediated salt stress tolerance, the authors expressed a complete and truncated form of SWI3A in *atdgcr14l* mutants. The non-truncated SWI3A increased salt tolerance of the *atdgcr14l* mutants, indicating that AtDGCR14L is required to express the active, constituently spliced form of SWI3A. The findings suggest that the AtDGCR14L plays a crucial role in the

crosstalk between mRNA splicing and salt stress tolerance (**Figure 1**). Furthermore, it provides additional clues to how the human DGCR14 protein might affect splicing.

Figure 1: The role of AtDGCR14L in pre-mRNA splicing and stress tolerance. Arabidopsis DGCR14L interacts with U1-70k to maintain splicing levels of mRNAs. Under salt stress, AtDGCR14L enhanced the expression of constitutive spliced forms such as SWITCH/SUCROSE NONFERMENTING (SWI3A) to provide salt stress tolerance. The figure is adapted from Xie et al. 2023 and created by BioRender.com.

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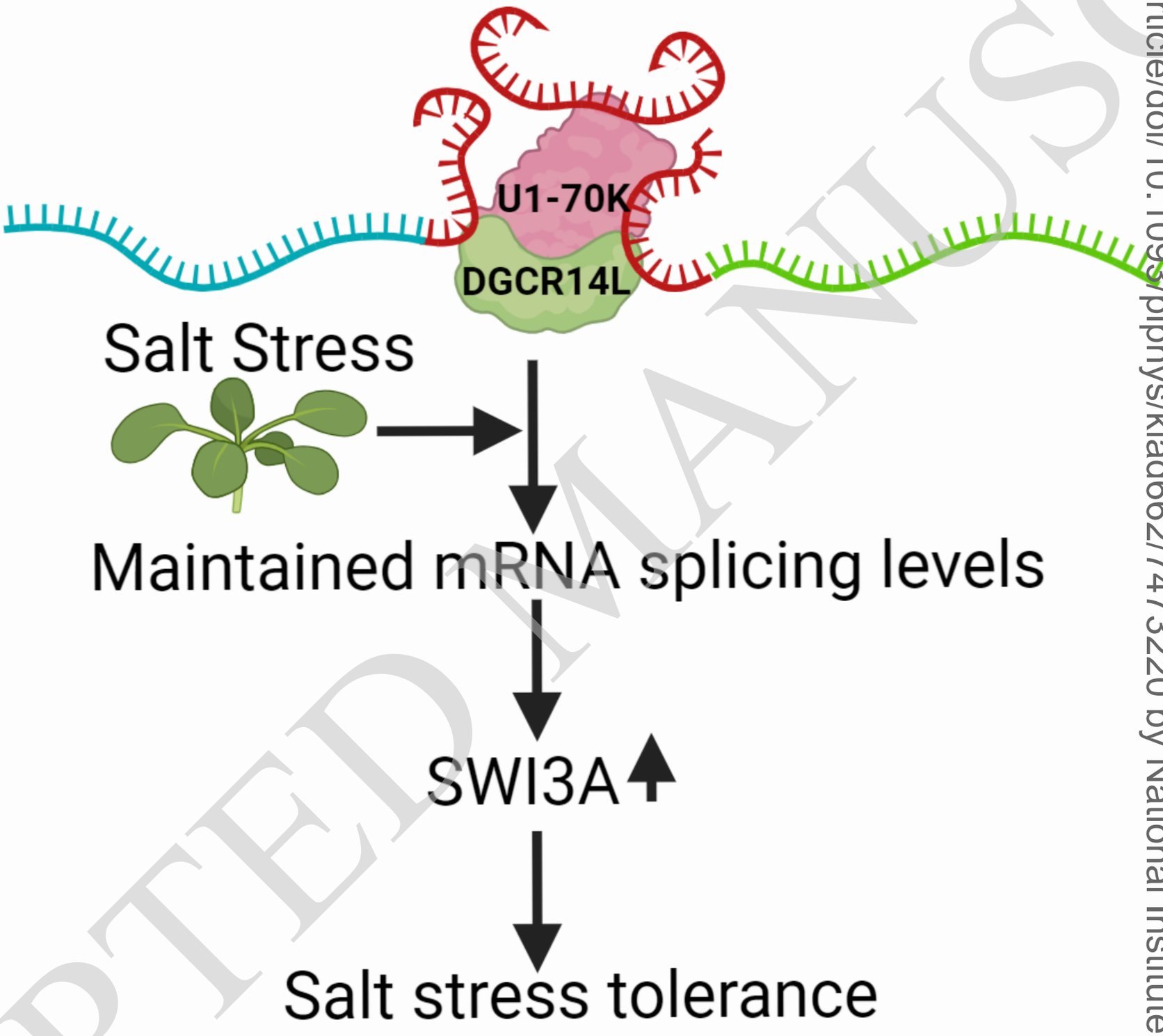

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