EDITORIAL: REFLECTIONS ON PLANT CELL CLASSICS

DREB Duo Defines Distinct Drought and Cold Response Pathways

Despite advances in agriculture over the millennia of human history, crop yields remain deeply dependent on climate and weather patterns. Abiotic stresses like drought, freezing, and flooding are dreaded for the devastation they can bring. Thus understanding plant response to abiotic stress has long been a primary goal in plant biology research, and it is perhaps not surprising that some of the most highly cited papers in the history of the journal relate to transcriptional regulation during abiotic stress conditions. Two of the most highly cited papers in *The Plant Cell* (Liu et al., 1998; and Yamaguchi-Shinozaki and Shinozaki, 1994) come from the laboratories of Kazuko Yamaguchi-Shinozaki (now at the University of Tokyo; then working at Japan International Research Center for Agricultural Sciences, Tsukuba), and Kazuo Shinozaki (RIKEN Center for Sustainable Resource Science, Yokohama).

First, Shinozaki-Yamaguchi and Shinozaki (1994) described the cis-acting element DEHYDRATION RESPONSE ELEMENT (DRE), found in the promoter of rd29A and shown to be involved in the rapid response in the expression of this gene to dehydration or high salt conditions. Liu et al. (1998) then extended this work by identifying two small families of transcription factors (TFs) in *Arabidopsis*—DREB1, which has three homologs, and DREB2, which has two homologs—that act in the regulation of two separate signal transduction pathways in response to low-temperature and dehydration conditions, respectively. One of the DREB1 proteins, DREB1B, and the DRE turned out to be the same as the CBF1 protein and a cold-regulated element (CRT), respectively, identified in independent studies carried out by Michael Thomashow and colleagues at Michigan State University (Baker et al., 1994; Stockinger et al., 1997).

There are, of course, many publications that uncovers aspects of transcriptional regulation under abiotic stress (far too many to cite here), and promoter deletion analysis had been in use in plants for some time prior to 1994. However, the Yamaguchi-Shinozaki and Shinozaki (1994) paper certainly is one of the finest examples of early work in plants that directly connected a cis-element to induction of gene expression with a change in environmental conditions, in this case dehydration and high salt, and should be on the required reading list as a classic study for students and researchers in this field. The authors first show that two genes, rd29a and rd29b, exhibit differential responses in expression to dehydration, high salt, or low temperature, with rd29a expression responding rapidly to these treatments and rd29b responding more slowly (dehydration and high salt treatments) or not at all (low temperature). Next, to pinpoint the region responsible for the rapid induction of rd29a, they conducted a classic example of promoter deletion assessment with a chimeric gene construct consisting of a series of deletion fragments from the rd29a and rd29b promoter regions fused to the GUS reporter gene and expressed in transgenic *Arabidopsis* and tobacco plants. This allowed the identification of a cis-acting, dehydration-responsive element, known as DRE, involved in the rapid response of rd29A to conditions of dehydration or high salt. They further showed that DRE is involved in the induction by low temperature but not in a slower ABA-responsive induction of rd29A.

Liu et al. (1998) extended this study by using yeast one-hybrid screening to identify two cDNA clones that encode the DRE binding proteins DREB1A and DREB2A, both of which bound specifically to the DRE sequence in vitro and activated the transcription of the GUS reporter gene driven by the DRE sequence in *Arabidopsis* leaf protoplasts. Interestingly, the two proteins showed no significant sequence similarity, except in their conserved DNA binding domains, and the expression of DREB1A and two homologous genes was induced by low-temperature, whereas expression of DREB2A and its single homologous gene was induced by dehydration in *Arabidopsis*. Thus they identified two independent families of DREB proteins, DREB1 and DREB2, that function as transcription factors in two different signal transduction pathways, regulating responses to different stresses—low-temperature and dehydration—integrated through the same element.

It has since been shown that the DREB proteins belong to a large family of over 100 plant-specific DNA binding proteins containing a highly conserved ERF/AP2 DNA binding domain. The DREB subfamily in *Arabidopsis* includes 56 members divided into 6 subgroups (A1-A6); the DREB1/CFB and DREB2 proteins are classified in the A1 and A2 subgroups, respectively (Sakuma et al., 2002). The DREB1/CFB proteins are now recognized as “master switches” constituting a “major hub” for gene regulation during cold acclimation (Kidokoro et al., 2017; Thomashow, 2010), whereas DREB2 proteins may function more specifically during drought and high salt conditions (Sakuma et al., 2002).

A seminal finding with major implications for crop improvement reported by Liu et al. (1998) was that overexpression of one TF alone, DREB1A, resulted in enhanced tolerance to both dehydration and freezing stress. It was also shown by the Thomashow group that overexpression of CBF1 enhanced freezing tolerance (Jaglo-Ottosen et al., 1998). Although the transgenic plants were stunted relative to wild type, this generated a lot of excitement, and early work on DREB/CFBs was cited as a promising avenue for engineering crop plants more highly tolerant of drought and other abiotic stresses (for example, Smirnoff and Bryant, 1999).

Many subsequent studies have sought ways of altering DREB/CFB expression to enhance stress tolerance without negatively affecting growth (for example, Kasuga et al., 1999). In the last 10 years since publication of these two studies, citations have picked up, reflecting the importance of
DREB/CBF pathways in plant stress tolerance and heightened efforts to achieve a breakthrough in overcoming the dichotomy between enhanced stress tolerance and growth retardation. The development of new methods and techniques, along with the characterization and deeper understanding of DREB/CBF pathways in different plant species (for example, Kudo et al., 2019, Li et al., 2019, Moon et al., 2019), gives renewed hope that such a breakthrough will not be far off.

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REFERENCES


