Cracking the code of bZIP dimerization in *Arabidopsis*

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S1 group Basic Leucine Zippe Domain (bZIP domain) transcription factors (bZIP1, bZIP2, bZIP11, bZIP44, bZIP53) form heterodimers with C group bZIP transcription factors (bZIP9, bZIP10, bZIP25, bZIP53). The dimers bind to ACGT core motives which have been identified in a multitude of plant genes regulated by diverse environmental, physiological and environmental cues. Specific S1/C dimer formation has been demonstrated using both Yeast two hybrid and Plant two hybrid analysis, but physiological relevance remained unclear. Our microarray analysis shows that different dimers regulate different set of genes in a specific manner. Interestingly, bZIP11 is affecting gene expression significantly more than other tested bZIP proteins both when over expressed alone or in combination with dimerizing partners. However, dimerization is in all cases enhancing activity of all bZIPs. Moreover, using gain and loss of function mutants reveal the importance of bZIPs dimer regulation in plants. Based on this, our proposed model suggests that the combinatorial control of amino acid metabolism and regulation of stress target genes are controlled by a network of specific heterodimers of bZIP transcription factors. This network gives the plant ample opportunity to fine-tune responses to a variety of factors by modulating the individual genes of bZIP proteins in the cell.