Identification of proteins interacting with the Sucrose Control peptide of bZIP11 to understand sucrose signaling

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Changed cellular sugar levels are dramatically affecting gene expression in plants. The bZIP11 transcription factor plays a part in this regulatory pathway by affecting genes encoding key enzymes in primary metabolism, thereby acting as a dominant regulator of metabolism (1). In response to high sucrose levels, bZIP11 is translationally repressed, which depends on the sucrose control (SC) peptide encoded by an upstream open reading frame (uORF) in the 5’-leader of bZIP11 mRNA (2). A likely model includes stalling of ribosomes on the bZIP11 mRNA due to sucrose-dependent interactions of the translated SC-peptide with ribosomal or ribosome associated factors (3). This regulatory principle is well conserved and unique to plants.

Transgenic Arabidopsis lines expressing an immuno-tagged SC peptide are being developed, allowing the enrichment and identification of interacting proteins. Additionally, a Yeast-2-Hybrid screening approach yielded several possible protein interactors of the SC-peptide. These experiments could lead to the identification of proteins or protein modifications involved in sucrose dependent stalling of translation and sugar signaling mechanisms in plants.