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News from the plant world: Listening to transcription

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There is a critical need to understand the mechanisms that plants use to tolerate stress and respond to environmental cues. Much of the food, fiber and fuel necessary for our society is derived from plants. We face a growing challenge of providing a secure food supply for a rapidly growing population while attempting to minimize adverse environmental effects of agriculture. We will need to meet this challenge by engineering plant systems that are resilient to environmental stresses. Agricultural crops of the future will need to tolerate droughts, floods, extreme temperatures and biotic pathogens while being highly efficient at nitrogen and phosphorous usage. Many animals have the potential to use behavior, or physical movement, to ameliorate environmental stresses. As sessile organisms, plants must rely upon changes in gene expression to tolerate environmental stresses. Plants must be able to influence development, metabolism or physiology in order to adapt to local conditions. As highlighted by the critical reviews provided by experts in this special issue of BBA Gene Regulatory Mechanisms, plants use some strategies shared by metazoans, while others appear to be unique to the kingdom. Lethi-Shiu and colleagues (2016) focus on the evolutionary history of transcription factor families, and how some families have diversified and expanded to accommodate plant domestication as well as developmental and biochemical novelty, while others transcription factor families present in metazoans are completely absent in the plants.

What DNA sequences transcription factors recognize *in vivo* as well as *in vitro*, and what are the tools available to determine preferred binding sites are the focus of the review by Franco-Zorrilla and Solano (2016). As in metazoans, chromatin immunoprecipitation (ChIP)-based methods often identify transcription factor binding sites that have little or no apparent consequence on the regulation of expression of the respective target gene. The authors also provide an up-to-date summary of the 500 or so plant transcription factors for which direct target have been identified. But transcription factors rarely control gene expression alone, frequently forming large complexes on the regulatory regions of the genes they control. How these complexes form in a combinatorial fashion, often involving proteins that recognize (readers) and/or modify (writers) specific histones is the focus of the review by Brkljacic and Grotewold (2016).

The application of systems biology approaches is likely to provide novel insights into the regulatory networks that control gene expression in plants. These approaches have been enabled by the presence of genome-scale data on gene expression combined with novel bioinformatics approaches to study the coordinate changes in gene expression throughout time or among diverse genotypes. Banf and Rhee (2016) provide a detailed overview of several approaches for documenting co-expression or gene regulatory networks in plants (Banf and Rhee 2016). This review also highlights on-going challenges related to integration of distinct data types and determining causality from networks. Schaefer and colleagues (2016) provide a description of efforts to use co-expression networks to document gene function in agricultural species. They provide a summary of available approaches and limitations for constructing co-expression networks. This review also highlights diverse biological applications of co-expression networks and how the combination of co-expression networks and GWAS can provide increased evidence for functional roles of specific genes. An in-depth description of the methods for generating transcription factor networks is provided by Muhammad et al. (2016). There are a variety of