

Genomic aspects of adaptation mechanisms to multiple environmental stresses in grasses

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Plants may experience multiple stresses during their lifecycle to which they have to adapt because they are sessile organisms and cannot escape easily. Different combinations of stress contribute to genotype by environment (GxE) effects, which are often non-linear and difficult to predict. Furthermore, the extent and variance of GxE effects may depend on the number and type of stresses. Currently, very little is known with respect to the cellular and molecular foundation of GxE effects. For this reason, these effects are difficult to incorporate into breeding methods such as genomic selection and more research is required to answer whether genomic selection works well with high GxE levels, and whether polymorphisms in stress-related genes predict phenotypes better than randomly selected markers. We have begun to investigate these questions by studying differentially adapted wild barley populations from Israel which differ in their response to drought stress. Using phenotypic and transcriptome analyses, we found candidate genes that are differentially affected by drought stress. We propose to investigate the function, expression and evolution of these genes in greater detail to understand their role in drought adaptation and to potentially exploit this information for breeding purposes.