

Poster 41. Transcript profiling identifies novel transcripts with unknown functions as a primary response components to dehydration stress in wheat (*Triticum aestivum* L.).

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Dehydration is among the major abiotic stresses that adversely impacts crop productivity and plants often display cultivar-dependent response. For understanding the molecular mechanism underlying differential dehydration tolerance of two wheat (*Triticum aestivum* L.) cultivars with contrasting stress adaptability, we compared transcriptomic changes occurring at early onset of dehydration and identified 107 nonredundant transcripts. Of these, most had unknown functions (~30%), signifying existence of putative novel wheat-specific genes reported here for the first time. Through macroarray analysis, ~64% clones were shown to differentially express (≥ 3 -fold) in response to dehydration and some highly upregulated known or unknown function transcripts was further confirmed by quantitative RT-PCR. Upon comparing with previous transcriptomic studies, 40% of these 107 dehydration stress-specific transcripts were found not to be documented. These new transcripts may therefore signify unexplored gene sources for specific responses to short-term dehydration stress in wheat. Expression analysis of the unknown function transcripts also revealed tissue- and other stress-specific differential regulation. Comparative *in silico* mapping of 107 wheat transcripts against the available mapping data of rice (40; ~37%), maize (34; ~32%) and sorghum (33; ~31%) revealed wheat orthologous sequences to be present in the respective cereals. This study provides interesting account of several unknown genes that in addition to genes with known functions may regulate stress dynamics and thus may be used as future candidates to improve stress adaptability through genetic manipulation.

Poster 42. Association mapping of Russian wheat aphid resistance in barley as a method to identify diversity in the National Small Grains Collection.

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Russian wheat aphid (RWA) infestations of barley cause chlorotic leaf spotting and streaking, and prevent unrolling of leaves which traps spikes and reduces grain yield. Resistant accessions identified in the NSGC were used to develop adapted, resistant germplasm and cultivars. This study identified loci affecting RWA resistance and diversity in the NSGC using association mapping. Resistant and susceptible accessions, breeding lines, and cultivars were genotyped with DArT markers and phenotyped for RWA responses. A core set of nine markers explained 83% of the variation for chlorosis. Most resistant and susceptible accessions had opposite genotypes at each of these markers. The six susceptible adapted cultivars were exceptions and shared the haplotype of the resistant accessions. Variability at four additional loci associated with resistance did not sufficiently explain phenotypic variability between resistant accessions and susceptible cultivars. Examining subsets of the data identified six additional markers associated with RWA response, which discriminated between resistant accessions and susceptible cultivars. Additional investigation is necessary to better understand the genetics of RWA resistance. However, this study provided useful information on diversity in the NSGC, and suggested that RWA resistance is a complex trait that may share physiological components with other characteristics that were selected during domestication.