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“Bridging the gap between increasing knowledge and decreasing resources”

Comparative Physiological and Molecular Response of Kenyan Barley (*Hordeum vulgare* L.) Cultivars in Response to Abiotic Stress

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Abstract

Abiotic stresses such as drought, salinity high temperatures, mineral deficiency and toxicity limits the growth and productivity of cereals globally accounting for 70% of yield losses. In Kenya barley is used as a source of malt for brewing, animal feed and is gradually gaining importance as a food security crop in the wake of pronounced climate change in sub-Saharan Africa. Exploitation of varietal diversity to identify cultivars with wider agroecological adaptability for enhanced selection for abiotic stress tolerance is essential. In this study, various physiological and molecular screening assays were performed in order to characterise Kenyan barley lines. Quantitative and qualitative changes in physiological parameters including ionic leakage damage, lipid peroxidation, chlorophyll content, metabolite accumulation of proline, sucrose and glycine betaine (GB) and expression profiles of major genes involved in abiotic response in barley such as dehydrin (*LEA II*), *Hordeum spontaneum* dehydration response gene (*Hsdr4*) and genes encoding transcription factors such as *HvDREB1* were evaluated. Twelve days old seedlings grown under controlled conditions were subjected to varying levels of salt and or combined with dehydration stress treatments. A phenotype assessment cluster was generated based on leaf colour, survival rate, tillering abilities emergence of the new apical leaf, and the ability to maintain “stay green trait”. Based on combined phenotype, physiological and biochemical assays, a cluster of representative putative tolerant and susceptible cultivars were generated. Response to abiotic stress was found to be genotype dependent and varied with the severity of stress especially salt. *HvBBD1* was strongly constitutively expressed in roots than in leaves while *HvBBD2* was strongly induced in leaves in response to stress suggesting the potential role of increased GB in osmotic adjustment. Low ion leakage, lipid peroxidation and increased GB, proline, chlorophyll was associated with abiotic stress tolerance. Dehydrin *Dhn1* and *Dhn9* genes were exclusively associated with dehydration response. *Dhn3*, *Dhn4* and *Dhn7* were induced by both dehydration and increased salt treatments. *Dhn8* were constitutively expressed. The results presented here are the first report on the status of abiotic stress tolerance in Kenyan cultivars and forms a basis for further improvement using both conventional and biotechnological approaches.

Keywords: Abiotic stress tolerance, barley, aldehydes, betain aldehyde dehydrogenase, compatible solutes, dehydrins, glycine betaine, *Hordeum vulgare*, transcription factors