Fayoum University
Faculty of Science
Botany Department

Association Mapping of Barley Phenotypic Traits under Drought Stress

By

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Summary and conclusion

Drought is among the harshest abiotic stresses hindering seed germination, plant growth, and crop productivity. Up to 28% of the usable land in the world is drought affected that prompt to find out strategies to minimize drought severity on crop development and productivity. Barley is considered as one of the most abiotic stresses tolerant among cereals. Therefore, elucidation of drought tolerance during seed germination in barley will pave the way to improve the performance in the remaining cereals. However, we still know relatively little about the genetic control of drought tolerance during seed germination phase.

Drought is one of the most important environmental stresses limiting crop production and yield of plants which becomes more common particularly in the arid and semiarid regions.Among the various abiotic factors challenging crop production globally, drought stress threats plant growth and development. Drought stress affects crop growth and yield during all developmental stages.

The effect of drought on yield is highly complex and involves processes as diverse as reproductive organs, gametogenesis, fertilization, embryogenesis, and seed development stress. Reproductive stages, such as flowering and seed development are especially sensitive to drought stress. A reduction in number of grains per spike, grain filling duration, and dry matter accumulation has already been reported to decrease grain weight in barley kernels.

Plant responses and adaptation to drought are achieved through a series of molecular, biochemical, and physiological processes including induction/ repression of various genes that cause accumulation of various osmolytes, improved antioxidant system, decreased transpiration, inhibited shoot growth, and reduced tillering.

In our study, 218 worldwide spring barley accessions were subjected to PEG-induced drought during seed germination. Drought stress "20% PEG" reduced the seed germination parameters and seedling related traits significantly. Genome-wide association scan was used to identify genomic regions associated with our trait of interest. Totally, 299

SNPs showed association with different traits which were distributed across the seven chromosomes of barley. Among them, 26 are associated with candidate genes. QTL detected genomic regions previously linked to natural variation of seed germination related traits under drought conditions as well as novel associations. Noteworthy, the identified QTL colocalized with a number of genes which are exclusively distributed on chromosomes 1, 2 and 5. The annotation of these genes shows their roles in drought tolerance through encoding different transcription factors. The function of the identified genes during seed germination was also confirmed by the annotation of their counterparts in *Arabidopsis*. The current analyses afford a significant genetic resource of developmental and adaptive traits in barley that is worth to be used in the future genetic and breeding work.

Finally, 121 worldwide spring barley accessions were grown under field-like conditions. Genome-wide association scan was used to identify genomic regions associated with our trait of interest. Totally, 101 SNPs showed association with different traits which were distributed across the seven chromosomes of barley. Among them, 16 are associated with candidate genes. The identified QTL colocalized with a number of genes which are exclusively distributed on chromosomes 2, 3, 4 and 6. The annotation of these genes shows their roles in drought tolerance through encoding different transcription factors.

- Traits with high heritability under drought such G% and root length, can be employed as selection parameters to test large number of genotypes in short time.

- Identification of drought stress-responsive genes encoding different proteins regulates the germination and post-germination events.

- The identified genes modulate the seed germination under control and drought in two different patterns; constitutively or adaptively.

- The constitutive genes can be harnessed for selection either under control or drought, especially those on chromosome 5.

- Genes on chromosome 2 are valuable for selection for yield-related traits such as Number of grains per spike "NGS" and Number of spikelets per spike "NSS".
- A large number of the stress-responsive genes are transcription factors regulating the variation in morphological and yield-related traits.
- The identified genes can be exploited to develop transgenics with higher tolerance to drought stress or for marker assisted selection “Marker Assisted Selection”.
- These genes representing a valuable base to improve drought tolerance in other cereals such as wheat.