

## Antioxidant capacity in seedling of colored-grain wheat under water deficit condition

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### Abstract

Nutritious and functional foods from crop have received great attention in recent years. Colored-grain wheat contains high phenolic compound and a large number of flavonoid. The anthocyanin and polyphenolic synthesis and accumulation is generally stimulated in response to biotic or abiotic stresses. Here, we analyzed genome wide transcripts in seedling of colored-grain wheat response to ABA and PEG treatment. About 900 and 1500 transcripts ( $p$ -value < 0.05) from ABA and PEG treatment were aligned to IWGSC1+popseq DB which is composed of over 110,000 transcripts including 100,934 coding genes. NR protein sequences of Poaceae from NCBI and protein sequence of transcription factors originated from 83 species in plant transcription factor database v3.0 were used for annotation of putative transcripts. Gene ontology analysis were conducted and KEGG mapping was performed to show expression pattern of biosynthesis genes related in flavonoid, isoflavonoid, flavons and anthocyanin biopathway. DroughtDB (<http://pgsb.helmholtz-muenchen.de/droughtdb/>) was used for detection of DEGs to explain that physiological and molecular drought avoidance by drought tolerance mechanisms. Drought response pathway, such as ABA signaling, water and ion channels, detoxification signaling, enzymes of osmolyte biosynthesis, phospholipid metabolism, signal transduction, and transcription factors related DEGs were selected to explain response mechanism under water deficit condition. Anthocyanin, phenol compound, and DPPH radical scavenging activity were measured and antioxidant activity enzyme assays were conducted to show biochemical adaptation under water deficit condition. Several MYB and bHLH transcription factors were up-regulated in both ABA and PEG treated condition, which means highly expressed MYB and bHLH transcription factors enhanced the expression of genes related in the biosynthesis pathways of flavonoids, such as anthocyanin and dihydroflavonols in colored wheat seedlings. Subsequently, the accumulation of total anthocyanin and phenol contents were observed in colored wheat seedlings, and antioxidant capacity was promoted by upregulation of genes involved in maintaining redox state and activation of antioxidant scavengers, such as CAT, APX, POD, and SOD in colored wheat seedlings under water deficit condition. This work may provide valuable and basic information for further investigation of the molecular responses of colored-grain wheat to water deficit stress and for further gene-based studies.

Keywords: colored wheat seedling, ABA, PEG, water deficit condition

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