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CHARACTERIZATION AND GENE EXPRESSION ANALYSIS OF ZINC FINGER RELATED GENES IN BREAD WHEAT (TRITICUM AESTIVUM)

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BIOCHEMICAL AND GENETIC ANALYSIS ON DROUGHT STRESS RELATED GENES IN BREAD WHEAT (TRITICUM AESTIVUM)

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ABSTRACT

Drought stress is an important problem that causes big losses in the economic yield of crops such as wheat (*Triticum aestivum*). Selection of wheat genotypes that can tolerate water stress would be helpful tools for breeding program to development drought tolerant genotypes by using relative water content (RWC) selection. The seven wheat genotypes were studied under drought stress 30% PEG-6000. The Relative water content (RWC) values decreased after 72h. DH4 exhibited the greatest value of water content with 86.6% while Gimmeza9 (sensitive) showed lowest water content with 64.2%, and the highest reduction value by 35.8%, while low reduction value was 13.4% appeared in DH4 the more tolerant than other genotypes. The first-strand cDNA synthesis was performed from total RNA isolated from roots of PEG-6000 treated wheat of four doubled-haploid bread wheat genotypes (DH1 to DH4) and three varieties (Sakha93, Sids1 and Gimmeza9), with molecular sizes 194, 234 and 204 bp representing the *WZY2*, *WUB3* and *TaOBF1b* genes respectively in all genotypes, the identification of genes involved in drought response can facilitate the genetic improvement of crops by molecular breeding.

Key words: drought stress, relative water content and drought related genes (WZY2, WUB3 and TaOBF1b) tritium aestivum, wheat.