Molecular Markers–Based Screening of Diversity for Drought Tolerance in Wheat (Triticum aestivum L.) Cultivars

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Abstract:

Drought stress can play an important role in the reduction of the plant growth and yield, specifically in arid and semi arid regions. The present study was carried out to screen 12 Sudanese wheat (*Triticum aestivum* L.) cultivars for their response to drought stress and to identify diverse sources that could accelerate the development of improved wheat varieties better adapted to meeting the challenges posed by dry climate in Sudan. For assessment, both physiological and molecular techniques were used. The effect of drought stress on the early growing stages was evaluated, in vitro, using five concentrations of Polyethylene glycol. Genetic diversity was studied using 24 allele specific simple sequence repeats (SSR) markers associated to drought tolerance in wheat. The presence of the drought genes and their chromosomal location was also investigated by isolating and sequencing of drehydration responsive element binding protein (dreb1). Results of the in vitro screening showed significant differences under different PEG concentration in all cultivars for all growth characters. The 24 drought specific SSR markers used revealed 50 alleles, with an average of 2.0 alleles per locus. Of these, 60% were polymorphic alleles with polymorphism information content (PIC) ranged from 0.16 to 0.89. A dendrogram based on the similarity values produced from the SSR data revealed three major clusters of wheat cultivars. Of the five specific primers for dreb1 genes, only primer P25F/PR has produced amplification products with the expected band sizes. Sequencing and BLAST results of the cloned fragments excised from the gels showed 99% homology to the dreb1 gene from genome A, chromosome 3 (3A) in wheat.