

Abstract

In the present study, the allelic variation within high-molecular-weight glutenins (HMW-Gs) was investigated in 30 durum wheat (*Triticum turgidum var durum*) wildtype genotypes using STS-PCR. Four pairs of primers from GLU-A1 and GLU-B1 genes were exploited for PCR. The results witnessed a remarkable variation among the studied durum wheat genotypes. The variation was analyzed using multivariate methods. Principal component analysis resulted in two principal components, explaining 66.9% of the variations collectively; where 41.38% and 25.52% of the variation was corresponded to first and second components, respectively. Cluster analysis was performed using UPGMA method. In 0.62 similarity coefficient (Jaccard's method) the genotypes were subdivided into eight subgroups. GLU-B1 locus expressed a considerable variation. The genotyped variation was partially correlated with geographical distribution.

Key words: STS, Molecular marker, genetic distance, Protein, glutenin



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