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THE ALLELIC STATE AT THE MAJOR LOW-MOLECULAR WEIGHT (LMW) AND HIGH-MOLECULAR WEIGHT (HMW) GLUTENIN SUBUNIT GENES IN A PANEL OF IRANIAN BREAD WHEAT CULTIVARS

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INTRODUCTION: The most important parts of the gluten complex in wheat are LMW-GS and HMW-GS proteins. They are encoded by a highly variable gene family. These proteins are held together by disulphide bonds to form gluten macropolymers, contribute to fundamental aspect of dough quality such as viscoelasticity, extensibility and consequently influence the end-use products of wheat. The purpose of this study was the application of PCR-based markers to discriminate different alleles at each of the LMW-GS and HMW-GS genes for the purpose of enhanced molecular marker-assisted breeding.

MATERIAL AND METHODS: A total 40 wheat improvd cultivars were obtained from gene bank of Ceral Research Instituts, Tehran, Iran. They came from the major varieties grown commercially in different zones in Iran for last decades. Genomic DNA was extracted from seeds using the CTAB procedure as reported by Gale (2005). Polymerase chain reaction (PCR) amplifications were performed in 20 µl reaction volume, consisting of 1U Taq DNA polymerase (Sinagene, Iran), 2.5 µl PCR buffer, 50 ng genomic DNA, 1.5 mM MgCl2 and 100 mM of each dNTP. PCR amplifications were conducted according to the following program: 95˚C for 4 min denaturation followed by 38 cycles of 60 s at 95˚C, 60 s at 50–70˚C (depending on the primer sets), and 120 s at 72˚C. PCR products were separated in 2% agarose gels. The allele-specific primers used in this study were adopted from Long et al. (2005) for LMW-GS. Group-specific primers of HMW-GS were designed based on the previous reported sequences of Ax2, Bx7 (Anderson & Greene, 1989), Ax1 (Halford et al. 1992), Bx17 and Dx5 (Anderson et al. 1989) by Ma et al. (2003).

RESULTS AND DISCUSSION: In this study nine specific LMW-GS and three specific HMW-GS primers, specifically amplify genes located on the A, B and D-genomes of hexaploid wheat cultivars. 11 alleles were detected in all cultivars for LMW-GS by nine pairs of specific primers and six alleles were detected in all accessions by three pairs of specific HMW-GS primers. A higher level of allelic variation of LMW-GS and HMW-GS were found in all cultivars with Nei's genetic variation index (H) of 0.73 and 0.58, respectively. A total of 39 patterns (30 for LMW-Gs and 10 for HMW-GS) resulted from the genetic combination of the alleles encoding at the glutenin loci. Although Glu-A, Glu-B and Glu-D loci were located on different chromosome arms and were theoretically independent, some cultivars were revealed due to pedigree relatedness between some Iranian wheat cultivars. The results of cluster analysis based on allelic variation for both HMW-GS and LMW-GS were also divided cultivars into three separate groups and indicated that most of genotypes that have same pedigree or geographical origin does not necessary in the same cluster grouping. This information could be useful to select Iranian varieties with improved quality and also as a source of genes to develop new lines when breeding for quality.

Keywords: LMW-GS, HMW-GS, PCR marker, Wheat (Triticum aestivum L.)