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The Genetic Potential of a Germplasm of Interspecific Crosses between Durum Wheats (*Triticum turgidum* L. ssp. *durum* (Desf.) Husn.) and their Relatives (*T. dicoccum* Schübl. and *T. polonicum* L.) in Five Glutenin Loci

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Wheat endosperm storage proteins are the major components of gluten. They play an important role in dough properties and in bread making quality in various wheat varieties. In the present study, the different alleles encoded at the 5 glutenin loci were identified from a set of 38 tetraploid wheat germplasm obtained from interspecific crosses between durum wheats (*Triticum turgidum* L. ssp. *durum* (Desf.) Husn.) and their relatives (*T. dicoccum* Schübl. and *T. polonicum* L.) using SDS-PAGE. At *Glu-A1* and *Glu-B1*, encoding high molecular weight glutenin subunits (HMW-GS), 2 and 4 alleles were observed, respectively. Low molecular weight glutenin subunits (LMW-GS) displayed similar polymorphism, as 3, 5 and 3 alleles were identified at loci *Glu-A3*, *Glu-B3* and *Glu-B2*, respectively. One new allele was detected at *Glu-B3* locus and appeared in nine accessions obtained from five crosses. This allele codes for five subunits (2 + 8 + 9 + 13 + 18), encoded by the *Glu-B3b* without subunit 16 plus subunits 2 and 18. A total of 38 patterns resulted from the genetic combination of the alleles encoding at the five glutenin loci. This led to a significantly higher Nei coefficient of genetic variation in *Glu-1*, *Glu-3* and *Glu-B2* loci (0.54). The germplasm analyzed exhibited allelic variation in HMW and LMW glutenin subunit composition and the variation differed from that of tetraploid wheats of other countries. The presence of high quality alleles in glutenin loci have led the accessions to be considered as an asset in breeding programs aimed for wheat quality.

Keywords: genetic diversity, glutenin subunits, polymorphism, durum wheats and relatives, interspecific crosses

Introduction

The wheat endosperm storage proteins are widely associated with the bread making quality (Wrigley et al. 2006). These studies suggest that the genetic variability for these proteins is highly eroded given the low frequency of some alleles (Caballero et al. 2009).

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Novel storage proteins are being screened in landraces of primitive agriculture for possible incorporation into the genomes of commercial wheats for developing new varieties with improved bread making quality (Payne 1987). Unfortunately, the improved materiel showed a narrowing in the genetic base for these genes due to the genetic drift process occurred during the genetic improvement (Gepts 1990). The loss of genetic diversity has promoted the search for new sources of variation that could help in plant breeding programs (Caballero et al. 2009). Therefore, the collection, conservation and use of both landraces and wild relatives of cultivated species were identified as a useful tool in the breeding programs (Brown et al. 1989). Wild emmer wheat has adapted to a broad range of environments and is rich in genetic resources that include drought and salt tolerances, herbicide tolerances, Zn and Fe contents, biotic tolerances, high quantity and high quality storage proteins and many others. They represent one of the best hopes for crop improvement (Ren et al. 2013). The aim of the current study is to describe the genetic diversity of high and low molecular weight glutenin subunits of 38 accessions derived from interspecific crosses between two Syrian varieties of durum wheat and two related species (*Triticum dicoccum* and *Triticum polonicum*).

Materials and methods

Plant material

Seeds from 38 accessions of sisters lines produced from the interspecific crosses between two Syrian varieties of durum wheat (*Triticum durum* Desf): Cham and Oum Rabi and two related species: *Triticum dicoccum* and *Triticum polonicum*, were analyzed in this study (Table S1*). These materials provided from the International Center for Agricultural Research in the Dry Areas (ICARDA) and were obtained by the Technical Institute of Field Crops (ITGC) Constantine; Algeria. Some durum wheat varieties and related species entering or not in the interspecific crosses (*T. dicoccum3*, Cham 1; Oum Rabi 5, Mohamed Ben Bachir, Waha, Ardente, Cirta, Hedba) were used as control, in addition to one accession of common wheat, *T. aestivum* L. cv. Chinese Spring (CS). At least three seeds were analyzed for each accession to assess its homogeneity.

Protein extraction, separation and nomenclature

Glutenins were extracted from a single half seed using the sequential procedure of Singh et al. (1991). Sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) was performed according to Singh et al. (1991). High molecular weight (HMW) glutenin alleles at *Glu-A1* and *Glu-B1* loci were identified using the nomenclature of Payne and Lawrence (1983) completed by Branlard et al. (2003). B-low molecular weight (B-LMW) glutenin alleles at *Glu-A3*, *Glu-B3* and *Glu-B2* loci were designated according to Nieto-Taladriz et al. (1997). Some standard tetraploid varieties were included to compare and classify the subunits detected.

*Further details about the Electronic Supplementary Material (ESM) can be found at the end of the article.

Data analysis

Allelic frequencies were calculated at each glutenin locus. The genetic diversity at each locus was calculated on the basis of Nei (1973) as follows: $H = 1 - \Sigma P_i^2$, with H denoting Nei's genetic variation index and P_i is the frequency of a particular allele at that locus. The polymorphism information content (PIC) was employed for each zone of the HMW and LMW glutenin subunits. The calculation of PIC for the i^{th} zone is $PIC = 1 - P_{ij}^2$, where P_{ij} is the frequency of j^{th} pattern for the i^{th} zone, and the summation extends over n patterns (Peng and Lapitan 2005; Dong et al. 2009). The similarity index was calculated according to Dedio et al. (1969). Cluster analysis based on HMW and LMW allelic frequencies was performed to determine the diversity among the accessions studied using the Euclidian distances method trough STATISTICA V.6.0 program.

Results

Variation of HMW and LMW glutenin subunits patterns

Seventeen different alleles at the *Glu-1*, *Glu-3* and *Glu-B2* loci (Table S1) were identified resulting in thirty-eight patterns in this collection. Sixteen patterns were specific to one accession (Table S1). Two and four HMW-GS were identified at the *Glu-A1* and *Glu-B1* loci, respectively. Eleven alleles encoding LMW glutenin subunits were observed in the collection.

Three, five and three alleles corresponded to the *Glu-A3*, *Glu-B3* and *Glu-B2* loci. Combination of these alleles gave seven HMW-GS patterns with the combinations *Glu-A1c/Glu-B1b* and *Glu-A1c/Glu-B1d* being the most common (26.31%), and eight LMW-GS patterns with the combination *Glu-A3h/Glu-B3new/Glu-B2a* being the most common (23.68%) (Table S1). The highest allelic variability for HMW and LMW-GS was found for chromosome 1B with four and five allelic forms at the *Glu-B1* and *Glu-B3* loci, respectively.

Glutenin diagram frequencies

Diagram frequencies observed for each zone of high and low molecular weight glutenin subunits are presented in Table S2, with a total of 21 bands and 3 null forms of silencing genes attributed to 38 diagrams that were detected for HMW and LMW glutenin subunits. Examples of glutenins and their diagrams are shown in Figure S1. In HMW-GS zone, 7 diagrams were revealed. The diagrams E (null + 7 + 8) and F (null + 6 + 8) were the most frequent in that zone with frequency 0.26, followed by the diagram A (1 + 7) with frequency 0.13. All other diagrams (B: 1 + 7 + 8, D: null + 7, G: null + 17 + 18) were accessions-specific at different levels of frequency (0.11 and 0.08, respectively). The C (1 + 17 + 18) diagram was shared by 2 accessions with frequency 0.05. For the LMW-GS zone, 15 bands and 2 null forms that attributed to 8 diagrams were recorded. The diagram H (null + 2 + 8 + 9 + 13 + 18 + 12) was the most frequentat frequency 0.24. The diagrams A (6 + 2 + 4 + 15 + 19 + 12), D (5 + 8 + 9 + 13 + 16 + 12) and E

(null + 4 + 6* + 15 + 19 + 12) were shared by 7 accessions at the 0.18 proportion. Diagrams C (6 + 2 + 4 + 15 + 17 + 19 + 12), B (6 + 8 + 9 + 13 + 16 + 12) and G (null + 4 + 6* + 15 + 19 + 12*) were considered to be rare or accessions-specific in the investigated material with relatively low frequencies (0.08 and 0.05, respectively), whereas the diagram F (null + 4 + 6* + 15 + 19 + null) was present only in one accession with frequency 0.03.

Phenotypic polymorphism

Table S2 represents the polymorphism information content (PIC) for each zone of high and low molecular weight glutenin subunits. Both zones were polymorphic. LMW-GS were considered to be the most informative with PIC value of 0.83 followed by the HMW-GS zone with PIC value of 0.81. On the other hand, this collection of accessions derived from interspecific crosses between two Syrian varieties of durum wheat and two related species (*Triticum dicoccum* and *Triticum polonicum*) disclosed important glutenin variability based on PIC values for each zone of HMW and LMW glutenin subunits.

Similarity indices

To quantify the analogy (or the dissimilarity) of diagrams, we calculate a similarity (or dis-similarity) index inspired by Dedio et al. (1969). The relative similarity index (RSI) is calculated by comparing the ASI (absolute similarity index) with the total number (N) of the components present in at least one diagram of the compared accessions, according to the following expression: RSI = (ASI/N) × 100. The ASI presents all the bands that are not significantly different between the two diagrams. Relative similarity indices (RSI) were calculated for paired comparisons of 38 accessions derived from interspecific crosses between two Syrian varieties of durum wheat and two related species (*Triticum dicoccum* and *Triticum polonicum*) based on the allelic composition and identity of all loci between each pair of accessions. The results are given in Table S3. The mean value of genetic similarity was 0.41, ranging between 0.00 and 1.00. Accessions with IRS = 0.00 (e.g. the pairs 8/1-2-13-14-15-16-18-23-28-29-34-35-38; 17/3-4-26; 7/9-10-13-14-15-23-28-29-34-35-37) displayed alternative alleles at both glutenin loci. Alternatively accessions with RSI = 1.00 (e.g., the pairs 2/23-35; 5/6; 10-11/21-25-32-36; 19/24; 21/32-36; 23/35; 25/31-35; 30/31; 32/36) shared the same range of allelic variation. Other pairs of accessions displayed such low or high glutenin variability in our study. Low values mean that diagrams have many dissimilarities. This is the case of the pairs with the RSI = 0.11, 0.25 and 0.43. Conversely, when the values of the RSI are high, the diagrams appear very close. For example the pairs with the RSI = 0.67. These accessions are always distinguishable because their diagrams have at least one difference in allelic composition.

Genetic distances

The calculation of the means of distances (similarity) of each accession with the others is given in Table S4. The result reveals that the accessions 7 and 8 (*T.DICOCCUM1* X CHAM1) have a genetic origin quite far from all the other accessions. On the other hand, the accessions 11 and 12 (*T.DICOCCUM3* X MRB5) have genetic kinships close to all the other accessions. According to Autran (1975), there is a relation between the electrophoretic heterogeneity of proteins and the genetic origin of wheat. The varieties whose diagrams are very close have, in fact, generally similar origins and naturally have both high genetic kinships and high similarity indices. Conversely, varieties with very different diagrams most often have distant genetic origins and lower similarity indices. In conclusion it can be said that the electrophoretic heterogeneity of glutenins constitute genetic markers and the similarity indices of diagrams would thus seem to express indirectly some form of kinship between varieties.

Allelic frequencies of HMW and LMW glutenin subunits

Allelic frequencies at Glu-1 loci

At *Glu-1* loci encoded for HMW-GS, each locus contains two tightly linked genes (Harberd et al. 1986) encoding subunits designated x- and y-type based on their molecular weights and biochemical characteristics (Payne et al. 1981). However, because of the silencing of some genes, only one to three HMW subunit genes are expressed in different durum wheat accessions: one or two subunits are always expressed by the *Glu-B1* locus, and one or none (the null allele) by the *Glu A1* locus. When only one subunit is expressed by *Glu-B1* or *Glu-A1* loci, this is always the x type (Shewry et al. 2003). Up to 6 allelic forms were detected at the *Glu-1* loci encoded for HMW-GS (Table S5). Two different alleles were detected at *Glu-A1* and four at *Glu-B1*. The null allele (*Glu-A1c*) was found in most accessions (71.05%), whereas the *Glu-A1a* allele was present only in eleven accessions. At *Glu-B1*, a total of four alleles were detected. Allele *Glu-B1b* was the most frequent at a frequency of 36.85%, followed by allele *Glu-B1d* with 26.31%. The alleles *Glu-B1a* and *Glu-B1i* were found in nine and five accessions with 23.68% and 13.16%, respectively.

Allelic frequencies at Glu-3 and Glu-B2 loci

The investigated material displays abundant allelic variation for LMW-GS. A total of 11 alleles were identified (Table S5). With the exception of one new allele, the identified LMW-GS were previously described by Nieto-Taladriz et al. (1997). The most common allele at *Glu-A3* was the null form (*Glu-A3h*) with a frequency of 50%, followed by *Glu-A3a* with 31.58%. Allele *Glu-A3b* was detected in only few accessions at frequency of 18.42%. At *Glu-B3*, a total of five alleles were detected, of which one allele has not been previously described. The most frequent allele was *Glu-B3j* with 26.31%, followed by *Glu-B3b* and the new one with 26.31% each. The other alleles (*Glu-B3a* and *Glu-B3d*)

were considered relatively abundant with 18.42% and 7.90%, respectively. With respect to the *Glu-B2* locus, 89.47% of the collection carries the *Glu-B2a* allele. The null allele (*Glu-B2b*) and *Glu-B2c* were present in 5.26% of the accessions. The new allele detected at *Glu-B3* locus appeared in nine accessions obtained from five crosses (*T.DICOCCUM3* X MRB5, *T.POLONICUM9* X CHAM1, *T.POLONICUM1* X MRB5, *T.DICOCCUM* X CHAM1, *T.DICOCCUM3* X MRB5) (Table S1). This allele codes for five subunits (2 + 8 + 9 + 13 + 18), encoded by the *Glu-B3b* without subunit 16 plus subunits 2 and 18.

Variation and distribution for glutenin genes

In order to assess the distribution of alleles in different populations, the classification of Marshall and Brown (1975) was used. This classification distinct among frequent (≥ 5%), rare (≤ 5%) and very rare (≤ 1%) by the presence, and wide or local distribution by the number and proximity of populations where appear. For the *Glu-1* loci (2 for *Glu-A1* and four for *Glu-B1*), all alleles were classified as frequent. For *Glu-3* and *Glu-B2* loci and according to Marshall and Brown classification, these loci presented frequent alleles (all for *Glu-A3*, 4 for *Glu-B3* and one for *Glu-B2*), relatively frequent allele (one for *Glu-B3*) and rare alleles (two for *Glu-B2*) (Table S5).

Genetic diversity

The indices (H) of genetic diversity at each of the fie loci of the 38 accessions derived from interspecific crosses between two Syrian varieties of durum wheat and two related species (*Triticum dicoccum* and *Triticum polonicum*) computed following Nei (1973) method are presented in Table S5. The collection dispalyed relatively high levels of genetic diversity. The mean index of genetic variation (H) for the germplasm analyzed was 0.54, ranging from 0.19 (*Glu-B2*) to 0.78 (*Glu-B3*). This locus was polymorphic. The mean H index at *Glu-1* was 0.57 (*Glu-A1*: 0.41, *Glu-B1*: 0.72). For *Glu-3* and *Glu-B2* loci, H indices ranged from 0.19 (*Glu-B2*) to 0.78 (*Glu-B3*), with a mean of 0.53 (*Glu-A3*: 0.62). On average, the genetic variability in *Glu-1* loci (0.57) was greater than that of *Glu-3* and *Glu-B2* loci (0.53). The higher H indices for *Glu-1* loci indicate that their alleles are relatively more distributed among the collection in a bimodal or trimodal shape, whereas the alleles in *Glu-1* are distributed in a unimodal shape.

Cluster analysis based on HMW and LMW allelic frequencies

Cluster analysis based on HMW and LMW allelic frequencies was performed to determine the diversity among the collection studied. The dendrogram (Figure S2) obtained from Euclidian distances of durum wheat accessions revealed three groups. At distance of 1.4, all accessions split into two groups (clusters I and II) that were the largest and composed of 18 and 19 accessions, respectively. Each one of clusters containing the accessions which have a high level of similarity, while the accession 26 (*T.POLONICUM1* X MRB5) is very different from other accessions and forms a group (cluster III) that was

linked to the other groups at a same distance of 2.0. Clusters I and II embodied each 11 accessions that were derived from interspecific crosses using *T. dicoccum*, the rest being derived from *T. polinicum*. The mean value of Euclidian distances was 1.0 (Figure S2), at this distance, the dendogram as a whole revealed high degree of similitude in the genetic diversity of proteins among the majority of accessions.

Discussion

In our study, we detected allelic variation at *Glu-1*, *Glu-3* and *Glu-B2* loci in 38 accessions derived from interspecific crosses between two Syrian varieties of durum wheat and two related species (*Triticum dicoccum* and *Triticum polonicum*). A total of 38 different glutenin patterns were detected, and 17 different alleles were identified for the five glutenin loci studied. The results obtained showed rather a high polymorphism in high and low molecular weight glutenin subunits variation, especially for the *Glu-B1* and *Glu-B3* loci.

For *Glu-A1* locus, the allele *Glu-A1c* is very frequent, encoding the null form. These results are in agreement with those of Nevo and Payne (1987) who found that this allele occurred in 95.7% and 79.7% of two populations analyzed of wild emmer from Israel, with those of Branlard et al. (1989) who studied a collection of 502 durum wheat varieties, with the result of Randhawa et al. (1997) who studied the polymorphism of HMW-GS of 144 accessions of relatives and cultivated wheats (25 accessions of *T. dicoccum* and 13 *T. durum*) and with those of Hamdi et al. (2010) who found that *Glu-A1c* was the most frequent (97.78%) in 856 accessions of durum wheat collected in Algeria. Similar results were obtained by Bellil et al. (2012, 2014) who found that this allele characterize 86.67% and 98.33% of the 30 varieties of Saharan durum wheat from Algerian oases and the 120 varieties of durum wheat (*Triticum turgidum* L. ssp. *durum* (Desf.) Husn.) germplasm grown in Algeria. The *Glu-A1a* encoding subunit 1 which occurs only in 28.95% of the collection analyzed, characterizes mostly the accessions obtained from crosses between *T. dicoccum* X CHAM 1. This allele appeared at lower frequencies (1.05% and 0.83%) in 856 accessions and 120 varieties of durum wheat collected in Algeria analyzed by Hamdi et al. (2010) and Bellil et al. (2014), respectively. The *Glu-A1a* was completely absent in a Saharan durum wheat from Algerian oases analyzed by Bellil et al. (2012) and in 5 populations of wild emmer from Israel analyzed by Nevo and Payne (1987). Branlard et al. (1989) showed that the subunit 1 is associated with the good wheat quality.

For *Glu-B1* locus, some alleles are very frequent, more particularly the allele *Glu-B1b* encoding subunit pairs 7 + 8. These results are in agreement with those of Bellil et al. (2014), who found that this allele occurred in 35% of the 120 varieties of durum wheat collected in Algeria, with those of Bellil et al. (2012) who studied 30 varieties of Saharan durum wheat from Algerian oases, with those of Moragues et al. (2006) who studied 63 durum wheat landraces from the Mediterranean basin and with the results reported by Carrillo (1995) who analyzed 200 varieties of Spanish durum wheat landraces. *Glu-B1b* was most frequent also in a collection of 120 Ethiopian tetraploid wheat germplasm (Hailu et al. 2006). These two subunits 7 and 8 originate from *T. dicoccum* species in this

collection. Perron et al. (1998) show that subunits Bx7 + By8 are associated with a high strength of pasta that was mesured by mixograph. Also, Khan et al. (1989) reported that subunits 7 + 8 characterize wheats with good quality. Most accessions analyzed have subunits 6 + 8 encoded by *Glu-B1d*, which is in agreement with the higher frequency of this allele found by Hamdi et al. (2010) in 856 accessions of durum wheat collected in Algeria. Similar results were observed by Branlard et al. (1989) who found also that *Glu-B1d* occurred in 26.3% of the 502 varieties of durum wheat originating from 23 countries. Cherdouh et al. (2005) studied 45 Algerian durum wheat landraces and old cultivars and found that *Glu-B1e* and *Glu-B1d* were the most frequent alleles with 32.7% each. The same results were observed by Aguiriano et al. (2008) in Spanish durum wheat landraces. Most cultivars of 120 durum wheat analyzed by Bellil et al. (2014) do not have subunits 6 + 8. Conversely, Bellil et al. (2012) and Hailu et al. (2006) found *Glu-B1d* with low frequencies. Khan et al. (1989) reported that subunits 6 + 8 are associated to wheats with bad quality. The alleles *Glu-B1a* (7) and *Glu-B1i* (17 + 18) were found in the present collection (23.68% and 13.16%, respectively). Conversely, the *Glu-B1i* allele was rare in the Algerian durum wheat genotypes analyzed by Hamdi et al. (2010) and *Glu-B1a* allele was completely absent in the other Algerian studies (Bellil et al. 2012, 2014). The allele *Glu-B1e* encoding subunit pairs 20x–20y which was the most frequent in the other studies (Bellil et al. 2014, 2012; Moragues et al. 2006; Carrillo 1995) was completely absent in all the accessions obtained from the crosses achieved despite being the only allele expressed at the *Glu-1* locus of the CHAM 1 variety used in crosses. In this case, we can talk about the dominance of genes from *T. dicoccum.* Similar results were obtained by Bellil et al. (2012); Aguiriano et al. (2008); Cherdouh et al. (2005) and Branlard et al. (1989).

For the B-LMW glutenins, three, five and three allelic variants were observed at *Glu-A3*, *Glu-B3* and *Glu-B2* loci, respectively. The alleles detected at *Glu-A3* locus were found by Bellil et al. (2012, 2014) in durum wheat collected in Algeria and Saharan wheats, by Hamdi et al. (2010) in Algerian local wheats, by Cherdouh et al. (2005) in Algerian landraces and by Nieto-Taladriz et al. (1997) in a collection of Spanish cultivars. The *Glu-A3h* allele was the most frequent in our study. Conversely, the *Glu-A3a* allele which occurs in 31.58% of the collection analyzed was the most frequent in Algerian studies (Bellil et al. 2014; Cherdouh et al. 2005; Hamdi et al. 2010), as well as in a collection of durum wheat cultivars grown in Portugal (Igrejas et al. 1999) and Spain (Nieto-Taladriz et al. 1997). The *Glu-A3c* allele which was completely absent in the germplasm analyzed was the most frequent in saharan durum wheat (Bellil et al. 2012). this allele was present with low frequency in the Algerian local and old durum wheat cultivars (Cherdouh et al. 2005; Hamdi et al. 2010; Bellil et al. 2014) and in the Spanish landraces (Aguiriano et al. 2008). The polymorphism found at the *Glu-B3* locus (five alleles) was higher than that detected at *Glu-A3*, and most of the accessions, 26.31%, had the *Glu-B3j* allele. This allele was completely absent in Algerian studies (Bellil et al. 2012, 2014; Cherdouh et al. 2005) and was to be among the rare LMW glutenin alleles that have only been found in old Spanish, Portuguese and Algerian cultivars (Nieto-Taladriz et al. 1997; Brites and Carrillo 2000; Hamdi et al. 2010). Among those rare alleles (*Glu-A3e, f, g, i, Glu-B3d, e, f, g, h, i, j, k*), *Glu-B3d* was detected in the germplasm analyzed. Most acces-

sions were characterized also by alleles *Glu-B3b* and the new one that occurred at frequency of 23.68% each. *Glu-B3b* was also present in a high frequency in Saharan durum (Bellil et al. 2012) and at low frequency in the other Algerian studies (Hamdi et al. 2010; Bellil et al. 2014). Conversely, the *Glu-B3a* allele which was present only in 18.42% of the accessions analyzed, was the most frequent in Algerian durum wheat (Bellil et al. 2014) and was also present in a very high frequency in Saharan durum wheat (Bellil et al. 2012), Algerian local and old cultivars (Hamdi et al. 2010; Cherdouh et al. 2005) and in Spanish and Portuguese collections (Igrejas et al. 1999; Aguiriano et al. 2008).

The genetic variability (H = 0.54) was higher than that obtained in cultivars from Portugal (Igrejas et al. 1999, H = 0.36) and Algeria (Bellil et al. 2014, H = 0.422; Hamdi et al. 2010, H = 0.34). Contrarily, it was lower than in durum wheat landraces from Spain (Aguiriano et al. 2008, H = 0.72), Mediterranean landraces (Moragues et al. 2006, H = 0.67) and Saharan durum wheat (Bellil et al. 2012, H = 0.63).

In conclusion, this study shows that the germplasm analyzed have extensive allelic variation in high and low molecular weight glutenin subunits including the new allele. This indicates that the germplasm analyzed have a potential value in wheat breeding. With respect to quality, accessions derived from interspecific crosses between two Syrian varieties of durum wheat and two related species (*Triticum dicoccum* and *Triticum polonicum*) have HMW and B-LMW glutenin alleles related to high grain quality such as *Glu-A1a* (Kaan et al. 1993) and *Glu-B1b,* but the HMW glutenin subunits appear to play a much less important role in the end-use quality of durum wheat (Du Cros 1987). B-LMW glutenin alleles related to high gluten strength were observed such as *Glu-A3a, Glu-A3h* and *Glu-B3a*, *Glu-B3c* (Carrillo et al. 2000). It would be interesting to make a quality evaluation of this germplasm, mainly to determine the effect on quality of the alleles and allele combinations for which no data are available. This information could be useful to select and create germplasm with improved quality.

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Electronic Supplementary Material (ESM)

Electronic Supplementary Material (ESM) associated with this article can be found at the website of CRC at http://www.akademiai.com/content/120427/

Electronic Supplementary *Table S1*. Allelic composition at the five glutenin loci found in 38 accessions derived from interspecific crosses between durum wheats and their relatives

Electronic Supplementary *Table S2*. Diagram frequencies and polymorphism information content (PIC) for each zone of HMW and LMW glutenin subunits in 38 accessions of tetraploid wheats studied

Electronic Supplementary *Table S3*. Relatives similarity indices (RSI) between 38 accessions of interspecific crosses between *T. durum* and their relatives (*T. dicoccum* and *T. polinicum*)

Electronic Supplementary *Table S4*. Genetic distances between 38 accessions of interspecific crosses between *T. durum* and their relatives (*T. dicoccum* and *T. polinicum*)

Electronic Supplementary *Table S5*. Allele frequencies of HMW and LMW glutenin and genetic index diversity at the *Glu-1*, *Glu-3* and *Glu-B2* loci of 38 accessions of interspecific crosses between *T. durum* and their relatives (*T. dicoccum* and *T. polinicum*)

Electronic Supplementary *Figure S1*. Examples of glutenins and their diagrams corresonding to HMW-GS encountered in 38 accessions of interspecific crosses between *T. durum* and their relatives (*T. dicoccum* and *T. polinicum*). Lane * is a common wheat, *T. aestivum* L. cv. Chinese Spring (CS) used as control

Electronic Supplementary *Figure S2*. Cluster analysis based on allele frequency in each accession of interspecific crosses between *T. durum* and their relatives (*T. dicoccum* and *T. polinicum*)