LMW Glutenin Subunits Variation in Persian and Polish Wheat

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Abstract: In the last years, one of the most important questions in the agriculture has been the evaluation and safeguard of genetic resources. The wild wheat relatives, together with the neglected wheat species and landraces, could be a rich source of genes for increasing the genetic base of the cultivated wheats. The LMW glutenin subunits composition of 140 accessions of Persian wheat (*Triticum turgidum* ssp. *carthlicum* (Nevski) A. Löve & D. Löve) and 159 accessions of Polish wheat (*T. turgidum* ssp. *polonicum* L. em. Thell) have been analysed by SDS-PAGE. The variability detected in these materials was greater than that detected in other hulled wheats. Twelve and seventeen different patterns have been found for the B-LMWGs zone in Persian and Polish wheat, respectively. The detected variability could be used to transfer new quality genes to cultivated wheat (durum and bread wheat) and widen their genetic base.

Keywords: *Triticum turgidum* ssp. *carthlicum*; *T. turgidum* ssp. *polonicum;* low molecular weight glutenin subunits; genetic resources

Plant breeding has eroded the genetic variability among and within cultivars in many crop species, including wheat, thereby reducing the possibility of further improvements. The lost of the genetic variability in the crops has been catalogued as a serious threat for biodiversity and for the maintenance or improvement of the crops.

In cereals, a useful tool for studies of genetic variability has been the analysis of the endosperm storage proteins or prolamins. The wheat prolamins are divided in two groups, gliadins and glutenins. Gliadins are monomeric prolamins, controlled by *Gli-1* and *Gli-2* loci located on the short arms of chromosomes of the homoeologous group 1 and 6, respectively (Payne 1987, Payne *et al*. 1982). Glutenins are divided in high molecular weight (HMW) and low molecular weight (LMW) subunits. These last can be divided in two zones: B-LMWGs and C-LMWGs, the most studied being the B-LMWGs. The genes that code for the LMW glutenin subunits are at the *Glu-3* loci. They are located on the short arms of group 1 homoeologous chromosomes and are tightly linked at the *Gli-1* loci that code some gliadins (Singh & Shepherd 1988, Pogna *et al*. 1990).

The search of the new alleles for gliadins and glutenins in wild wheat relatives neglected wheat and landraces could increase the genetic basis of wheat. Between these neglected wheats, we have incorporated two new species of naked tetraploid wheats as Persian wheat (*T. turgidum* ssp. *carthlicum* Nevski em. A. Löve et D. Löve) or Polish wheat (*T. turgidum* ssp. *polonicum* L. em. Thell.). Although both species were cultivated in the past, nowadays the major part of the genetic resources for these species are conserved only in Germplasm Banks, where they are condemned to a slow but inexorable lost of germinating power due to the scarce interest showed in these wheats during the 20th Century (Hammer 2003).

The main goal of this study was to evaluate the polymorphism of the B-LMWGs zone present in two world collections of Persian and Polish wheat.

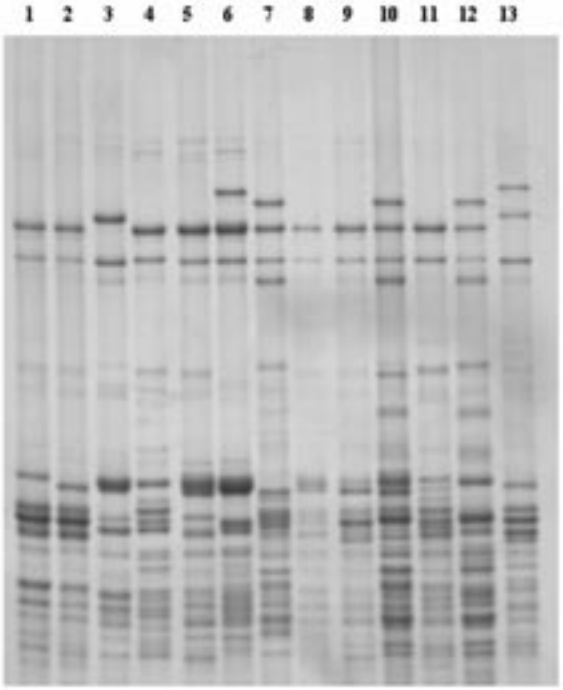

Figure 1. SDS-PAGE (10%) of a representative sample of the variability found in Persian wheat. Lanes as follow:1 – B1 (PI-78812); 2 – B2 (PI-78813); 3 – B3 (CItr 7665); 4 – B4 (PI-70738); 5 – B5 (PI-115816); 6 – B6 (PI-168672); 7 – B7 (PI-272522); 8 – B8 (PI-532500); 9 – B1 (PI-532509); 10 – B9 (PI-532511); 11 – B10 (TRI-17820); 12 – B11 (C0200512); 13 – B12 (CGN-8358)

MATERIAL AND METHODS

One hundred forty Persian wheat accessions and one hundred fifty-nine Polish wheat accessions obtained from the National Small Grain Collection (Aberdeen, USA), Genebank Gasterleben (Gasterleben, Germany), Genebank of Research Institute of Crop Production (Prague-Ruzyne, Czech Republic) and Centre for Genetic Resources (Wageningen, Netherlands) were analysed in this study.

Proteins were extracted according to the protocol described by Alvarez *et al*. (2001). Glutenin subunits were separated by electrophoresis in vertical SDS-PAGE slabs in a discontinuous Tris-HCl-SDS buffer system (pH: 6.8/8.8) at polyacrylamide concentration 10% (w/v, C: 1.28%).

RESULTS AND DISCUSSION

In this study, we analysed only the B-LMWGs zone. Because the information available on their allelic segregation in these species is very limited; we considered each group as a block. This approximation, although it is not genetically the most correct, is frequently used in the variability studies. A great variation has been detected. A representative sample of the variation detected for both species are shown in Figure 1 and 2.

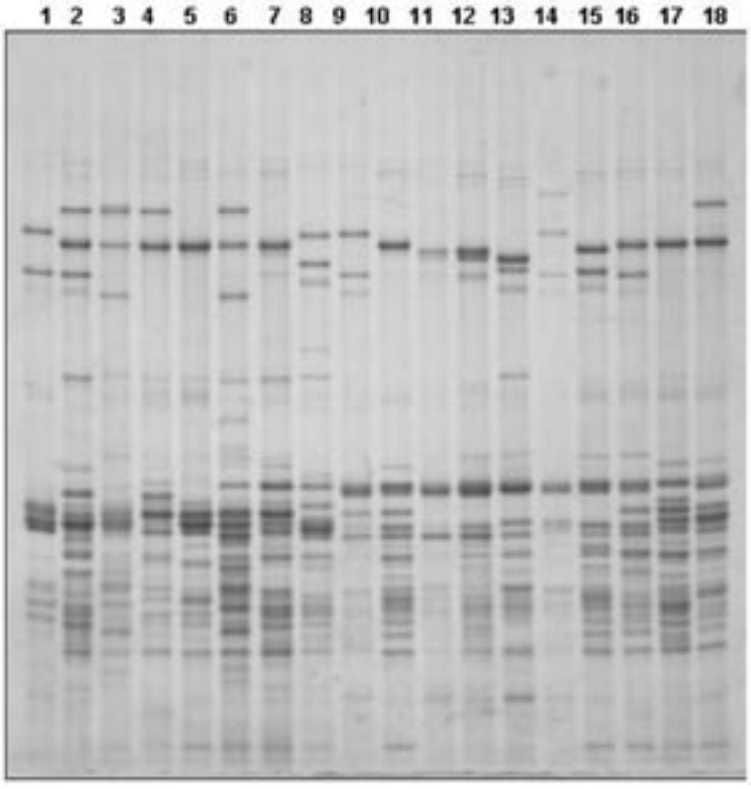

Figure 2. Representative sample of the Polish wheat variability for the B-LMWGs in SDS-PAGE (10%). Lanes as follow: 1 – B1 (CItr13919); 2 – B3 (CItr14803); 3 – B7 (PI-191620); 4 – B3 (PI-191881); 5 – B7 (PI-191893); 6 – B13 (PI-585015); 7 – B10 (TRI-6961); 8 – B17 (CGN12292); 9 – B5 (CItr5023); 10 – B2 (CItr14139); 11 – B6 (CItr7070); 12 – B12 (CItr7071); 13 – B14 (TRI-1897); 14 – B4 (PI-286547); 15 – B8 (PI-191823); 16 – B9 (PI-191823); 17 – B18 (PI-191890); 18 – B11 (PI-191903)

Table 1. Frequencies of different patterns of B-LMWGs among 140 Persian wheat accessions

Patterns	No.	%	Accession standards
1	47	33.57	PI-78812
2	34	24.29	PI-78813
3	2	1.43	Citr 7665, TRI-9535
4	2	1.43	PI-70738, PI-532518
5	46	32.86	PI-115817
6	4	2.86	PI-168672
7	1	0.71	PI-532499
8	1	0.71	PI-532511
9	1	0.71	CO204376
10	1	0.71	C0200512
11	1	0.71	CGN-6596
12	1	0.71	CGN-12284

Twenty-one bands were detected in Persian wheat; these formed up to 12 different patterns. In Polish wheat we detected only 18 bands, but they formed 17 patterns. The patterns present in Persian wheat were formed with four to eight bands, with patterns having five bands being the most frequent. The B1, B5 and B2 patterns were the most frequent, appearing in 47, 46 and 34 accessions respectively. By contrast, six out 12 patterns can be considered as rare or very rare, appearing in only one accession. The frequencies of the patterns are given in Table 1. For Polish wheat, the patterns were formed by two to seven bands, with six bands being the common number. Eight out 17 patterns appeared only in one accession. The B6 and B2 patterns were the most frequent, being detected in 72 and 41 accessions, respectively (Table 2).

Several patterns presented common bands, e.g., the bands present in the B1 and B2 patterns in Persian wheat (Figure 1, lanes 1 and 2, respectively) or in the B12 and B13 patterns of Polish wheat (Figure 2, lanes 12 and 13, respectively).

Table 2. Frequencies of different patterns of B-LMWGs among 159 Polish wheat accessions

Patterns	No.	%	Accession standards
1	1	0.63	Citr-13919
2	41	25.79	Citr-14139
3	2	1.26	Citr-14803, PI-191881
4	15	9.43	PI-384266, PI-384267
5	9	5.66	Citr-5023, PI-191837
6	72	45.28	Citr-7070, Citr-7071
7	3	1.89	PI-191893, CGC-12289
8	1	0.63	PI-191823
9	1	0.63	PI-191826
10	4	2.52	PI-191890, TRI-17209
11	3	1.89	PI-191903, TRI-3550
12	1	0.63	PI-349052
13	2	1.89	TRI-18271, C0201091
14	1	0.63	TRI-1897
15	1	0.63	TRI-3248
16	1	0.63	TRI-4466
17	1	0.63	CGN-12292

Other patterns were very similar with small differences such as one or two additional bands or change in the mobility of one band. For example, the B9 pattern that has one band more than the B11 pattern in Polish wheat (Figure 2, lanes 9 and 11, respectively).

In studies carried out with other tetraploid wheats, greater variation was found. For instance, in *T. turgidum* ssp. *dicoccum* (Pflüger *et al*. 2001) up to 23 different B-LMWGs patterns were detected. Nieto-Taladriz *et al*. (1997) found a similar number of patterns in durum wheat to that found in Polish wheat.

In conclusion, the low frequency of some patterns confirms the necessity of protection and conservation of these accessions, because the possibility of finding the same alleles in other material is very low. For this reason, these materials are being regenerated and multiplied for maintaining their variability. Further analysis of their agronomic characters, including bread making quality, must be undertaken. Their variability could be used to increase the genetic base of the modern cultivated wheats by introgression.

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