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SHORT COMMUNICATION

Relationships between the HMW- and LMW-glutenin Subunits and SDS-Sedimentation Volume in Spanish Hulled Wheat Lines

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Abstract: Emmer and spelt are two hulled wheats that were widely grown in Spain until the latter 1960s. Twenty-nine emmer and twenty-six spelt lines obtained from Spanish accessions of these hulled wheats were analysed for quality traits and endosperm storage protein composition. The results showed a wide range of variability in these traits. Likewise, a certain association between some alleles of these proteins and the SDS-sedimentation volume has been detected.

Keywords: emmer wheat; genetic resources; bread-making quality; spelt wheat

Emmer (*Triticum dicoccon* Schrank) and spelt (*T. spelta* L.) are two hulled wheats that were once widely cultivated in Spain. Since 1970 these crops have been displaced by semi-dwarf wheats bred by the International Maize and Wheat Improvement Centre (CIMMYT). Fortunately, many of these materials had previously been collected and stored in Germplasm Banks. In 2001, a broad sample of the Spanish stored materials for both species in Germplasm Banks (102 accession for emmer and 405 ones for spelt) was analysed for their endosperm storage protein composition (Caballero *et al.* 2001; Pflüger *et al.* 2001). These materials showed a high variability in these proteins with new alleles that were not detected in wheat previously. Some of these novel alleles appeared at a low frequency, which suggests a possible loss of allelic variants previously to their collection.

Nowadays, these crops are becoming popular again in some Spanish regions, mainly in Asturias (North of Spain), where they are generically named *escanda*. These materials derive from seed conserved by small farmers, who maintained its crop due to diverse cultures and customs. Recently, other farmers have begun to cultivate this *escanda*, mainly for home consumption. In these cases, the materials were obtained by way of exchange between farmers.

Our studies have confirmed the great genetic erosion that has depleted these crops (Caballero *et al.* 2007, 2008). Emmer is now rarely seen in the fields (Caballero *et al.* 2007), while in spelt, up to four alleles for the *Glu-B1* locus and five for the *Glu-D1* locus have been lost in current populations (Caballero *et al.* 2008).

The aim of the present study was to evaluate the relationships between the high-molecular-weight (HMW) and low-molecular-weight (LMW) glutenin subunits and the SDS-sedimentation volume in escanda.

Twenty-nine emmer and twenty-six spelt lines obtained from self-pollinated individual plants

Table 1. Mean values of SDS sedimentation and QI for each allele and locus in the evaluated emmer lines

Locus	Allele	Subunit	SDSs (ml)	QI (ratio)
Glu-A1	*Glu-A1a*	1	5.4a	32.5a
	Glu-A1c	*null*	4.4a	21.9b
	Glu-A1j	III	5.1a	29.5a
	Glu-A1v	VII	5.5a	30.3a
Glu-B1	*Glu-B1b*	7+8	5.2ab	33.0a
	Glu-B1d	6+8	3.8cd	25.4b
	Glu-B1n	II	6.0a	30.9a
	Glu-B1q	V	3.0d	17.0c
	Glu-B1ax	XV	4.1cd	10.1c
	Glu-B1az	XVII	5.8ab	31.5a

Mean values in each locus followed by the same letter are not significantly different at the 5% level of probability.

during two generations were analysed. These lines were obtained by single seed selection from the equal number of original accessions evaluated by Pflüger *et al.* (2001) and Caballero *et al.* (2001). The storage protein composition of these lines was analysed according to Alvarez *et al.* (2001). These lines were grown during 2005/2006 in a 1 m, one-row plot of an unreplicated trial in the Guadalquivir River Valley (Cordoba, Spain) with standard agronomic practice for the region (175 kg/ha N, 90 kg/ha P, and 90 kg/ha K) at the CIFA-IFAPA experimental station at Cordoba, Spain.

Samples were milled using a cyclone mill fitted with a 0.5 mm sieve. Protein content was deter-

Table 2. Mean values of SDS sedimentation and QI for each *Glu-3* pattern in the evaluated emmer lines

Locus	Pattern[a]	SDSs (ml)	QI (ratio)
Glu-3	1	5.9ab	33.7ab
	2	4.8abc	26.1b
	3	4.1bc	26.9ab
	4	4.0bc	26.1b
	5	6.2ab	36.5ab
	6	4.0bc	24.2b
	7	8.0a	54.0a
	8	6.3ab	35.5ab
	9	5.8abc	26.9ab
	10	3.8bc	25.4b
	11	5.8abc	25.7b
	12	4.3bc	25.5b
	13	3.5bc	23.9b
	14	4.5abc	27.8ab
	15	2.8c	16.8b

[a]according Pflüger *et al.* (2001)

Mean values in each locus followed by the same letter are not significantly different at the 5% level of probability

mined by the Kjeldahl method (%N × 5.7, dry matter). Gluten strength was estimated by the SDS-lactic sedimentation volume (SDSs) according to Peña *et al.* (1990). The quality index (QI), which represents the volume of sedimentation per unit of protein (ml/g protein), was calculated (Halverson & Zeleny 1988). All determinations were performed in duplicate. The data were analysed by one-way ANOVA and the least significant differences in SDSs and QI were calculated per each locus and species.

Given the high values for protein content detected in both crops (17.3 ± 2.6 for emmer and 18.0 ± 0.8 for spelt), the QI was used as the correction of SDS volume. The values for SDSs and QI were higher in the spelt lines than in the emmer lines.

Several studies in durum and common wheat indicated that the HMWGs synthesised by the *Glu-B1* locus play an important role in gluten strength (Payne *et al.* 1988; Pogna *et al.* 1990; Peña *et al.* 1994). In emmer, the allelic variants for the *Glu-A1* locus did not present any significant differences for SDSs; however, for QI, the *Glu-A1c* allele presented values significantly lower than the rest (Table 1). The *Glu-B1* alleles presented differences in both parameters, the differences being clearer for QI. According to this parameter, the alleles *Glu-B1q* (subunit V) and *Glu-B1ax* (subunit XV) were associated with a low SDS-sedimentation volume, whereas the alleles *Glu-B1b* (subunit 7+8), *Glu-B1n* (subunit II) and *Glu-B1az* (subunit XVIII) were associated with a high SDS-sedimentation volume. The new allele, *Glu-B1az* (subunit XVII), presented similar values for both parameters to the *Glu-B1b* allele (subunits 7+8).

Because the LMWGs (*Glu-3* loci) were related with gluten strength in durum wheat (Carrillo *et al.* 1990), these proteins were also analysed in emmer. In these lines, clear differences in both parameters were found, pattern 7 being associated with a high SDS-sedimentation volume and pattern 15 with a low SDS-sedimentation volume (Table 2).

In spelt, the *Glu-A1* alleles presented clearer differences in both parameters. The *Glu-A1a* and *Glu-A1b* alleles (subunits 1 and 2*, respectively) had similar values for SDSs and QI, but different with the *Glu-A1c* allele (Table 3). For the *Glu-B1* locus, the highest values were detected for subunits 13+16, 13+18 and 13*+16 (alleles *Glu-B1f*, *Glu-B1at* and *Glu-B1ba*, respectively), the other three alleles being associated with a low SDS-sedimentation volume (Table 3).

The *Glu-D1an* allele shows the highest values of all the alleles evaluated for the *Glu-D1* locus,

Table 3. Mean values of SDS sedimentation and QI for each allele and locus in the evaluated spelt lines

Locus	Allele	Subunit	SDSs (ml)	QI (ratio)
Glu-A1	*Glu-A1a*	1	13.7a	75.8a
	Glu-A1b	2*	13.1a	72.5a
	Glu-A1c	*null*	9.5b	54.8b
Glu-B1	*Glu-B1an*	6	10.8b	61.9b
	Glu-B1at	13+18	13.4a	76.1a
	Glu-B1e	20	10.9b	61.6b
	Glu-B1f	13+16	14.5a	80.1a
	Glu-B1bb	6+18‘	11.3b	57.6b
	Glu-B1ba	13*+16	13.5a	74.3a
Glu-D1	*Glu-D1a*	2+12	13.0b	71.9b
	Glu-D1b	3+12	13.8b	75.9b
	Glu-D1d	5+10	13.4b	77.3b
	Glu-D1an	2+12*	17.3a	98.8a
	Glu-D1ap	2.5+12	13.9b	78.4b

Mean values in each locus followed by the same letter are not significantly different at the 5% level of probability

the rest of the alleles presenting similar values among them. Seven out of these alleles (*Glu-B1an*, *Glu-B1e*, *Glu-B1bb*, *Glu-B1ba*, *Glu-D1d*, *Glu-D1an* and *Glu-D1ap*) have not been found in the current Spanish populations (Caballero *et al.* 2008), which makes the conservation of these lines very important.

In conclusion, the results of the present study show that these materials have a wide range of variability in SDS-sedimentation volume, which is associated with the presence of alleles not found in the current populations of *escanda* and in modern durum and common wheats. Because these data are preliminary, further works must be carried out to determine the association between these alleles and the gluten strength measured by rheological and baking techniques. These novel alleles could be transferred to modern wheats for enlarging the genetic pool of seed storage proteins in these wheats. Likewise, this information could be used for the quality improvement of these crops and contribute to their on-farm conservation.

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