6-24-1994

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ABSTRACT

Variation in high molecular weight glutenin subunit composition among 177 durum wheat genotypes, derived from a collection of durum wheat landraces from Jordan, was investigated using one-dimensional sodium dodecyl sulphate polyacrylamide gel electrophoresis. A total of 22 alleles, in addition to the null allele, Glu-A1c, were identified; three and seven novel variants were identified at the Glu-A1 and Glu-B1 loci, respectively. The null allele, Glu-A1c, had the highest (76.1%) frequency, followed by Glu-B1b (34.7%). Two loci at the Glu-B1 locus were lacking, these were Glu-B1c and Glu-B1i. Glu-A1b was present with low (6.7%) frequency in this collection, however, it might have a positive effect on gluten strength of the end products of durum wheat. Polymorphism (H_e) at the Glu-A1 and Glu-B1 loci averaged 0.2610.04 and 0.7330.02, respectively. H_e for Glu-A1 was negatively ($r=-0.467$; P) correlated, while H_e for Glu-B1 was positively ($r=0.615$; P), correlated with altitude of collection site. However, both H_e estimates were positively and significantly correlated with rainfall quotient.

INTRODUCTION

BRANLARD et al. (1989) pointed out that our present knowledge of high molecular weight (HMW) glutenin subunit variation in durum wheat (*Triticum durum* Desf.), as compared to that of bread wheat (*Triticum aestivum* L.), is very limited. Nevertheless, new information on these storage proteins is emerging from studies on durum wheat landraces (van Hintum and Elings, 1991) and improved cultivars (du Cross, 1987; Margiotta *et al.*, 1988; Ng *et al.*, 1989). In a recent review, Perreno and Porceddu (1990) concluded that genetical and biochemical studies, carried out on durum wheat accessions collected from several Mediterranean countries, revealed the presence of a broad genetic diversity of HMW glutenins. This variation is due to allelic genes which occur at two compound loci, i.e., Glu-A1 and Glu-B1 (Payne and Lawrence, 1983).

Studies on the HMW glutenin subunits provided useful information on genetic variation in the evolution and domestication of wheat (Galili and Feldman, 1983); enhanced the genetic variability available to improve its industrial quality (Vallega abd Waines, 1987; du Cross, 1987; Ng *et al.*, 1989), were instrumental in the assessment of genetic diversity of wild wheat (Levi and Feldman, 1988), domesticated landraces (Lagudah *et al.*, 1987; van Hintum and Elings, 1991), and improved durum wheat cultivars (Ng *et al.*, 1989; Branlard *et al.*, 1989).

This paper reports on the Glu-1 allele composition of landrace genotypes of durum wheat from Jordan, which are genetically diverse for developmental (Jaradat, 1991a) and morphological and yield-related traits (Jaradat, 1991b).

MATERIALS AND METHODS

A total of 177 landrace genotypes, derived from a collection of durum wheat landraces from Jordan (Jaradat, 1991a), were used in this study. Landrace genotypes were grouped according to agroecological characteristics of their collection sites. Rainfall quotient, which combines rainfall and mean maximum temperature effects, mean minimum temperature and elevation of collection sites, were used in characterizing collection sites (N.A.J., 1984). A total of 42 collection sites in 6 agroecological zones were identified (Table 2). Four zones (Irbid, Karak, Tafilah and Shoubak) were found within the Mediterranean semiarid bioclimate and the remaining two (Ajlun and Salt) were found within the Mediterranean semihumid bioclimate. Total proteins

were extracted from ground kernels of each landrace genotype and fractionated by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) using 17.5% polyacrylamide gels as described by Ng and Bushuk (1987). The Canadian bread wheat cultivar "Marquis" (genotype: Glu-A1a, Glu- B1c and Glu-D1d) was used as a reference in each gel. Gels were fixed and stained following the procedure of Blakesley and Boezi (1977). Identification and nomenclature of the HMW glutenin subunits followed the systems of Payne and Lawrence (1983) and Vallega and Waines (1987). Allelic frequencies and genic diversity (H_e) at Glu-A1 and Glu-B1 loci were estimated (Nei, 1972). Diversity indices, by agroecological zone, were subjected to analysis of variance. Spearman correlations were computed between all variables and multiple regression analysis was employed to determine whether agroecological factors were associated with allelic or genic diversity.

RESULTS AND DISCUSSION

Five HMW subunits, in addition to the null allele, Glu-A1c, were detected at the Glu-A1 locus (Table 1). Two of the five HMW subunits have been previously identified (Branlard *et al.*, 1989) in durum wheats, the remaining three subunits could be explained by assuming three new Glu-A1 alleles. The nomenclature of Vallega and Waines (1987) was utilized for these alleles. The new alleles accounted for 4.5% of total allelic frequency at the Glu-A1 locus. Glu-A1c, the null allele, had the highest frequency (76.1%), while the frequency of Glu-A1a and Glu-A1b were 12.7 and 6.7%, respectively. Ng *et al.* (1988) reported that all Canadian durum wheat cultivars contain the null allele Glu-A1c, which is also the most commonly occuring allele in commercial durum wheats grown throughout the world. Glu-A1b has a positive effect on gluten strength as speculated by du Cross (1987).

Seventeen HMW subunits were detected at the Glu-B1 locus (Table 1). Ten of these subunits have been previously described by Payne and Lawrence (1983) and Branlard *et al.* (1989). The remaining seven subunits could be explained by assuming five new alleles at the Glu-B1 locus. These five alleles accounted for 9.1% of total allelic frequency at this locus. Frequencies of the remaining alleles ranged from 1.2 (Glu-B1h) to 34.7% (Glu-B1b). This collection was lacking alleles Glu-B1c and Glu-B1i, and the frequency of Glu-B1a (2.9%) is low, however, this frequency is reasonably higher than the one (0.8%) reported by Branlard *et al.* (1989).

The frequencies of alleles in the collection were compared according to geographical distribution. Four alleles (Glu-A1c, Glu-B1b, Glu-B1d, and Glu-B1e) were common and widely distributed. The alleles Glu-A1a and Glu-A1b were common in only two restricted zones. All new alleles at the Glu-B1 locus were rare and restricted to the southern part of the country, especially with high (1000 m above sea level) elevation. Finally, the Glu-B1a, Glu-B1f, Glu-B1h and all new alleles at the Glu-A1 locus were rare and appeared in at least four of the six agroecological zones.

Polymorphism (H_e) at the Glu-A1 locus ranged from 0.0930.08 to 0.5780.04, and averaged 0.2610.04, whereas H_e at the Glu-B1 locus ranged from 0.6250.04 to 0.8390.02 and averaged 0.7330.02 (Table 2). Average H_e over both loci was 0.6090.025. Two of the agroecological zones (Salt and Shoubak in Table 2) exhibited very low diversity indeces for Glu-A1 due to the high frequency of the null allele, Glu-A1c.

Table 1. Allelic frequency at 2 glutenin loci for 177 landrace genotypes of durum wheat collected from Jordan.

Locus	Allele	Frequency (%)
Glu-A1	a	12.7
	b	6.7
	c	76.1
New alleles	I	1.5
	II	0.7
	III	2.3
Glu-B1	a	2.9
	b	34.7
	d	21.1
	e	27.5
	f	3.5
	h	1.2
New alleles	I	0.5
	II	1.2
	III	0.7
	IV	3.8
	V	2.9

Table 2. Characteristics of 6 ecogeographical zones and H_e estimates of two Glu-1 loci for 177 durum wheat landrace genotypes collected from Jordan.

No.	Zone	Long.	Lat.	Alt.	H_e Glu-A1	H_e Glu-B1
1	Irbid	Min. 35 40	32 30	450	0.145±0.07	0.646±0.09
		Max. 36 00	32 39	675		
2	Ajlun	Min. 35 35	32 24	700	0.366±0.09	0.747±0.03
		Max. 36 04	32 30	1000		
3	Salt	Min. 35 42	32 11	600	0.076±0.05	0.625±0.04
		Max. 35 54	32 22	1100		
4	Karak	Min. 35 44	32 00	620	0.255±0.09	0.735±0.04
		Max. 35 47	32 08	980		
5	Tafilah	Min. 35 41	31 17	700	0.578±0.04	0.839±0.02
		Max. 35 51	31 50	960		
6	Shoubak	Min. 35 28	31 04	1080	0.093±0.08	0.780±0.02
		Max. 35 41	31 04	1600		
Average					0.261±.040	0.733±.02

Analysis of variance for H_e of both loci revealed significant differences among agroecological zones. A larger portion (77%) of total variance in H_e for Glu-B1 was found within agroecological zones as compared to 55% for Glu-A1 (Table 3).

Altitude (750 m above sea level) of collection sites was a major factor in influencing H_e estimates for both loci (Table 4). H_e for Glu-A1 was negatively and significantly ($r=-0.467$;P) correlated with altitude of collection sites. On the other hand, H_e for Glu-B1 was positively and significantly ($r=0.615$; P) correlated with altitude of collection site. Both diversity indices for Glu-A1 and Glu-B1 loci were positively and significantly correlated with rainfall quotient (Table 4). Earlier findings in bread wheat (Laghudah *et al.*, 1987) indicated that variation occurs at the Glu-B1 locus in both the altitudinal set and geographical sites of landrace collections whereas allelic variation at the Glu-A1 locus was only found at the geographical set of the collection sites.

Altitude and rainfall quotient (Q) of collection sites explained 34.9% of the variability in glutenin diversity. However, when only genotypes collected from sites 750 m

Table 3. Analysis of variance for H_e estimates for Glu-A1 and Glu-B1 loci in 177 landrace genotypes of durum wheat from Jordan.

Source of variation	Glu-A1 MS	Glu-A1 % Variance	Glu-B1 MS	Glu-B1 % Variance
Among Zones	0.283 **	45	0.047**	23
Within zones	0.041	55	0.015	77

*, ** :significant at the 5% and 1% levels of probability, respectively.

Table 4. Pairwise correlation coefficients between H_e estimates for two Glu-1 loci and each of altitude and rainfall qoutient (Q) of collection sites of 177 landrace genotypes of durum wheat from Jordan.

H_e	Altitude (m) <750	Altitude (m) >750	Rainfall qoutient (Q)
Glu-A1	0.071 ns	-0.467*	0.563 **
Glu-B1	0.296 ns	0.615 **	0.451 *

ns: not significant, *, **: significant at the 5 and 1% levels of probability, respectively.

Table 5. Multiple regression analysis for H_e estimates for each of Glu-1, Glu-A1 and Glu-B1 loci in a collection of durum wheat landrace genotypes from Jordan.

Source of variation	MS Glu-1	MS Glu-A1	MS Glu-B1
Regression	0.370	0.263	0.043
Residual	0.072	0.041	0.013
P	<0.012	<0.005	<0.05
R^2	43.5%	49.8%	21.4%

above sea level were considered, both altitude and Q explained 43.5% of the variability in glutenin diversity. When each locus was considered separately, R^2 values for Glu-A1 and Glu-B1 were 49.8 and 21.4%, respectively (Table 5).

Glutenin diversity index for durum wheat landraces collected in Syria, was found to be highly correlated with geographical and climatological characteristics of their collection sites; similarly, it was highly correlated with a phenotypic diversity index based on ten phenological and morpholgical traits (van Hintum and Elings, 1991). However, other studies reported no significant differences in allelic frequencies of HMW glutenins due to geographical locations of bread wheat landraces from Afghanistan (Laghudah *et al.*, 1987) or from Nepal (Margiotta *et al.*, 1988).

This collection of durum wheat landrace genotypes from Jordan presents a wealth of quantitative and qualitative diversity for Glu-1 locus in durum wheat, as compared with a total of 18 different alleles identified in 502 durum wheats (Branlard *et al.*, 1987).

Quantitative and qualitative variation in HMW glutenin subunits of these landrace genotypes of durum wheat can be exploited in wheat breeding programs (Lukow *et al.*, 1992), and will be useful in developing countries for specialty end-use cultivars of durum wheat.

LITERATURE CITED

Branlard, G, J.C. Autran, and P. Monneveux, 1989. High molecular weight glutenin subunits in durum wheat (*Triticum durum*). Theor. Appl. Genet. 78:353-358.

Blakesley, R.W. and J.A. Boezi, 1977. A new staining technique for proteins in polyacrylamide gels using Comassie Brilliant Blue G250. Anal. Biochem. 82:580-582.

du Cross, D.L., 1987. Glutenin proteins and gluten strength in durum wheat. J. Cereal Sci. 5:3-12.

Galili, G. and M. Feldman, 1983. Genetic control of endosperm protein in wheat I. The use of high resolution one-dimensional gel electrophoresis for the allocation of genes coding for endosperm protein subunits in the common wheat cultivar Chinese Spring. Theor. Appl. Genet. 64:97-101.

Jaradat, A.A., 1991a. Breeding potential of durum wheat landraces from Jordan I. Phenotypic diversity. Hereditas 116:301-304.

Jaradat, A.A., 1991b. Breeding potential of durum wheat landraces from Jordan II. Differential responses to drought. Hereditas 116:305-309.

Lagudah, E.S., R.G. Flood and M. Halloran, 1987. Variation in high molecular weight glutenin subunits in landraces of hexaploid wheat from Afghanistan. Euphytica 36:3-9.

Levi, A.A. and M. Feldman, 1988. Ecogeographical distribution of HMW glutenin alleles in populations of the wild tetraploid wheat *Triticum turgidum* var *dicoccoides*. Theor. Appl. Genet. 75:651-658.

Lukow, O.M., S.A. Forsyth and P.I. Payne, 1992. Overproduction of high molecular weight glutenin subunits coded on chromosome 1B in common wheat, *Triticum aestivum*. J. Genet. & Breed. 46:187-192.

Margiotta, B., D. Lafiandra, C. Tomassini, P. Perrino and E. Porceddu, 1988. Variation in high molecular weight glutenin subunits in a hexaploid wheat collection from Nepal. *In:* T.E. Miller and R.M.D. Koebner (eds) Proc. of the 7th International Wheat genetics Symposium, Cambridge. pp 975-980.

National Atlas of Jordan, 1984. Climate and agroclimatology. Part I. Jordan National Geographic Center, Amman, pp 135.

Nei, M., 1972. Genetic distances between populations. Am. Nat. 106:283-292.

Ng, P.K.W. and F. Bushuk, 1987. Glutenin of Marquis wheat as a reference for estimating molecular weights of glutenin subunits by SDS-PAGE. Cereal Chem. 64:324-327.

Ng, P.K.W., N.E. Pogna, F. Mellini and F. Bushuk, 1989. Glu-1 allele composition of the wheat cultivars registered in Canada. J. Genet & Breed. 43:53-59.

Payne, P.I. and G.J. Lawrence, 1983. Catalogue of alleles for the complex gene loci Glu-A1, Glu-B1 and Glu-D1 which code for high-molecular weight subunits of gluten in hexaploid wheat. Cereal Res. Commun. 11:29-35.

Perrino, P. and E. Porceddu, 1990. Wheat genetic resources in Ethiopia and the Mediterranean region. *In:* J.P. Srivastava and A.B. Damania (eds). Wheat genetic resources: meeting diverse needs. pp 161-178.

Vallega, V. and J.G. Waines, 1987. High-molecular-wieght glutenin subunits in *Triticum turgidum* var *dicoccum*. Theor Appl Genet 74:706-710.

van Hintum, T.H. J.L. and A. Elings, 1991. Assessment of glutenin and phenotypic diversity of Syrian durum wheat landraces in relation to their geographical origin. Euphytica 55:209-215.