



High molecular weight glutenin subunit composition in wheat (*Triticum aestivum* L.)

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The suitability of a wheat (*Triticum aestivum* L.) cultivar for different end uses, viz., bread, chapathi, biscuit, noodle and pasta products is determined to a large extent by its seed protein composition [1]. Glutenin proteins of wheat endosperm form polymeric aggregates that vary widely in molecular size and that confer unique viscoelastic properties on wheat flour dough. The high molecular weight subunits of glutenin are of special significance because, despite constituting only about 10% of the total flour protein, they make a profound contribution to dough strength [2]. These subunits are encoded by genes at the Glu-A1, Glu-B1, and Glu-D1 loci on the long arm of homoeologous chromosomes 1A, 1B and 1D respectively. The subunits are highly polymorphic and a number of alleles have been identified at each of the homoeo loci [3]. These alleles have different effects on dough viscoelastic properties. Hence, these subunits are useful not only for the identification of wheat cultivars, but can also be used by breeders in choosing parental lines and selecting progenies with superior gluten quality. Although India is the second largest producer of wheat in the world, limited information is available on the allelic variation for these proteins among the Indian wheat cultivars [4].

The experimental material for the investigation comprised of 49 strains of bread wheat which includes 8 commercial cultivars and 41 advanced breeding lines. All the strains were collected from wheat quality laboratory and wheat breeding section of Division of Genetics, IARI and IARI Regional Station, Wellington. All the strains were analysed for protein percentage and high molecular weight glutenin subunit composition (HMW-GS). The Kjeldahl method given by A.O.A.C. (1965) was used to determine the percentage of protein [5]. Total seed proteins were extracted from half kernels with sample buffer (0.2ml) containing 4% (w/v) SDS, 15% (v/v) glycerol, 0.001% (w/v) bromophenol blue,

2% (v/v) 2-mercapto-ethanol and 0.06 N Tris-HCL, pH 6.8, at 60°C for 1 hour and then centrifuged at 12000 g for 10 min. Aliquots (10 ul) of the supernatant were loaded into the sample wells of the gel for SDS-PAGE separation of high molecular weight glutenin subunits. At least 10 kernels of each cultivar were analysed to check for homogeneity. The discontinuous SDS-PAGE system used was based on that of Lawrence [6], with the following modifications. The stacking gel had 3% acrylamide, 2.6% C (bis-acrylamide-to-acrylamide ratio), 0.1% (w/v) SDS and 0.125 N Tris-HCL, pH 6.8, The separating gel (150×150×1.5 mm) contained 10% acrylamide, 1.5% C, 0.1% (w/v) SDS and 0.375 N Tris-HCl, pH 8.9. Electrophoresis was performed for 18 hours at 8 mA per gel [8].

Amongst the 49 strains examined, only one allele was identified for the Glu-A1 locus (2*). Three alleles (7+8, 7+9 and 17+180 at Glu-B1 locus and two alleles (2+12 and 5+10) at Glu-D1 locus were identified. The identity of individual subunits was determined by comparison with standard cultivars having known subunits e.g. Kundan (2*, 17+18, 5+10), VL 401 (1, 7+8, 2+12), NI-917C (null, 7+9, 2+12) and so on. All the high molecular weight subunits, except 2 and 2*, were clearly separated in a 10% acrylamide gel with 1.5% C. However, an indication of the likely presence of subunit 2* could be obtained from the comparative strength and width of band 2, which was noticeably broader when present with 2*. These two subunits were easily distinguished by employing an 8% acrylamide gel (1.5% C), in which 2* had a higher electrophoretic mobility than subunit 2. The allelic composition at the Glu-A1, Glu-B1 and Glu-D1 loci of each of the 49 cultivars is shown in Table 1.

Subunits 2+12 for the Glu-D1 locus, 7+8 for the Glu-B1, locus and 2* for the Glu-A1 locus were the

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Table 1. The HMW-GS composition of 49 strains of wheat

Sl. No.	Strains	Protein Percent	HMW-GS Composition			Glu-1 Quality Score	Total
			1A	1B	1D		
1.	Kalyansona	13.0	2*	17+18	2+12	3+3+2	8
2.	HW 2061	12.5	2*	17+18	2+12	3+3+2	8
3.	HW 2002A	12.6	2*	17+18	2+12	3+3+2	8
4.	Sonalika	13.2	2*	7+9	2+12	3+2+2	7
5.	HW 2031	12.7	2*	7+9	2+12	3+2+2	7
6.	HW 2001 A	12.3	2*	7+9	2+12	3+2+2	7
7.	HD 2329	13.7	2*	7+9	2+12	3+2+2	7
8.	HW 2037	12.3	2*	7+9	2+12	3+2+2	7
9.	HW 2007	13.1	2*	7+9	2+12	3+3+2	7
10.	HW 2046	12.4	2*	7+9	2+12	3+3+2	8
11.	HD 2285	13.0	2*	7+8	2+12	3+2+2	8
12.	HW 2038	12.5	2*	7+8	2+12	3+3+2	8
13.	HW 2008	12.8	2*	7+8	2+12	3+3+2	8
14.	Lok 1	10.9	2*	17+18	2+12	3+3+2	8
15.	HW 2032	11.0	2*	17+18	2+12	3+3+2	8
16.	HW 2006	11.2	2*	17+18	2+12	3+3+2	8
17.	HW 2041	11.0	2*	17+18	2+12	3+3+2	8
18.	WH 147	11.7	2*	7+8	2+12	3+3+2	8
19.	HW 2042	12.0	2*	7+8	2+12	3+3+2	8
20.	PBW 226	11.9	2*	7+8	2+12	3+3+2	8
21.	HW 2044	12.0	2*	7+8	2+12	3+3+2	8
22.	HUW 234	11.9	2*	7+8	2+12	3+3+2	8
23.	HW 2043	11.4	2*	7+8	2+12	3+3+2	8
24.	P 271-4	12.6	2*	17+18	2+12	3+3+2	8
25.	P 421-7	15.3	2*	7+9	2+12	3+2+2	7
26.	P 425-23	17.2	2*	7+8	2+12	3+3+2	8
27.	HW 2047	15.1	2*	7+9	2+12	3+2+4	9
28.	HW 2048	14.4	2*	17+18	5+10	3+3+4	10
29.	HW 2045	12.2	2*	7+8	2+12	3+3+2	8
30.	T 2669	11.7	2*	7+8	2+12	3+3+2	8
31.	1536	14.9	2*	7+8	2+12	3+3+2	8
32.	1544	14.4	2*	17+18	5+10	3+3+4	10
33.	2104	14.0	2*	17+18	5+10	3+3+4	10
34.	2103	13.6	2*	17+18	5+10	3+3+4	10
35.	21	14.0	2*	7+9	5+10	3+2+4	9
36.	2160	12.9	2*	7+9	5+10	3+2+4	9
37.	2173	11.2	2*	7+8	2+12	3+3+2	8
38.	2233	12.0	2*	7+8	2+12	3+3+2	8
39.	2175	15.5	2*	7+8	2+12	3+3+2	8
40.	2206	12.0	2*	7+8	2+12	3+3+2	8
41.	2219	11.1	2*	7+8	2+12	3+3+2	8
42.	P 319-9	13.6	2*	7+8	2+12	3+3+2	8
43.	P 331-57	16.9	2*	7+8	2+12	3+3+2	8
44.	P 424-7	12.7	2*	7+8	2+12	3+3+2	8
45.	P 416-8	14.0	2*	7+8	2+12	3+3+2	8
46.	P 427-11	13.2	2*	17+18	2+12	3+3+2	8
47.	P 414-5	13.0	2*	7+8	2+12	3+3+2	8
48.	P 414-8	13.9	2*	7+8	2+12	3+3+2	8
49.	P 389-2	13.7	2*	17+18	2+12	3+3+2	8

predominant alleles among the Indian wheat. The most frequent combinations of subunits were 2*, 7+8, 2+12 and 2*, 17+18, 2+12. The predominance of these two combinations of subunits is not pedigree related as the cultivars in the two groups have diverse origins. Since the Indian wheat breeders lines are tested extensively for their chapathi-making quality before release, these combinations of subunits may have been selected for their favourable effect on quality.

On summation of Glu-1 quality scores [7] assigned to individual subunits [Table 2], four strains had a maximum Glu-1 score i.e. '10', possible for any variety best suited for breadmaking. All these four lines recorded a protein per cent more than 13 indicating that they

are highly suitable for breadmaking. All these lines possess 5+10 subunit at Glu-D1 locus. Three more lines also possess 5+10 subunit at Glu-D1 locus but ended up with a Glu-1 quality score 9 because of the presence of a poor subunit (7+9) at their Glu-B1 loci.

Table 2. Quality scores assigned to individual or pairs of HMW Glutenin subunits

Score	Chromosome		
	1A	1B	1D
4	-	-	5+10
3	1	17+18	-
3	2*	7+8	-
2	-	7+9	2+12
2	-	-	3+12
1	Null	7	4+12
1	-	6+8	-

Though selection has not been applied for bread making quality, four lines qualified the test for bread making quality. A clue for wheat breeders who wish to develop varieties with improved bread making quality is therefore to cross genotypes that have complementary good quality subunits coded by different loci and to select progeny with high Glu-1 quality scores.

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