
Development of a new marker system for identifying the complex members of the low-molecular-weight glutenin subunit gene family in bread wheat (*Triticum aestivum* L.)

Theoretical and Applied Genetics

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Supplementary Table 1 Identification of the LMW-GS genes in Chinese Spring with the marker system developed in the present study

Chromosome ^a	LMWGS1	LMWGS2	LMWGS3a	LMWGS3b	LMWGS3c	Accession No. ^b
1A	391	485	375	--	--	--
1D	385	492	383	--	--	AK330800 ^e
1D	393	499	390	--	--	--
1D	394	501	393	--	--	DQ457417 ^f
1A	402	509	402	--	--	--
1D	441	547	441	--	--	FH615311
1A	N ^c	N	-- ^d	--	537	--
1D	525	632	531	--	--	DQ357052/AY214450
1B	530	637	--	537	--	X84960
1B	549	655	--	556	--	--
1D	575	N	--	583	--	X84961
1B/1D	578	684	--	586	--	DQ357057
1D	590	695	--	600	--	--
1B	593	700	--	608	--	--
1A	620	725	--	--	666	AT453154/FJ876821
1B	624	729	--	639	--	--

^a Chromosome locations of the DNA fragments from Chinese Spring were identified with its nullisomic–tetrasomic lines N1AT1D, N1BT1D and N1DT1B

^b The LMW-GS genes/alleles, identified from Chinese Spring reported in GenBank, share the same size and/or high identity with the DNA fragments detected in the present study

^c not detected

^d not applicable

^e from the cDNA clone in Chinese Spring, which was not annotated to be the LMW-GS gene

^f having high sequence identity with the sequences of the corresponding DNA fragment, but containing some deletions in the repetitive region

Supplementary Table 2 Comparison of the DNA fragments with the LMW-GS gene sequences reported in GenBank from Xiaoyan 54, Norin 61, Glenlea and Chinese Spring

Xiaoyan 54			Norin 61			Glenlea		Chinese Spring	
Gene	Size ^a	Accession No. ^b	Size	Accession No.	Type	Size	Accession No.	Size	Accession No.
<i>LGS2-477</i>	477	--	460	--	--	477	--	485	--
<i>D3-4</i>	492	FJ755311	492	AB062873	Group 8	492	EU189090/ EU189091/ EU189092	492	AK330800 ^e
<i>D3-5</i>	499	FJ755312	499	--	--	499	--	499	--
<i>D3-7</i>	501	FJ755314	501	AB062872	Group 7	501	EU189093	501	DQ457417 ^d
<i>A3-1</i>	509	FJ755302	506	AB062868	Group 6	515	--	509	--
<i>D3-2</i>	538	FJ755315	538	AB062875	Group 10	538	EU189094	547	FJ615311/ DQ357054
<i>LGS2-590</i>	590	--	590	--	--	596	--	596	--
<i>D3-6</i>	632	FJ755313	632	AB062865	Group 5	635	EU189098	632	AY214450/ DQ357052
<i>B3-1</i>	637	FJ755306	637	AB062852 ^d	Group 2	637	EU189089/ EU189097	637	X84960
<i>LGS2-651</i>	-- ^c	--	--	--	--	651	EU189088	--	--
<i>LGS2-655</i>	655	--	655	--	--	655	--	655	--
<i>A3-3</i>	672	FJ755305	672	AB062876 ^d	Group 11	--	--	--	--
<i>A3-2</i>	675	FJ755304	675	--	--	--	--	--	--
<i>D3-1</i>	682	FJ755310	682	AB062851	Group 1	682	EU189096	682	X84961
<i>D3-3</i>	684	FJ755316	684	DQ357058	Group 4	684	EU189095	684	DQ357057
<i>LGS2-690</i>	690	--	695	--	--	695	--	695	--
<i>LGS2-700</i>	--	--	--	--	--	--	--	700	--
<i>A3-4</i>	768	FJ755303	768	AB062877 ^d	Group 12	750	EU189087	725	AY453154
<i>B3-2</i>	792	FJ755309	792	AB062855 ^d	Group 3	726	--	729	--
<i>B3-3</i>	--	FJ755307	795	AB062853	Group 3	--	--	--	--

^a Sizes of the DNA fragments were represented with data from the primer LMWGS2

^b LMW-GS genes/alleles identified from Xiaoyan 54 (Dong et al. 2010), Norin 61 (Ikeda et al. 2002), Glenlea (Huang and Cloutier 2008) and Chinese Spring reported in GenBank share the same size and/or high sequence identity with the DNA fragments detected in the present study

^c not applicable

^d having high sequence identity with the sequences of the corresponding DNA fragment, but containing some deletions in the repetitive region

^e from the cDNA clone in Chinese Spring, which was not annotated to be a LMW-GS gene