Protein and Quality Characterization of Triticale Translocation Lines in Breadmaking

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ABSTRACT

Introduction of high molecular weight glutenin subunits (HMW-GS) from the *Glu-D1d* locus of wheat into triticale restores the genetic constitution of high molecular weight glutenin loci to that of wheat and subsequently improves the breadmaking quality of triticale. One means of achieving such restoration of the genetic constitution is through the use of translocation lines. The aim of this study was to evaluate and compare the performance of translocations 1A.1D and 1R.1D with HMW-GS 5+10 and 2+12 in terms of physical dough tests and baking quality using four different sets of triticale lines, GDS7, Trim, Rhino, and Rigel. In general, significantly lower milling quality (flour yield), very low mixing times with lower loaf volume were typical of all the triticales studied except 1A.1D 5+10 lines, when compared to hard wheat flour (Pegaso). Among the lines studied, significantly higher loaf volume, mixograph dough development time (MDDT), and maximum resistance to extension (R_{max}) were observed with 1A.1D 5+10 lines indicating that translocation of the *Glu-D1d* allele with HMW-GS 5+10 was beneficial in terms of improving the quality attributes. Although pure triticale flour from these lines did not possess the functional characteristics for good quality bread, the translocation 1A.1D that contains HMW glutenin subunits 5+10 showed significant improvement in quality characteristics, and could reasonably be expected to yield commercially satisfactory bread loaves when combined with bread wheat flour. Significantly higher UPP, R_{max}, and MDDT values along with a lower gliadin-to-glutenin ratio in 1A.1D 5+10 of GDS7 and Rigel sets indicate that the molecular weight distribution was shifted to higher molecular weights, resulting in greater dough strength associated with 5+10 subunits.

Triticale (X *Triticosecale* Wittmack), the first man-made cereal, is a hexaploid that combines the A and B genomes from wheat (*Triticum* spp.) and the R genome of rye (*Secale cereale*) to obtain the high yield potential and good grain quality of wheat with the disease and environmental resistance of rye.

The FAO (http://faostat.fao.org/site/567/DesktopDefault.aspx?PageID=567) reported the worldwide acreage of triticale was 3.9 million ha. This is an increase of 1.6 million ha over 1998 with a production of 14 million tons of grain. Triticale has remained stable and even showed a slight increased in acreage worldwide due to use as forage and feed. Triticale does have limited application in food but is not expansive because of the deficiency in gluten. Triticale does have better agronomic properties (Martinek et al 2008); the crop may have application if modification of the triticale genome incorporates genes contributing to breadmaking quality from wheat.

Cultivated hexaploid triticale lines have the genomic constitution AABBRR. They differ from bread wheat (AABBDD) by a replacement of the D genome of wheat with the R genome from rye (*Secale cereale* L.). Consequently, triticale has one-third fewer loci coding for important gluten storage proteins and contains less gluten (Lukaszewski 1998). The genes coding for wheat storage proteins that confer breadmaking properties are located on group 1 and 6 chromosomes. High molecular weight glutenin subunits (HMW-GS) are encoded by genes (*Glu-1)* on the long arms of group 1 chromosomes. Most of the low molecular weight glutenin subunits (LMW-GS) are encoded at the *Glu-3* loci on the short arms of chromosome 1, as are the major gliadins (*Gli-1*). Additional gliadins (Gli-2) are encoded on the short arms of group 6 chromosomes. The R genome of rye contributes the secalin loci, *Sec-3* (on 1RL), *Sec-1* (on 1RS), and *Sec-2* (on 2 RL) into triticale (Shewry et al 1984; Lukaszewski 2001). Thus the absence of the D genome results in the poor breadmaking quality of triticale (Zeller and Hsam 1984). However, secalins are not entirely detrimental to breadmaking quality; *Sec-3* had some positive effects on dough properties (Kumlay et al 2003); no effect of *Sec-2* on any dough properties has been reported so far (Gupta et al 1989).

Nevertheless, in comparing contributions of individual group-1 chromosomes to breadmaking quality of triticale, rye chromosome 1R has always been placed higher than wheat chromosome 1A (Kazman and Lelly 1996; Lukaszewski 1996, 1998; Kumaly et al 2003).

The restoration of the genetic constitution of the wheat storage protein loci (i.e., the *Glu-D1d* gene that encodes HMW-GS 1Dx5 and 1Dy10) of triticale is paramount to becoming a commercially viable cereal (Shewry et al 1995). This may be achieved in several different ways: 1) transformation with known storage protein loci from the D-genome of wheat and concomitant silencing of the detrimental secalin loci (Shewry et al 1995); 2) chromosome substitution, or cytogenetic engineering of specific segments of chromosomes that carry important loci (Lukaszewski 2006).

Lafferty and Lelley (2001) reported three possible substitutions, 1D(1A), 1D (1B), and 1D(1R) that lead to significant increase in the Zeleny sedimentation value. The difference between two gluten alleles *Glu-D1a* (HMW-GS 2+12) and *Glu-D1d* (HMW-GS 5+10) was not as obvious as in wheat. Besides a high cytological stability and minimal effect on agronomic performance, substitution with 1D(1A) appears to be the most desirable in triticale breeding, whereas the other two substitutions 1D(1B) and 1D(1R) showed considerable yield loss (Lukaszewski 1990).

Brezinski and Lukaszewski (1998) reported that the baking quality of substitutions 1D(1R) and 1D(1A) was comparable to a wheat check cultivar and showed improvement over previous triticale lines. Replacement of 1A or 1B by 1D does not eliminate the effect of chromosome 1R and rye secalins in triticale.

To improve the breadmaking performance of triticale, Lukaszewski and Curtis (1992, 1994) used chromosomal engineering to transfer a segment of a chromosome 1D of bread wheat with the *Glu-D1d* allele encoding HMW-GS 5+10 to chromosome 1R of the triticale Rhino. Using the same approach, *Glu-D1a* (2+12) and *Glu-D1d* (5+10) alleles were introduced into chromosome 1A of the same triticale line.

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The hypothesis of the study was that modification of triticale translocation lines will improve bread quality. The objective was to evaluate and compare the performance of translocations 1A.1D and 1R.1D with HMW-GS 5+10 and 2+12 in terms of physical dough tests and baking quality using four different sets of triticale lines, GDS7, Trim, Rhino, and Rigel.

MATERIALS AND METHODS

Development of Triticale Samples

The translocated Rhino triticale lines (1R.1D$_{5+10}$, 1A.1D$_{5+10}$, and 1A.1D$_{2+12}$ were provided by A. Lukaszewski from the Department of Botany and Plant Sciences, University of California, Riverside, CA. These lines were crossed and backcrossed at least four times with three other triticales (GDS7, Trim, and Rigel) to transfer translocated segments in different backgrounds and evaluate the effect of the specific translocation types on breadmaking performance. After each backcross, analysis of HMW-GS were conducted on 10% SDS-PAGE as described in Pirozi et al (2008) and seeds with subunits 5+10 or 2+12 were planted and backcrossed again with GDS7, Trim, and Rigel. At the end of the backcrossing, material was increased and all the translocated lines along with the Rhino triticale lines described above were field-grown for one year in Viterbo (Central Italy) in randomized triplicate plots (1.5 m × 5 m). Descriptions of the lines along with HMW-GS compositions are presented in Table I. All the triticale lines studied possess HMW-GS 13+16 subunits at the *Glu-B1* loci.

Further information about Materials and Methods used in this study are described in a companion article (Jonnala et al 2010).

Test Baking

Bread loaves were baked according to the breadmaking test for 10 g of flour described by Shogren and Finney (1984). Bread loaves were made in duplicate for each wheat sample and the average data was reported. All ingredients were mixed together to optimum gluten development according to the mixograph mixing times. Developed doughs were sheeted, folded twice, and placed in an open container and fermented for 120 min in a proofing

TABLE I
Selected Triticale Translocation Lines Used in Production and Evaluation of Bread

		HMW Glutenin Subunits on Chromosome		
	Translocation	1A	1B	1R
GDS7 set				
GDS7	Parent line	Null	13+16	
GDS7 1R.1D 5+10	1R.1D	Null	13+16	5+10
GDS7 1A.1D 2+12	1A.1D	2+12	13+16	
GDS7 1A.1D 5+10	1A.1D	5+10	13+16	
Trim set				
Trim	Parent line	1	13+16	
Trim 1R.1D 5+10	1R.1D	1	13+16	5+10
Trim 1A.1D 2+12	1A.1D	2+12	13+16	
Trim 1A.1D 5+10	1A.1D	5+10	13+16	
Rhino set				
Rhino	Parent line	Null	13+16	*Sec-3*
Rhino 1R.1D 5+10	1R.1D	Null	13+16	5+10
Rhino 1A.1D 2+12	1A.1D	2+12	13+16	*Sec-3*
Rhino 1A.1D 5+10	1A.1D	5+10	13+16	*Sec-3*
Rigel set				
Rigel	Parent line	Null	13+16	
Rigel 1R.1D 5+10	1R.1D	Null	13+16	5+10
Rigel 1A.1D 2+12	1A.1D	2+12	13+16	
Rigel 1A.1D 5+10	1A.1D	5+10	13+16	

TABLE II
Physical Characterization, Hardness Index (HI), and Flour Properties of Selected Triticale Translocation Lines[a]

		Milling Yield (%)				
	HI	Break Flour	Total Flour	Bran	% Flour Protein	% Flour Moisture
GDS7 set						
GDS7	52	34.7	40.1	59.8	9.0a	14.9a
GDS7 1R.1D 5+10	58	32.6	37.8	62.2	8.3bc	14.1a
GDS7 1A.1D 2+12	60	27.6	32.6	67.3	8.4b	14.6a
GDS7 1A.1D 5+10	58	34.7	41.0	58.9	8.3c	14.5a
Trim set						
Trim	57	31.8	37.8	62.2	7.9c	13.7a
Trim 1R.1D 5+10	68	33.9	38.8	61.2	9.6a	13.9a
Trim 1A.1D 2+12	55	30.1	35.9	64.1	8.9b	14.3a
Trim 1A.1D 5+10	56	27.3	32.5	67.4	8.1c	14.6a
Rhino set						
Rhino	63	37.9	43.6	56.4	7.4a	13.9b
Rhino 1R.1D 5+10	62	35.4	40.9	59.2	6.9c	14.6a
Rhino 1A.1D 2+12	53	34.8	42.3	57.7	6.9c	14.1ab
Rhino 1A.1D 5+10	53	39.5	46.2	53.8	6.9b	14.3ab
Rigel set						
Rigel	59	40.4	46.2	53.8	7.2c	13.5c
Rigel 1R.1D 5+10	54	29.7	34.1	65.9	10.3a	14.2ab
Rigel 1A.1D 2+12	51	39.5	45.5	54.5	7.4c	13.7bc
Rigel 1A.1D 5+10	64	31.8	36.8	63.1	9.1b	14.9a

[a] Values in each set followed by the same letters in the same column are not significantly different at $P < 0.05$.

chamber maintained at 30 ± 1°C and 95 ± 1% rh. Punch times were 69, 103, and 120 min during fermentation. Doughs were then resheeted, molded using a 10-g molder, and proofed for 40 min at 30°C and baked at 232°C for 13 min. Loaf volumes were assessed using rapeseed displacement (AACC Approved Method 10-05.01) after cooling bread for 2 hr. All loaves of developed lines were compared against bread from parent lines.

C-Cell Image Data Analysis

Bread quality factors such as crumb grain, crumb texture, and other characteristics were assessed using the C-Cell image analysis technique and the data was analyzed using the C-cell software (Calibre Control International, Warrington, UK). Image analysis of crumb grain was performed on 10-g bread loaves ≈12 hr after baking. Loaves were sliced using a rotary disk blade cutter (unserrated Graef blade), and measurements were conducted on central slices 15-mm thick from each loaf. Two slices from each bread loaf was used for analysis. Thus, the C-Cell data reported was an average of four slices from each triticale sample. Loaf and cell characteristics such as loaf weight, slice area, loaf height, number of cells, wall thickness, and cell diameter measured by image analysis were correlated with quality and protein characteristics.

Comparison to Hard Wheat Flour

Baking and flour quality tests results in the present study were compared to Pegaso wheat, a typical Italian bread wheat cultivar (Jonnala et al 2008). For convenience of the readers, important flour quality data of Pegaso wheat is hardness index 62, milling yields (47.7% bran, 52.6% total flour, and 46.3% break flour), HPLC-SEC data (UPP 42.1%, PPP 40.5%, and gliadin 39.1%), mixograph test (MDDT 4.7 min) and micro-extension values (R_{max} 299 mN).

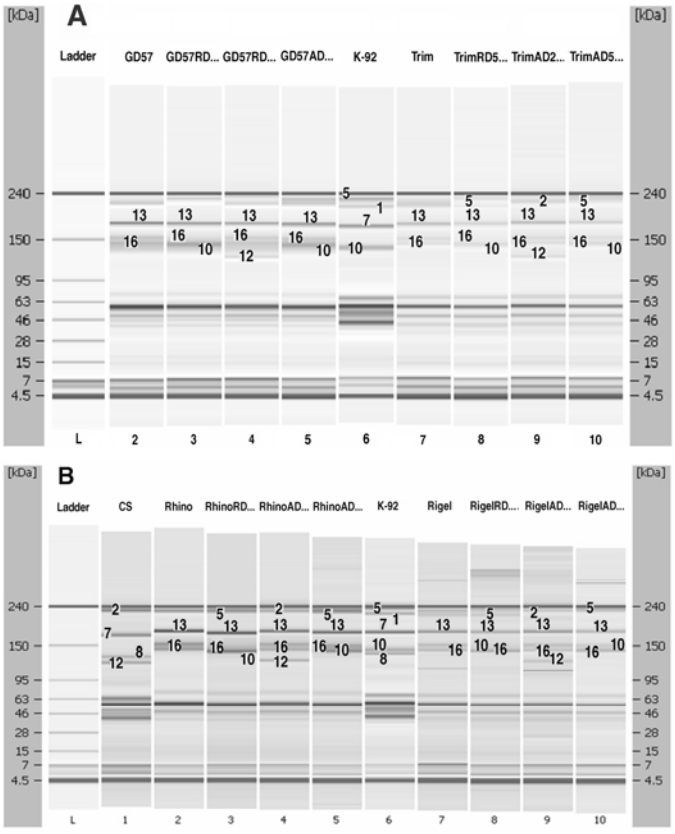

Fig. 1. High molecular weight glutenin subunit composition of four triticale translocation lines as identified by Lab-on-a-Chip methodology.

Statistical Analyses

All analyses were conducted at least in duplicate and in randomized order and reported with mean values. All developed lines in each set were compared statistically with the parent line considered the control. Analysis of variance (ANOVA) of the results was performed using the General Linear Model procedure of SAS (v.9.1. SAS Institute, Cary, NC). Statistical significance was declared at $P < 0.05$. Linear regression and correlation were also performed using SAS procedures.

RESULTS AND DISCUSSION

Initial Physical Tests

Results of the milling yield and flour protein content of the selected triticale translocated lines are presented in Table II. The hardness index (HI) was 51–68 with an average value of 58; milling quality of all samples was poor with lower flour yield (34–46%) and higher bran (53–67%) than values routinely obtained from hard wheat. There was no specific trend observed for flour protein content. The protein contents of 1R.1D 5+10 were highest in Trim and Rigel sets compared to other lines.

High bran yields and poor flour yields obtained with triticale samples were in agreement with previous studies (MacRitchie 1980; Weipert 1986; Pena and Amaya 1992). Typical grain morphological characteristics in triticale (long, shriveled, with deep creases) are less favorable for the production of flour than wheat (Weipert 1986). MacRitchie (1980) reported that triticale cultivars possess soft endosperm, a characteristic responsible for the poor flour flow properties that negatively affect flour sifting during milling and flour yield. Additionally, Pena and Amaya (1992) observed that semi-hard triticales exhibited poorer milling properties than the soft wheat samples. However, the defects in grain morphology of triticale predominated over grain hardness in defining the milling performance. Co-milling of wheat and triticale may be a good practice to improve the milling performance of triticale.

Flour protein content was 6.9–10.3 in all the different groups. Pomeranz (1985) reported that flour protein content was important because almost all flour properties (gluten content, water absorption, MDDT, and loaf volume) were highly correlated with protein content.

Electrophoretic Characterization of HMW-GS Using Lab-on-a-Chip Method

HMW-GS composition of triticale samples was analyzed using Lab-on-a-Chip method (Fig. 1). Apparent molecular sizes of subunits are shown in Table III. All the triticale lines have 13+16 subunits at the *Glu-B1* loci in common. Samples with known subunit composition were used as a control to identify specific HMW-GS. These were Chinese Spring (null, 7+8, 2+12) and Karl-92 (1, 7+8, 5+10).

Electrophoregrams of triticale sets were similar to rye and wheat samples, where HMW-GS from wheat and HMW secalins from rye were observed (Fig. 1). Tohver et al (2005) reported that

TABLE III
Apparent Sizes (kDa) of Triticale High Molecular Weight (HMW) Glutenin Subunits Determined Using the Lab-on-a-Chip Method

	Glu-A1	A/R Genome				*Glu-B1*				R Genome
Subunit	1	2	5	10	12	7	8	13	16	HMW Secalin
Size (kDa)	202	214.4	214	135.7	121.6	165.6	130.6	181.9	144.5	Varies

glutenin patterns of most of the triticale cultivars were similar to the glutenin pattern of rye, whereas some were closer to that of wheat using SDS-PAGE. The migration sequence of HMW-GS on the chip system was 12, 8, 10, 16, 7, 13, 1, 4, 5, and 2, which was the same as reported by Uthayakumaran et al (2006). However, apparent sizes of corresponding subunits did not match exactly the previous results (Uthayakumaran et al 2006) because the protein chip used in the present study has a higher molecular range (230+ kit) compared to the 210+ kit that they used.

Protein Composition and Physical Dough Tests

Triticale protein compositional data analyzed by SE-HPLC are presented in Table IV. Although there were significant differences among triticale lines in each set, there was no specific pattern observed for any of the parameters measured. However, for the GDS 7 set, 1A.1D 5+10 had a significantly higher UPP compared to the other lines. There was no significant difference for protein fractions in triticale compared to regular wheat samples (Jonnala et al 2008). Higher amounts of albumins and globulins were found with GDS7 and Trim sets that were similar to results previously reported (Naeem et al 2002).

Dough quality measurements including MDDT, R_{max}, and extensibility are presented in Table V. Micro-extensibility tests were performed to measure R_{max} and extensibility. Generally, MDDT measured by the mixograph were significantly lower compared to Pegaso bread wheat (Jonnala et al 2008) with the exception of the GDS7 and Rigel sets in which 1A.1D 5+10 had higher MDDT. Translocation 1A.1D 5+10 samples in all triticale sets were sig-

TABLE IV
Comparison of Protein Compositional Data of Selected Triticale Translocation Lines Using Size-Exclusion High-Performance Liquid Chromatography[a,b,c]

	GGR	LMW/HMW	% UPP	% PPP	% Gliadin	% Albumin + % Globulin
GDS7 set						
GDS7	0.9	1.3	40.6b	46.2a	35.7a	16.6ab
GDS7 1R.1D 5+10	0.9	1.0	41.6b	44.8a	38.2a	14.1b
GDS7 1A.1D 2+12	0.9	1.6	42.9b	44.5a	38.4a	17.1a
GDS7 1A.1D 5+10	0.8	1.0	48.5a	42.3a	39.3a	18.4a
Trim set						
Trim	1.2	1.9	36.9bc	35.2c	46.3ab	18.5a
Trim 1R.1D 5+10	1.4	3.6	33.3c	33.1d	47.5a	15.5b
Trim 1A.1D 2+12	1.0	1.3	42.3ab	36.4a	44.5b	19.0a
Trim 1A.1D 5+10	1.0	2.0	45.3a	35.4b	44.9b	15.3b
Rhino set						
Rhino	1.7	1.4	24.1b	41.9a	41.2a	13.4b
Rhino 1R.1D 5+10	1.1	1.5	35.6a	42.6a	38.6ab	14.8a
Rhino 1A.1D 2+12	1.1	1.7	35.1a	43.6a	37.9b	14.5a
Rhino 1A.1D 5+10	1.1	1.4	37.0a	45.6a	39.2ab	14.8a
Rigel set						
Rigel	0.9	1.1	40.6bc	47.4a	35.7b	13.3b
Rigel 1R.1D 5+10	0.9	1.1	38.3c	42.9c	41.9a	12.2c
Rigel 1A.1D 2+12	0.9	1.2	46.4a	44.2bc	36.6b	14.8a
Rigel 1A.1D 5+10	0.8	1.2	42.4b	46.2ab	36.7b	13.5b

[a] GGR, gliadin-to-glutenin ratio; LMW/HMW, ratio of low molecular weight glutenins to high molecular weight glutenins; UPP, % unextractable polymeric protein; PPP, % polymeric protein.
[b] Values in each set followed by the same letters in the same column are not significantly different at $P < 0.05$.
[c] LMW/HMW ratio calculated from Lab-on-a-Chip analysis.

TABLE V
Comparison of Physical Dough Testing Properties of Selected Triticale Translocation Lines[a]

	Mixograph		Extensibility	
	MDDT[b] (min)	Width (at 8 min)	R_{max}[b] (mN)	Extensibility(mm)
GDS7 set				
GDS7	1.5c	12.5b	232d	26.8a
GDS7 1R.1D 5+10	4.1b	18.6ab	269c	19.9bc
GDS7 1A.1D 2+12	1.7c	16.4ab	296b	18.4c
GDS7 1A.1D 5+10	7.4a	22.5a	393a	20.8b
Trim set				
Trim	1.2ab	9.4ab	195d	22.6a
Trim 1R.1D 5+10	1.2ab	8.9b	217c	20.6b
Trim 1A.1D 2+12	1.0b	14.0a	253b	21.7ab
Trim 1A.1D 5+10	1.6a	11.5ab	289a	22.1ab
Rhino set				
Rhino	1.6ab	9.4a	128c	28.9a
Rhino 1R.1D 5+10	2.2a	15.5a	248a	18.6c
Rhino 1A.1D 2+12	1.0b	10.0a	216b	19.4bc
Rhino 1A.1D 5+10	2.2a	12.4a	251a	21.0b
Rigel set				
Rigel	1.2b	13.9ab	247b	23.4b
Rigel 1R.1D 5+10	1.7b	17.3a	202c	26.2ab
Rigel 1A.1D 2+12	1.5b	12.3b	197c	26.5a
Rigel 1A.1D 5+10	7.7a	16.4ab	295a	24.2ab

[a] Values in each set followed by the same letters in the same column are not significantly different at $P < 0.05$.
[b] MDDT, mixograph peak dough development time; R_{max}, maximum resistance to extension.

TABLE VI
Correlation Matrix for Various Quality Parameters and Protein Composition of Selected Triticale Translocation Lines[a,b,c]

	R_{max}	Ext	LV	PPP	FPP	UPP	GGR	FP	LMW/HMW
MDDT	0.678***	–0.083	0.472*	0.219	0.145	0.512** (0.478)	–0.419	0.176	–0.348
R_{max}	1.000	–0.538	0.466*	0.088	0.011	0.779*** (0.575)	–0.662	0.112	–0.208
Ext		1.000	0.053	0.163	0.378 (0.263)	–0.184	0.178	0.211	–0.257
LV			1.000	–0.265	0.272 (0.272)	0.522**	–0.314	0.169	–0.185
PPP				1.000	–0.087	0.146	–0.498	–0.358	0.706***
FPP					1.000	0.411	–0.336	0.784***	–0.144
UPP						1.000	–0.903	0.345	–0.376
GGR							1.000	–0.146	0.543**
FP								1.000	0.204
LMW/HMW									

[a] MDDT, mixograph dough development time; R_{max}, maximum resistance to extension test; Ext, extensibility; LV, loaf volume; PPP, % polymeric protein; FPP, flour polymeric protein; UPP, unextractable polymeric protein; GGR, gliadin-to-glutenin ratio; FP, flour protein; LMW/HMW, ratio of low molecular weight glutenins to high molecular weight glutenins.
[b] Values in parentheses normalized to flour protein content.
[c] *, **, ***, Significant at $P > 0.1$, 0.05, 0.01, respectively.

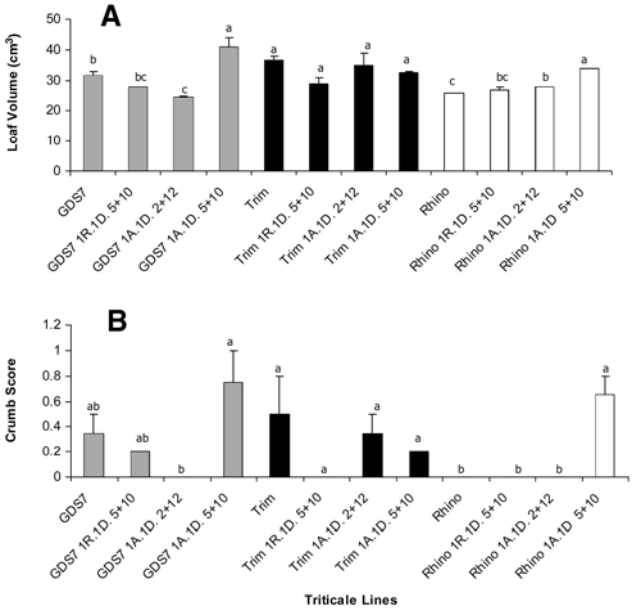

Fig. 2. Comparison of loaf volume (cm^3) (**A**) and crumb scores (**B**) of micro-breads baked from selected triticale sets.

nificantly higher in MDDT over other lines. R_{max} and extensibility values of triticale lines were 195–393 mN and 18.4–28.9 mm, respectively. Both MDDT and R_{max} followed a similar trend in which 1A.1D 5+10 had the highest values among all the samples. Triticale doughs developed readily with low stability and fast breakdown, suggesting that they were deficient in gluten protein quantity and quality. Weaker gluten, lower water absorption and lower dough mixing tolerance with significantly lower mixing times for triticales have been reported previously (Seguchi et al 1999; Serna-Saldivar et al 2004).

The correlation matrix between various protein composition and physical dough test parameters are shown in Table VI. Dough strength as measured by MDDT (r = 0.51) and R_{max} (r = 0.78) were significantly correlated with UPP. Loaf volume, an important breadmaking parameter was also strongly correlated (r = 0.52) with UPP. Extensibility (r = 0.38) was correlated positively with FPP. Naeem et al (2002) reported similar results with triticale samples in which the extensibility (r = 0.96) was highly correlated with FPP. Gupta et al (1993) observed a similar trend with wheat flour.

High UPP, R_{max}, and MDDT values with a lower gliadin-to-glutenin ratio (in 1A.1D 5+10 of GDS7 and Rigel sets) indicate that the molecular weight distribution was shifted to a higher molecular weight. The resulting dough exhibited greater strength associated with 5+10 subunits. Similar findings were reported by MacRitchie and Lafiandra (2001).

The important quality attributes such as MDDT, R_{max}, extensibility, and loaf volume were normalized to flour protein content to eliminate the effect of variation in protein amounts. These correlation values are indicated in parentheses in Table VI. However, there were no differences in correlation trends observed after normalization.

Test Baking Results

Micro-bread loaves (10 g of flour) were baked from only three triticale sets and the loaf volume results are shown in Fig. 2A. The correlation matrix among various protein composition, physical dough test characteristics, and C-cell parameters were evaluated (data not shown).

As shown in Fig. 2B, crumb scores indicate that bread made from pure triticale flour was not acceptable. However, consistent with the results from physical dough tests, loaf volume of 1A.1D 5+10 was significantly higher among all the lines. Average loaf volume and crumb score of 31 and 0.3 were observed with triticale samples against 61 and 2.2, respectively, for Pegaso bread wheat (Jonnala et al 2008).

Researchers reported that bread loaves made from pure triticale flour have significantly lower loaf height (Naeem et al 2002) and loaf volume (Doxastakis et al 2002). Substantial improvements in loaf volumes with substitution and translocation lines of triticales were previously reported by Lafferty and Lelley (2001) and Wos et al (2002). Although the crumb scores were low from breads made with triticales in the current study, crumb structure as well as crumb appearance observed (Fig. 3) were satisfactory. These results were in agreement with previous studies (Pena and Amaya 1992; Doxastakis et al 2002). Test baking results from the current triticale lines show promising breadmaking potential for these flours when blended with bread wheat flours. In particular, translocation lines at 1A.1D with subunits 5+10 have shown better breadmaking properties. The observations made above need further study on different levels of triticale-wheat flour blends to evaluate the level of triticale flour addition required to make commercial breads.

Mean flour absorption values of 56.4% were observed with triticales. Kasearu et al (1997) reported that an acceptable water absorption was 55–65%. Water absorption values were negatively correlated (r = –0.47) with loaf volume, which is in accordance with previous results (Kasearu et al 1997).

Loaf volume was significantly correlated with important dough parameters such as MDDT (r = –0.47), R_{max} (r = –0.46), and UPP (r = –0.52), whereas poor correlation was observed with extensibility (r = 0.05) and FPP (r = 0.27). Most of the crumb grain char-

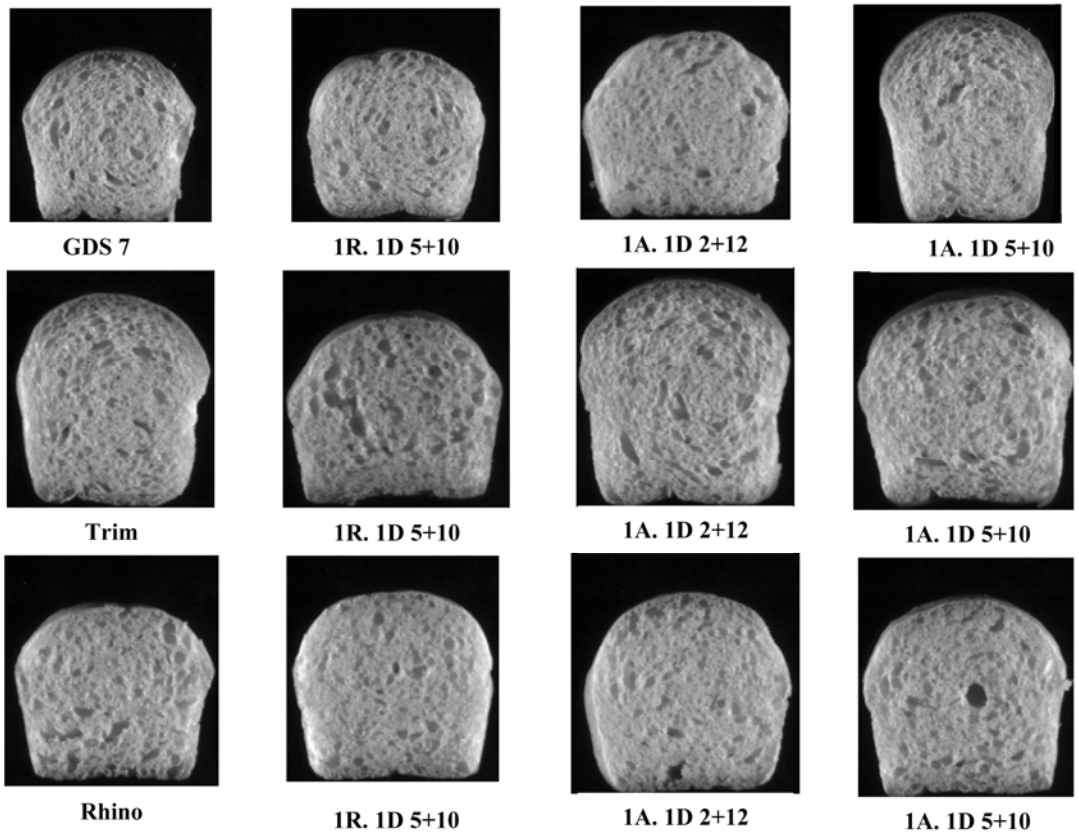

Fig. 3. C-cell images of micro-bread loaves baked from different triticale sets comparing breads in each group in a row.

acteristics measured by the C-cell analysis such as loaf height, slice area, number of cells, and cell diameter were positively correlated with each other (data not shown).

C-cell images (Fig. 3) of triticale breads are presented for comparison. All triticale breads were round in shape with improper shred and break. Crumb structures appeared to be poor (with open grain and unevenly distributed gas cells). Similar results were reported by Pena and Amaya (1992) with triticale loaves.

CONCLUSIONS

Pure triticale flours from translocation lines evaluated in this study did not possess the functional characteristics to make a commercially viable bread.

However, translocations at 1A.1D with subunits 5+10 have significantly higher loaf volumes along with satisfactory bread crumb characteristics which indicate that these translocation lines, when combined with bread wheat flour at different levels, would yield commercially satisfactory bread loaves. Evaluation of the promising breadmaking potential characteristics of these specific translocation lines needs further attention.

Poor milling quality (flour yield) and very low mixing times (MDDT) with lower loaf volume were typical of all the triticales studied except 1A.1D 5+10 lines. However, high loaf volume with MDDT and R_{max} were observed with 1A.1D 5+10 translocation lines in all the triticale sets, indicating that translocation of the *Glu-D1d* allele with HMW-GS 5+10 is beneficial in improving the quality attributes. Dough strength measurements such as MDDT, and R_{max} correlated well with loaf volume.

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