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Research Article

Distribution of the Chromosomal Translocation 1BL/1RS and the Allelic Combinations 7+9/j and 7+8/j in a Set of Dihaploid Lines of Common Wheat

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Abstract

The influence of wheat-rye translocation 1BL/1RS and allelic combinations of 7+9/j and 7+8/j on the genetic degradation of wheat dihaploid lines was studied.

The results of the study showed close to normal genetic degradation, which is assessed on the basis of the presence or absence of 1BL/1RS translocation in the DH lines obtained from eight hybrid combinations.

Due to the association between the allele encoding the Glu-B1 high-molecular fraction 7+9 and the low-molecular allele 'j' from the locus Glu-B3, dihaploid lines were obtained with certain combinations of high-(HMW) and low-(LMW) molecular weight glutenin configurations. This phenomenon could significantly limit the possibilities of combinational selection in some cases.

Keywords: Common Wheat; 1BL/1RL Translocation; Dihaploid Lines (DH); HMW- and LMW- Glutenin Configurations

Introduction

Wheat breeding is mainly aimed at creating varieties with good productivity and high quality. Combining classic breeding with the new biochemical and biotechnological methods, it could speed up the accomplishment of this task by shortening the breeding process and introducing new points in qualitative assessment. The wheat grain reserve proteins are used as genetic markers to select quality genotypes early in the selection process. Electrophoresis applied to their separation is a fast and relatively inexpensive method. The quality data obtained with the help of these markers is stable regardless of the influence of the external conditions. An essential point of an improved technology for the selection of wheat, associated with the application of genetic markers is the use of the anther culture method to create dihaploid lines (DH). The main advantage of this method is the rapid and complete alignment of the offspring, resulting in the accelerated creation of new lines. The application of the anther culture method in selection is closely linked to the wheat-rye translocation *1BL/1RS*. Most wheat varieties bearing the *1BL/1RS* translocation have been found to have high androgenic responsiveness. The genes controlling this responsiveness are located in the 1R translocation arm [1,2]. However, the authors admit that there is another genetic system for high responsiveness. The different responsiveness of the parental forms of the hybrid combinations from which the dihaploid lines are derived is a cause of deviation from normal genetic decay. It limits the possibilities of combinational selection due to the elimination of genotypes with valuable economic traits.

Aim of the Study

The aim of this study is to determine the effect of wheat rye translocation *1BL/1RS* and some allelic combinations of high and low molecular weight glutenins on the genetic breakdown of wheat dihaploid lines derived from F1 crosses between high quality varieties and high yield varieties, carriers of the above translocation.

Material and Methods

Material

F1 plants from the following crosses Albena x Svilena, Albena x Crystal, Albena x Enola, Aglika x Svilena, Aglika x Crystal, Aglika x Enola, Milena x Svilena, Milena x Crystal and Milena x Enola were used to obtain the dihaploid (DH) lines.

The selection of parental hybridization forms is consistent with the fractional composition of the reserve proteins, quality, productive potential and responsiveness to anther cultivation. The paternal varieties Svilena, Crystal and Enola are carriers of the wheat-rye translocation *1BL/1RS*.

Methods

Anther culture method

The dihaploid lines were obtained by the anther culture method. Potato 2 nutrient solution was used to induce embryogenic structures (calluses and embryoids) and plant regeneration was performed on nutrient medium 190-2.

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Electrophoretic methods

The extraction of glutenins was performed by the method of Singh., *et al* [3]. The electrophoresis run on vertical apparatus in two ways: a) classical one-dimensional 12% polyacrylamide gel [4]; b) one-dimensional 10% polyacrylamide gel SDS-PAGE with addition of 4M urea (Lafiandra., *et al*. 1993).

Arrangement and numbering of HMW-GS in wheat was carried out according Payne and Lawrence [5]. LMW-GS nomenclature in wheat [6] and combined method for LMW-GS and gliadin identification were adopted [7].

Results

The distribution of the wheat-rye translocation *1BL/1RS* in the 665 dihaploid lines of the eight crossings is very close to the theoretical expectation of 50%: 50% (Table 1).

Cross	Total number of DH lines	DH lines with 1BL/1RS		DH lines with 1BL/1BS	
		Number	%	Number	%
Albena x Svilena	125	70	56.0	55	44.0
Albena x Crystal	83	41	49.4	42	50.6
Albena x Enola	60	29	48.3	31	51.7
Aglika x Svilena	175	95	54.3	80	45.7
Aglika x Crystal	139	59	42.4	80	57.6
Milena x Svilena	39	15	38.5	24	61.5
Milena x Cristal	35	24	68.6	11	31.4
Milena x Enola	9	7	77.8	2	22.2
Total	665	340	51.1	325	48.9

Table 1: Relative share of dihaploid lines with 1BL/1RS and with 1BL/1BS chromosome.

Some exceptions are the Milena crosses with the Svilena, Crystal and Enola varieties due to the smaller number of dihaploid lines obtained.

It can be assumed that the highly responsive translocation varieties Svilena and Kristal in the anther culture method would displace the normal distribution to increasing the number of dihaploid lines with translocation. The absence of such deviation from the normal distribution indicates the absence of gametic breeding *in vitro* cultivation.

The study of a large number of Bulgarian and foreign varieties and lines of wheat [8] showed that almost all samples, carriers of the wheat-rye translocation *1BL/1RS* (low molecular weight allele j in the Glu B3 locus), contain the fraction pair 7 + 9 in the locus Glu B1. While translocation samples of wheat containing the 7 + 8 fractional pair at the same locus are an exception. A similar phenomenon was observed in the present study in the dihaploid lines from the Albena (Glu B1 -7 + 8 and Glu B3-b) crosses with the Svilena, Crystal and Enola varieties (Glu B1-7 + 9 and Glu B3-j). The 7 + 9/*j* combination was found to be average in 92.9% of the dihaploid lines, while the 7 + 8/*j* combination was only 7.1% (Table 2).

Cross	Total number of DH lines	DH lines with translocation		7+9/*j*		7+8/*j*	
		Number	%	Number	%	Number	%
Albena x Svilena	125	70	56.0	69	98.6	1	1.4
Albena x Cristal	83	41	49.4	34	82.9	7	17.1
Albena x Enola	60	29	47.3	27	93.1	2	6.9
Total	268	140	52.2	130	92.9	10	7.1

Table 2: Relative share of combinations 7+9/j (1BL/1RS) and 7+8/j (1BL/1RS) in translocation lines.

This phenomenon is reflected in the distribution of the dihaploid lines with certain high- and low-molecular configurations at the crosses between translocation samples - *1BL/1RS* and samples with normal wheat chromosome 1BL/1BS. Because the parental varieties of the Albena x Svilena cross differ in alleles at five loci - Glu-A1, Glu-B1, Glu-D1, Glu-A3 and Glu-B3, theoretically possible combinations of high- and low molecular weight glutenins are 32. However, in practice, certain combinations are missing or obtained in a minimal number of dihaploid lines (Table 3). This fact can be explained by the dominance of the combination 7 + 9/*j* over 7 + 9/b and 7 + 8/b over 7 + 8/*j*, which is the result of the above-mentioned natural link of the high molecular weight couple 7+ 9 and the wheat-rye translocation *1BL/1RS* (j). A similar situation was found at the crosses of the Albena variety with the translocation varieties Crystal and Enola (data not shown).

Table 4 lists the theoretically possible combinations of high- and low-molecular-weight glutenin alleles from cross Aglica (Glu B1-7 + 9 and Glu B3-b) x Svilena (Glu B1-7 + 9 and Glu B3-j). At this cross there are dihaploid lines of all possible combinations.

Therefore, the absence of the high-molecular fraction pair 7 + 8 in this case, and the presence of only 7 + 9, results in a near-normal distribution of the 7 + 9/*j* and 7 + 9/b combinations in the dihaploid lines. A similar situation was found at the crosses of the Aglica variety with the translocation varieties Crystal (data not shown).

Discussion

The results of the study indicate close to normal genetic degradation estimated based on the presence or absence of *1BL/1RS* translocation in DH lines derived from eight hybrid combinations. In a number of studies, other authors [1,9] found some deviation from normal disintegration, with preferential production of DH lines with chromosomal translocation *1BL/1RS*, whereas normal distribution of lines with and without translocation is relatively rare [10].

The established association of the allele encoding the high molecular weight fraction pair 7 + 9 of the Glu-B1 locus with the low molecular weight allele j of the Glu-B3 locus limits the production of dihaploid lines with certain combinations of high and low

	HMW			LMW		Parents/number of DH lines
Glu-A1	Glu-B1	Glu-D1	Glu-A3	Glu-B3	Glu-D3	
N 1	7+8 7+9	5+10 2+12	f e	b j	c c	Albena Svilena
1	7+9	2+12	e	j	c	5
N	7+9	2+12	e	b	c	-
N	7+9	2+12	f	j	c	5
N	7+9	2+12	f	b	c	-
N	7+9	5+10	e	j	c	12
N	7+9	5+10	e	b	c	1
N	7+9	5+10	f	j	c	21
N	7+9	5+10	f	b	c	1
N	7+8	2+12	e	j	c	-
N	7+8	2+12	e	b	c	4
N	7+8	2+12	f	j	c	-
N	7+8	2+12	f	b	c	4
N	7+8	5+10	e	j	c	-
N	7+8	5+10	e	b	c	3
N	7+8	5+10	f	j	c	-
N	7+8	5+10	f	b	c	10
1	7+9	2+12	e	j	c	3
1	7+9	2+12	e	b	c	1
1	7+9	2+12	f	j	c	5
1	7+9	2+12	f	b	c	1
1	7+9	5+10	e	j	c	12
1	7+9	5+10	e	b	c	1
1	7+9	5+10	f	j	c	6
1	7+9	5+10	f	b	c	-
1	7+8	2+12	e	j	c	-
1	7+8	2+12	e	b	c	4
1	7+8	2+12	f	j	c	1
1	7+8	2+12	f	b	c	6
1	7+8	5+10	e	j	c	-
1	7+8	5+10	e	b	c	13
1	7+8	5+10	f	j	c	-
1	7+8	5+10	f	b	c	6
Total						125

Table 3: High- (HMW) and low- (LMW) molecular weight glutenin composition of dihaploid (DH) wheat lines from Albena x Svilena cross.

molecular weight glutenin configurations. Such a relationship is also found by Trethowan., *et al.* [11] when analyzing 1267 lines of common wheat. Obviously, this phenomenon would in some cases significantly limit the possibilities of combinational breeding. However, its nature can hardly be explained from a genetic point of view. These loci are known to be located, respectively, in the long and short arm of wheat chromosome 1B, at a considerable distance from each other [12] which eliminates the possibility of associated inheritance of the alleles located therein. Apparently, the nature of the established link between the high molecular weight glutenin allele c encoding the 7 + 9 fraction pair and the low molecular weight glutenin allele j can be established by in-depth genetic and biochemical studies.

Conclusion

The results of the study showed close to normal genetic disintegration, which is assessed on the basis of the presence or absence of *1BL/1RS* translocation in the DH lines obtained from eight hybrid combinations.

Due to the association between the allele encoding the Glu-B1 high-molecular fraction 7+9 (allele ‘c’) and the low-molecular allele ‘j’ from the locus Glu-B3, dihaploid lines were obtained with

	HMW			LMW		Parents/number of DH lines
Glu-A1	Glu-B1	Glu-D1	Glu-A3	Glu-B3	Glu-D3	
2*	7+9	5+10	c	b	c	Aglika
1	7+9	2+12	e	j	c	Svilena
1	7+9	2+12	e	j	c	8
1	7+9	2+12	e	b	c	5
1	7+9	2+12	c	j	c	13
1	7+9	2+12	c	b	c	4
1	7+9	5+10	e	j	c	11
1	7+9	5+10	e	b	c	21
1	7+9	5+10	c	j	c	9
1	7+9	5+10	c	b	c	10
2*	7+9	2+12	e	j	c	7
2*	7+9	2+12	e	b	c	12
2*	7+9	2+12	c	j	c	16
2*	7+9	2+12	c	b	c	8
2*	7+9	5+10	e	j	c	18
2*	7+9	5+10	e	b	c	12
2*	7+9	5+10	c	j	c	13
2*	7+9	5+10	c	b	c	8
Total						175

Table 4: High- (HMW) and low- (LMW) molecular weight glutenin composition of dihaploid (DH) wheat lines from Aglika x Svilena cross.

certain combinations of high-(HMW) and low-(LMW) molecular weight glutenins configurations. This phenomenon could significantly limit the possibilities of combinational breeding in some cases.

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Bibliography

1. Agache S., *et al*. "Genetic analysis of anther culture response in wheat using aneuploid, chromosome substitution and translocation lines". *Theoretical and Applied Genetics* 77.1 (1989): 7-11.

2. Foroughi-Wehr B and Zeiier FJ. "*In vitro* microspore reaction of different German wheat cultuvars". *Theoretical and Applied Genetics* 79.1 (1990): 77-80.

3. Singh NK., *et al*. "A Simplified SDS-PAGE Procedure for Separating LMW Subunits of Glutenin". *Journal of Cereal Science* 14.3 (1991): 203-208.

4. Laemmli UK. "Cleavage of structural proteins during the assembly of bacteriophage T4". *Nature* 227.5259 (1970): 680-685.

5. Payne PI and Lawrence GJ. "Catalogue of alleles for the complex gene loci, Glu - A1, Glu - B1 and Glu - D 1 which code for high-molecular-weight subunit in hexaploid wheat". *Cereal Research Communication* 11.1 (1983): 29-35.

6. Gupta RB and Shepherd KW. "Two-step one-dimensional SDS-PAGE analysis of LMW subunits of glutenin". *Theoretical and Applied Genetics* 80 (1990): 65-74.

7. Jackson EA., *et al*. "Proposal for combining the classification systems of alleles of Gli-1 and Glu-3 loci in bread wheat (*Triticum aestivum* L.)". *Journal of Genetics and Breeding* 50.4 (1996): 321-336.

8. Todorov DI. "Study on grain storage proteins and their use as genetic markers in wheat breeding". Author of dissertation for doctor of sciences (2006).

9. Henry Y., *et al*. "Nuclear gametophytic genes from chromosome arm 1RS improve regeneration of wheat microspore-derived embryos". *Genome* 36.5 (1993): 808-814.

10. Tuversson IKD., *et al*. "An effect of the 1BL/1RS chromosome on albino frequency in wheat (*Triticum aestivum* L.) anther culture". *Journal of Genetics and Breeding* 45 (1991): 345-348.

11. Trethowan RM., *et al*. "The effect of indirect tests for grain quality on the grain yield and industrial quality of bread wheat". *Plant Breeding* 120.6 (2001): 509-512.

12. Payne PI. “Genetics of Wheat Storage Proteins and the Effect of Allelic Variation on Bread-Making Quality”. *Annual Review of Physiology* 38 (1987): 141-153.

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