Meiotic Stability and Characteristics of Rye Genome and Productivity of Bulgarian Hexaploid Triticale Lines

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Abstract


The hexaploid triticale lines C₁ and C₂ were investigated. The lines are of high meiotic stability as 83.51% - 91.22% of the tetrads have no micronuclei and are highly productive. Plants of line C₁ are characterized with long spike (10.62 cm), average number of spikelets (26.50) and average number of florets (97.80) while these of C₂ - (9.61 cm ) long spike, (26.20) average number of spikelets and (92.92) average number of florets. The mean grain number per main spike varying from 49.83 to 52.08 and the mean mass from 2.06 to 2.41 g.

Differential staining analyses showed the presence of 14 rye chromosomes and no reduction in telomere heterochromatin content. Both lines possess all A- and B- wheat chromosomes in their genomes. Line C₁ carries the dominant gene for spring type of development while C₂ has the dominant gene for winter type of development.

Key words: triticale, meiotic stability, rye chromosomes, productivity

Introduction

The synthetic species triticale introduced variety into the group of cereal crops and successfully grow in regions with poor soil. Triticale plants are resistant to certain economically important fungal deseases and the grains are of high crude protein contents, triticale protein being rich in lysine.

The studies on meiosis help to better understand the interrelationship between the extent of damaging and the yield as well as to clarify which chromosomes might be affected by the damages more frequently (Fedorova, 1985; Papa et al., 1990; Prasanna et al., 1994; Maich and Ordonez, 2003).

Genome analyses support the breeding process aiming to increase the diversity of hexaploid triticale and grain production. Badaeva et al. (1986) reported more intensive bands in 1R, 2R and 3R chromosomes than in those of the parental rye. The breeding pressure is thought to tend to preserve all seven rye chromosomes (Seal and Bennett, 1981). Semyonov and Semyonova (1983) most frequently supposed to decline 1R, 2R and 3R chromosomes for which chromosomes from the
D genome substituted. The 2R/2D substitution was related to the introduction of a gene for plant response to day length and is closely related to grain number per ear (Lukaszewski and Apolinarska, 1994; Pilch, 1994).

Reddy (1992) and Reddy and Edwin (1993a,b) established substitutions of 2R, 3R, 5R, 4R/7R. The substitution of fourth, sixth and seventh homeologous chromosome groups improves grain quality. A possible role of heterochromatin for a better balanced nuclear type along with triticale selection has been proposed (Garsia and Soler, 1989).

According to (Rogalska et al., 1999) the amount and distribution of heterochromatin in rye chromosomes do not affect grain mass in hexaploid triticale.

The aim of the present investigation is to assess the meiotic stability, the productivity and the relationship between them in hexaploid triticale, bred in Institute of Genetics in Bulgaria. The analysis of the rye chromosomes by means of differential staining clarify their number in triticale lines genomes.

**Material and Methods**

Two lines were assessed: C1 – a complex cross between triticale form AD 2/4 and the hybrid between AD 208 and wheat cultivar Priboy and C2 - a cross between AD 18 x wheat cultivar Levent. The data of productivity elements being analysed by the variation-statistic method (Lidansky, 1988). For meiotic analysis, spikes were fixed in 3:1 (ethanol:acetic acid). Aceto-carmine staining was used for observations (Guedes-Pinto, 1988). About 40 cells were recorded for diakinesis, 102-105 for metaphase I, 189-239 for anaphase I and 189-205 tetrads for telophase II. Rye chromosomes were stained using the brief C-method (Gill et al., 1991) by the following parameters: treatment in Ba(OH)2 for 12 min, washing with tap water, air drying, treatment for 9 min in 2x SSC at 49-50°C, rinsing with distilled water and staining for 3 min in Hamatology Giemsa with a double dose of Tris-buffer.

**Results and Discussion**

In both triticale lines (C1 and C2) 21 bivalents were recorded in diakinesis (Figure 1). Metaphase I with univalents and anaphase I with laggards are shown on Figures 2 and 3. Lower mean number of univalents per cell in metaphase I, lower percentage of lagging chromosomes in anaphase I and higher percentage of tetrads lacking micronuclei providing higher meiotic stability characterize triticale line C2 (Table 1).

![Fig. 1. Diakinesis with 21 bivalents](image)
Differential rye chromosome staining reveals availability of all 7 rye chromosome couples both in C1 and C2 and shows that there is no substitution of rye chromosomes for wheat chromosomes. Four chromosomes with two telomere heterochromatin blocks and three with one heterochromatin block were established. There is an intercalar heterochromatin block near the telomere block on the long arm of 1R chromosome only in the case of smaller chromosome shortening.

About 1.66% and 2.60% shriveled grains were scored in lines C1 and C2, respectively. Possibly there exists certain relation between the presence of large heterochromatin blocks and endosperm shrivelling. Papa et al. (1990) proposed that the heterochromatin blocks in 4R and 5R chromosomes cause grain shriveling in rye addition lines.

The large telomeric blocks are considered to be a reason for anaphase bridges in rye chromosomes, resulting into aber-

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**Table 1**

Analysis of meiosis in triticale C1 and C2 lines

<table>
<thead>
<tr>
<th>Triticale lines</th>
<th>Univalents average number in metaphase I</th>
<th>Percentage of cells with lagging chromosomes in anaphase I</th>
<th>Telophase II-percentage of tetrads with micronuclei</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>0</td>
</tr>
<tr>
<td>C1</td>
<td>2.14</td>
<td>38.18</td>
<td>83.15</td>
</tr>
<tr>
<td>C2</td>
<td>0.65</td>
<td>18.61</td>
<td>91.22</td>
</tr>
</tbody>
</table>
rant nuclei in endosperm cells. After deletions of telomere heterochromatin blocks in 2R, 3R and 7R/4R the number of those nuclei decreases significantly (Fedoro-
va,1985).

Another reason for grain shriveling is a β-amilase increased activity causing distur-
bances in aleuronic layer formation (Fedorova, 1985). Since no reduction in telomere heterochromatin content has been established in C1 and C2 grain shriv-
eling should be considered as resulting from a complex of factors.

The genomes of both triticale lines contain all chromosomes from wheat subge-
nomes as in diakinesis are recorded 21 bivalents out of which 14 are rye and no multivalent associations are observed in the triticale genome analyzed. Con
tcharov (1988) and Gontcharov and Efimov (2003) have found that the genes coding grain number per ear are located in 1A, 2A, 3A, 4A and 5A chromosomes as well as in 1B, 2B, 3B, 5B, 6B and 7B chromosomes. The genes coding grain mass per ear are located in 1A, 2A, 3A and 5A chromosomes as well as in 1B, 4B and 5B chromosomes. The combination of the above chromosomes in the genomes of C1 and

<table>
<thead>
<tr>
<th>Triticale Lines</th>
<th>Spike length, cm</th>
<th>Spikelets number per spike</th>
<th>Florets number per spike</th>
<th>Grains number per spike</th>
<th>Mass of grains, g</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>M ± m VC%</td>
<td>M ± m VC%</td>
<td>M ± m VC%</td>
<td>M ± m VC%</td>
<td>M ± m VC%</td>
</tr>
<tr>
<td>C1</td>
<td>9.68±1.56 8.08</td>
<td>26.20±0.48 9.08</td>
<td>92.92±1.89 10.21</td>
<td>49.83±1.73 17.08</td>
<td>2.06±0.78 18.47</td>
</tr>
<tr>
<td>C2</td>
<td>10.62±2.75 12.98</td>
<td>26.56±0.82 15.45</td>
<td>97.80±2.84 14.53</td>
<td>52.08±1.48 13.93</td>
<td>2.41±0.83 16.76</td>
</tr>
</tbody>
</table>

Vrn1 from chromosome 5A long arm is dominant for spring type of development while gene Vrn2 from chromosome 5B is dominant for winter type of development. It was found that after spring sowing vernalization proceeds within a shorter period of time in triticale C1 than in triticale C2. The plants of earing was over in 90% of the C1 plants and only in 50% of the C2 plants. These data suggest that the line C1 carries the dominant gene for spring type of development while C2 has the dominant gene for winter type of development. The line C1 winters successfully due to the presence of all rye chromosomes into its genome.

No germination of the grains in the spikes occurred before harvest.
Conclusions

Hexaploid triticale lines C₁ and C₂ carry all 14 rye chromosomes as well as the chromosomes of wheat A- and B- subgenomes. The balanced chromosome composition is determined by high meiotic stability. The lower percent of tetrads without disturbances in line C₁, probably, is due to weaker relationships between rye – and wheat- chromosomes in triticale genomes.

The triticale lines, newly created in Bulgaria are suitable for growing in practice because of their improved spike seed set and absence of kernel shriveling.

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References


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