Cytogenetical characteristic of the introgressive common wheat lines including and lacking the 4S1 chromosome

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Abstract. The lines Tritium aestivum/Aegilops sharonensis were explored in regard to presence of introgressions in line genome, their amount and belonging to definite homoeologous group. The results of studying of chromosome associations in M1 of PMC in the hybrids between lines with each other and with recurrent common wheat genotype Aurora were compared with the data of the line assessment for the chromosomal biochemical and morphological markers. 26 lines were distinguished between six groups with specific genome rearrangement regard to recurrent genotype.

Introduction. In recent years, introgressive plant material, including wheat plant material, is actively used for the development of mapping populations. Using the mapping population for gene linkage determination, the comparison between the empirical and theoretical ratios of phenotypic classes is carried out. When calculating the theoretical class volume we need to be sure the meioses in the F1 plants proceeds without abnormalities, otherwise, we can obtain the artifacts.

The group of introgressive lines Tritium aestivum/Aegilops sharonensis with certain alien characters was investigated. These lines are able to be used for genetic analysis of wheat for genes that control alien gradation of characters. Detailed genetic examination of introgressive lines concerning their cytological stability is the first and necessary step when using such lines for development of mapping population. Moreover, the cytogenetical peculiarities of the F1 hybrids from crosses of the lines with each other, which are the direct source of the mapping population, should be also studied.

Results and Discussion. Introgressive lines which phenotype differs from phenotype of variety Aurora concerning one of the spike morphology characters (Tables 1).

Table 1. Number of chromosome rearrangement in the introgressive lines

<table>
<thead>
<tr>
<th>Hybrid number</th>
<th>Chromosome number variation</th>
<th>Hybrid number</th>
<th>Chromosome number variation</th>
</tr>
</thead>
<tbody>
<tr>
<td>112</td>
<td>39-44</td>
<td>198</td>
<td>49-44</td>
</tr>
<tr>
<td>122</td>
<td>40-44</td>
<td>150</td>
<td>44-44</td>
</tr>
<tr>
<td>78</td>
<td>39-43</td>
<td>109</td>
<td>43-45</td>
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</tbody>
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Results of microsatellite analysis for introgressive lines and parental introgressive lines. Microsatellite analysis indicated presence of introgression of chromosome S1 in hybrid between lines with each other. The number of chromosome rearrangement in the introgressive lines can be detailed using as a base the meiosis M1 pattern in hybrids F1 between lines with each other. These results demonstrated what kind of introgression characterizes the line, chromosome substitution or translocation. In addition to cytological characterization, the line were analyzed with the use of biochemical markers that are specific for definite homoeologous chromosome group of Triticeae. Lines with similar genome structure form 21 closed bivalent. If four univalents occur in metaphase 1 of meiosis in the F1 hybrid between lines, each out of the lines has alien chromosome substitution, but the lines differ from each other concerning homoeologous belonging of alien chromosomes. Our results allow us to characterize each line regarding alien chromosome presence, their homoeologous belonging, and translocation presence. Homoeologous belonging of translocations was only to be presumed in most cases. It suggests that efficacy of the biochemical marker method decreases when not the whole alien chromosome but only its portion as a translocation in the wheat chromosome or as a telocentric chromosome is present in the line genome. This portion may not contain the gene that marks definite chromosome. That is why microsatellite markers attract our attention, as they may be used as markers for different parts of alien chromosomes. It is essential that the use of microsatellite markers requires meticulous prior selection of chromosome specific primers.

Experimental design and plant material development.

In the F1 hybrid between the chromosome substitution line and variety Aurora the chromosome sets of the A and S genomes out of the same homoeologous group can not pair with each other and keep as univalents. Chromosomes of the A and B genomes should be paired without irregularities, although marginal probability of association between the S-chromosomes and the chromosomes from the A, B, and D genomes may be left. The triploid hybrid Tetra-Aurora x Ae. sharonensis (ABS1) was shown to form 0.06 trivalents per cell. Moreover, it is important to examine associations between homoeologous chromosomes and heteromorphic bivalents. Although, pairing between wheat and alien (Ae. sharonensis) chromosomes is extremely reduced, it occurs with minor frequency. So, number of bivalents and univalents under highest chromosome association in meiosis M1 of hybrid between the introgressive line and variety Aurora and knowledge about homoeologous belonging of introgressions remain to be major sources of information about line genome structure. The number of open bivalents indicates presence of translocations in line genome. These translocations can include alien genetic material, but they also, can be extreme wheat-wheat. Some hybrids between introgressive lines and cultivated Aurora are characterized by greater number of closed bivalents, than in variety Aurora. It does not contradict the data about recessiveness of desynapsis genes, which presence was shown for variety Aurora.

Results of mitochondrial gene analysis for introgressive lines.

The number of closed bivalents, than in variety Aurora. It does not contradict the data about recessiveness of desynapsis genes, which presence was shown for variety Aurora.

Conclusions. Data presented concerning the chromosome association in M1 of PMC in F1 hybrids from crosses between introgressive lines and variety Aurora and with each other and, and electrophoretic spectra of proteins prove the changes of 1-4 chromosomes in the line genomes in comparison with the variety Aurora genome.

The number of closed bivalents in the introgressive wheat line with or without 4S1 chromosome were showed. Wheat chromosomes are either substituted with chromosome S1 from the same homoeologous group or a rearrangement through translocations (alien-wheat or wheat-wheat) takes place.

Contrary to the use of microsatellite markers specific for the 4D chromosome it was proved that determination of translocation arm specificity is possible only for gametocidal chromosome 4S1.