A cytogenetic map on the entire length of rye chromosome 1R, including one translocation breakpoint, three isozyme loci and four C-bands

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Summary. A cytogenetic map of the whole 1R chromosome of rye has been made, with distances between adjacent markers shorter than 50% recombination. Included in the map are isozyme loci Gpi-R1, Mdh-R1 and Pgd2, the telomere C-bands of the short arm (tsl) and the long arm (tll), two interstitial C-bands in the short arm proximal to the nuclear organizing region (NOR) (is1) and in the middle of the long arm (ill), respectively, and translocation T273W (Wageningen tester set). By means of electron microscope analysis of spread pachytene synaptonemal complexes, the breakpoint of this translocation was physically mapped in the short arm of 1R, proximal to NOR, and in the long arm of 5R (contrary to previous assumptions). The data indicated the marker order: tsl - Gpi-R1 - is1 - T273W/Mdh-R1 - ill - Pgd2 - tll. A comparison between genetic and physical maps revealed that recombination is mainly restricted to the distal regions of both arms. For the translocation T273W, in heterozygotes no recombinants were observed between the translocation breakpoint and its two adjacent located markers (is1 and Mdh-R1), but recombination was not reduced in the distal regions of the chromosome. The segregations of several other isozyme and C-band markers also analyzed in the investigation presented here were consistent with observations of earlier authors concerning chromosome assignment and linkage relationships.

Key words: Rye - Cytogenetic maps - Isozymes - C-heterochromatin bands - Translocation

Introduction

In recent years, an increasing number of investigations have been carried out on the construction of genetic maps in rye. These have involved different combinations of markers, including those for morphological traits, isozymes, RFLPs, endosperm proteins, disease resistances, the nucleolus organizer region (NOR), the centromeres, translocation breakpoints, and C-bands (for references see Figueiras et al. 1989; Benito et al. 1990, 1991; Vaquero et al. 1990; Carrillo et al. 1990; Sybenga et al. 1990; Gustafson et al. 1990; Singh et al. 1990; Wang et al. 1991).

The best known chromosome in this species is most likely chromosome 1R, in which integrations between genetic and physical maps, providing relevant information about the frequency and distribution of crossing-over along the chromosome length, have been attempted in several instances. Cytological markers as the nucleolus organizer (Lawrence and Appels 1986) and the telomeric C-band of 1RS (Singh et al. 1990) have been used to construct cytogenetic maps for the short arm of this chromosome. Structural changes, including telocentrics and translocations, have also been used as cytological markers (Figueiras et al. 1985, 1989; Sybenga et al. 1990). However the comparison between the genetic distances in these cases with the ones obtained in karyotypically normal plants can present some problems, and in most cases the exact locations of the breakpoints of the translocations used have not been clearly determined. The genetic distances between six C-bands located along the whole length of chromosome 1R were reported by Kalisikas et al. (1986), with values lower than 50% recombination not being observed between all pairs of consecutive C-bands.
The present article reports on a map of the whole 1R chromosome i.e., from telomere to telomere, with all consecutive markers located at distances of lower than 50% recombination. The map includes three isozyme loci (Pgi-RI, Mdh-R1 and Pgd2), the C-bands of the two telomeres and two interstitial C-bands located, respectively, in the short and long arm of this chromosome. In addition, a comparison has been made between the maps including these markers in plants heterozygous for a translocation (T273W) involving chromosomes 1R and 5R and in normal, non-translocated plants. The translocation breakpoint has been physically mapped with respect to other features of chromosome 1R by means of electron microscope analysis of spread pachytene synaptonemal complexes.

Material and methods

Plant material

Different crosses involving plants from cv 'Ailés', cv 'Merced', inbred line E (Giraldez et al. 1979) and a line homozygous for translocation T273W (involving chromosomes 1R and 5R; translocation tester set; Sybenga and Wolters 1972) were made in order to obtain plants heterozygous for different markers, including those for isozymes, C-bands and translocation T273W.

From these crosses, six multiple heterozygous plants were selected (Table 1). The segregation analysis was made in the six progenies (backcross-like) that were obtained from the crosses between these multiple heterozygous plants and homozygous plants for all markers (the line homozygous for translocation T273W indicated above or a line double ditelocentric for chromosome 3R obtained from J. Sybenga). The multiple heterozygous plants were used as females in plants 9-15, 13-13 and 14-25, and as both males and females in plants 5-22, 13-14 and 13-24. In these three plants differences between male and female segregations were not significant.

A line ditelocentric for chromosome 1R obtained from J. Orellana was also used in the synaptonemal complex analyses.

All plants were grown in a climate chamber under identical conditions during their life cycle. During meiosis, a temperature of 18–20°C and a photoperiod of 14 h light/10 h dark were maintained.

Iszyme assays

Six isozymatic systems from extracts of leaf tissue, phosphoglucone mutase (PGM, EC 2.7.5.1), glucosephosphate isomerase (GPI, EC 5.3.1.9), malate dehydrogenase (MDH, EC 1.1.1.37), phosphogluconate dehydrogenase (PGD, EC 1.1.1.44), glutamic oxaloacetic transaminase (GOT, EC 2.6.1.1) and aconitase (ACO, EC 4.2.1.3), were assayed following electrophoresis of the extracts on horizontal 12% starch gel. The buffers and staining methods were as described by Figueiras et al. (1985) and Chenieck and Hart (1987).

Mitotic and meiotic metaphase C-banding analysis

Root tips were immersed in tap water at 0°C for 24 h to shorten the chromosomes and fixed in acetic acid: alcohol 1:3. Anthers having PMCs at metaphase I were fixed in acetic acid: alcohol 6:9.

Table 1. Genotypes of the multiple heterozygous plants used as parents of the six segregating progenies analyzed. These plants were crossed by the lines diteloc-3R and/or hom-T273W, whose genotype for the different markers is also shown.

Plant

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Pgm-R1</th>
<th>Gpi-R1</th>
<th>Mdh-R1</th>
<th>Pgd2</th>
<th>Got-R3</th>
<th>Aco-R3</th>
<th>C-bands</th>
</tr>
</thead>
<tbody>
<tr>
<td>9-15</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>++/++</td>
</tr>
<tr>
<td>13-13</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>++/++</td>
</tr>
<tr>
<td>14-25</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>++/++</td>
</tr>
<tr>
<td>5-22</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>++/++</td>
</tr>
<tr>
<td>13-14</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>++/++</td>
</tr>
<tr>
<td>13-24</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>++/++</td>
</tr>
<tr>
<td>13-25</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>I/I</td>
<td>++/++</td>
</tr>
</tbody>
</table>

The number before the hyphen refers to the cross from which the plant was obtained. The order in which the different alleles are written (before or after the bar) indicates their parental origin.