CYTOLOGICAL STUDIES ON SOME X-RAY MUTANTS OF BARLEY

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I. INTRODUCTION

That X-rays can produce hereditary changes—mutations—is known already from the investigations of Muller and Stadler, carried out at the end of the twenties. About 1930 Nilsson-Ehle and Gustafsson started to apply X-ray treatment for practical plant breeding purposes among others in Golden barley. This variety is a pure line derived from an old Gotland indigenous variety (Tedin 1913). It is practically 100 per cent homozygous and true breeding. Thus all aberrant types appearing after X-ray treatment of kernels of this line could be taken as mutations. In the second generation (X₂) of the first experiments after the treatment, a number of viable mutants were found of which in eleven cases the density of the spike was affected. These mutants were called erectoides and numbered from 1 to 11. Subsequently however, it was found that mutations of this kind seemed to be rather common. Some 40 erectoides mutants have been thus far recorded. A review of this work has been given by Gustafsson (1947).

Many problems connected with the mutations are of great interest for instance: What has happened cytologically in these mutants? Why especially were these erectoides mutations so common? And lastly: What is the behaviour of the mutants in respect to general vitality and single characters in heterozygous as well as homozygous conditions? The present paper is an attempt to try to connect the properties «erectoides 1» and «erectoides 7» with pure cytological data in order to get a first approach to the mapping of the barley chromosomes. No such map is thus far known to us for barley, although many characters have been studied (Robertson et al., 1941).

In a preliminary paper a short account has been given previously by the authors (Hagberg and Tjo, 1950) on the localization of the translocation point of erectoides 7. New data have been gathered about it, which will be included in this paper.

II. MATERIAL AND METHOD

The material for these studies was kindly put at our disposal by prof. Gustafsson. It consists of Golden barley, erectoides 1 and 7, while F₁-hybrids were obtained from the reciprocal crosses erectoides 7 × Golden barley. Hereafter the following abbreviations will be used: G. b. for Golden barley, er. 1 for erectoides 1 and er. 7 for
erectoides 7. As has been mentioned before, the mutants have been derived from the X₂ progeny of the first experiments with X-ray treatment carried out at Svalöv. They have been isolated for more than 10 generations.

For the degree of fertility the frequency of good pollen and seed set is taken. Pollen fertility is determined from aceto carmine-glycerine preparations. Fruit set is determined from the percentage of normally developed kernels on the total amount of florets found on the full grown spikes.

For meiosis studies whole spikes were fixed in Carnoy (3:1) for 3-4 hours and kept in 70 per cent alcohol. Feulgen smear preparations were made. The somatic chromosomes were studied from orcein smear preparations, made according to the oxyquinoline method (Tjio and Levan, 1950). This method proved to be very suitable for getting excellent analysable metaphase plates. Chromosome measurements were made of the following number of metaphase plates: 31 metaphases of G. b., 10 metaphases of er. 7 and 4 metaphases of F₁ hybrid er. 7 × G. b. Measurements were made from drawings of single chromosomes which are drawn in the following way. The chromosomes in a metaphase plate are numbered. Each chromosome is then moved to the center of the microscopic field and drawn separately with great care. In this way the amount of errors is limited.

III. SOME CYTO-GENETIC DATA

Hagberg (unpublished) has since 1946 carried out a series of cyto-genetic studies on the present material. Some of his data connected with our problem therefore will be given here.

Several crosses have been made between G. b. and its erectoides mutants, especially to study the effect of dominance relations (super-dominance, see Gustafsson et al., 1950) and the possible existence of single factorial heterosis in the F₁ hybrids of the respective combinations. For this purpose the vitality character as well as the fertility (both pollen and seed set) were determined. Table 1 shows the fertility frequencies for the years 1948 and 1949.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Per cent good pollen 1948</th>
<th>Per cent good pollen 1949</th>
<th>Per cent fruit set 1948</th>
<th>Per cent fruit set 1949</th>
</tr>
</thead>
<tbody>
<tr>
<td>Golden barley</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Erectoides 1</td>
<td>93</td>
<td>98</td>
<td>97</td>
<td>90</td>
</tr>
<tr>
<td>Erectoides 7</td>
<td>92</td>
<td>99</td>
<td>97</td>
<td>88</td>
</tr>
<tr>
<td>F₁ hybrid er. 1 × G. b</td>
<td>86</td>
<td>93</td>
<td>83</td>
<td>77</td>
</tr>
<tr>
<td>» er. 7 × G. b.</td>
<td>82</td>
<td>85</td>
<td>76</td>
<td>72</td>
</tr>
<tr>
<td>» er. 1 × er. 7</td>
<td>—</td>
<td>78</td>
<td>—</td>
<td>56</td>
</tr>
</tbody>
</table>
Fig. 1. Photograph showing spikes of Golden barley (no. 1 and 10), erectoides 1 (no. 3), erectoides 7 (no. 8), F₁ hybrid erectoides 1 × Golden barley (no. 2), F₁ hybrid erectoides 7 × Golden barley (no. 9) and F₁ hybrid erectoides 1 × erectoides 7 (no. 4-7).

As can be seen from Table 1, the frequencies are quite comparable within each year. The low values for seed set in 1949 is due to a heavy rust attack which apparently decreased the seed set. The fertility relation between the parent plants and its F₁ hybrids however remains, unchanged. There is therefore no doubt that it is here not a question of pure gene differences between the two mutants and G. b. but that obviously structural differences are involved.

In Fig. 1 the types of spikes of G. b., er. 1, er. 7 and the F₁ hybrids of er. 1 × G. b., er. 7 × G. b. and er. 1 × er. 7 are depicted. Spike 1 and 10 are of G. b. They are two rowed, of the mutans type and with kernels of the β type (see ABERG, 1946). The dense spike 3 and 8 are er. 1 and er. 7 respectively. They are both very easy to distinguish from G. b. but it is difficult to keep them from each other. G. b. is semi-dominant over er. 1 and er. 7. This can be seen from the appearance of spike number 2 and 9 in Fig. 1. They are respectively spikes of the F₁ hybrids er. 1 × G. b. and er. 7 × G. b. Er. 1 and er. 7 are obviously not multiple alleles, because the F₁ hybrid of er. 1 × er. 7 has lax spikes almost like G. b. (spike no. 4-7, Fig. 1). The fertility relations can be also appreciated from the spikes shown in Fig. 1.

During a study of the meiosis of the F₁ hybrid er. 1 × G. b. and er. 7 × G. b. in 1948 amphibivalent configurations were found in
Fig. 2. First metaphase in side view in P.M.C. smears. — a: Golden barley, 2n = 14:7H; b: erectoides 7, 2n = 14:7H, note the smallest bivalent, drawn in black; c and d erectoides 1 × Golden barley, 2n = 14:1IV, 5H; e: erectoides 7 × Golden barley, 2n = 14:1IV, 5H; f: erectoides 1 × erectoides 7, 2n = 14:2IV, 3H; g: photograph of the same plate as is drawn in f. × 2650
both hybrids. The mutants are obviously homozygous for reciprocal translocations as compared with G. b. Whereas the F₁ hybrids are heterozygous for one translocation, which gives amphibivalents in metaphase I. The fertility disturbances are lowest in er. 1 × G. b. as can be seen from Table 1. This is presumably because the segments which are interchanged are very small. This is also supported by the fact that in M. 1 besides ring amphibivalents chains of 4 chromosomes were also found in a certain, although low, frequency (Fig. 2 c and d). In the F₁ hybrid er. 7 × G. b. no chain amphibivalents have been encountered. The F₁ hybrid er. 1 × er. 7 however showed the configurations 2^IV + 3^II which suggested that different chromosome pairs are involved in the two translocations (see Fig. 2 f and g). As has been stated in our previous paper (Hagberg and Tjørn, 1950) a particular small bivalent was found in metaphase I of er. 7 (Fig. 2 b). This was much smaller than the smallest bivalent in G. b. (Fig. 2 a). It was thought that it would be possible to find out, which chromosomes have been translocated. In a genetical analysis of the progeny of the hybrid er. 7 × G. b. and also of er. 1 × G. b. not a single case of crossing-over between the locus for spike density and the respective translocation points have been encountered. The «genes» have presumably been mutated in connection with the chromosome breaks and reunion of chromatids and are situated at the translocation points.

IV. OBSERVATIONS OF THE KARYOTYPES

As has been mentioned before, it was the size difference between the smallest bivalent of G. b. and er. 7 that stimulated us to look for structural differences of the somatic chromosomes with the use of the oxyquinoline method. It was thought to be possible to localize the translocation points of er. 1 and er. 7. The method proved to give striking results; not only excellent metaphase plates but also quite good prophases and anaphases were obtained. Prophases show often very delicate structures (Fig. 3 a, b). Even anaphase stages are often so good that also at this stage the chromosome types could be recognized (Fig. 3 c).

The quadruple structure of the centromere is also often seen (Fig. 4 a). In many metaphase plates the different karyotypes could be quite easily analysed. Very often the chromosomes are lying on the same plane, completely separated from each other, quite flat and straight. This facilitates very much the obtaining of correct measurements of the chromosome arms.

GOLDEN BARLEY

As is wellknown the chromosome number of barley is 2n = 14. Of the 7 pairs two have a satellite, four are nearly of the same size and with almost the same position of the centromere, while the seventh pair is decidedly smaller than the others. Various authors
(Bhaduri and Sharma, 1949 and others) have studied the karyotypes of several *Hordeum* spp. The idiogram of Golden barley has been described rather superficially previously by Tjio and Levan (1950) and Hagberg and Tjio (1950). An attempt is now made to analyze statistically the different types of chromosome pairs. This is especially important to distinguish the four longest chromosomes from each other. The statistical treatment of the measurements of the chromosomes is as follows:

As a standard measure for the chromosome length, a *relative value* is used. Its absolute length is expressed as the percentage of the total sum of the lengths of all chromosomes in each metaphase plate. Otherwise it would have been quite impossible to compare the different karyotypes as the variations between the plates are rather great.

The ratio between short and long arm of the chromosome is used as its *index*. If the chromosomes and its arms keep its length ratio in plates of different contraction stages was afterwards controlled. Although some variation occurred, no indication was found that certain chromosome pairs contract more than others. The relative ratio between the arms and between the various chromosomes remain obviously constant, independent of the degree of contraction.

The gathered data on relative length and index of the chromosomes were dotted on a point diagram of which the X-axis represents the relative length (percentage of total length) and the Y-axis the index (ratio short on long arm). By studying this diagram it was possible to get an idea of the approximate position of the mean values of the relative length and index, especially important for the classification of chromosome I-IV. The identification of V, VI and VII does not produce any difficulties as they have clear morphological differences (the satellite of VI and VII) but it is often difficult to do it for I, II, III and IV. The four longest chromosomes could however be classified into I, II, III and IV by considering both relative length and index. The means can afterwards be calculated. It is however, not possible to use the standard error to the means of the four longest chromosomes as such a standard error would underestimate the real variability of the material. But for chromosome pair V, VI and VII where there are clear morphological differences the standard error can obviously be applied.

The karyotype of Golden barley can be summarized as follows:

Pair I: Longest chromosome pair. Relative length 16.6. Index 0.75. The centromere is submedially attached. Sometimes a secondary constriction could be found at the terminal third of the long arm.

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Fig. 3. Root tip squashes of *Hordeum* showing prophase and metaphase chromosomes after 4 hours' treatment with 0.002 mol/l 8-oxquinoline.—a: prophase of Golden barley; b: prophase of *erectoides* × Golden barley; c: anaphase of Golden barley.
Fig. 5. Metaphases from root tip squashes. — a: *erectoides* 7 × Golden barley; b: Golden barley × *erectoides* 7.

Pair II: Long chromosome. Relative length 16.0 and index 0.86. Thus, submedially attached centromere.

Pair III. Long chromosome. Relative length 14.3 and index 0.92, which implies that the centromere is almost medially attached.

Pair IV: Long chromosome. Relative length 14.4 and index 0.77. Submedian centromere.

Pair V: Shortest chromosome without satellite. Relative length 12.7 and index 0.73. Centromere submedially to subterminally attached.

Pair VI: Chromosome with biggest satellite. Relative length 12.1 and index 0.61. Almost subterminally attached centromere.

Pair VII: Chromosome has a smaller satellite than VI. Relative length 13.4. Index 0.41. Thus, subterminal centromere. The long arm is equal to the long arm of pair 1. It is also the longest arm in the karyotype.

The satellite length is not included in the chromosome length. Table 2 gives the absolute measurements of the chromosomes of one typical plate which is shown in Fig. 4 a.

<table>
<thead>
<tr>
<th>Pair No.</th>
<th>Member 1</th>
<th></th>
<th></th>
<th>Member 2</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Long arm</td>
<td>Short arm</td>
<td>Sat.</td>
<td>Total</td>
<td>Long arm</td>
<td>Short arm</td>
</tr>
<tr>
<td>I</td>
<td>4.5</td>
<td>3.6</td>
<td>8.1</td>
<td>4.7</td>
<td>3.5</td>
<td>8.2</td>
</tr>
<tr>
<td>II</td>
<td>4.2</td>
<td>3.8</td>
<td>8.0</td>
<td>4.1</td>
<td>3.8</td>
<td>7.9</td>
</tr>
<tr>
<td>III</td>
<td>4.0</td>
<td>3.8</td>
<td>7.8</td>
<td>4.0</td>
<td>3.7</td>
<td>7.7</td>
</tr>
<tr>
<td>IV</td>
<td>4.1</td>
<td>3.0</td>
<td>7.1</td>
<td>4.3</td>
<td>3.1</td>
<td>7.4</td>
</tr>
<tr>
<td>V</td>
<td>3.7</td>
<td>2.9</td>
<td>6.6</td>
<td>3.5</td>
<td>2.7</td>
<td>6.2</td>
</tr>
<tr>
<td>VI</td>
<td>3.2</td>
<td>2.2</td>
<td>5.4</td>
<td>3.4</td>
<td>2.3</td>
<td>5.7</td>
</tr>
<tr>
<td>VII</td>
<td>4.7</td>
<td>2.0</td>
<td>(1.0)</td>
<td>6.7</td>
<td>4.8</td>
<td>2.2</td>
</tr>
</tbody>
</table>

The satellites are not included into the total length.

Fig. 6. Diagram of the mean values for the relative chromosome length (X-axis) and index of short arm on long arm (Y-axis) of the karyotypes of Golden barley, erectoides 1 and 7. Note the positions of chromosomes 1 and V of erectoides 7.
ERECTOIDES 7.

The data of the karyotypes of the mutants are treated in the same way as those of Golden barley, by means of the point diagram. The mean values of the chromosome types of G. b., er. 1 and er. 7 are shown in the diagram of Fig. 6. The general impression gathered from this is that the means are lying in groups which are especially clear for chromosome pair IV-VI.

It can be immediately seen from the diagram that er. 7 has a different pair V and I in its karyotype than G. b. Especially the position of pair V of er. 7 diverges clearly from that of G. b. This pair can be also immediately detected from the photographs in Fig. 4 a-b and 7 a-b, its short arm being extremely short. In many good plates it can be also observed that the long arm of pair I is longer in er. 7 than in G. b. and that it is the piece terminal to the secondary constriction which is increased in length. The constriction is lying in G. b. in the terminal third of the long arm, whereas in er. 7 it is almost medially situated. The difference in pair I and V between G. b. and er. 7 can be also clearly seen from the following Table.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Pair I</th>
<th></th>
<th>Pair V</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Rel. length</td>
<td>Index</td>
<td>Rel. length</td>
</tr>
<tr>
<td>Golden barley</td>
<td>16.6</td>
<td>0.75</td>
<td>12.7</td>
</tr>
<tr>
<td>Erectoides 7</td>
<td>17.7</td>
<td>0.69</td>
<td>10.8</td>
</tr>
<tr>
<td>F&lt;sub&gt;1&lt;/sub&gt; hybrid er. 7 × G. b. (a)</td>
<td>16.5</td>
<td>0.75</td>
<td>13.1</td>
</tr>
<tr>
<td>(b)</td>
<td>17.5</td>
<td>0.70</td>
<td>10.1</td>
</tr>
</tbody>
</table>

- a means of chromosome member received from father plant
- b » » » » » » mother »

The other 5 pairs are of the G. b. type.

F<sub>1</sub> HYBRID ERECTOIDES 7 × GOLDEN BARLEY

The karyotype of the F<sub>1</sub> er. 7 × G. b. clearly shows, as is to be expected, that the chromosomes of pair V are unequal. On closer study, pair I can also be detected as being heterogenous. In Table 3 the relative length and index of the members of pair I and V of the F<sub>1</sub> hybrid er. 7 × G. b. are given in comparison with its parent plants. As can be seen there is a good agreement between the members of the F<sub>1</sub> hybrid and their respective parent karyotypes. It may be stated here that the F<sub>1</sub> hybrid of the reciprocal cross (G. b. × er. 7) has also given exactly the same karyotype (see Fig. 5 a-b, 7 c and 8 b).
To demonstrate that the variation between the members in the
caryotype is greatest in pair I and V the following Table 4. is given.
The means of the relative lengths and indexes are given.

<table>
<thead>
<tr>
<th>Pair No.</th>
<th>Mean of relative length</th>
<th>Mean of index</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Member 1*</td>
<td>Member 2*</td>
</tr>
<tr>
<td>I</td>
<td>17.5</td>
<td>16.5</td>
</tr>
<tr>
<td>II</td>
<td>15.8</td>
<td>15.3</td>
</tr>
<tr>
<td>III</td>
<td>15.3</td>
<td>14.9</td>
</tr>
<tr>
<td>IV</td>
<td>15.3</td>
<td>15.0</td>
</tr>
<tr>
<td>V</td>
<td>13.1</td>
<td>10.1</td>
</tr>
<tr>
<td>VI</td>
<td>12.8</td>
<td>12.0</td>
</tr>
<tr>
<td>VII</td>
<td>13.7</td>
<td>13.0</td>
</tr>
</tbody>
</table>

(*) The mean of member 1 is the mean value of the long chromosomes and
that of member 2 is the mean value of the short ones of the same pair.

The difference is greatest for pair I and V. Especially for pair V
it is very clear but not so great in pair I. It may be due to a differ-
ence in contraction of the different arms.

ERECTOIDES 1.

It was thought that it would be possible also to localize the trans-
location point of er. 1 in the same way as in er. 7. It seemed at first
to be simple, as two pairs could be already excluded viz. pair I and V.
As is mentioned before, a configuration $2^V + 3^I$ was found in
meiosis of the F$_1$ hybrid er. 1 × er. 7 (Fig. 2 f, g). This implies that 2
different chromosome pairs were involved in the translocation which
produced er. 1. Furthermore amphib valents as chains of 4 chromo-
somes have been found in the F$_1$ hybrid er. 1 × G. b. (Fig. 2 d). This
suggests that the interchanged segments were apparently very small
or anyhow one of them.

The mean values of the relative length and index are given in
the diagram of Fig. 6. As can be seen from it, there is a general
agreement with the standard karyotype (G. b.). The greatest diver-
gence is found in pair I which has a lower index than in G. b. This
chromosome ought however, to be unchanged. It is also impossible
that another pair has become longer than I by a translocation, as
in this case the original longest one which is now nominated II.
would be too short.

Fig. 7. Root tip squashes showing metaphase chromosomes.—a: Golden barley;
b: erectoides 7; c: erectoides 7 × Golden barley. Note chromosome pair V.
V. DISCUSSIONS

X-ray treatment often produces a high frequency of chromosome breaks (see for instance Lea, 1947 and Muller, 1950 for details). This is often followed by various structural rearrangements. It would be expected that the most common type of rearrangements which can produce viable cells, cell tissues and individuals, would be reciprocal translocations. This is evidently also the case. Of the 59 chromosomal alterations Randolph (1950) found in this X-rayed maize 44 were translocations, 8 were inversions, and 7 were deletions. And of the 89 alterations he found in his Bikini material 61 were reciprocal translocations, 15 were inversions and 13 were deletions. Luther Smith (1950) found in the same Bikini test also a high frequency of translocations in barley. Nynom (unpublished) and also Hagberg (unpublished) have found various translocations after X-ray treatment of barley but no inversions. Many such translocations are connected with morphological changes. They are of the homozygous phenotype, which are morphological vital mutations as for example, er. 1 and er. 7. The genes er. 1 and er. 7 are apparently completely linked with their respective translocation points. It is very likely that some kind of chemical change of the locus —«gene»— has taken place in connection with the chromosome breakage or at the rearrangement. It may also be that the changed reaction of the gene is caused by the new gene environment after rearrangement i. e. a position effect.

That it has been possible to localize the translocation point linked with er. 7 in somatic chromosomes is because the interchanged segments were apparently of different sizes. Of these one must be somewhat smaller than the other. The biggest segment must be, at the very most, as long as the short arm of chromosome V in G. b. The difference is, however, evidently big enough that it could be detected. The translocation linked with er. 1, however, could not be localized in the somatic chromosomes. Its karyotype did not show great differences from the standard type (see Fig. 8 a, c and 9 a, b). They were almost perfectly in agreement with each other. It is most likely that the interchanged segments were of such a size that the length ratio of the chromosomes is almost unchanged. This may be achieved in at least two ways: Either the interchange segments are of the same size or they may be of different size but the points of translocation are on the same level in relation to the centromere. In the last case the unbroken arms of the two chromosomes involved ought to be of the same size. The segments are also apparently small (or at least one of them) because in metaphase I of F₁ hybrid er. 1 × G. b. open amphibuvalents were found now and then (Fig. 2 d).

Fig. 8. Metaphases from root tip squashes. — a: erectoides 1; b: erectoides 7 × Golden barley; c: Golden barley.
Chiasma formation obviously sometimes failed between the translocation points. This is to be expected if at least one of the interchanged segments is very small.

Obviously other methods have to be applied to localize er. 1. The somatic prophases as is shown in Fig. 3 a, b, very often show delicate structures, which might be a very useful help in analyzing certain chromosomes. It may also help to localize er. 7 more exactly. No attempt has as yet been made in this direction as the stay at Svalöv of one of us has been limited. Another, and perhaps better method, to come nearer to a solution of this problem is of course to analyze the pachytene, as is known in Zea mays (RHOADES, 1950). Barley pachytene chromosome are however not very suitable to analyse although of course not quite impossible. An analysis of the pachytene chromosomes of the F₁ hybrids er. 1 × G. b. and er. 7 × G. b. would most likely give the most exact cytological localization of the gene er. 1 and er. 7.

Although, we realize very well, that our method is far from perfect, it is at least of interest that by this study a possibility is created to connect linkage groups of genes or gene maps on the 7 barley chromosome types by pure cytological data. It would be possible now to start examining which of the chromosomes correspond to the linkage-groups. The present investigation is just an initial step towards this goal. Meanwhile several other translocation cases have been found in the mutation material at Svalöv. It is very likely that certain suitable translocations of this material could be connected to certain chromosomes which again would be a further help for the cytological mapping of linkage groups in barley.

Acknowledgment.—We wish to express our sincere thanks to Dr. LEVAN and Prof. GUSTAFSSON for criticism and encouragement.

SUMMARY

A cytological study has been carried out in Golden barley and its X-ray mutants, erectoides 1, erectoides 7 and the reciprocal F₁, hybrids erectoides 7 × Golden barley. A short account is given of genetical and meiosis data. The somatic chromosomes have been studied by means of the oxyquinoline method. An analysis is given of the karyotypes of Golden barley, erectoides 1, erectoides 7 and the reciprocal hybrids erectoides 7 × Golden barley. An attempt is made to localize the translocation points for erectoides 1 and erectoides 7 which are strongly linked with the «gene» er. 1 and er. 7 respectively. The translocation point of erectoides 7 was found to be situated

Fig. 9. Root tip squashes showing metaphase chromosomes.—a: erectoides 1; b: Golden barley. Note the similarity of both karyotypes.
on the proximal part of the short arm of chromosome V and on the long arm of chromosome I between the secondary constriction and its terminal end. It has not been possible to localize the translocation point of *erectoides* 1.

**RESUMEN**

(ESTUDIOS CITOLOGICOS SOBRE ALGUNOS MUTANTES POR RAYOS X, DE CEBADA)

Se ha realizado un estudio citológico con la variedad de cebada «Golden» y sus mutantes, provocados con rayos X, *erectoides* 1 y *erectoides* 7, junto con la F1 de los híbridos *erectoides* 7 × Golden y el recíproco. Se da una breve indicación de la meiosis y datos genéticos. Los cromosomas somáticos se han estudiado utilizando el método de la oxiquinolina, realizándose un análisis de los cariotipos correspondientes a la variedad, mutantes y recíprocos indicados. Se intenta localizar los puntos de translocación para los mutantes, que están intímicamente ligados con los genes *er*. 1 y *er*. 7, respectivamente. El punto de translocación del *erectoides* 7 se encuentra que está situado en la parte proximal del brazo corto del cromosoma V, y entre la constricción secundaria y el extremo del brazo largo del cromosoma I. No ha sido posible localizar el punto de translocación del mutante *erectoides* 1.

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CONTENTS

1. Introduction ........................................... 149
2. Material and method ................................... 149
3. Some cytogenetic data ................................ 150
4. Observations of the karyotypes ........................ 153
   Golden barley ........................................ 153
   Erectoides 7 ....................................... 159
   F1, Hybrid Erectoides 7 x Golden Barley ............. 159
   Erectoides 1 ....................................... 161
5. Discussions ........................................... 163
   Summary ............................................. 165
   Resumen en español .................................. 166
   Literature cited ..................................... 166