

LINKAGE RELATIONS OF creep ON CHROMOSOME 5

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Plants of the EMS-induced mutant creep (1) grow prostrate along the ground. This distinctive behavior establishes creep as a worthy seedling marker as well as a candidate for physiological studies. The type of line for this mutant, WL 5859, is tall (Le.) and lacks anthocyanin pigmentation (a), the mutant having been induced in the variety 'Torstag'. I crossed WL 5859 with one of my own le A lines preparatory to attempting linkage studies. The A line had speckled seeds but it was unknown at the time whether its genotype was F, Fs, F fs, or f Fs.

As expected, the F1's of the initial cross were wild type with respect to height, flower color, and habit, i.e. Le/- .A/- .Creep/-. The F1's also had speckled seed. The of a small field population grown in 1980 and scored for Creep-creep and for speckled vs. non-speckled seed showed the segregation pattern indicated in Table 1. This F2 also segregated for A-a but the .a/a plants were not included in the summary.

Table 1. Joint segregation of Creep and a seed speckling gene (either F or Fs)

| Population   | <u>Creep</u> |              | <u>creep</u> |              | Total | Chi-square   |                |         | Recomb. fract. |
|--------------|--------------|--------------|--------------|--------------|-------|--------------|----------------|---------|----------------|
|              | Speckled     | Non-speckled | Speckled     | Non-speckled |       | <u>Creep</u> | Seed speckling | Linkage |                |
| B280-457-460 | 68           | 11           | 5            | 16           | 100   | 0.85         | 0.21           | 29.9    | 16.8 ± 4.2     |

It is clear that only one of the polymeric genes for seed speckling segregated, but it still was unknown whether the segregating locus in question was F or Fs. However, since the Creep A parent was either F or Fs but not both, it is evident from the results that the creep a parent was homozygous recessive for both f and fs. Therefore, the segregation data in Table 1 suggest the possibility of linkage between creep and f on chromosome 3 or fs on chromosome 5.

F3 plants were grown from F2 segregants with the genotype A, creep, f, f.s. To test whether creep was linked with f on chromosome 3 or with Fs on chromosome 5, the creep F3 plants were crossed reciprocally with each of two marker lines. The first marker line carried st-b-chi-6. (f being closely linked with st). This first marker line had speckled seeds, resulting from the presence of Fs alone, i.e. it was known to be f. Fs. Reciprocal crosses were also made between the creep F3 line and a ce (A) line, .ce residing near fs on chromosome 5. The ce line had colorless seeds (f, fs). The relevant genic makeup of the two crosses was as follows:

First cross  
f-st-b-chi-6-Fs-Cr/cr Creep  
 x  
F-St-B-Chi-6-fs-Cr/Cr creep

Second cross  
f fs Cr Ce Creep  
 x  
f fs Cr ce creep

All F1's from the crosses involving the chromosome 3 markers had speckled seeds, whereas all F1's from the ce. crosses had colorless seeds, and all F1's from both crosses had a normal (Creep/-) growth habit. The F1's from both series of crosses were scored in the field in 1981 (Table 2).

Table 2. Distribution of phenotypes in F<sub>2</sub> of two sets of crosses, both sets having one parent in common. The relevant genotype of the common parent was creep fs Cr Ce f St. The genotype of the parent in one set of crosses was st f Fs Cr/cr. The parent of crosses in the second set was ce, f, fs. Data not arranged by cross but by presence or absence of linkage between markers.

| Gene pair | Phase | XY  | Xy  | xY  | xy  | Total | Chi-squares |      |         | Recomb. fract. |
|-----------|-------|-----|-----|-----|-----|-------|-------------|------|---------|----------------|
|           |       |     |     |     |     |       | X           | Y    | Linkage |                |
| Creep-Ce  | R     | 140 | 83  | 73  | 3   | 299   | 0.03        | 2.26 | 33.67   | 17.9 ± 5.6     |
| Creep-Fs  | C     | 441 | 49  | 50  | 128 | 668   | 0.97        | 0.80 | 253.79  | 15.7 ± 1.6     |
| Creep-Cr  | R     | 89  | 43  | 35  | 2   | 169   | 0.87        | 0.24 | 10.60   | 22.8 ± 7.2     |
| Cr-Fs     | R     | 85  | 33  | 40  | 5   | 163   | 0.59        | 0.25 | 5.40    | 34.4 ± 6.8     |
| St-Creep  | R     | 600 | 209 | 201 | 53  | 1063  | 0.69        | 0.07 | 2.45    | ---            |
| St-Fs     | R     | 368 | 135 | 120 | 43  | 666   | 0.98        | 1.06 | 0.02    | ---            |

Direct and indirect evidence from both crosses show that creep is situated in chromosome 5. One piece of direct evidence comes from the cross involving st. The calculated estimate of linkage between creep and st was  $17.9 \pm 5.6$  (Table 2). Additional direct evidence came from the cross involving the st parental line. Since the st line carried Fs (but not F), the line provided a chromosome 5 marker as well as the chromosome 3 markers. The Fs-creep linkage estimate was  $15.7 \pm 1.6$ .

The st. line also provided corroborating negative evidence inasmuch as st shown to be independent not only of creep but also of Fs. Moreover, the st-b-chi-6 parent was heterozygous for Cr (Cr/cr). so some of the data could be used in a three-point analysis involving cr, creep. and fs. Although the data are meager, there is evidence of repulsion phase linkage between creep and cr. in this cross.

The data are considered insufficient to establish gene order because these crosses did not allow a direct test of linkage intensity between ce. and fs. But the recovery of ce-creep-fs segregants in provided the genotype for three-point coupling phase crosses now in progress.

1. Sidorova, K. K. 1975. PNL 7:57-58.