

## SUPPLEMENTAL LINKAGE DATA FOR CHROMOSOMES 1 AND 5

Marx, G. A. NYS Agricultural Experiment Station, Geneva, NY USA

**Creep-Ce-Fs**

In 1982 (5) I reported evidence showing that creep is situated on chromosome 5. With respect to other markers on that chromosome, the following order was suggested: Cr-Creep-Fs-Ce. A line homozygous recessive for creep ce fs was recovered from the above study and was used in the three-point test reported here (Table 1.) The present data confirm the previous findings in all essential respects except that the intensity of linkage among creep, ce and fs is stronger in this study and that the order apparently is creep-ce-fs rather than creep-fs-ce. The order indicated by the present data conforms with the order given in Lamprecht's 1968 map [see (1)].

Table 1. Analysis of the F<sub>2</sub> of a three-point cross Creep Ce Fs x creep ce fs and reciprocal. Data<sup>2</sup> collected from field (Fld) and glasshouse (GH) populations.

| Loci        | Number |     |          | Chi-squares |      |         | Recomb. fract. | S.E.         |      |
|-------------|--------|-----|----------|-------------|------|---------|----------------|--------------|------|
|             | Field  | GH  |          | X           | Y    | Linkage |                |              |      |
| Creep Ce Fs | 245    | 116 |          |             |      |         |                |              |      |
| Creep Ce fs | 1      | 1   | Creep-Ce | Fld         | 0.16 | 0.01    | 167.28**       | 12.08        | 1.87 |
| Creep ce Fs | 0      | 0   |          | GH          | 3.12 | 1.05    | 67.56**        | 8.42         | 2.36 |
| Creep ce fs | 22     | 8   |          |             |      |         |                |              |      |
| creep Ce Fs | 18     | 4   | Creep-Fs | Fld         | 0.16 | 0.05    | 165.45**       | 12.34        | 1.89 |
| creep Ce fs | 0      | 0   |          | GH          | 3.12 | 0.70    | 65.80**        | 8.93         | 2.43 |
| creep ce Fs | 0      | 0   |          |             |      |         |                |              |      |
| creep ce fs | 67     | 25  |          |             |      |         |                |              |      |
|             | 353    | 154 | Ce-Fs    | Fld         | 0.01 | 0.05    | 354.33**       | 0.01         | 0.06 |
|             |        |     |          | GH          | 1.05 | 0.70    | 123.66**       | no           |      |
|             |        |     |          |             |      |         |                | recombinants |      |

(B283-156-158)

(C282-154-157)

The data are divided into two separate analyses because the overall experiment was conducted in part in the glasshouse and in part in the field. There was some question about the genotype of 18 F<sub>2</sub> segregants, so these plants were progeny tested to verify their genotype. There were only two Ce fs crossover F<sub>2</sub> plants in the combined populations comprising 507 plants.

Cov Fs

Evidence adduced previously has indicated that cov, a chlorophyll gene which confers a distinct blue-green foliage color (but without affecting pod color), is located on chromosome 5 in the vicinity of cr and gp (3,4). These results lead to the expectation, demonstrated herein, that cov should show evidence of linkage with fs (Table 2).

Table 2. Analysis of the F<sub>2</sub> of a repulsion phase cross Cov fs x cov Fs.

| Cov Fs | Cov fs | cov Fs | cov fs | Total | Chi-squares |      |         | Recomb. |      |
|--------|--------|--------|--------|-------|-------------|------|---------|---------|------|
|        |        |        |        |       | Cov         | Fs   | Linkage | Fract.  | S.E. |
| 139    | 51     | 49     | 5      | 244   | 1.07        | 0.55 | 7.35**  | 32.5    | 5.6  |

A-Af-I-Am-1

Preliminary data on a cross involving three genes on chromosome 1, af-i-am-1, was reported last year (6). Larger populations of the same cross were grown and evaluated in the field in 1983. In this case, however, the seeds from the F<sub>1</sub> plants (i.e. F<sub>2</sub> seeds) were sorted prior to planting for yellow (I) and green (i) cotyledon color. Because, as the analysis of the glasshouse populations demonstrated, the three genes are rather tightly linked, the I seeds, except for a few crossovers, were expected to produce plants with normal (Af/-) foliage but to segregate for A-a, for I-i, and for Am-1-am-1. The am-1/am-1 plants were expected to be I/I but only the A plants of this group are expected to show the seed disorder (sd-1) associated with am-1 (that is, sd-2 expression is blocked in the presence of a/a). The second group of seeds, the ii seeds, were expected to produce (except for crossovers) afila (af) plants segregating for A-a but not for am-1 and its associated seed disorder. These expectations were fulfilled in the field populations (Tables 3 and 4), the only exceptions arising from crossover events.

Table 3. Segregation for flower color in F<sub>2</sub> of cross A Af I am-1 x a af i Am-1. Populations of the cross were grown in the field (Fld) and in the glasshouse (GH).

|      | Wild-type | White |       | Totals |                              |
|------|-----------|-------|-------|--------|------------------------------|
|      |           | a     | am-1  |        |                              |
| Fld  | 188       | 83    | 58    | 329    | $\chi^2_{(9:7)} = 0.78^{ns}$ |
| GH   | 125       | 71    | 54    | 250    |                              |
| Obs. | 313       | 154   | 112   | 579    |                              |
| Exp. | 325.7     | 144.7 | 108.6 | 579    |                              |

Table 4. Analysis of the  $F_2$  of a four-point cross  
 A Af I am-1 x a af i Am-1. Populations of the cross were grown in  
 the field (Fld) and in the glasshouse (GH).

| Loci    |     | XY  | Xy | xY | xy | Total | Chi-squares |      |          | Recomb.<br>fract. | S.E. |
|---------|-----|-----|----|----|----|-------|-------------|------|----------|-------------------|------|
|         |     |     |    |    |    |       | X           | Y    | Linkage  |                   |      |
| A-Af    | Fld | 190 | 61 | 64 | 19 | 334   | 0.00        | 0.20 | 0.07     | 48.90             | 4.15 |
|         | GH  | 136 | 43 | 52 | 19 | 250   | 1.54        | 0.01 | 0.22     | 47.97             | 4.64 |
| Af-I    | Fld | 240 | 10 | 8  | 70 | 328   | 0.26        | 0.06 | 225.56** | 5.69              | 1.32 |
|         | GH  | 181 | 7  | 3  | 59 | 250   | 0.01        | 0.26 | 206.72** | 3.72              | 1.22 |
| Af-Am-1 | Fld | 132 | 58 | 61 | 0  | 251   | 0.07        | 0.48 | 22.41**  | <13               |      |
|         | GH  | 82  | 54 | 43 | 0  | 179   | 0.09        | 2.55 | 27.11**  | <13               |      |
| Am-1-I  | Fld | 126 | 64 | 57 | 0  | 247   | 0.49        | 0.11 | 25.27**  | <13               |      |
|         | GH  | 79  | 46 | 54 | 0  | 179   | 2.55        | 0.05 | 30.32**  | <13               |      |

Although the cross represents a four-point linkage test, the data are presented as combinations of specific gene pairs. In view of the complexity that is introduced by various forms of epistasis it is easier to comprehend the relationships among all the genes by considering them in pairs.

Wild-type vs white flower color: The two parents in the cross were white flowered, one because of a and the other because of am-1. The F1 plants bore wild-type flowers and the overall F2 population satisfactorily fit a 9:7 for colored vs white flowers, the white flowered class being composed of a/a and am-1/am-1 plants (Table 3).

Normal (Af) vs afila (af) habit and yellow (I) vs green (i) cotyledons: Since i is linked in coupling phase with af in this cross, nearly all ii seeds gave rise to af plants, but some crossovers were recovered and the calculated linkage intensity between af and i was 3.72 in the glasshouse population and 5.60 in the field populations (Table 4).

Af-af vs Am-1-am-1: These two genes were in repulsion phase and no crossover plants were recovered in the F2 of either the glasshouse or field populations (Table 4). This result is consistent with a previous study (2) involving a comparable number of plants. In both cases progeny tests were required to extract af - am-1 recombinants. In the present case, 32 am-1 F2 segregants were progeny tested and, of those, five progenies segregated for Af-af, the estimated recombination fraction being 9 + 4% (vs 8 + 3% for the 1969 experiment).

Am-1-am-1 vs I-i: These two genes also were in repulsion and, again, no am-1-i plants were recovered in F2 (Table 4). The progeny tests which were performed to recover af-am-1 plants (described in previous paragraph) were not all carried into the adult plant stage so no estimate of the intensity of linkage between am-1 and i is possible from these studies, except that the combined F2 populations indicate that the value is less than 13%. However, one crossover progeny was found among a group of selected plants that were grown to maturity.

1. Blixt, S. 1972. *Agri Hort. Genet.* 30:1-293.
2. Marx, G. A. 1969. PNL 1:9-10.
3. Marx, G. A. 1972. PNL A:30-31.
4. Marx, G. A. 197A. PNL 6:30-31.
5. Marx, G. A. 1982. PNL 14:41-42.
6. Marx, G. A. 1983. PNL 15:43-45.