Genetic Analysis of Seed-Weight in Reciprocal Crosses of Flax (Linum usitatissimum L.)

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Summary. Materials used in this study consisted of small and large seeded flax varieties Redwing and Beta 210, and of their reciprocal crosses and backcrosses. The seed weight means (mg’s/seed) of reciprocal crosses were the same in F1, but significantly different in F2 and F3 generations indicating thus their nonequivalence with respect to this character. This nonequivalence was detectable also in the backcross reciprocals. On the assumption that Redwing and Beta 210 have different plasmatypes and the hybrid has the same plasmatype as its female parent, the available 24 families, including the parents as sells, were grouped into two genomically the same but plasmatically supposedly different sets. A detailed analysis of the family means in these two sets led to the conclusion that the inheritance of the character considered was rather complicated. In F1 generation the Beta 210 set of genes was partially dominant over its allelic Redwing set (|k| < |d|). In the subsequent generations the Beta 210 set of genes has sustained a certain degree of loss of expressivity. This loss was 73% in the plasmatypically Redwing set of families and 20% in the plasmatypically Beta 210 set of families. This difference in the loss of expressivity and the gene-dosis effects, detected mainly in the plasmatypically Beta 210 set of families, indicated that the nature of the reciprocal cross nonequivalence observed in this study was both cytoplasmic and nuclear.

Introduction

The mode of the inheritance of seed weight in reciprocal crosses of flax (Linum usitatissimum L.) dealt with in this study, has been briefly reported by Smith and Fitzsimmons (1964, 1965). In their 1965 paper the authors have pointed out that the seed weight in the reciprocal flax crosses they were dealing with, was inherited in a manner similar to that reported by Chandraratna and Sakai (1960) for reciprocal rice crosses. As in rice, the seed weight differences between the reciprocals appeared to be controlled both plasmatically and genotypically. However, in contrast with rice, the nonequivalence of reciprocals with respect to seed size, expressed itself beginning with the second and not the first filial generation. This failure of expression of reciprocal differences in the F1 generation was not explained satisfactorily at that time.

Materials and Methods

At the time when the typescript of the previous paper (1965) was submitted for publication, the compilation of data on seed-weight was not complete. For the present paper all the seed-weight data obtained for flax varieties Redwing and Beta 210, and for their reciprocal crosses and backcrosses were used. All the family means, including those for which there were no additional data, were calculated anew. The standard errors of the generation, or family, means were obtained from the corresponding “within family — between plot” variances. It was assumed that the parents Redwing and Beta 210 were different for seed-weight both plasmatically and genotypically, and that the hybrid and its female parent had the same plasmatype. Therefore, the families were grouped into two supposedly plasmatically different sets, as given in Table 1, where “set of π(R) families” and “set of π(B) families” refer, respectively, to families assumed to have the same plasmatype as Redwing (R) and to those assumed to have the same plasmatype as Beta 210 (B).

Experimental Results

From the data in Table 1 it is obvious that the seed-weight means of the varieties Redwing and Beta 210, referred to hereafter as R and B, are different, and that the means of reciprocal crosses (RB) and (BR) in the first filial generation are the same, viz., \( \bar{x}(RB) F_1 = \bar{x}(BR) F_1 = 0.12 \pm 0.13 \).

With this information alone one would be inclined to conclude that the parents R and B were genotypically different but plasmatically the same with respect to seed-weight. Such a conclusion would be valid if the equality of the seed-weight means of reciprocals were preserved in the subsequent generations of selfing. The differences \( \bar{x}(RB) F_3 - \bar{x}(BR) F_3 = -1.60 \pm 0.29 \) and \( \bar{x}(RB) F_3 - \bar{x}(BR) F_3 = -1.14 \pm 0.15 \) calculated from the data (Table 1) show this not to be so. This quantitative genetic nonequivalence of the reciprocals, which in the present case...
Table 1. Mean Seed-Weights of Redwing (R) and Beta 210 (B) and of their Reciprocal Crosses and Backcrosses

<table>
<thead>
<tr>
<th>Set of Families</th>
<th>No. of Plots</th>
<th>Mean Seed-Weight (mg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(R)</td>
<td>30</td>
<td>4.91 ± 0.04</td>
</tr>
<tr>
<td>(RB) F₁</td>
<td>6</td>
<td>8.13 ± 0.08</td>
</tr>
<tr>
<td>(RB) F₂</td>
<td>3</td>
<td>6.09 ± 0.28</td>
</tr>
<tr>
<td>(BR) F₁</td>
<td>11</td>
<td>5.74 ± 0.15</td>
</tr>
<tr>
<td>(BR) F₂</td>
<td>5</td>
<td>5.20 ± 0.15</td>
</tr>
<tr>
<td>(RB) F₁</td>
<td>11</td>
<td>5.74 ± 0.15</td>
</tr>
<tr>
<td>(BR) F₂</td>
<td>5</td>
<td>5.20 ± 0.15</td>
</tr>
<tr>
<td>(RB) F₁</td>
<td>10</td>
<td>5.77 ± 0.18</td>
</tr>
<tr>
<td>(BR) F₂</td>
<td>5</td>
<td>5.73 ± 0.19</td>
</tr>
<tr>
<td>(RB) F₁</td>
<td>12</td>
<td>8.79 ± 0.13</td>
</tr>
<tr>
<td>(BR) F₂</td>
<td>5</td>
<td>7.83 ± 0.18</td>
</tr>
</tbody>
</table>

1 The parental, F₂ and F₃ plots were considerably larger than those of F₁'s (≠ 40—100 plants as compared to 7—9 plants, respectively). The entire experiment consisted of 6438 plants.

manifested itself beginning with the F₂ generation, implies that the parents R and B probably differ with respect to seed weight both genotypically and plasmatypically. Furthermore, 

\[
\bar{x}(RB) F₂ - \left( \frac{1}{4} \right) \left[ \bar{x}(R) + 2\bar{x}(RB) F₁ + \bar{x}(B) \right] = -1.58 ± 0.29***
\]

but

\[
\bar{x}(BR) F₂ - \left( \frac{1}{4} \right) \left[ \bar{x}(R) + 2\bar{x}(BR) F₁ + \bar{x}(B) \right] = 0.08 ± 0.40**
\]

Since the reciprocal crosses R x B and B x R involve the same set of differential loci, the disagreement between the differences (1) and (2) confirms the plasmatypic inequality of the parents R and B \([\pi(R) \neq \pi(B)] in Aksel's (1974) notation\). It also indicates that the set of genes contributed by B to R x B hybrids has been affected by \(\pi(B)\) but its allelic set contributed by R to B x R hybrids has not been affected by \(\pi(B)\). In other words, since \(\bar{x}(RB) F₁ - \bar{x}(BR) F₁ = 0.12 ± 0.13\) and the difference (2) = 0.08 ± 0.40**, the difference (1) = -1.58 ± 0.29*** has to be attributed to both \(\pi(R) \neq \pi(B)\) and the \(\pi(R), \varphi(x) k\) — sensitivity of the set of genes contributed by B to the R x B hybrids, and not to epistasis. Let us consider the two sets of families individually.

Set of \(\pi(R)\) families. In regard to this set it is assumed that the differential genes of B were affected in \(\pi(R)\) when contributed either by \(RB) F₁ or \(BR) F₁, and were not affected when contributed directly by B itself (Aksel 1974, assumption 6c). Consequently, the system of linear equations for this set will be as given in Table 2, where the parameters \(m, [d], [h] = (\bar{h} - \bar{A})\) and \(\bar{A}\) in the corresponding equation in Table 2. The observed mean of the ith family \((i = 1, 2, \ldots, 12)\) deviates from its expected value by \(e_i\). The adequacy of the genetical model was tested by \(\chi^2 = \sum w_i e_i^2\) with \(n - k\) degrees of freedom \((n = \text{no. of equations}, k = \text{up. of parameters to be fitted to them})\). The data in this particular case fits the model: \(\chi^2 = 7.8393; DF = 7; 0.30 < P < 0.50\).

Set of \(\pi(B)\) families. It was shown that 

\[
\bar{x}(BR) F₁ - \bar{x}(RB) F₁ \approx 0
\]

and

\[
\bar{x}(BR) F₂ - \left( \frac{1}{4} \right) \bar{x}(BR) F₁ - \left( \frac{1}{4} \right) \left[ \bar{x}(R) + \bar{x}(B) \right] \approx 0,
\]

i.e., as far as the F₁ and F₂ generations of the B x R cross are concerned, there was no indication of \(\pi(B)\) effect on \(U_k(r)_k\) or of non-allelic interaction. Consequently, \(\bar{x}(BR) F₂\) and its expected value

\[
\left( \frac{1}{4} \right) \left[ \bar{x}(R) + 2\bar{x}(BR) F₁ + \bar{x}(B) \right],
\]

or

\[
\left( \frac{1}{4} \right) \left[ 3\bar{x}(R) + 2(\bar{BR}) F₁ + 3\bar{x}(B) \right],
\]

would be the same. However, this happens not to be the case, since the pertinent data from Table 1