Linkage relationship between the loci Twt and Vam

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Earlier we have shown that the loci Variomaculata (Vam) [3] and Twisted tendrils (Twt) [1, 2, 4] reside in the proximal part of the long arm of chromosome II (here we use chromosome numbers coinciding with those of linkage groups). However, their positions with respect to each other remained unclear. Moreover, the precision of mapping was reduced because the mutant alleles of both loci were in a repulsion phase to other markers segregating in the cross. For this reason we obtained a tester useful for more precise mapping. We examined several hundred F1 plants resulting from the cross described in (3) and found among them a single cross-over plant with the phenotype (a vam), from which a stock OK16 (a, vam, twt) was derived by selfing (in this work this stock was used at the F6 generation).

The mutation Twt appeared simultaneously with the Twt-translocation between chromosome II and VI (2, 4). A heterozygote for this translocation produces tertiary trisomics possessing an interchange extra chromosome with a frequency of 3-5% (2). In a progeny produced by the selfing of such a trisomic, a diploid plant was found which carried the gene Twt on a non-translocated chromosome II (1). This plant gave rise to the isogenic line TWT-D (A, Vam, Twt).

A cross OK16 x TWT-D produced seven F1 plants with phenotype (A Vam Twt). Segregation in F2 and linkage data derived are shown in Table 1. Joint segregation analysis of the data generate the following map segment.

\[
\begin{array}{ccc}
A & Vam & Twt \\
7.0 & 5.1 & 10.8 \\
& \text{cM}
\end{array}
\]

Table 1. Segregation of phenotypes in F2 progeny of the cross OK16 (a, vam, twt) x Twt-D (A, Vam, Twt). N=116.

<table>
<thead>
<tr>
<th>Gene pair</th>
<th>Number of progeny</th>
<th>A/B</th>
<th>A/b</th>
<th>a/B</th>
<th>a/b</th>
<th>Joint Chi-sq.</th>
<th>Recomb. Fract.</th>
<th>St. Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>a Twt</td>
<td>80 7 5 24</td>
<td>62.00***</td>
<td>10.79</td>
<td>3.08</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>a vam</td>
<td>81 6 2 27</td>
<td>79.41***</td>
<td>6.97</td>
<td>2.47</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Twt vam</td>
<td>81 4 2 29</td>
<td>88.08***</td>
<td>5.12</td>
<td>2.11</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Capital letters A and B stand for dominant alleles, lowercase letters for recessive alleles. Calculations of recombination fractions and their standard errors were made with the maximum likelihood method using the program ‘Cros’.

*** - probabilities less than 0.0001.

Thus, the mutant genes vam and Twt can be used as convenient markers of the centromeric region of the chromosome II long arm because both mutant phenotypes are easily scored at the seedling stage.

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