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 F_3 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 F_6 generation).

The mutation *Twt* appeared simultanously 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 F_1 plants with phenotype (*A Vam Twt*). Segregation in F_2 and linkage data derived are shown in Table 1. Joint segregation analysis of the data generate the following map segment.

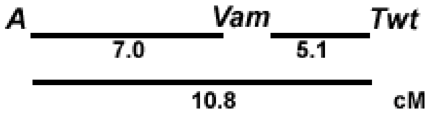

Table 1. Segregation of phenotypes in F_2 progeny of the cross *OK16 (a, vam, twt)* x Twt-D (*A, Vam, Twt*). N=116.

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

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.

Acknowledgement: The work was partly supported by the Russian State Program 'Russian Fund for Fundamental Research'.

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3. Rozov, S.M. and Gorel', F.L. 1994. Pisum Genetics 26: 26-27.
4. Temnykh, S.V., Gorel', F.L., Berdnikov, V.A. and Weeden, N.F. 1995. Pisum Genetics 27: 23-24.