Mapping of the breakpoints of the *Twt*-translocation

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In 1992 we described a dominant mutation *Twt* (*Twisted tendrils*) found in the M_2 population after treatment of seeds of the line Sprint2 with EMS (1). Surprisingly, this mutation appeared to be connected with one of the breakpoints of a new reciprocal translocation found in the same plant and which most probably arose from the same mutation event. In subsequent experiments we have not observed the translocation without *Twt*. Thus, the Twt mutation is a marker of the new translocation, which we called *Twt*-translocation. We have shown that the locus *Twt* resides on the long arm of chromosome II (for simplicity, here we use the numerals of linkage groups to designate chromosomes), about 8 cM from the locus *A* towards the telomere (1, 2). Later we found pseudo-linkage (18% crossing-over) between *Twt* and the locus *D* (4), a marker on chromosome I not far from the telomere (5). Thus, the *Twt*-translocation involves chromosomes I and II.

For a more precise location of the breakpoint on chromosome I we crossed our line Twt-T (being a structural homozygote for *Twt*-translocation originating from cross VIR3953 x Sprint2 *Twt/twt* described in ref. 1) with line WL6115 (*a, twt, brac*). The locus *Brac* shows linkage to *D* (27.5 % of crossing-over, ref. 3). It should be noted that among plants with *Twt* phenotype the homozygotes *Twt/Twt* can be easily distinguished from heterozygotes *Twt/+* by pollen fertility, heterozygotes exhibiting 50% sterile pollen. The data presented in Table 1 show that all the three segregating loci, *A, Twt* and *Brac*, are tightly linked. The strongest linkage (0.8%) is found between the loci *Twt* and *Brac*. Fig. 1 shows the presumed position of the recessive allele *brac* on chromosome I with a dashed oval.

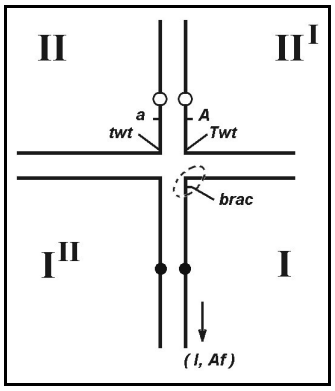

*Fig. 1. Scheme of a translocation cross formed in meiosis of F_1 (*Twt-T *x WL6115).*

A more precise location of *Brac* was achieved by trisomic analysis. Earlier (1) we have shown that in the progeny of structural heterozygotes for the *Twt*-translocation there occur tertiary trisomics that possess a standard diploid karyotytpe plus a small interchange chromosome II^I. In the F_2 population analyzed, we found two such trisomics (their karyoptype was supported by analysis of PMC). The plants displayed the phenotype *A Twt brac*. Thus, the recessive allele *brac* was not covered by the extra chromosome II^I. Instead, it is situated on chromosome I more proximally (lower on the diagram) than the translocation breakpoint.

Table 1. Segregation data for F_2 progeny of the cross Twt-T (*A, Twt, Brac*) x WL6115 (*a, twt, brac*)

Locus pairs		Number of progeny with designated phenotypes[1]						Joint Chi-sq.	Recomb. Fract.	Standard error
		A/B	A/h	A/b	a/B	a/h	a/b			
Brac	***Twt***	**17**	**68**	**1**	**0**	**0**	**27**	**107.70*** **	**0.81**	**0.85**
A	***Twt***	**17**	**66**	**4**	**0**	**2**	**24**	**82.69*** **	**5.05**	**2.10**
Brac	***A***	**83**	**-**	**3**	**4**	**-**	**24**	**77.42*** **	**6.55**	**2.42**

[1]Designations: A,a - first gene; B,b - second gene; capital letters stand for dominant alleles, h - heterozygous.
***** probability less than 0.0001.**
All calculations were done by the maximum likelihood method with the use of the program 'Cros'.
Two trisomic plants were excluded from the analysis.

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