

Gene *Twt* (*twisted tendrils*) decoupled from the translocation breakpoint became a convenient dominant marker on chromosome 1.

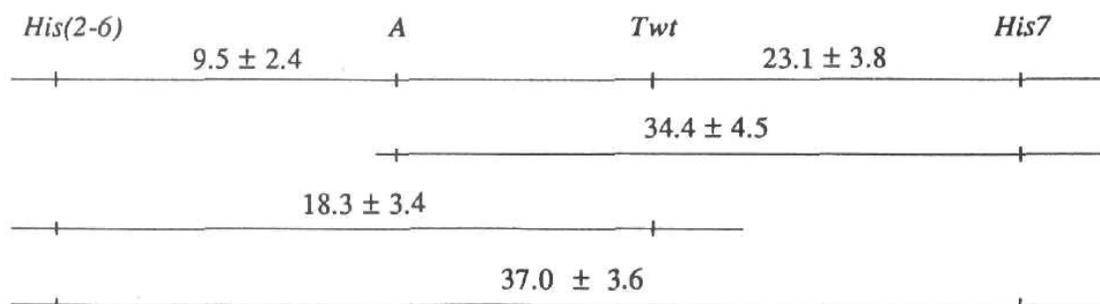
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Earlier we described a new dominant mutation *Twt* (*twisted tendrils*) (1) tightly linked to the break point of a translocation which arose simultaneously with the mutation. The translocation involves chromosome 1 and an unidentified chromosome. Among 106 plants obtained by setting of a structural heterozygote (1), all 43 plants with normal tendrils had fertile pollen, while all 52 plants with phenotype *Twt* had semisterile pollen. We concluded that gene *Twt* must be located in close proximity (less than 1 cM) to the break point. In the progeny of a cross between the structural heterozygote and plants possessing a normal karyotype, the tertiary trisomic ($2n + 1-X$) was identified (1). The additional chromosome, 1-X, carried a fragment of chromosome 1, with genes *A* (*anthocyanin*), *His(2-6)* (encoding subtypes 2-6 of histone H1), and *Twt*. Trisomic plants had phenotype *Twt* and fertile pollen, but were inferior to their $2n$ siblings in vigour and fertility. Selfing of these trisomic plants should have produced the following karyotypic classes: trisomics, structural heterozygotes, homozygotes for reciprocal translocations, or homozygotes for normal karyotype; the latter class of plants should have phenotype *twt* and the others phenotype *Twt*. However, one fertile and vigorous plant with phenotype *Twt* was detected in the progeny of a trisomic. It gave 249 seeds in contrast to the 5-10 seeds ordinarily produced by trisomics. This exceptional plant turned out to be heterozygous for loci *a* and *His(2-6)* [phenotype 1021/1133, for designation of H1 haplotypes see (1)] and homozygous for gene *His7* (allele 2) encoding H1 subtype 7 (2).

We examined 216 individual progeny from this plant. All progeny proved to be fully fertile and showed segregation for phenotypes $A : a$ and $Twt : twt$. Chromosome analysis of pollen mother cells of representatives of all the phenotypic classes showed the presence of the common, seven bivalent configuration at meiotic metaphase I. The pattern of phenotypic segregation (Table 1) allowed us to consider gene *Twt* as a dominant factor linked to genes *a* and *His(2-6)*. The calculated recombination fractions for gene pairs *His(2-6) - a* and *His(2-6) - Twt* are 5.5 ± 1.6 and 12.5 ± 2.4 , respectively.

One of these plants with phenotype $His(2-6)^{1133}$, a , *Twt*, $His7^2$ was crossed with the line WL1255 with genotype $His(2-6)^{1221}$, A , *twt*, $His7^3$. Among five F_1 plants, three had phenotype *Twt* and two had phenotype *twt* indicating the parental plant was heterozygous at this locus. The three *Twt* plants were selfed and the resulting F_2 scored for segregating linkage group I markers. The combined data are presented in Table 2. Recombination fractions \pm SE were obtained using the method of maximum likelihood with the aid of the computer program CROS developed by S.M. Rozov. The results can be presented as the following segment of the genetic map for linkage group 1:



(The distance between genes *a* and *Twt* appeared to be zero due to their repulsion phase and the absence of double cross-overs with phenotype *a twt*; it is impossible to estimate the actual distance between closely linked loci in such a cross). This map corresponds well to the recently reported (2) normal order of genes *His(2-6)*, *A*, and *His7*.

Table 1. Joint segregation of loci *His(2-6)*, *a*, and *Twt* in the progeny of the exceptional trisomic descendant with normal fertility and karyotype. (The total number of plants is 216).

<i>Anthocyanin</i> <i>His(2-6)</i>	<i>a</i>			<i>A</i>		
	<i>1021</i>	<i>1021/1133</i>	<i>1133</i>	<i>1021</i>	<i>1021/1133</i>	<i>1133</i>
<i>Twt</i>	36	7	0	4	92	8
<i>twt</i>	2	0	0	0	17	50

Table 2. Joint segregation of loci *Twt*, *A*, *His(2-6)*, and *His7*. (Total number of plants is 159).

<i>His(2-6)</i> <i>Anthocyanin</i>	<i>His7</i> <i>Twisted tendrils</i>	<i>1133</i>		<i>1133/1221</i>		<i>1221</i>	
		<i>A</i>	<i>a</i>	<i>A</i>	<i>a</i>	<i>A</i>	<i>a</i>
3	<i>Twt</i>	1	2	12	0	4	0
	<i>twt</i>	0	0	11	0	13	0
2/3	<i>Twt</i>	5	14	36	2	7	0
	<i>twt</i>	0	0	1	0	9	0
2	<i>Twt</i>	2	11	21	1	4	1
	<i>twt</i>	0	0	1	0	1	0

The cause of the observed separation of gene *Twt* from the translocation breakpoint is not clear, it might be crossing over or some reverse translocation. Anyway, this gene became a convenient dominant marker on chromosome 1. Moreover, the line appears to possess a normal karyotype.

1. Gorel, F.L., Temnykh, S.V., Lebedeva, I.P. and Berdnikov, V.A. 1992. *Pisum Genetics* 24:48-51.
2. Kosterin, O.E. 1992. *Pisum Genetics* 24:56-59.