TENDRILLED ACACIA (tac): AN ALLELE AT THE Uni LOCUS

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Tendrilled acacia (tac) recently has been found to be situated in chromosome 3 (5), toward the M end of the chromosome (6). To fix its position more precisely, tac was crossed with lines which were known or thought to reside in the segment between st and uni. It became apparent from these crosses that tac and uni are allelic.

Analysis of crosses involving st apu tac and M (Table I) revealed a rather close linkage between M and tac, and the close association between st and apu, reported previously (5), was confirmed. Since earlier evidence (3,4) indicated that we1 is located close to st, in the region between st and M, we1 was also used in crosses with tac. The present evidence, however, indicates that wel lies toward the b end of chromosome 3 rather than toward the M end. The substantial population size in the present studies and the fact that the cross is a four point cross lends considerable credence to the new findings.

Tables 3-4 provide additional linkage data for chromosome 3 markers collected in the course of pursuing studies not directly related to this investigation.

Since M and uni are known to be closely linked (2) and inasmuch as tac and M are closely linked (Table 1), tac and uni were expected to be closely linked as well. To test this assumption, tac was crossed with WL 187 (type line for uni), seeds of which were kindly supplied by Dr. Blixt. Since uni/uni plants are sterile, it was necessary to use a number of phenotypically normal segregants in WL 187 as parents to ensure recovering the uni allele from a heterozygous plant. A total of 73 F1 seeds from 11 individual F1 plants were planted. Six of the F1 progenies contained wild-type plants exclusively whereas five progenies contained plants of two different phenotypes: some wild type and some resembling a combination of tac and uni. In plants of the latter class the early-formed leaves were unifoliate; later leaves became tripartite, followed by two pairs of leaflets and a terminal leaflet. These plants characteristically had no terminal tendrils, but rarely an odd subterminal tendril did appear. Flowers on the affected plants were somewhat malformed In contrast to the flowers borne on sibling plants. The malformation notwithstanding, the flowers more closely resembled normal flowers than the distinctively sterile inflorescences of uni/uni plants. Fertility was only somewhat impaired. The described plants were interpreted as carrying the tac allele and the uni allele together in the same plant, thus evidencing alleles at a single locus.

To pursue this supposition further, and to demonstrate that the plants in question were not selfs, I grew the selfed seed of two of the F1's showing the described hybrid phenotype. One population contained 44 F2 plants (one died early), the second 18 plants (Table 5). The spectrum of plant phenotypes was the same in both populations. There were no normal, wild-type plants in either population. Most plants resembled tac (some with typical subterminal tendrils) and a minority resembled the distinctive phenotype conferred by uni/uni, including the typical malformed, sterile

inflorescences (Table 6). The tac allele apparently is dominant to the uni allele but the dominance is incomplete and the heterozygotes usually can be distinguished from tac homozygotes (and readily from uni homozygotes). Segregation for these phenotypes was accompanied by normal segregation for other markers present in the cross (Table 6); segregation also occurred at the R and I loci.

Even before recognizing the stated allelism certain similarities were evident between tac and uni plants in the early seedling stage. The first true leaf of tac plants often is unlfoliate and, conversely, uni typically bears some tripartite leaves, although later in development.

Another feature of tac plants is the reduced number of leaflet pairs. In fact, this is a convenient means to distinguish tac tl from Tac tl in segregating populations. Sharma (7) has already pointed out that the terminal leaflet of tac plants is not appreciably reduced in size as is typically the case in _t_l plants. In plants homozygous for tac and for tl, the pair of subterminal tendrils (characteristic of tac) are absent, thus for this property tl is epistatic to tac. However, tac Tl plants often show variability of expression with respect to the subterminal tendrils; not infrequently the leaves have only one tendril or they may have none. Thus the absence of subterminal tendrils is by itself not a sure way to distinguish between tac t1 and Tac t1 plants. Such a distinction can confidently be made, however, by observing differences in the number of leaflet pairs per leaf. Plants with the tac t1 combination have fewer leaflet pairs than those with tl alone; thus, in this respect, tac is epistatic to tl. In an af_ background the distinction between tac tl and tac Tl/- is unmistakable. Moreover, the difference between af tac tl and af Tac tl is evident by the larger and fewer laminae in the former than in the latter. (This difference evidently was also recognized by Sharma (7) because, in his diagramatic illustrations, he depicts the leaflet size of af tac t1 plants as larger than af Tac t1 plants). Thus, tac is an interesting and powerful mutant gene in a number of respects.

There remains the question of symbolization. Because the discovery of unifoliata (1) antidates tendriled acacia, perhaps the symbolization should be: Uni, Uni^{tac}, uni. According to Sharma and Kumar (8) there already exist two alleles of tac: tac^{b}, and tac^{s}. Whether Uni is a classical multiple allelic locus or a complex locus remains to be seen.

1. Lamprecht, H. 1933. Hereditas 28:269-296.
2. Lamprecht, H. 1948. Agri Hort. Genet. 6:10-48.
3. Marx, G. A. 1972. PNL 4:30-31.
4. Marx, 6. A. 1974. PNL 6:30-31.
5. Marx, G. A. 1984. PNL 16:46-48.
6. Marx, G. A., N. F. Weeden, and R. Provvidenti. 1985. PNL 17:57-60.
7. Sharma, B. 1981. Pulse Crops News1. 1(1):56-57.
8. Sharma, B. and S. Kumar. Pulse Crops Newsl. l(3):2 1-22.

Table 1. Analysis of F_2 populations derived from the cross A M Tac Apu St x A m tac apu st.

Gene combinations St	Apu	Tac	M	No.
+	+	+	+	209
+	+	+	-	10
+	+	-	+	7
+	+	-	-	35
+	-	+	+	10
+	-	+	-	0
+	-	-	+	1
+	-	-	-	8
-	+	+	+	11
-	+	+	-	0
-	+	-	+	0
-	+	-	-	0
-	-	+	+	49
-	-	+	-	3
-	-	-	+	4
-	-	-	-	19
				366

Gene pair	Chi-squares X	Y	Linkage	Recomb. fract.	S.E.
St Apu	0.44	0.09	217.28**	8.3	1.5
St Tac	0.44	4.46*	2.97ns	-	-
St M	0.44	3.97*	1.79ns	-	-
Apu Tac	0.09	4.46*	14.98**	36.0	3.3
Apu M	0.09	3.96*	10.13**	38.3	3.4
Tac M	4.46*	3.96*	228.05**	7.7	1.5

(Population : B285-436-449)

Table 2. Analysis of F_2 populations derived from the cross Tac Apu St wel x tac apu st Wel.

Gene combinations Wel	St	Apu	Tac	No.
+	+	+	+	231
+	+	+	-	55
+	+	-	+	8
+	+	-	-	6
+	-	+	+	10
+	-	+	-	1
+	-	+	-	1
+	-	-	+	91
+	-	-	-	69
-	+	+	+	130
-	+	+	-	27
-	+	-	+	2
-	+	-	-	3
-	-	+	+	0
-	-	+	-	0
-	-	-	+	3
-	-	-	-	0
				636

Gene pair	X	Y	Linkage	Recomb. fract.	S.E.
Wel St	0.30	1.89	78.84**	12.5	3.9
Wel Apu	0.30	4.44*	61.61**	19.8	3.8
Wel Tac	0.30	0.03	6.17*	42.3	3.2
St Apu	1.89	4.44*	496.37**	4.5	0.8
St Tac	1.89	0.03	30.23**	36.4	2.5
Apu Tac	4.44*	0.03	41.50**	33.9	2.4

(Population: B285-450-472)

Table 3. Analysis of populations derived from three crosses of the constitution: apu tac x Apu Tac,

Gene pair	XY	Xy	xY	xy	Tot.	Chi-square X	Chi-square Y	Chi-square Linkage	Recomb. fract.	S.E
Apu Tac	45	9	7	13	74	0.16	0.88	19.51**	23.0	5.
(Population: B285-507-511)										
Apu Tac	97	21	17	18	153	0.37	0.02	15.27**	29.5	4.
(Population: B285-341-349)										
Apu Tac	38	20	3	8	69	3.02	8.93**	5.61*	29.1	6.
(Population: B285-413-416)										

Table 4. Analysis of three F2 populations derived from three-point crosses (a) st apu tac x St Tac St, (b) St_ a£u tac x st Apu Tac, and (c) st Apu Tac x St apu tac.

(a)

Apu	Tac	St	No.
+	+	+	75
+	+	-	5
+	-	+	24
+	-	-	2
-	+	+	1
-	+	-	8
-	-	+	7
-	-	-	19
			141

Gene pair	Chi-square X	Chi-square Y	Chi-square Linkage	Recomb. fract.	S.E.
Apu Tac	0.00	10.61**	27.98**	23.4	4.2
Apu St	0.00	0.06	69.51**	11.4	2.9
Tac St	10.61**	0.06	11.92**	31.9	4.9
(Population: B285-418-423)					

(b)

St	Apu	Tac	No.
+	+	+	121
+	+	-	41
+	-	+	43
+	-	-	43
-	+	+	79
-	+	-	9
-	-	+	1
-	-	-	1
			338

Gene pair	Chi-square X	Chi-square Y	Chi-square Linkage	Recomb. fract.	S.E.
St Apu	0.48	0.19	38.45**	14.3	5.3
St Tac	0.48	1.42	18.62**	30.9	4.8
Apu Tac	0.19	1.42	32.41**	31.9	3.2
(Population: A285-363-364)					

(c)

St	Apu	Tac	No.
+	+	+	52
+	+	-	15
+	-	+	19
+	-	-	14
-	+	+	29
-	+	-	4
-	-	+	0
-	-	-	1
			133

Gene pair	Chi-square X	Chi-square Y	Chi-square Linkage	Recomb. fract.	S.E.
St Apu	0.00	0.00	14.34**	<23.2	8.7
St Tac	0.00	0.00	3.75ns	-	-
Apu Tac	0.00	0.00	7.22**	34.7	5.3
(Population: A285-351)					