Inheritance of the Two-points Pattern of Partly Colored Seedcoats in Common Bean

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ABSTRACT. Common bean (*Phaseolus vulgaris* L.) seedcoats can have partly colored patterns such as the new two-points pattern, which has an unknown genotype. The gene t^{cf} (derived from PI 507984) expresses partly colored seedcoat pattern with colored flowers. A genetic tester stock t^{cf} two-points BC₃ 5-593 was derived from PI 507984 by backcrossing to the recurrent parent, Florida dry bean breeding line 5-593, which has black self-colored seeds and purple flowers due to the genotype $T P V$. A series of test crosses were made between t^{cf} two-points BC₃ 5-593 and three genetic tester stocks: $t z j^{ers}$ white BC₃ 5-593, $t z bip$ bipunctata BC₃ 5-593, and $t z virgarcus$ BC₃ 5-593. All three test crosses were studied in F₁ and F₂ populations, and the latter test cross in F₃ progenies derived from 80 randomly selected F₂ plants. The two-points pattern was never observed with white flower plants expressed by t/t , supporting the hypothesis that t^{cf} is necessary for two-points expression. The complete genotype for two-points was found to be $t^{cf} z j^{ers}$. The t^{cf} gene expresses more extensive colored zones in partly colored seedcoats than t . For example, $t^{cf} z J$ expresses self-colored seedcoats, whereas $t^{cf}/t z J$ expresses white ends pattern and $t z J$ expresses virgarcus. Similarly, the $t^{cf} z j^{ers}$ genotype expresses two-points pattern, whereas $t z j^{ers}$ expresses white seedcoat; and $t^{cf}/- z J/j^{ers}$ expresses PI type pattern, whereas $t z J/j^{ers}$ expresses weak virgarcus pattern.

In common bean (*Phaseolus vulgaris* L.), the t allele of the T locus expresses two pleiotropic effects, viz., partly colored seedcoats and white flowers (Leakey, 1988). The term “partly colored” denotes a seedcoat pattern, part of which is white, whereas the remainder is any nonwhite color. Bassett et al. (1999) presented data supporting the hypothesis that a second recessive allele exists at the T locus with gene symbol t^{cf} , which permits expression of colored flowers and partly colored seedcoats. The gene t^{cf} was derived from the Plant Introduction (PI) accession 507984, which has partly colored seedcoats that are highly sensitive to environmental conditions. The seedcoat expression can vary from self-colored to partly colored patterns that range from extensively colored to its most limited expression, the latter pattern referred to as “PI type” in this paper (Fig. 1). The development of a genetic stock, t^{cf} two-points BC₃ 5-593 is described below. When the two dots are coalesced at the micropyle, the pattern was named unipunctata by Lamprecht (1934). When the two dots are completely separate in the micropyle area, the new pattern is given the name two-points (Fig. 2) in this paper. Lamprecht (1934) was not able to provide a genetic explanation of the unipunctata pattern, which also co-segregated with bipunctata (Fig. 3) in his material. The objectives of this research are to investigate the inheritance of the two-points pattern of partly colored seedcoats derived from PI 507984 and to compare the effects of t^{cf} (vs. t) on the extent of colored zones in partly colored seedcoat patterns.

Materials and Methods

DEVELOPMENT OF GENETIC TESTER STOCKS. Florida dry bean breeding line 5-593 has the black seedcoat genotype $T Bip P [C r] Z J G B V R k$ (Bassett, 2003) and has been used for many years as a recurrent parent in a program to produce genetic tester

Fig. 1. A ventral view (left seed) and a side view (right seed) of PI 507984 with the “PI type” pattern of partly colored seeds of common bean typical of 1) seed grown at Pullman, Wash. or 2) expressed by genotypes $t^{cf}/- z J/Bip/Bip J/j^{ers}$ when grown at Gainesville, Fla.

Fig. 2. A ventral view (left seed) and a side view (right seed) of the two-points pattern of partly colored seeds of common bean expressed by genotype $t^{cf} z Bip j^{ers}$.

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Fig. 3. A ventral view (left seed) and a side view (right seed) of the bipunctata pattern of partly colored seeds of common bean expressed by genotype $t z \text{ bip } J$.

Fig. 4. A ventral view (left seed) and a side view (right seed) of the virgarcus pattern of partly colored seeds of common bean expressed by genotype $t z \text{ Bip } J$.

stocks. These stocks contain one or more recessive marker genes backcrossed into 5-593 with selection against all other marker genes (Bassett, 1994). Line 5-593 has colored (purple) flowers due to the genotype $T P V$ (Leakey, 1988).

Development of the genetic tester stocks with the partly colored seedcoat patterns virgarcus ($t z \text{ virgarcus } BC_3 \text{ 5-593}$) (Fig. 4) and bipunctata ($t z \text{ bip } bipunctata BC_3 \text{ 5-593}$) have already been described (Bassett, 1996). Similarly, development of the genetic tester stock with white seedcoats, $t z \text{ jers } white BC_3 \text{ 5-593}$, has also been previously described (Bassett, 1997a).

PI 507984 has (under growing conditions at Pullman, Wash.) a partly colored seedcoat pattern (Fig. 1) referred to as "PI type" in this paper, but has bishops violet flowers rather than the white flowers expected with t . The crosses PI 507984 $\times t z \text{ bip } bipunctata BC_3 \text{ 5-593}$ and PI 507984 $\times 5-593$ were made in 1989; and data were recorded on segregation for flower color and seedcoat pattern in the F_2 progenies, which were grown in the field in Spring 1990. With further inbreeding and selection from the PI 507984 $\times t z \text{ bip } bipunctata BC_3 \text{ 5-593}$ cross, a true breeding F_5 selection designated as " $F_5 t^{cf}$ two-points bishops violet (BV) flowers" was made in 1992. The subsequent cross $F_5 t^{cf}$ two-points BV flowers $\times 5-593$ produced the true breeding F_3 selection t^{cf} two-points $BC_1 \text{ 5-593}$ in 1993. An additional backcross to 5-593, viz., t^{cf} two-points $BC_1 \text{ 5-593} \times 5-593$, produced (after inbreeding and selection) the true breeding selection t^{cf} two-points $BC_2 \text{ 5-593}$ in 1994. Similarly, a final backcross to 5-593 created the genetic stock t^{cf} two-points $BC_3 \text{ 5-593}$ in 1995.

CROSSES USED IN THE INHERITANCE STUDY. The cross t^{cf} two-points $BC_3 \text{ 5-593} \times t z \text{ jers } white BC_3 \text{ 5-593}$ was made in the greenhouse in Fall 1996, and the F_2 progeny were planted in the field in Spring 1997. Data were recorded on segregation for flower color and seedcoat pattern in F_1 and F_2 . The crosses t^{cf} two-points $BC_3 \text{ 5-593} \times t z \text{ virgarcus } BC_3 \text{ 5-593}$ and $t z \text{ bip } bipunctata BC_3 \text{ 5-593} \times t^{cf}$ two-points $BC_3 \text{ 5-593}$ were made in the greenhouse in Fall 1995, and the F_2 progenies from both crosses were grown in the field in Spring 1996. Data were recorded on segregation for flower color and seedcoat pattern in F_1 and F_2 .

From remnant F_2 seed of the cross t^{cf} two-points $BC_3 \text{ 5-593} \times t z \text{ virgarcus } BC_3 \text{ 5-593}$, 80 randomly selected plants were grown in the greenhouse in Fall 1996. The resulting 80 F_3 progenies were grown in the field in Spring 1997. Data were recorded on segregation for flower color and seedcoat pattern in F_2 and F_3 . The

basis for choosing 80 F_2 parents for the F_3 progeny test was as follows. For the anticipated segregation for two genes (T and J), the least frequent F_2 genotypes would occur at a 1/16 frequency. For approximately a 95% level of probability of obtaining at least one such F_2 parent, the sample size is $3 \times 16 = 48$. With 80 F_2 parents, the probability of observing all segregation patterns is $>95\%$.

Results and Discussion

The genetic hypothesis for the two-points seedcoat pattern is presented in advance to make the paper easier to follow (Table 1). Two-points can only express with $t^{cf} z \text{ jers}$. The cross $t^{cf} (z \text{ jers})$ two-points $BC_3 \text{ 5-593} \times t z \text{ jers } white BC_3 \text{ 5-593}$ was made to test the genetic hypothesis given above for two-points. The F_1 progeny ($t^{cf}/t z \text{ jers}$) had nearly white seedcoats, which agrees with the expected phenotype (Table 1) for that genotype (data not shown). In terms of the genetic hypothesis for two-points, the F_2 segregated only at T , and not at Z or J (Table 2). Plants with purple flowers expressed only two phenotypic classes for seedcoats: 27 two-points pattern ($t^{cf}/t^{cf} z \text{ jers}$) and 42 nearly white ($t^{cf}/t z \text{ jers}$). Plants with white flowers and seedcoats were interpreted to have the genotype $t z \text{ jers}$, which is known to express white flowers and seedcoats (Bassett, 1997a; Bassett et al., 2002). Seedcoats with genotype $t^{cf}/t z \text{ jers}$ are not entirely white, but are very nearly so. The faint markings on the nearly-white seedcoat class are always clearly distinct with respect to the two-points pattern. The hypothesis is that genotype t^{cf}/t greatly suppresses seedcoat color expression compared to t^{cf}/t^{cf} . The traces of very pale color in the hilum ring or very fine dots observed are described in the footnote to Table 1. The gene t^{cf} is fully dominant for flower color, but has only a very weak dominance for seedcoat pattern with $t^{cf}/t z \text{ jers}$.

Thus, the test cross (Table 2) acted as an allelism test for z and $jers$, and the results confirmed the hypothesis of allelism. If $t z J$ had been present, segregation for expansa pattern would have been observed. If $t z J$ had been present, segregation for virgarcus pattern would have been observed. Thus, the t^{cf} two-points $BC_3 \text{ 5-593}$ parent does not carry genotype Z or J . Although the above genetic hypothesis for two-points is consistent with the data in Table 2, the hypothesis needs further testing for confirmation.

The F_1 plants from the test cross $t z (J) \text{ bip } bipunctata BC_3 \text{ 5-593} \times t^{cf} (z \text{ jers } Bip)$ two-points $BC_3 \text{ 5-593}$ expressed bipunctata

Table 1. The expected genetic and phenotypic segregation for common bean seedcoat patterns in F₂ and F₃ (in the presence of $\bar{z}/\bar{z}$) obtained when F₁ genotype $t^{cf}/t \ J/j^{ers}$ is self-pollinated.

Genotypes	Fre- quency	Expected segregation classes	
		In F ₂ progeny	In F ₃ progeny
$t^{cf}/t^{cf} \ J/J$	1	Self-colored	All self-colored
$t^{cf}/t^{cf} \ J/j^{ers}$	2	PI type	1 self-colored:2 PI type:1 two-points
$t^{cf}/t^{cf} \ j^{ers}/j^{ers}$	1	Two-points ^z	All two-points ^z
$t^{cf}/t \ J/J$	2	White ends	1 self-colored:2 white ends:1 virgarcus
$t^{cf}/t \ J/j^{ers}$	4	PI type	Recapitulation of the F ₂ distribution
$t^{cf}/t \ j^{ers}/j^{ers}$	2	Nearly white ^z	1 two-points:3 nearly white or white ^z
$t/t \ J/J$	1	Virgarcus	All virgarcus
$t/t \ J/j^{ers}$	2	Weak virgarcus	1 virgarcus:2 weak virgarcus:1 white
$t/t \ j^{ers}/j^{ers}$	1	White	All white

^zThe “nearly white” seedcoats are not entirely white, but only careful inspection (often with magnification needed) can detect the following (with variable expression); very pale gray hilum ring, minute dots of color at the caruncula and sometimes at the micropyle (not a two-points pattern), and, infrequently, very fine dots widely distributed over the entire seedcoat.

Table 2. Segregation in common bean for flower color and partly colored seedcoat patterns observed in the F₂ from the cross $t^{cf} \ (\bar{z} \ j^{ers})$ two-points BC₃ 5-593 $\times$ $t \ \bar{z} \ j^{ers}$ white BC₃ 5-593.

Purple flowers ^z		White flowers ^z		χ^2	<i>P</i>
t^{cf}/t^{cf}	t^{cf}/t	t/t			
Two-points seed	Nearly white seed	White seed	1:2:1		
27	42	19	1.636	0.44	

^zFor the data 69 ($t^{cf}/-$) and 19 (t/t), the χ^2 (3:1) = 0.546, *P* = 0.46.

Fig. 5. A side view (left seed), a ventral view (middle seed), and the opposite side view (right seed) of the white ends pattern of partly colored seeds of common bean expressed by genotype $t^{cf}/t \ \bar{z}/\bar{z} \ Bip/Bip \ J/J$.

seedcoat pattern with fine dots over the remainder of the seedcoat (data not shown). The F₂ segregated for plants with purple flowers and several seedcoat patterns that could not always be unambiguously classified, viz., self-colored, white ends (Fig. 5), and PI type (Table 3). Those classes were genetically interpreted as expression of $t^{cf}/- \ \bar{z}/\bar{z} \ J/-$ (Tables 1 and 3). F₂ plants with white flowers (t/t) also segregated for two seedcoat patterns that could not be unambiguously classified, viz., weak virgarcus (Fig. 6) and

bipunctata (Table 3). The bipunctata and virgarcus classes required $t \ \bar{z} \ J/-$ for expression, whereas weak virgarcus specifically required $t \ \bar{z} \ J/j^{ers}$ for expression (Bassett, 1997a; Bassett et al., 2002).

Segregation for two-points with t/t white flowers was not observed, and neither was segregation for virgarcus, weak virgarcus, or bipunctata with purple flowers ($t^{cf}/-$). Clearly, the partly colored seedcoat pattern virgarcus expressed by $t \ \bar{z} \ J$ is permitted much greater expansion of the colored zone with genotype $t^{cf} \ \bar{z} \ J$, viz., as self-colored (Tables 1 and 3). Similarly, the weak virgarcus pattern expressed with $t \ \bar{z} \ J/j^{ers}$ is permitted much greater expansion of the colored zone with genotype $t^{cf}/- \ \bar{z} \ J/j^{ers}$, viz., as the PI type pattern. Segregation at *Bip* did not express a novel phenotypic class with $t^{cf}/-$. The genotype for two-points pattern (with $t^{cf}/-$) expressed as white seed with t/t . In general, t^{cf} permitted greater expansion of the colored zone than t did for any of the genotypes at *Z*, *J*, and *Bip* that were tested. The four phenotypic classes observed gave a satisfactory fit to the expected 9:3:3:1 genetic segregation ratio for the gene combinations $t^{cf}/- \ \bar{z} \ J/-$, $t^{cf}/- \ \bar{z} \ j^{ers}/j^{ers}$, $t/t \ \bar{z} \ J/-$, and $t/t \ \bar{z} \ j^{ers}/j^{ers}$, respectively (Table 3).

The F₁ plants from the test cross $t^{cf} \ (\bar{z} \ j^{ers})$ two-points BC₃ 5-593 $\times$ $t \ \bar{z} \ (J)$ virgarcus BC₃ 5-593 expressed seedcoats with bipunctata pattern with fine dots over the remainder of the seedcoat, where the caruncula dot was much smaller than the two,

large, coalesced dots at the micropyle (data not shown). The F₂ segregated for the expected classes with genotype $t^{cf} \ \bar{z} \ J/-$, viz., self-colored, white ends and PI type (Table 4). With $t^{cf} \ \bar{z} \ j^{ers}$, the expected two-points and nearly-white seed classes were observed, and the expected segregation ratio of 1 two-points ($t^{cf}/t^{cf} \ \bar{z} \ j^{ers}$) to 2 white ($t^{cf}/t \ \bar{z} \ j^{ers}$) was observed. The plants with white flowers (t/t) segregated for virgarcus, weak virgarcus, and white seed in a 1:2:1 ratio, respectively (Table 4). The segregation for all

Table 3. Segregation in common bean for flower color and partly colored seedcoat patterns observed in the F₂ from the cross *t z (J) bip* bipunctata BC₃ 5-593 × *t^{cf} (z^{jers} Bip)* two-points BC₃ 5-593.

Purple flowers <i>t^{cf}/-</i>		White flowers <i>t/t</i>		χ^2 (9:3:3:1) ^w	<i>P</i>
Self-colored to PI type seed ^z <i>J/-</i>	Two-points or nearly white seed ^y <i>j^{ers}/j^{ers}</i>	Partly colored seed ^x <i>J/-</i>	White seed <i>j^{ers}/j^{ers}</i>		
208	82	62	16	5.295	0.22

^zThere was continuous variation from self-colored to the white ends pattern to the PI type pattern, i.e., white ends and PI type patterns were highly variable.

^yThere were 30 two-points (*t^{cf}/t^{cf} z jers*) and 52 nearly white (*t^{cf}/t z jers*) observations; and for the data 30 and 52, the χ^2 (1:2) = 0.390, *P* = 0.53.

^xThe classes included bipunctata, weak virgarcus, and virgarcus; unambiguous classification of the first two classes was not possible.

^wSegregation for flower color, 290 purple *t^{cf}/-* and 78 white *t/t*, gave χ^2 (3:1) = 2.841, *P* = 0.09. Segregation at *J*: with *t^{cf}/-*, 208 *J/-* and 82 *j^{ers}/j^{ers}* gave χ^2 (3:1) = 1.660, *P* = 0.20; and with *t/t*, 62 *J/-* and 16 *j^{ers}/j^{ers}* gave χ^2 (3:1) = 0.838, *P* = 0.36.

Fig. 6. Five ventral views showing the range of variability of the weak virgarcus pattern of partly colored seeds of common bean expressed by genotype *t/t z/z Bip/Bip J/j^{ers}*.

five phenotypic classes (or groups of classes) observed in the F₂ failed to fit the expected segregation ratio 9:3:1:2:1 (Table 4). Most of the large chi-square value was due to highly disturbed segregation at *T*, viz., for *t^{cf}/-* vs. *t/t* the χ^2 (3:1) = 22.36, *P* < 0.001. The tendency for disturbed segregation at *T* associated with *t^{cf}* has been reported before (Bassett et al., 1999). Segregation at *J* was normal (Table 4).

The development of *t^{cf}* two-points BC₃ 5-593 began with the cross PI 507984 × *t z bip* bipunctata BC₃ 5-593, and a question arises about a possible role for the *bip* gene in two-points expression. If two-points BC₃ 5-593 carried *bip*, then the cross *t z virgarcus* BC₃ 5-593 × *t^{cf}* two-points BC₃ 5-593 should segregate in F₂ for bipunctata pattern seeds with genotype *t/t*. The bipunctata pattern was not observed with *t/t* (Table 4); and, therefore, *t^{cf}* two-points BC₃ 5-593 does not have genotype *bip*.

The 80 randomly selected F₂ progeny from the cross *t^{cf} (z^{jers})* two-points BC₃ 5-593 × *t z (J)* virgarcus BC₃ 5-593 segregated into five phenotypic classes (Table 5). Each of the five classes had a unique segregation pattern in F₃ progeny except for the PI type class, which had two dif-

ferent segregation patterns (Table 5). Thus, a total of six unique segregation patterns was observed. Hypothetical genotypes were assigned to the six classes based on the model in Table 1 and the segregation data presented above for other test crosses. The four F₂ parents with self-colored seedcoat (*t^{cf}/t^{cf} J/J*) were true breeding in F₃. One of the PI type classes (*t^{cf}/t^{cf} J/j^{ers}*) segregated for only two classes (self-colored or PI type vs. two-points) with disturbed segregation at *J*. The other PI type class (*t^{cf}/t J/j^{ers}*) recapitulated the F₂ segregation pattern of five phenotypic classes. For the second PI type class, there was disturbed segregation at *T* (χ^2

(3:1) = 5.504, *P* = 0.019) and disturbed segregation at *J* for the *t^{cf}/-* plants (χ^2 (3:1) = 4.301, *P* = 0.038) but not for the *t/t* plants (χ^2 (1:2:1) = 2.260, *P* = 0.32) (Table 5). Disturbed segregation at *T*, when *t^{cf}* was involved, was previously reported (Bassett et al., 1999). Disturbed segregation at *J* (vs. *j^{ers}*), involving a surplus of *j^{ers}/j^{ers}* (as in Table 5), was previously reported (Bassett, 1997a). The seedcoat pattern class white ends (*t^{cf}/t J/J*) always segregated for two classes, which fit the expected 3:1 segregation ratio for 3 self-colored or white ends to 1 virgarcus, respectively. The F₂ parents with two-points pattern (*t^{cf}/t^{cf} j^{ers}/j^{ers}*) were always true breeding in F₃, whereas the F₂ parents with nearly white seedcoats (*t^{cf}/t j^{ers}/j^{ers}*) always segregated 3:1 for *t^{cf}/-* two-points or nearly white to *t/t* white seed, respectively (Table 5). The frequency of the six classes of F₂ plants fit the expected ratio of 1:2:1:2:4:2 for their respective genotypes and expected F₃ segregation patterns (Table 5). The above results strongly support the genetic hypothesis for the two-points pattern (Table 1). Thus, the genotype *t^{cf} z jers* for two-points pattern was confirmed.

The F₂ plants with PI type seedcoat pattern were always expressions of heterozygosity at *J* (Table 5), whereas when PI 507984 is grown at Pullman, Wash., the PI type pattern is true breeding (due to a homozygous genotype). The author's hypothesis is that the PI type pattern of PI 507984 has a different genotype at the *Z* locus compared with the heterozygous PI type materials presented in Table 5. The cross PI 507984 × *t z bip* bipunctata BC₃ 5-593 segregated in F₂ (111 total progeny) for partly colored seedcoat patterns (Bassett, 1996, 1997b) known to require either *Z* (self-colored, expansa or ambigua, 34 plants) or *z^{sel}* (sellatus, 21 plants) for their expression (data not shown). The cross PI 507984 × 5-593 segregated in F₂ (184 total progeny) for only eight partly colored progeny, which were all of the expansa class. From the first cross, plants with white flowers (*t/t*) did not segregate for the expected piebald pattern (Bassett, 1997b) expressed by genotype *t/t z^{sel}/z J/J Bip/Bip* (data not shown). The data were not sufficient to develop a conclusive genetic hypothesis for the genotype of PI 507984 at the *Z* locus. On the basis of the data in Tables 2 through 5, we can conclude that PI 507984 would express two-points pattern if it carried *z*, which conclusively rules out that genotype. The genotype at the *Z* locus in PI 507984 remains uncertain. Future experimental work should be done to determine the seedcoat pattern expression of genotype *t^{cf} z^{sel} jers*, which is the more plausible candidate genotype (vs. *t^{cf} Z jers*) for the true breeding PI type pattern. Alternatively, PI 507984 may have a novel allele at *Z*, one which has not been reported.

Table 4. Segregation in common bean for flower color and partly colored seedcoat patterns observed in the F₂ from the cross *t z* (*J*) *virgarcus* BC₃ 5-593 x *t^{cf}* (*z j^{ers}*) two-points BC₃ 5-593.

Purple flowers (<i>t^{cl}/-</i>) ^z		White flowers (<i>t/t</i>) ^z			χ^2 9:3:1:2:1 ^w	<i>P</i>
Self-colored to PI type seed ^y <i>J/-</i>	Two-points or nearly white seed ^x <i>J^{ers}/J^{ers}</i>	Virgarcus seed <i>J/J</i>	Weak virgarcus <i>J/J^{ers}</i>	White seed <i>J^{ers}/J^{ers}</i>		
430	161	33	64	27	24.598	< 0.001

^zSegregation for flower color, 591 *t^{cf}/-* and 124 *t/t*, gave χ^2 (3:1) = 22.36, *P* < 0.001. For the *t^{cf}/-* data, segregation at *J* for seedcoat pattern was 430 *J/-* and 161 *j^{ers}/j^{ers}*, giving the χ^2 (3:1) = 1.584, *P* = 0.21. For the *t/t* data, segregation at *J* for seedcoat pattern was 33 *J/J*, 64 *J/j^{ers}*, and 27 *j^{ers}/j^{ers}*, giving the χ^2 (1:2:1) = 0.710, *P* = 0.70. Thus, disturbed segregation at *T* was entirely responsible for the failure of the model.

^yThere was continuous variation from self-colored to white ends pattern to the PI type pattern.

^xWithin the *t^{cf}/-* *j^{ers}/j^{ers}* class, there were 64 two-points (*t^{cf}/t^{cf} j^{ers}/j^{ers}*) and 97 nearly white seedcoat (*t^{cf}/t j^{ers}/j^{ers}*) plants, giving χ^2 (1:2) = 2.985, *P* = 0.08.

Table 5. Segregation in common bean for flower color and seedcoat pattern observed in F₃ progenies from 80 F₂ parents selected for purple flowers (*t^{cf}/-*) but randomly selected for seedcoat pattern from the cross *t^{cf}* (*z j^{ers}*) two-points BC₃ 5-593 x *t z* (*J*) *virgarcus* BC₃ 5-593.

Segregation in F ₃							
			Purple flowers (<i>t^{cf}/-</i>)		White flowers (<i>t/t</i>)		
Class no.	F ₂ parents, phenotypes and genotypes ^z	No. of F ₃ plots	Self-colored to PI type seed ^y <i>J/-</i>	Two-points and nearly white seed <i>j^{ers}/j^{ers}</i>	Virgarcus seed <i>J/J</i>	Weak virgarcus seed <i>J/j^{ers}</i>	White seed <i>j^{ers}/j^{ers}</i>
1	Self-colored seed <i>t^{cf}/t^{cf} J/J</i>	4	280 ^x				
2	PI type seed ^w <i>t^{cf}/t^{cf} J/j^{ers}</i>	12	497	212			
3	Two-points seed <i>t^{cf}/t^{cf} j^{ers}/j^{ers}</i>	12		538 ^x			
4	White ends seed ^v <i>t^{cf}/t J/J</i>	13	608		187		
5	PI type seed ^u <i>t^{cf}/t J/j^{ers}</i>	30	995	376	105	208	87
6	Nearly white seed ^t <i>t^{cf}/t j^{ers}/j^{ers}</i>	9		310			124

^zFor the observed class frequencies 4, 12, 12, 13, 30, 9, the χ^2 (1:2:1:2:4:2) = 7.30, *P* = 0.20.

^yThree seedcoat classes were combined: self-colored seeds, white ends, and PI type.

^xAll F₃ plots were true breeding only for the indicated seedcoat phenotype of the F₂ parent.

^wThose PI type (Fig. 1) F₃ progenies segregated for two classes: 1) self-colored or PI type, and 2) two-points. For the data 497 and 212 (*J/-* vs. *j^{ers}/j^{ers}*), the χ^2 (3:1) = 9.084, *P* = 0.003 and χ^2 (9:7) = 55.25, *P* = 0.001.

^vWhite ends (Fig. 5) segregated for two classes: 1) self-colored or white ends, and 2) virgarcus. For the data 608 and 187, the χ^2 (3:1) = 0.926, *P* = 0.34.

^uThose F₃ progenies recapitulated the F₂ segregation. For the data 995, 376, 105, 208, and 87, the χ^2 (9:3:1:2:1) = 11.98, *P* = 0.017. For the data 995 and 376 (*J/-* vs. *j^{ers}/j^{ers}*), the χ^2 (3:1) = 4.301, *P* = 0.038. For the data 105, 208, and 87, the χ^2 (1:2:1) = 2.260, *P* = 0.32. For the data 1371 and 400 (*t^{cf}/-* vs. *t/t*), the χ^2 (3:1) = 5.504, *P* = 0.019.

^tNearly white progenies segregated for two classes: 1) two-points or nearly white, and 2) white seed. For the data 310 and 124, the χ^2 (3:1) = 2.952, *P* = 0.09.

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