

IDENTIFICATION AND INHERITANCE OF A NEW DWARFING GENE IN PIGEONPEA

S. C. GUPTA, R. K. KAPOOR, T. P. RAO AND R. P. ARIYANAYAGAM

Legumes Program, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru 502324

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ABSTRACT

A spontaneous dwarf (D_{11}) mutant was identified in an advanced line ICPL 146. In order to study inheritance of the dwarfness in D_{11} and its allelic relationship to the D_1 dwarfing gene, D_{11} was crossed with three tall lines (ICPL 146, ICPL 85024, ICPL 85037) and a D_1 dwarf (ICPL 85059) in 1986. The segregation patterns in F_1 , F_2 backcrosses to both the parents and F_3 progenies suggested that D_{11} dwarfness is governed by a single recessive gene in homozygous condition (t_3t_3). The genes in D_{11} and D_1 were found to be nonallelic.

Key words *Cajanus cajan*, dwarf mutant, inheritance

The excessive vegetative growth related to tallness of traditional pigeonpea [*Cajanus cajan* (L.) Millsp.] cultivars leads to reduced harvest index and hinders efficient crop management practices. Delayed plantings can result in reduced height [1]. However, Mohammed and Ariyanayagam [2] argued that the use of genetic dwarfs would be a more desirable approach to reduce plant height.

A bushy dwarf pigeonpea with brittle branches and condensed internodes was reported [3-5]. They found that the dwarfness was controlled by a single recessive gene. Twelve sources of dwarfism (D_0 to D_{11}) in pigeonpea are available at ICRISAT Center. Genetic studies of the D_0 indicated that the dwarfness was controlled by two nonallelic recessive genes t_{11} and t_{22} [6]. Jain [7] found that dwarfing in D_1 was controlled by a single recessive gene (t_4t_4). Inheritance of dwarfness D_6 , PD_1 (D_7) and $PBNA$ (D_8) indicated that the dwarf phenotype in each of the three lines was controlled by a single recessive gene in homozygous state [8]. They also reported that D_6 and PD_1 had similar alleles (t_3t_3) and $PBNA$ had a different allele ($t_3^h t_3^h$) for dwarfness.

During 1986 rainy season a spontaneous dwarf mutant plant was identified at the ICRISAT Sub-Center, Hisar in an advanced short duration pigeonpea line ICPL 146. Its

height at maturity was 35 cm as against the 130 cm of ICPL 146. This dwarf was designated as D_{11} . The present study was conducted to study the inheritance pattern of the dwarfing gene in D_{11} and its allelic relationship to the gene controlling dwarfness in the D_1 dwarf, an extensively used parent in the crossing program at ICRISAT.

MATERIALS AND METHODS

Two dwarf (D_1 and D_{11}) and three tall (ICPL 146, ICPL 85024 and ICPL 85037) pigeonpea lines were included in this study. Characteristics of these dwarf and tall parents are summarized in Table 1. The D_{11} dwarf was the shortest parent with a mean height of 39.5 cm and ICPL 85037 was the tallest with a mean height of 120 cm. The mean plant height of D_1 dwarf (ICPL 85059) and tall parent ICPL 85024 was about the same (Table 1), however, the branching pattern and the internode length in these two parents were significantly different. ICPL 85024 had on an average 7.2 primary branches per plant at mean internode length of 5.3 cm, while ICPL 85059 (D_1 dwarf) had on an average 12.8 primary branches per plant at mean internode length of 1.9 cm. The internodes in D_1 dwarf are condensed so that acute branches radiate from a narrow region about 10 to 15 cm above the ground level. The main branches are brittle.

Table 1. Characteristics of the parents used in the study on pigeonpea

Parent	Plant height (cm)	No. of primary branches	Internode length (cm)	Days to flowering
D_{11} dwarf	39.5 ± 1.7	5.8 ± 0.3	3.0 ± 0.1	61.8 ± 0.4
D_1 dwarf (ICPL 85059)	85.7 ± 1.4	12.8 ± 0.7	1.9 ± 0.1	64.1 ± 0.6
ICPL 146	106.4 ± 0.9	7.9 ± 0.4	7.2 ± 0.2	66.5 ± 0.4
ICPL 85024	85.6 ± 1.0	7.2 ± 0.3	5.3 ± 0.2	58.5 ± 0.5
ICPL 85037	120.0 ± 0.6	9.0 ± 0.4	8.7 ± 0.2	63.6 ± 0.4

Each of the two dwarf lines was crossed to all the three tall parents and also among themselves to study allelic relationship. The F_1 s were grown during 1987 at Hisar to produce F_2 seed and to backcross with both the parents. The parents, F_1 , F_2 and backcross to both the parents were grown during 1988 at Hisar. The parents, F_1 , and the backcrosses were planted in one row and F_2 populations were grown in 20 row plots of 9 m length. The rows were spaced 60 cm apart with intra-row spacing of 15-20 cm. The number of dwarf and tall plants in each generation for each of the four crosses were recorded. In each of the three F_2 populations involving crosses between D_{11} dwarf and the three tall parents, 20-50 and 52-231 tall plants were selected randomly to study the segregation pattern in the F_3 generation. In the 1989 rainy season F_2 -derived F_3 progenies were grown at Hisar, along

with their respective parents, in 9 m long one row plots. The observation on segregation of tall and dwarf plants in each single plant progeny was recorded separately for each of the three crosses. The chi-square test was applied to test the significance of segregation ratios.

RESULTS AND DISCUSSION

INHERITANCE

The F₁ plants of all the three crosses involving D₁₁ dwarf and the three tall parents resembled their tall parents, suggesting that D₁₁ dwarf is inherited as a recessive trait. In the F₂ populations obtained by crossing D₁₁ dwarf with tall parents, the observed segregation of tall and dwarf plants fitted the expected 3 tall : 1 dwarf ratio indicating that the D₁₁ dwarf phenotype was controlled by a single recessive gene in homozygous state (Table 2). This was further confirmed by the phenotypic segregation patterns in the backcrosses (Table 2) and F₃ progenies (Table 3). The backcross of F₁ to tall parent produced only tall progenies. Segregation in the test cross (F₁ × D₁₁ dwarf) progenies of all the three crosses showed a good fit to the expected ratio of 1 tall : 1 D₁₁ dwarf (Table 2). As expected within each cross, all the F₃ progenies of D₁₁ dwarf F₂ plants bred true for dwarfness. However, two-thirds of F₃ progenies of tall F₂ plants segregated for D₁₁ dwarf and tall plants and the remaining one-third bred true for tallness (Table 3). Within each segregating progeny, good fit for 3 tall : 1 D₁₁ dwarf was found. The data pooled over the segregating F₃ progenies in each of the three crosses (Table 4) also showed a good fit for the expected 3 tall : 1 D₁₁ dwarf ratio. These observations confirmed that D₁₁ dwarfness was governed by a single recessive gene which we designate as t5t5. The dwarf stature in pigeonpea has been reported to be controlled by a single recessive gene [3-5, 7-9].

Table 2. Phenotypic classification of F₂ and test cross progenies between D₁₁ dwarf and three tall pigeonpea lines

Generation and cross	Number of plants					Ratio	χ^2	P
	total	observed		expected				
		tall	dwarf	tall	dwarf			
F ₂ : D ₁₁ × ICPL 146	1211	909	302	908.25	302.7	3:1	0.003	0.90-0.95
BC : F ₁ × D ₁₁	21	11	10	10.50	10.5	1:1	0.047	0.80-0.90
F ₂ : D ₁₁ × ICPL 85024	1257	952	305	942.75	314.2	3:1	0.362	0.50-0.60
BC : F ₁ × D ₁₁	23	13	10	11.50	11.5	1:1	0.391	0.50-0.60
F ₂ : D ₁₁ × ICPL 85037	1661	1262	399	1245.75	415.2	3:1	0.848	0.30-0.40
BC : F ₁ × D ₁₁	19	10	9	9.50	9.5	1:1	0.052	0.80-0.90
Pooled : F ₂	4129	3123	1006	3096.75	1032.2	3:1	0.889	0.30-0.40
F ₁ × D ₁₁	63	34	29	31.50	31.5	1:1	0.397	0.50-0.60

Table 3. Segregation in F₃ progenies grown from random tall F₂ plants of the crosses between D₁₁ dwarf and three tall parents of pigeonpea

Cross	total	Number of F ₃ progenies				Ratio tested	χ^2	P
		observed		expected				
		segregating	non-segregating (tall)	segregating	non-segregating (tall)			
D ₁₁ × ICPL 146	98	63	35	65.3	32.7	2:1	0.252	0.60-0.70
D ₁₁ × ICPL 85024	231	149	82	154.0	77.0	2:1	0.486	0.40-0.50
D ₁₁ × ICPL 85037	52	32	20	34.7	17.3	2:1	0.616	0.30-0.40
Pooled	381	244	137	254.0	127.0	2:1	1.180	0.20-0.30

ALLELIC RELATIONSHIP WITH D₁ DWARF

The allelic relationship of D₁₁ and D₁ (ICPL 85059) dwarfs was studied in F₁, F₂ and backcrosses to both the dwarf parents. All the plants in F₁ between D₁ and D₁₁ dwarfs were tall, indicating that they have separate genes controlling their dwarfness designated as t4t4 and t5t5, respectively. Out of 1482 plants studied in F₂, 830 were tall, 386 were of D₁ dwarf type and 266 were of D₁₁ dwarf type (Table 5) fitting the expected segregation ratio of 9:3:4. Presence of both the dominant genes (T₄ - and T₅ -) resulted in tall plants. Plants having t5t5 in recessive homozygous form in the absence of t4t4 (T₄-t5t5) were of D₁₁ dwarf types and the plants having t4t4 in recessive homozygous form (t4t4T₅-and t4t4t5t5) were of D₁ dwarf types. In double homozygous recessive plants (t4t4t5t5), t4t4 masked the effect of t5t5 resulting in D₁ dwarfs. As expected backcross of F₁ with D₁ dwarf segregated into 1 tall : 1 D₁ dwarf and with D₁₁ dwarf into 1 tall : 1 D₁₁ dwarf, respectively (Table 5). These observations confirmed that the D₁ and D₁₁ dwarfness in pigeonpea was controlled by two different recessive genes t4t4 and t5t5, respectively in homozygous state.

Table 4. Pooled segregation for tall and D₁₁ dwarf types within the tall F₃ segregating progenies from the crosses between D₁₁ dwarf and three tall parents of pigeonpea

Cross	No. of F ₃ progenies	Number of plants					Ratio tested	χ^2	P
		total	observed		expected				
			tall	dwarf	tall	dwarf			
D ₁₁ × ICPL 146	63	2216	1680	536	1662.0	554.0	3:1	0.779	0.30-0.40
D ₁₁ × ICPL 85024	149	5523	4161	1362	4142.3	1380.7	3:1	0.339	0.50-0.60
D ₁₁ × ICPL 85037	32	1097	833	264	822.7	274.3	3:1	0.510	0.40-0.50
Pooled	244	8836	6674	2162	6627.0	2209.0	3:1	1.333	0.20-0.30

Table 5. Segregation pattern in F₁, F₂ and backcross between D₁ and D₁₁ dwarfs of pigeonpea

Generation and cross	Number of plants						Ratio	χ^2	Probability	
	total	observed			expected					
		tall	D ₁₁ dwarf	D ₁ dwarf	tall	D ₁₁ dwarf				D ₁ dwarf
F ₂ : D ₁ x D ₁₁	1482	830	266	386	833.6	277.9	370.5	9:3:4	1.166	0.60-0.70
BC: F ₁ x D ₁	27	15	—	12	13.5	—	13.5	1:1	0.333	0.50-0.60
BC: F ₁ x D ₁₁	23	13	10	—	11.5	11.5	—	1:1	0.391	0.50-0.60

The d₁₁ dwarf provides an additional source of dwarfness in pigeonpea. Unlike ICPL 85059 (D₁ dwarf) its branches are not brittle. However, its usefulness and linkages with other characteristics has yet to be studied.

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FERTILITY RESTORATION CAPACITY OF FOUR RESTORERS IN HYBRIDS WITH CMS LINES HAVING TRITICUM TIMOPHEEVI CYTOPLASM

P. P. SINGH AND R. K. S. RATHORE

Department of Agriculture Botany, R. B. S. College, Bichpuri, Agra 283105

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ABSTRACT

Fertility restoration capacity of four exotic Rf-sources (W 8156, 3401/478466, PE/YQ and R3-401) in five CMS lines (msHD 2204, msHD 2260, msHP 1102, msUP 368 and msWH 157) with *T. timopheevi* cytoplasm and their reciprocal crosses was studied in two sets during 1983 and 1984. The set I included A x R and set II R x B crosses. The significant differences in the fertility restoration capacity of all the Rf-sources studied were observed in both the years. R x B crosses showed better seed set than their respective A x R crosses. During both crop seasons msHD 2204 x PE/YQ in set I gave the highest seed set while msUP 368 gave consistently high seed set with all restorers.

Key words. CMS lines, Rf-sources, *T. timopheevi*

Complete restoration of pollen fertility in the F₁ generation is essential for the production of hybrid wheat. Fertility restoring (Rf) genes for cytoplasm i.e. male sterile lines with *T. timopheevi* cytoplasm have been found in various tetraploid and hexaploid wheats [1-7]. The fertility restoration capacity primarily depends on the effect of Rf-genes present and their interaction with the cytoplasm of the CMS lines [8]; it can also be influenced by the environment and the nuclear genes of the CMS lines [9]. Therefore, detailed investigations on the fertility restoration capacity of different restorers are necessary for various CMS lines. This investigation was aimed to study the level of fertility restoration in the F₁ generation of five CMS lines (msHD 2204, msHD 2260, msHP 1102, msUP 368 and msWH 157) after pollination with four restorer lines (W 8156, 3501/478466, PE/YQ, and R3-401) in wheat.

MATERIALS AND METHODS

The five *T. timopheevi* derived CMS lines (A lines) were used as females and four exotic restorers (R lines) as male parents [10]. Hybrid seed was produced by crossing each of the five CMS lines with four restorer lines, the latter were also emasculated and crossed with