# Inheritance of Resistance to Blight in Pigeonpeas

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**ABSTRACT**

Sharma, D., Kannaiyan, J., and Reddy, L. J. 1982. Inheritance of resistance to blight in pigeonpeas. Plant Disease 66:22-25.

Sources of resistance to isolate P2 of the fungus *Phytophthora drechsleri* f. sp. *cajani* have been identified in pigeonpea (*Cajanus cajan*). Observations on $F_1$ and $F_2$ progenies and on backcrosses of resistant and susceptible parents studied by use of the pot culture technique indicated that resistance is governed by a single dominant gene, which is designated $Pd_1$. The $F_1$ and $F_2$ progenies of resistant parents were all resistant, showing that the gene for resistance is the same in all the parents. Field screening of $F_3$ progenies of another set of susceptible × resistant crosses showed a good fit for a 1:2 ratio of true breeding to segregating for resistance in five of the nine crosses. In all nine crosses, most of the individual segregating progenies in $F_3$ showed a good fit to a 3:1 ratio of resistant to susceptible, confirming monogenic dominant inheritance of resistance. All seven resistant parents were of diverse origin, and their $F_1$ progeny showed a high degree of specificity of reaction to isolate P2.

A number of *Phytophthora* spp. cause stem blight, canker, or stem rot in pigeonpeas (*Cajanus cajan* (L.) Millsp.) in India, Puerto Rico, the Dominican Republic, and Trinidad (3). In India, *P. drechsleri* Tucker var. *cajani* Pal, Grewal and Sarbhoy was identified as the causal agent of stem rot in pigeonpeas (4), which is now designated as *P. drechsleri* Tucker f. sp. *cajani* Kannaiyan et al (2).

Pal et al (4) described the symptoms of the disease, the conditions that favor its development, and the effect on plants. The incidence of disease varies from season to season but was high at Hyderabad during 1976 and 1977 (Fig. 1) when July and August were very wet.

Cultivars differ in their reaction to the fungus (4), but little systematic work has been done to screen pigeonpea germ plasm and identify sources of resistance. Kannaiyan et al (1) developed a pot screening technique and screened 2,835 lines of pigeonpea germ plasm, of which 80 were resistant to isolate P2 (isolated from diseased plants obtained from ICRISAT) of the fungus (1). However, lines that were resistant to isolate P2 were not resistant to an isolate of the fungus from Kanpur (Uttar Pradesh), India.

This study was undertaken to determine the mode of inheritance and allelic relationships of genes for resistance to isolate P2 in different sources of resistance and to determine the reaction of combined sources of resistance to the Kanpur isolate of the fungus.

## MATERIALS AND METHODS

**Pot screening.** The pot culture technique (1) was used to identify susceptible and resistant plants. Plastic pots 20 cm in diameter were filled with red soil of the Alfisols group (60% sand,

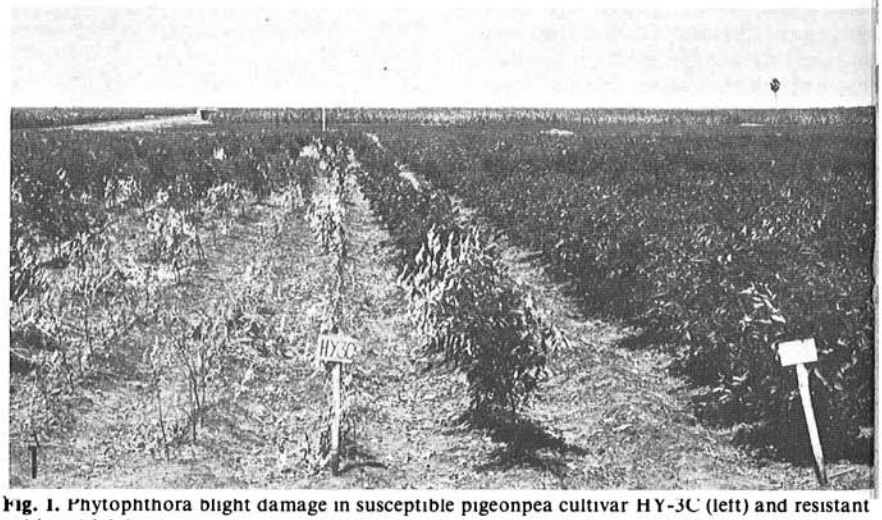


Fig. 1. Phytophthora blight damage in susceptible pigeonpea cultivar HY-3C (left) and resistant cultivar (right).

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**Table 1.** Pigeonpea lines used to study the inheritance of resistance to Phytophthora blight

| Source | Pedigree[a] | Origin | Disease reaction[b] | |
|---|---|---|---|---|
| | | | Isolate P2 | Kanpur isolate |
| Pant A-3 | ICP-6974-28⊠-1⊠-B⊠-B⊠-B⊠-B⊠ | Pantnagar, U.P. | R | S |
| Pusa Ageti | ICPL-7 (ICP-28-24⊠-1⊠-3⊠-2⊠-B⊠-B⊠-B⊠-B⊠) | IARI, Delhi | R | S |
| UPAS-120 | ICPL-1 (ICP-6971-32⊠-83⊠-3⊠-5⊠-3⊠-B⊠-B⊠-B⊠-B⊠) | Pantnagar, U.P. | S | S |
| No.148 | ICP-7120-51⊠-4⊠-1⊠-B⊠-B⊠ | Maharashtra | S | S |
| BDN-1 | ICP-7182-9⊠-1⊠-B⊠-B⊠ | Maharashtra | R | S |
| Germ plasm | ICP-6997-108⊠-2⊠-1⊠-B⊠-B⊠ | Bangladesh | S | S |
| Germ plasm | ICP-231 (2366-IP5⊠-B⊠) | APAU, A.P. | R | S |
| Germ plasm | ICP-2376 (P2 resistant control) | APAU, A.P. | R | S |
| NP-69 | ICP-4779-73⊠-1⊠-3⊠-B⊠-B⊠ | IARI, Delhi | R | S |
| Germ plasm | ICP-7065-29⊠-3⊠-1⊠-B⊠-B⊠ (P2 resistant control) | Madhya Pradesh | R | S |
| Prabhat | ICP-7220 | IARI, Delhi | S | S |
| HY-3C | ICP-7119 (P2 susceptible control) | IARI, Hyderabad | S | S |

[a] ⊠ = selfed lines.
[b] R = resistant, S = susceptible.

33% clay, 7% silt), and 25 seeds were sown in each pot.

*P. drechsleri* f. sp. *cajani* was grown in petri plates on V-8 juice agar (V-8 juice, 100 ml; $CaCO_3$, 2 g; agar, 20 g; distilled water to make 1,000 ml [5]). One 5-mm disk of a 1-wk-old culture was transferred to a 250-ml flask containing 100 ml of V-8 juice broth (same composition as juice agar but without agar). The broth cultures were incubated at 28–30 C for 15 days. The inoculum was prepared by macerating the fungus mats in water and blending the mats in a Waring Blendor with 100 ml of water per mat for 2 min. A quantity of water equal to the blended material was added; 100 ml of the prepared inoculum was poured in each pot containing 5- to 10-day-old seedlings.

The pots were watered three times a day to encourage development of the disease, and observations were recorded 10 days after inoculation. HY-3C (a susceptible line) and ICP-7065 or 2376 (resistant lines) were maintained as uniform controls with each inoculated batch.

Early in our study, we observed that the incidence of the disease on known genotypes varied considerably, and the proportion of susceptible and resistant $F_2$ plants fluctuated among batches. Repeated subculturing of the pathogen might have resulted in reduced virulence; therefore the pathogen was frequently isolated afresh from diseased seedlings to maintain the original virulence. The isolate was tested for virulence on susceptible and resistant lines before use. Optimum temperature conditions (25–35 C) were maintained for development of the disease (2,6).

**Field screening.** The inoculum was multiplied on V-8 juice agar for 1 wk and was mixed well with the medium after 600-mesh Carborundum was added. Individual 30-day-old seedlings were inoculated at the collar region. The field was flood-irrigated twice with a week's interval between irrigations to create conditions favorable for disease development.

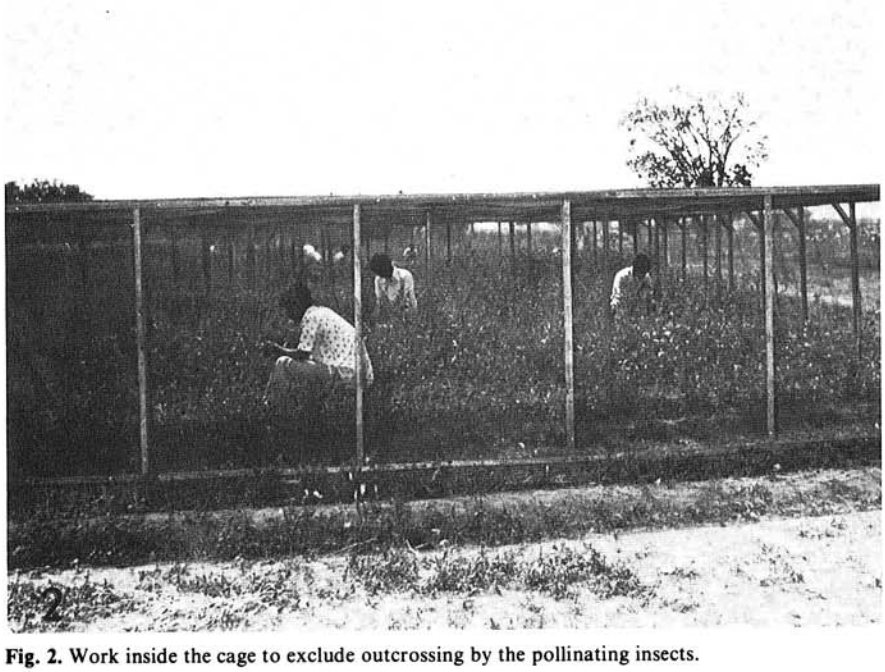

**Fig. 2.** Work inside the cage to exclude outcrossing by the pollinating insects.

**Table 2.** Reaction of $F_1$ hybrids of a 10 parent diallel including seven resistant and three susceptible lines

| Pedigree[a] | Disease reaction | | | |
|---|---|---|---|---|
| | Isolate P2 | | Kanpur isolate | |
| | Resistant | Susceptible | Resistant[b] | Susceptible |
| Susceptible × susceptible[c] | | | | |
| ICPL-1 × No. 148 | 1[b] | 14 | 0 | 9 |
| ICPL-1 × ICP-6997 | 0 | 15 | 0 | 10 |
| No. 148 × ICP-6997 | 0 | 14 | 1 | 9 |
| Resistant × susceptible | | | | |
| Pant A-3 × ICPL-1 | 14 | 1[d] | 0 | 6 |
| Pant A-3 × No. 148 | 15 | 0 | 3 | 7 |
| Pant A-3 × ICP-6997 | 15 | 0 | 1 | 8 |
| ICPL-7 × ICPL-1 | 15 | 0 | 1 | 9 |
| ICPL-7 × No. 148 | 15 | 0 | 2 | 8 |
| ICPL-7 × ICP-6997 | 15 | 0 | 1 | 9 |
| ICPL-1 × BDN-1 | 15 | 0 | 2 | 8 |
| ICPL-1 × ICP-231-P5⊠ | 13 | 0 | 0 | 10 |
| ICPL-1 × ICP-2376 | 13 | 0 | 3 | 7 |
| NP-69 × ICPL-1 | 12 | 0 | 0 | 9 |
| ICP-7065 × ICPL-1 | 15 | 0 | 0 | 10 |
| No. 148 × BDN-1 | 15 | 0 | 2 | 8 |
| No. 148 × ICP-231-P5⊠ | 15 | 0 | 1 | 9 |
| No. 148 × ICP-2376 | 14 | 1[d] | 0 | 10 |
| No. 148 × NP-69 | 15 | 0 | 3 | 7 |
| No. 148 × ICP-7065 | 15 | 0 | 1 | 9 |
| BDN-1 × ICP-6997 | 15 | 0 | 2 | 8 |

(*continued on next page*)

**Table 2.** (*continued from preceding page*)

| Pedigree[a] | Disease reaction: Isolate P2 Resistant | Isolate P2 Susceptible | Kanpur isolate Resistant[b] | Kanpur isolate Susceptible |
|---|---|---|---|---|
| ICP-231-P5⊠ × ICP-6997 | 14 | 0 | 1 | 9 |
| ICP-6997 × ICP-2376 | 15 | 0 | 1 | 9 |
| ICP-6997 × NP-69 | 15 | 0 | 0 | 9 |
| ICP-6997 × ICP-7065 | 15 | 0 | 0 | 10 |
| Resistant × resistant | | | | |
| Pant A-3 × ICPL-7 | 15 | 0 | 1 | 6 |
| Pant A-3 × BDN-1 | 15 | 0 | 3 | 7 |
| Pant A-3 × ICP-231-P5⊠ | 15 | 0 | 1 | 9 |
| Pant A-3 × ICP-2376 | 15 | 0 | 1 | 8 |
| NP-69 × Pant A-3 | 10 | 0 | 1 | 9 |
| ICP-7065 × Pant A-3 | 15 | 0 | 1 | 9 |
| ICPL-7 × BDN-1 | 15 | 0 | 0 | 10 |
| ICPL-7 × ICP-231-P5⊠ | 15 | 0 | 1 | 9 |
| ICPL-7 × ICP-2376 | 15 | 0 | 0 | 10 |
| NP-69 × ICPL-7 | 15 | 0 | 1 | 6 |
| ICP-7065 × ICPL-7 | 14 | 0 | 3 | 6 |
| BDN-1 × ICP-231-P5⊠ | 13 | 0 | 0 | 10 |
| BDN-1 × ICP-2376 | 15 | 0 | 1 | 9 |
| NP-69 × BDN-1 | 7 | 0 | 1 | 6 |
| BDN-1 × ICP-7065 | 15 | 0 | 1 | 9 |
| ICP-231-P5⊠ × ICP-2376 | 15 | 0 | 0 | 10 |
| NP-69 × ICP-231-P5⊠ | 15 | 0 | 1 | 8 |
| ICP-7065 × ICP-231-P5⊠ | 15 | 0 | 2 | 7 |
| NP-69 × ICP-2376 | 14 | 0 | 1 | 8 |
| ICP-7065 × ICP-2376 | 15 | 0 | 0 | 10 |
| NP-69 × ICP-7065 | 15 | 0 | 0 | 9 |
| ICP-7065 (resistant check)[c] | 15 | 0 | 0 | 15 |
| HY-3C (susceptible check) | 0 | 15 | 0 | 15 |

[a] ⊠ = selfed progenies.
[b] Escapes in subsequent tests.
[c] To isolate P2.
[d] Possible result of chance impurity of seed.

**Table 3.** Reaction of $F_2$ and backcross populations to isolate P2

| Cross[a] | Reaction: Resistant | Reaction: Susceptible | Expected ratio | $\chi^2$ Probability |
|---|---|---|---|---|
| Resistant × susceptible $F_2$ | | | | |
| Pant A-3 × ICPL-1 | 152 | 44 | 3:1 | 0.40–0.30 |
| ICPL-7 × ICPL-1 | 145 | 50 | 3:1 | 0.90–0.80 |
| BDN-1 × ICPL-1 | 143 | 44 | 3:1 | 0.70–0.50 |
| Resistant × resistant $F_2$ | | | | |
| Pant A-3 × BDN-1 | 182 | 0 | ... | ... |
| (Resistant × susceptible) × susceptible $BC_1$ | | | | |
| (Pant A-3 × ICPL-1) × ICPL-1 | 38 | 35 | 1:1 | 0.80–0.70 |
| (ICPL-7 × ICPL-1) × ICPL-1 | 16 | 10 | 1:1 | 0.30–0.20 |
| (BDN-1 × ICPL-1) × ICPL-1 | 46 | 46 | 1:1 | 1.0 |
| (Resistant × resistant) × resistant $BC_1$ | | | | |
| (Pant A-3 × BDN-1) × Pant A-3 | 78 | 0 | ... | ... |
| (Pant A-3 × BDN-1) × BDN-1 | 68 | 0 | ... | ... |
| (Resistant × susceptible) × resistant $BC_1$ | | | | |
| (Pant A-3 × ICPL-1) × Pant A-3 | 73 | 0 | ... | ... |
| (ICPL-7 × ICPL-1) × ICPL-7 | 39 | 0 | ... | ... |
| (BDN-1 × ICPL-1) × BDN-1 | 69 | 0 | ... | ... |
| Control | | | | |
| ICP-2376 (resistant) | 25 | 0 | ... | ... |
| HY-3C (susceptible) | 0 | 25 | ... | ... |

[a] Parentage of the crosses is given as the source or as ICP/ICPL number.

Typical blight symptoms appeared within 10 days after inoculation. One month after the first inoculation, the disease-free plants were reinoculated to minimize the chances of escapes. Also, the effectiveness and uniformity of the inoculation across the field were monitored by growing the susceptible check cultivar HY-3C after every 10 test rows. Test material was planted in one or two rows 5 m long. Resistant plants for advancing to the next generation were selected only from areas in the field where the susceptible check showed more than 90% incidence of disease.

**Materials screened.** Seven resistant and three susceptible parents were crossed in diallel to test allelic relationships of the genes from different sources of resistance (Table 1). Eight backcrosses and four $F_2$ populations involving three resistant parents and a susceptible parent were screened to determine the mode of inheritance of resistance. All the crossing and growing of $F_1$ progeny was done in a cage (Fig. 2) to avoid any chance of outcrossing by pollinating insects, and all material was screened by pot culture. The disease reaction was noted as resistant (surviving) and susceptible (dead plants).

In addition, $F_2$ and $F_3$ generations of nine crosses involving nine susceptible parents and the resistant parent ICP-7065 were studied in the field.

## RESULTS AND DISCUSSION

**Pot screening.** *Inheritance.* The $F_1$ hybrids of susceptible parents were all susceptible, and the $F_1$ hybrids of resistant × susceptible and resistant × resistant parents were all resistant (except two plants) to isolate P2 (Table 2), indicating that resistance to isolate P2 was completely dominant over susceptibility. Chance impurity of the seeds could have produced the susceptible $F_1$ plant in Pant A-3 × ICPL-1 and the plant in No.148 × ICP-2376.

The dominant nature of resistance was further confirmed by the backcrosses to the resistant parent, which did not segregate (Table 3). Three $F_2$ populations of resistant and susceptible crosses segregated in a 3:1 ratio of resistant to susceptible (Table 3); thus a single dominant gene controlled resistance in these three parents. Backcrosses to the susceptible parent segregated as expected in a 1:1 ratio of resistant to susceptible, which further confirmed monogenic dominant inheritance of resistance to isolate P2.

Although a few $F_1$ plants of some crosses possessed apparent resistance to the Kanpur isolate (Table 2), subsequent tests showed that they were all escapes.

*Allelic relationships.* The $F_1$ plants of all crosses among resistant parents were resistant for isolate P2 (Table 2). The reactions of the $F_1$ hybrids of two parents, both of which have a dominant gene for resistance, provide no information on the allelic relationships of the resistance genes. There was no segregation in the $F_2$ populations of crosses among resistant parents except in two cases (Table 4). In $F_2$ populations of Pant A-3 × BDN-1 and ICP-231-P5⊠ × ICP-7065, a few plants were susceptible, perhaps as a result of chance contamination of seeds. From these data, we concluded that the genes controlling resistance in the seven resistant parents were at a common locus.

**Field screening.** $F_2$ populations of nine crosses involving nine susceptible parents and the resistant parent ICP-7065 were screened in the blight nursery and the individual resistant plants were selfed. For each cross, about 100 individual $F_2$s were selfed and raised as $F_3$ progenies in the blight nursery. However, selfing could not be done in three crosses

**Table 4.** Reaction of $F_2$ populations from resistant crosses studied by pot screening

| Pedigree[a] | Reaction to isolate P2 | |
|---|---|---|
| | Resistant | Susceptible |
| Pant A-3 × ICPL-7 | 52 | 0 |
| Pant A-3 × BDN-1 | 192 | 2[b] |
| Pant A-3 × ICP-231-P5⊠ | 190 | 0 |
| Pant A-3 × ICP-2376 | 129 | 0 |
| NP-69 × Pant A-3 | 93 | 0 |
| ICP-7065 × Pant A-3 | 71 | 0 |
| ICPL-7 × BDN-1 | 164 | 0 |
| ICPL-7 × ICP-231-P5⊠ | 143 | 0 |
| ICPL-7 × ICP-2376 | 107 | 0 |
| BDN-1 × ICP-231-P5⊠ | 179 | 0 |
| BDN-1 × ICP-2376 | 151 | 0 |
| BDN-1 × ICP-7065 | 79 | 0 |
| ICP-231-P5⊠ × ICP-2376 | 189 | 0 |
| ICP-231-P5⊠ × ICP-7065 | 171 | 5[a] |
| ICP-231-P5⊠ × NP-69 | 153 | 0 |
| NP-69 × BDN-1 | 144 | 0 |
| NP-69 × ICPL-7 | 137 | 0 |
| ICP-7065 × ICPL-7 | 104 | 0 |
| ICP-2376 × ICP-7065 | 128 | 0 |
| ICP-2376 (resistant control) | 25 | 0 |
| HY-3C (susceptible control) | 0 | 25 |

[a] ⊠ = selfed progenies.
[b] Possible result of chance impurity of seeds.

**Table 5.** Reaction of $F_3$ progenies of susceptible × resistant crosses by field screening for isolate P2

| Pedigree | No. of progenies | | | | $\chi^2$ value (1:2) | Probability |
|---|---|---|---|---|---|---|
| | Total | Escapes[a] | Homozygous resistant | Segregating | | |
| Prabhat × ICP-7065 | 100 | 2 | 20 | 78 | 7.37 | 0.01–0.005 |
| UPAS-120 × ICP-7065 | 87 | 4 | 22 | 61 | 1.74 | 0.25–0.1 |
| ICP-1 × ICP-7065 | 100 | 3 | 17 | 80 | 10.9 | <0.005 |
| No.148 × ICP-7065 | 91 | 9 | 30 | 52 | 0.39 | 0.75–0.5 |
| C-11 × ICP-7065 | 100 | 2 | 25 | 73 | 2.70 | 0.25–0.1 |
| ICP-102 × ICP-7065 | 99 | 10 | 23 | 66 | 2.25 | 0.25–0.1 |
| ICP-6997 × ICP-7065 | 93 | 9 | 4 | 80 | 30.86 | <0.005 |
| ICP-7035 × ICP-7065 | 97 | 18 | 20 | 59 | 2.28 | 0.25–0.1 |
| HY-3C × ICP-7065 | 96 | 25 | 13 | 58 | 7.22 | 0.01–0.005 |

[a] Progenies that showed more than 85% susceptibility.

involving ICP-1, C-11, and Prabhat, and only open-pollinated seeds were used in these cases.

For the genetic analysis of the $F_3$ progenies, those that had more than 85% susceptible plants were treated as escapes and those that had less than 10% susceptible plants as resistant progenies. Of the nine crosses, five crosses segregated in a 1:2 pattern of true breeding resistant to segregating progenies (Table 5). Similarly, more than 50% of the segregating progenies in all nine crosses showed very good fit to a 3:1 ratio for resistance and susceptibility (Table 6). These observations on $F_3$ progenies closely agree with those on parents, $F_1$s, and $F_2$s studied by the pot culture technique and confirm the monogenic dominant nature of resistance to *Phytophthora*. The large number of departures from the 1:2 ratio of true breeding to segregating progenies

**Table 6.** Goodness of fit of the segregating $F_3$ progenies to 3:1 ratio (resistant/susceptible) by field screening for isolate P2

| Pedigree | Segregating progenies (no.) | Progenies fitting 3:1 ratio |
|---|---|---|
| Prabhat × ICP-7065 | 78 | 53 (68.0%) |
| UPAS-120 × ICP-7065 | 61 | 48 (78.7%) |
| ICP-1 × ICP-7065 | 80 | 61 (76.3%) |
| No.148 × ICP-7065 | 52 | 31 (59.6%) |
| C-11 × ICP-7065 | 73 | 55 (75.0%) |
| ICP-102 × ICP-7065 | 66 | 39 (59.0%) |
| ICP-6997 × ICP-7065 | 80 | 48 (60.0%) |
| ICP-7035 × ICP-7065 | 59 | 46 (78.0%) |
| HY-3C × ICP-7065 | 58 | 30 (51.7%) |

in a few crosses and departures from the 3:1 ratio in the segregating $F_3$ progenies in the field could have resulted from impurity of parental stocks, chance outcrossing of the $F_1$s, or mistakes in classification.

A high degree of specificity of reaction to isolate P2 by resistant lines from diverse sources suggests that this resistance would be of limited use in a breeding program. A systematic search for new genes for resistance to different races of *P. drechsleri* f. sp. *cajani* is essential for developing cultivars with wide adaptability.

The common gene in the seven resistant parents studied is designated as $Pd_1$. Neither the parents nor their $F_1$s were resistant to the Kanpur isolate, indicating the possibility of more than one race of *P. drechsleri* f. sp. *cajani*.

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