



Analyzing the genetic relatedness of pigeonpea varieties released over last 58 years in India

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(Received: September 2019; Revised: January 2020; Accepted: February 2020)

Abstract

The genetic base of 150 pigeonpea varieties released in India during 1960 to 2018 was examined. Of these, 89, 57, three, and one variety were developed by pedigree selection, pureline selection, mutation and population improvement, respectively. Examination of pedigree records of 89 pigeonpea varieties developed through pedigree breeding method between 1971 and 2018 traced back to 113 ancestors. The highest mean genetic contribution was recorded for the genotype T 190 (0.051) accompanied by UPAS 120 (0.049) and ICP 8863 (0.043). The ancestor T 190 appeared with highest frequency of 21, directly as one of the parent (male/female) in four varieties and indirectly in the development of 17 varieties. Similarly, the ancestors UPAS 120 and ICP 8863 were more frequently used (in nine varieties) as direct parents followed by T 21 and C 11 (in five varieties). The variety PRG 176 involved the highest number (9) of ancestors during the course of its development followed by the variety VBN (Rg) 3 with eight ancestors. Results indicated that 51.69% (46 of the 89 varieties) of released varieties were developed through biparental crossing whereas 48.31% involved multiple parents. The frequent use of a limited number of ancestors has caused the narrow genetic base of released pigeonpea varieties. We recommend large-scale deployment of novel germplasm resources for generating broad-base breeding populations. This will help to obtain improved pigeonpea cultivars with high grain yield, biotic tolerance and climate adaptation.

Key words: *Cajanus cajan*, Diversity, Genetic base, Pedigree, Pigeonpea

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millspaugh], also called redgram, tur or arhar is predominantly an annual food legume, which is grown in different cropping systems as *kharif* crop in the Indian sub-continent. Pigeonpea

is the second most important pulse crop in India (Bohra et al. 2020). As an integral part of the human diet pigeonpea serves as an affordable and rich source of proteins and essential micronutrients, particularly in India. Other diverse usages of pigeonpea include fodder and feed for animals, fuel wood for rural households, soil binder to protect soil erosion and as border crop to protect the main crop.

Pigeonpea is grown as sole crop or inter crop in varying agro-eco systems. In India, pigeonpea is cultivated in five distinct agro-ecological zones viz., Hilly, North-Western Plain, North-Eastern Plain, Central and South Zones. Different maturity groups of pigeonpea viz., extra-early (110-120 days), early (121-150 days), mid-early (151-165 days), medium (166-185 days) and late (>200 days) show adaptability to a particular agro-ecology. For instance, medium duration pigeonpea is cultivated in Central and South zones, whereas late-maturing pigeonpea is particularly suited to North-Eastern Plain Zone. Pigeonpea area in India is dominated by medium maturity group followed by early cultivars. In view of the geographical variations of these zones, pigeonpea is restricted to distinct maturity groups pertaining to the zone of cultivation. (AICRP on Pigeonpea Project Coordinator Report, 2018-19).

Developing cultivars with enhanced seed yield has been the topmost objective ever since the organized breeding programme initiated in pigeonpea. The pigeonpea breeding is dominated by hybridization between high-value parents for generating segregating populations, which in turn leads to recovery of superior segregates to practice the selection. The conscious

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process of parental selection for breeding inadvertently causes a higher probability of selecting related parents for hybridization, a bottleneck that reflects in the narrow genetic base of the released varieties of pigeonpea (Singh et al. 2015; Bohra et al. 2010, 2017; Saxena et al. 2018).

Several high-yielding cultivars of pigeonpea have been developed and released for cultivation at farmers' field following establishment of AICRP on Pulses in 1960. This has caused replacement of traditional landraces that represented the major cultivated forms of pigeonpea, thus decreasing the genetic base of pigeonpea. This renders improved varieties vulnerable to outbreak of evolving insect-pests, diseases and climatic uncertainties. Therefore, efforts were made in the recent past to increase the genetic diversity of pigeonpea by incorporating more elite genotypes and wild accessions of pigeonpea including tertiary gene pool. Pre-breeding attempts were made to incorporate the pod borer resistance from *Flemingia* spp (Mallikarjuna et al. 2007), pod fly resistance from *Rhynchosia bracteata* (Sharma et al. 2003), photoperiod insensitivity from *Rhynchosia rothii* (Pundir and Singh 1987), early flowering and *Phytophthora* blight resistance from *Cajanus platycarpus* (Mallikarjuna et al. 2006), Bruchid and water logging tolerance form *Cajanus sericeus* (Mallikarjuna et al. 2011) and high protein content from *Cajanus scarabaeoides* (Saxena et al. 2002).

Keeping track of the breeding history of the current cultivars and breeding lines is important to enhance the use of germplasms. Estimation of ancestor-kinship relationship ensures genetic diversity in the developed cultivars via measurement of relative or mean genetic contribution (MGC) (Lin 1991). For estimating genetic base, the MGC has been widely used in cereals (Cox et al. 1986; Lin 1991) and pulses (Dixit and Katiyar 2004; 2006; Katiyar et al. 2007; 2008; Srivastava et al. 2017; Katiyar and Tripathi 2018). A systematic analysis of the genetic base of pigeonpea cultivars developed by various national and state research partners is important to promote enhanced use of novel germplasms to widen the genetic base of current breeding programmes. In view of this, the present study was conducted to determine the genetic diversity among the released pigeonpea varieties and further assessed the frequencies of ancestor in the pedigree and estimated the relative genetic contribution of ancestors in the entries evaluated during 2007 to 2018 in initial varietal trial (IVT) under AICRP-

Pigeonpea and varieties released (from 1960 to 2018) from state and central varietal release.

Materials and methods

A total of 150 pigeonpea varieties released during 1960-2018 and 520 IVT entries of AICRP evaluated from 2007 to 2018 were included in the present study. Of these, 89 released varieties and 455 IVT entries developed through pedigree method were used for analysis of different genetic parameters. All the released varieties were grouped into five time periods (10 year interval) to make it simpler to study the change of genetic diversity over time. There were one, 26, 35, 26, 35 and 27 varieties released in the periods of 1960-69, 1970-79, 1980-89, 1990-99, 2000-09 and 2010-till date, respectively. Pedigree analysis was performed to identify the ancestors of the varieties developed through hybridization. Indigenous varieties/landraces/genotypes of unknown ancestry were considered as ancestors for itself. For each variety the pedigree tree was drawn till the available final ancestor root.

Using path coefficient analysis described by Wright (1922), the RGC of different ancestors towards a given variety were computed. As shown in Fig. 1,

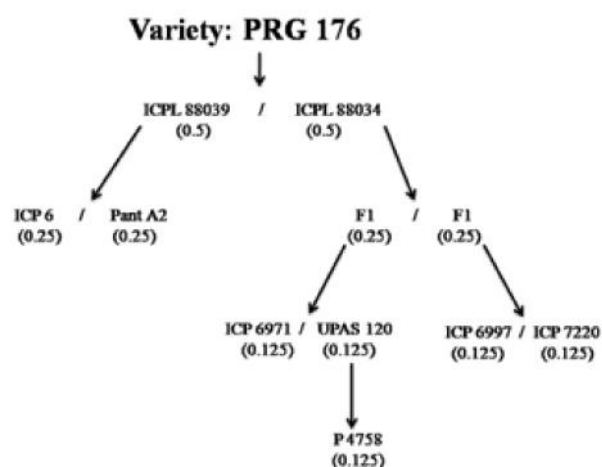


Fig. 1. Schematic representation for estimation of theoretical values for RGC in a pedigree tree

RGC partitions the genetic constitute of each variety into theoretical percentages attributable to different ancestors based on their level of involvement in the pedigree tree of varietal development process. Each value of RGC is recorded as variety versus ancestor in data file for further computation. The mean RGC of a given ancestor was estimated by the mean of the RGC of particular ancestor to all varieties released in

a certain time period. The successive sum of mean RGC generated the cumulative RGC over time. For computation of genetic contributions, it is assumed that a genotype derived from a cross/hybridization receives half of its genetic material from each parent, with all ancestors unrelated to each other. These estimates, therefore, remain statistical representations, not the real nuclear compositions (Lin 1991).

Results and discussion

The pedigrees of 150 pigeonpea varieties released during 1960 to 2018 were traced back to 168 ancestors. Of the total released varieties, 89, 57, 3 and one were developed following pedigree, pureline selection, mutation and population breeding approaches, respectively. The 89 varieties developed through artificial hybridization accompanied by pedigree method were reverted to 113 ancestors. Similarly, the data analyzed for IVT-AICRP entries (2007 to 2018) suggested a strong inclination (455 entries) towards hybridization coupled with pedigree method. Medium and early maturing pigeonpea representing the largest groups in India comprised of 48 released and 182 IVT entries, and 33 released and 142 IVT entries, respectively (Table 1). The higher number of varieties for these groups is directly proportional to acreage under cultivation.

As inferred from Table 2, pedigrees of 89 hybridization derived varieties traced back to 113 ancestors (Table 2), of which 72 were used only once in the hybridization. Although greater numbers of ancestors were integrated into breeding programme in recent years (Fig. 2), only 25 ancestors had higher mean cumulative genetic contribution of 0.55 for the total released varieties from 1960 to 2018 (Table 3).

The genotype T 190 contributed high mean genetic contribution of 0.051, with highest percent occurrence (7.34) in the total released varieties. T 190 (21) appeared directly as one of the parents (male/female) in four varieties and indirectly in 17 varieties. Two genotypes UPAS 120 and ICP 8863 were used as direct parents in nine varieties, with mean genetic contributions of 0.05 and 0.04 respectively. This is followed by T 21 and C 11 (in 5 varieties) with mean genetic contributions of 0.03 each. Recurrent exploitation of a limited number of ancestors in varietal development could be attributed to important breeding traits that they carry such as higher grain yield, disease and insect resistance, earliness, quality etc (Table 4). In congruence with our findings, Saxena et al. (2018)

Table 1. Classification of pigeonpea varieties released from 1960 to 2018 and IVT-AICRP entries evaluated between 2007-2018 based on maturity groups and breeding method used

Breeding method	Maturity group	No of released entries (from 1960 to 2018)	No of IVT entries (from 2007 to 2018)
Hybridization	Extra early	-	13
	Early	33	142
	Mid early	-	59
	Medium	48	182
	Late	8	59
	Total	89	455
Pureline selection	Extra early	-	1
	Early	14	24
	Mid early	-	9
	Medium	33	18
	Late	10	4
	Total	57	56
Mutation breeding	Early	2	5
	Mid early	-	1
	Medium	1	2
	Total	3	8
Population improvement	Extra early	1	
Somoclonal variant	Medium	-	1
Grand total		150	520

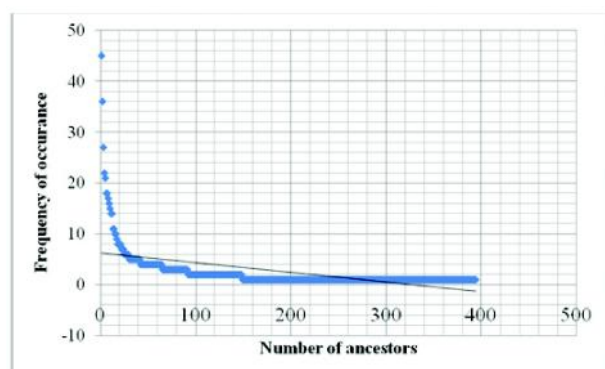
have also found pigeonpea genotypes T 190 and C 11 as among the top six founders contributing to current genetic base of pigeonpea varieties following analysis of 63 varieties with 50K SNP array. Similar reports documenting repeated use of fewer donors were also available in other legume crops like chickpea (Srivatsav et al. 2017), groundnut (Knauft and Gorbet 1989), soybean (Delannay et al. 1983; Sneller 1994), mungbean (Katiyar et al. 2007), urdbean (Katiyar et al. 2008) and in lentil (Katiyar and Tripathi 2018).

The variety UPAS 120 is a pureline selected from P 4768 in 1976 for its traits like, indeterminate growth habit, semi-spreading, early maturity and tolerance to pod borer. This was initially released for cultivation in NEPZ; however, the pedigree records of IVT AICRP entries (2007-2018) reflects its wider adaptation to various agro-ecologies in India and encouraged its repeated direct use (36 times) as ancestor with 3.64% occurrence.

Table 2. List of ancestors and their frequency of occurrence in pedigree of 89 pigeonpea varieties released from 1971 to 2018 in India

Ancestor	Ancestor	Ancestor	Ancestor	Ancestor
T 190 (21)*	NPWR 15 (3)	B 517 (1)	ICP 6971 (1)	MS Pusa 33 (1)
T 1 (18)	Pant A2 (3)	B 7 (1)	ICP 7035-1 (1)	PD 1 (1)
UPAS 120 (13)	Pusa Ageti (3)	Bhavani Shankar Local (1)	ICP 7220 (1)	Personal (1)
P 4768 (13)	T 2 (3)	BRG 2 (1)	ICP 8862 (1)	Plant 142 (1)
T 21 (12)	TT 6 (3)	BRG 3 (1)	ICPL 151 (1)	Prabhat DT (1)
ICP 8863 (10)	BRG 1 (2)	BSMR 198 (1)	ICPL 161 (1)	Pusa 9 (1)
C 11 (9)	BSMR 736 (2)	BSMR 65 (1)	ICPL 269 (1)	Sel. 90310 (1)
ICP 6 (9)	EE 76 (2)	BWR 24 (1)	ICPL 341 (1)	T 15-15 (1)
GP No. 148 (7)	GNP 357 (2)	CMS 2043 (1)	ICPL 383 (1)	T 8 (1)
BDN 2 (6)	ICP 3673 (2)	CMS BSMR 736 (1)	ICPL 83027 (1)	TA 277 (1)
Brazil 1-1 (6)	ICP 87051 (2)	Co 5 (1)	ICPL 85024 (1)	TS 3 (1)
Bahar (5)	ICPL 99046 (2)	CO 6 (1)	ICPL 85063 (1)	Vamban 1 (1)
BDN 1 (5)	MA 2 (2)	DA 6 (1)	ICPL 87 (1)	WRG 13 (1)
Hy 3C (5)	PT 221 (2)	DL 78-1 (1)	ICPL 87051 (1)	
Prabhat (5)	Pusa Sweta (2)	GAUT 85-21 (1)	ICPL 88034 (1)	
Asha (4)	QLP 200 (2)	GAUT 87-20 (1)	ICPL 88039 (1)	
ICP 7217 (4)	2740R (1)	GP No. 81 (1)	ICPL 96058 (1)	
ICPL 7336 (4)	AC 314 (1)	GS 1 (1)	JA 275 (1)	
BSMR 853 (3)	AK 101 (1)	GT 288A (1)	JA 277 (1)	
Hosakote Local (3)	AK 2 (1)	GTR 11 (1)	Kanke 1 (1)	
ICP 6997 (3)	AKMS 2 (1)	Gulbarga Local (1)	Khargone 2 (1)	
ICPL 332 (3)	AL 16 (1)	H 88-45 (1)	KPBR 80-1 (1)	
ICPL 84008 (3)	AL 688 (1)	H 89-5 (1)	KPBR 80-2-1 (1)	
LRG 41 (3)	Allapur local (1)	ICP 11204 (1)	LRG 30 (1)	
MS Prabhat DT (3)	APK 1 (1)	ICP 525427 (1)	MA 166 (1)	

*Numbers in parenthesis indicate the frequency of occurrence of that ancestor in 89 pedigrees

**Fig. 2.** Number of ancestors and their frequency of occurrence in the pedigree of 455 pigeonpea IVT entries from 2007 to 2018

Examination of pedigree records of IVT AICRP entries from 2007 to 2018 reveals the pigeonpea variety UPAS 120 as the most widely used cytoplasmic parent (25 entries) followed by Asha (ICP 87119) with genetic contributions towards 24 entries (Fig. 3). With 27% frequency of occurrence in IVT entries, another popular pigeonpea variety ICP 8863 has been used 18 times as male and nine times as cytoplasmic parent in breeding cultivars of different maturity groups like early, medium and late. ICP 8863, also called as Maruti, is a pureline selection from Hyderabad landrace released in 1986 for cultivation in south zone for its high yield and wilt resistance. Similarly, the variety Asha (ICP 87119) also stands at top in terms of appearance as parent (44 times).

Table 3. Relative genetic contribution, mean genetic contribution and frequency of occurrence for the top 24 ancestral contributors of the varieties released from 1960 to 2018

Ancestor	Mean genetic contribution	Cumulative mean genetic contribution	Frequency of occurrence	Occurrence (%)
T 190	0.051	0.051	21	7.34
UPAS 120	0.049	0.099	13	4.55
ICP 8863	0.043	0.142	10	3.50
T 1	0.040	0.182	18	6.29
T 21	0.037	0.219	12	4.20
C 11	0.032	0.251	9	3.15
ICP 6	0.029	0.280	9	3.15
P 4768	0.024	0.304	13	4.55
GP No. 148	0.024	0.328	7	2.45
Bahar	0.020	0.348	5	1.75
BDN 2	0.020	0.369	6	2.10
Brazil 1-1	0.020	0.389	6	2.10
Asha	0.018	0.407	4	1.40
Prabhat	0.015	0.422	5	1.75
BSMR 853	0.014	0.435	3	1.05
ICPL 332	0.014	0.449	3	1.05
ICPL 84008	0.014	0.462	3	1.05
LRG 41	0.014	0.476	3	1.05
MS Prabhat DT	0.014	0.490	3	1.05
NPWR 15	0.014	0.503	3	1.05
Pusaageti	0.014	0.517	3	1.05
TT 6	0.014	0.530	3	1.05
Hy 3C	0.011	0.541	5	1.75
Pant A2	0.011	0.553	3	1.05

Released in 1986, the variety Asha has been derived from the hybridization between C 11 as cytoplasmic parent and ICP 6 as male parent. Unlike UPAS 120 which was donor for most of early and medium group, Asha has been used additionally for late maturity group too; this indicates wider adaptability of Asha as both cytoplasmic and nuclear parent.

The present study confirms the recurring exploitation of few ancestors that has caused narrow genetic base. This narrow genetic base enhances the susceptibility of pigeonpea cultivars to growing climatic vagaries and resistance breakdown in cultivars upon

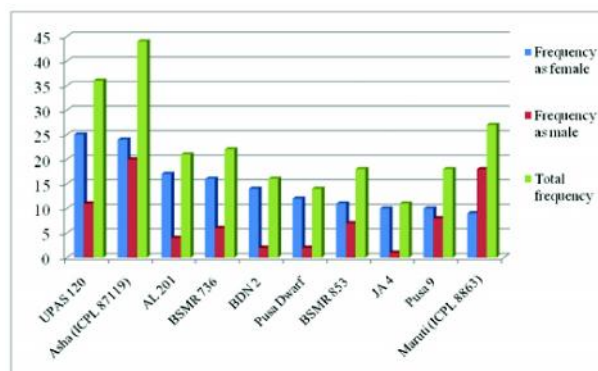


Fig. 3. Frequency of top ten ancestors used in IVT, AICRP entries from 2007 to 2018

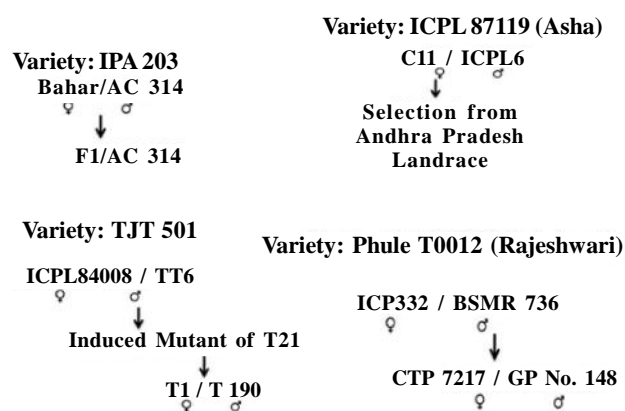


Fig. 4. Pedigree tree of popular pigeonpea varieties namely IPA 203, ICPL 87119 (Asha), TJT 501 and Phule T 0012 (Rajeshwari)

emergence of new races of biotic stresses. Further, limited utilization of genetic variability led in reduction of development of varieties for wider adoptability. Similar trend suggesting a smaller number of ancestors causing narrow genetic base has been evident in other legume crops as well such as lentil (Katiyar and Tripathi 2018).

The pattern of genetic diversity estimated though ancestral genetic contribution matrix may not always be conclusive for distance estimation among the released varieties. Therefore, cluster analysis of genetic contribution derived dissimilarity values was used to study diversity among the released cultivars. The analysis of all varieties broadly separated into four clusters and two outliers at the distance of 0.04 to 0.07 on Grower similarity index. Cluster-II being the largest cluster with 29 varieties is followed by the cluster-I, III and IV having 27, 18 and 13 varieties, respectively. The extremely close proximity of varieties

Table 4. Important characteristics of top five high frequency ancestral genotypes

S.No.	Genotype name	Pedigree	Important features
1	T 190	Selection from	Late Maturing, indeterminate growth habit, semi-spreading braches with 45-Landrace 60° angle from stem, high number of primary and secondary branching, brown seed coat, tolerant to wilt
2	UPAS 120	Selection from	Early maturing (135-150 days), indeterminate growth habit, semi-spreading P 4758 braches with 45-60°angle from stem, synchronous in maturity, tolerant to pod borer, brown seed coat, yields 1.38-1.8 t/ha
3	ICP 8863	Selection from Landrace	Medium maturing (170-180 days), indeterminate growth habit, semi-spreading braches with 45-60° angle from stem, high number of primary and secondary branches, wilt resistant, yields 1.8-2.5 t/ha
4	T 21	T 1 x T 190	Mid-early maturing (150-160 days), indeterminate growth habit, semi-spreading braches with 45-60° angle from stem, high number of primary branching, small seeded, 7-7.5 g (100 seed), tall plant type
5	C 11	Selection from Andhra Pradesh Landrace coat	Late maturing (200-220 days), indeterminate growth habit, spreading braches with >60° angle from main stem, high number of primary branching, brown seed tolerant to wilt, plant grows 3-4 meters of height

like Sharda and Mukta indicates their identical pedigrees. The variety Vipula an outlier remains between the cluster –II and III as a bridging entity. Variety PRG 176 connects cluster-IV with other three clusters. The pedigree record of PRG 176 revealed that, it is the only pigeonpea variety with the highest number (9) of parental genotypes contributing towards its development. Therefore, the involvement of more number of ancestors could be a reason for it being the connecting link among different clusters. Earlier, Sneller (1994) has reported similar case in soybean cultivars released in North and South America.

The results reveal that 51.69 % of released 89 varieties were developed through bi-parental crossing, while development of 41 varieties involved three to six parents. Among all released varieties, PRG 176 and VBN (rg)3 with nine and eight ancestors, respectively involve the highest number of parents.

In summary, breeding strategy based on crossing with only few distant ancestors to widen the genetic base may limit the success and future gain from selection. Pigeonpea has the total collection of about 19,276 unique germplasm accessions in India. Of which National Bureau of Plant Genetic Resources (NBPGR), New Delhi, is maintaining the national stock of 5,644 accessions and also a repository of donors for resistance to several biotic stresses like *Fusarium* wilt, *Phytophthora* blight, sterility mosaic disease and resistant lines for different abiotic stresses. Likewise, ICRISAT has global active collection comprising

13,632 accessions and mini core set of 146 accessions that show wide spectrum of variation for grain yield and component traits (Bohra et al. 2010). Besides, ICAR-IIPR, Kanpur has nearly 1,300 working collection of pigeonpea. Taken together, the pigeonpea germplasm repository has no dearth of valuable germplasm resources for deployment in pigeonpea genetic enhancement.

Notwithstanding a limited number of parents involved in current cultivated base of pigeonpea, recent trends towards utilizing diverse germplasm resources are encouraging. Integration of new accessions has not caused broadening of the genetic base of released pigeonpea varieties due to: i) frequent use of same sources of superior genes/alleles and ii) limited use of distantly-related genotypes (Bohra et al. 2017). Current study offers insights into genetic relatedness of varieties by dissecting their pedigree. Knowledge and understanding on the degree of relatedness among the varieties is useful in choosing potential yet genetically diverse parents for generating broad-base breeding populations.

Authors' contribution

Conceptualization of research (SJSN); Designing of the experiments (SJSN, AB, IPS); Contribution of experimental materials (IPS, FS, DD); Execution of field/lab experiments and data collection (SSJN, ST, AKM); Analysis of data and interpretation (SSJN, AB, AKM); Preparation of manuscript (SSJN, AB, NP).

Declaration

The authors declare no conflict of interest.

Acknowledgments

The authors are thankful to the ICAR, New Delhi and ICAR-IIPR, Kanpur for financial support and project AICRP on Pigeonpea for providing the basic data on pedigree.

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