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Pigeonpea improvement through conventional breeding

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Abstract

Contributions made through conventional breeding have been of great significance in the development of pigeon varieties for diverse agro ecological regions in the country. The available genetic variability has been exploited to its full potential for enhancing trait based genetic improvement. However, the on farm productivity and production has remained low due to several constraints including the plant architecture, early maturity, disease and insect pest resistance. Hence, to breed cultivars having high agronomic performance with broad genetic base for specific regions, new sources of genetic variability need to be tapped. Wild species of *Cajanus* present a vast reservoir of useful genes for pigeonpea improvement. Heterosis breeding has enormous scope to break the yield barrier and enhancing potential but there is great need to identify heterotic parents to be used as MS lines and their respective restorers. However the major challenges are still being faced to answer genetic solutions for achieving yield potential through early maturity restructuring the plant type and resistance breeding to pave the way for sustainability in pigeon pea production.

Key words: Pigeonpea, conventional breeding, early maturity, heterosis breeding

Introduction

Pulses are major source of nutrition and bear health significance among Indian population and has a prominent place in diet of African and sub-Saharan people. India is a major producer and consumer of pulses but at the same time its production and productivity is low and not fully realized. Among pulse crops, pigeonpea occupy a significance place. Traditionally, pigeonpea is being grown in many production systems under a range of agroecological conditions and rainfed farming. However, presently, it has secured a place in irrigated system based on sprinkler or drip with high-tech applications. Historically, it was cultivated for centuries on less productive and marginal soil with minimal or no inputs like manures, fertilizer etc. under subsistence farming. It was mostly grown as a companion crop under mix or inter-cropping with other *kharif* crops. There are some reports to believe that historical exposure of the pigeonpea over the years of adaptation and selection led to the development of characteristics in the germplasm, more useful to develop competitive ability for survival and perpetuation, rather than high productivity in terms of grain yield (Ariyanayagam et al. 1997). However, it may not be appropriate, to say that production can not be enhanced through conventional breeding. There have been examples that selection from the local germplasm, like C11 or ICP 8863 demonstrated the productivity as high as 2 t/ha under front line demonstrations. If the pigeonpea is considered in terms of total energy harvested in the form of grain, in terms of proteins and carbohydrate content, it can't be considered as poor yielder as compared to cereals. Moreover, its wider adaptation under harsh environments provided safety to have better place under rainfed conditions. The conventional breeding involving selection from cultivar/germplasm had been productive to provide stable variety like C11, which occupied large area for more than 60 years in central India. The other part of conventional breeding is recombination of favorable traits like disease resistance. It is a matter of satisfaction that the serious malady of *Fusarium* wilt could be resolved through this approach and resistant lines have been adopted by farmers in central and south India during past four decades on a very large scale. The variety T-21 bred at Kanpur in 1960s remained unbeaten in the respective maturity group, for so many years. When new technologies able to produce polyploidy, mutation,

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hybrids (on commercial scale), transgenics etc. emerged, and currently being used in plant breeding, the old methodologies like selection, hybridization, population improvement are thrown in the category of conventional breeding. The conventional breeding in pigeonpea progressed to yield many suitable varieties for farmers across the country, although new techniques helped in improving the speed in expeditious mission. Thus, it would be interesting to go through the conventional breeding strategies adopted in past and think about the future. No technology of plant modification is absolutely perfact and obsolete. The present article deals with improvement in pigeonpea and possible use of its wild species, attempts made in cytogenetical investigations for searching useful traits to enhance yield potential under diverse agro-ecological conditions.

Origin, domestication and distribution

Pigeonpea, *Cajanus cajan* L. belongs to the subtribe Cajaninae comprised of 13 genera. Earlier, the genus *Atylosia* and *Cajanus* were considered closely related, however, during taxonomic revision in 1986, Van der Maesen merged many of the wild relatives of the pigeonpea, formerly in *Atylosia* W. & A. into *Cajanus* DC. Subsequently, the genus *Cajanus* has been classified into 32 species, 18 of which are endemic to Asia and 13 to Australia and one to western Africa (Van der Maesen 1986). Apart from these, there are other related genera, namely *Rhynchosia*, *Dunbaria*, *Flemingia*, *Paracalyx*, *Eriosema*, *Adenodolichos*, *Bolusafra*, *Carissoa*, *Chrysoscias* and *Baukea*.

Wild species are important sources of resistance to biotic and abiotic stresses as they have evolved to survive droughts, floods, extremes of temperature (heat/ cold), and have the capability to withstand damage by insect pests and diseases that cause heavy losses to cultivated species. Consequently, these species are likely to possess a great potential for successful introgression of economic and useful desirable traits for pigeonpea improvement.

Natural occurrence of different wild relatives, diverse genetic variability in the gene pool and some historical and archaeological records support Indian origin of pigeonpea and Africa is considered as the secondary centre of origin (Vavilov, 1951; Van der Maesen, 1980, 1986, 1990) as only a few wild relatives *viz*., *C. kerstingii* is reported to occur in West Africa and *C. scarabaeoides* restricted to the coastal areas only. However, Australia is also considered as the centre of diversity for pigeonpea. Contrary to that, Kassa et al. (2012) observed very low level of molecular genetic diversity, using SNP markers among the wild Australian species. *C. cajan* with pan tropical presence is the only cultivated species of the genus *Cajanus*. Domestication of pigeonpea traced back to around 3,500 years ago (Vavilov, 1951; De, 1974; Royes, 1976). *C. cajanifolius* is accepted as putative progenitor of present day cultivated pigeon pea, based on the different morphological features (De, 1974; Van der Maesen, 1986, 1990). *C. cajan* and *C. cajanifolius* have stark similarity in different morphological attributes other than the strophiole characteristics (De, 1974). Based on the variation in esterase enzyme examined in the seed extracts of *C. cajan* (T21) and six wild species, Krishna and Reddy (1982) postulated that *C. cajanifolius* is the closest wild relative of *C. cajan*. Similarly, close proximity of *C. cajan* with *C. cajanifolius* was also demonstrated by Jha and Ohri (1996) through developing seed protein profiles of different cultivated and wild accessions. Pundir and Singh (1985) proposed that *C. cajanifolius* is closest wild relative of *C. cajan*. Durgesh at al. (2015) reported ten alleles unique to inter-specific derivetives of *C. cajan* x *C. scarabaeoides*. The presence of alleles unique to specific population or group indicates an inimitable genetic variability at certain loci. This information is valuable to categorize interspecific hybrids with exclusive genetic variability, whose selection can increase the allele richness of breeding population. Lakshmi et al. (2000), advocated *C. cajanifolius* as the maternal parent by using PCR-RFLP technique different genera of sub tribe *Cajaninae*

Cytological investigation of pigeonpea dates back to 1930s, when Roy (1933) reported the chromosome number of pigeonpea as 2n=2x=22 for the first time and also described the development of its embryo sac. Krishnaswamy and Ayyangar (1935) confirmed the count and suggested that 11 was the basic number of the entire tribe. Later reports suggested that the somatic chromosome number to be 2n=2x=22 (Naithani, 1941) with notable exception of one African species *C. kertsingü* with n=16 (Gill and Hussaini, 1986). Naithani (1941) also described size of pigeonpea somatic chromosomes as “very small” (1.35-2.7µ).

Polyploidy in pigeonpea rarely occurs in nature. However, three spontaneous polyploids including tetraploids, n=22, 2n=4x=44 (Saxena et al. 1982) and a hexaploid, n=33 (Pathak and Yadava, 1951) were

first identified in the field on the basis of their morphological features and poor pod set. There are many reports on artificial induction of tetraploidy using colchicine (Kumar et al. 1945; Bhattacharjee, 1956; Shrivastava et al. 1972) and X-ray treatment (Chopde et al. 1979). It is believed that no identified stocks of aneuploids is available till date. Only two cases of aneuploidy have been reported in pigeonpea with 2n=23 (D'Cruz and Jadhav, 1972) and anther-derived callus (no plantlets were raised) with chromosome numbers varying from 2n=8 to 28 (Bajaj et al. 1980). Pigeonpea exhibits normal synapsis or "perfect pairing" (Reddy and De, 1983) with eleven bivalents at metaphase I and the chiasma frequency per bivalent is reported to be 1.46 (Mukhopadhyay, 1986). However, Krishnaswamy and Ayyangar described the larger metaphase I chromosomes of the pigeonpea as having more than four chiasmata in 1935. Several methods for studying the somatic chromosomes of pigeonpea have been used. Root sections (Naithani, 1941; Kumar et al. 1958), squashes of root tips etc. pretreated with chemicals or temperature shock to arrest cell division fixed in an organic acid-alcohol mixture and staining in an acid-based dye solution have been utilised. Sharma and Sharma (1980) have published a number of schedules for handling plant chromosomes. Lavania and Lavania (1982) were the first to achieve characterization of pigeonpea chromosomes using C-banding. They could distinguish only one pigeonpea chromosome by applying C-banding technique to pigeonpea somatic chromosomes.

Meiotic studies involved sectioning flower buds and use of different types of dyes/stains e.g., Heidenhain's ironalum haematoxylin (Roy, 1933; Krishnaswamy and Ayyangar, 1935), aceto-carmine (Singh et al. 1942) and propionic-carmine stain, the best to study all stages of meiosis, including pachytene (Reddy, 1981a, b, c; Dundas et al. 1983, 1988). Pollen viability has been studied using toluidine blue stain under ultra-violet (UV) radiation and aceto-carmine under fluorescence microscope. The first detailed attempt at karyotype analysis was made by Deodikar and Thakar (1956) and they reported the total length (75.4µ) of chromatin, the length of each chromosome, and positions of primary and secondary constrictions. The considerable varietal difference with respect to total chromatin length was explained by Sinha and Kumar (1979) as the chromosome structural change was associated with varietal development.

Though, accurate recognition of pigeonpea chromosomes always remain a challenge due to their small size and lack of distinguishing features like arm ratio or chromosome length. The patterns of pachytene chromosomes proved to be the most genuine feature to identify pigeonpea chromosomes. In such chromosomal morphology, pachytene is the stage of choice to study karyotype. Genomic *in situ* hybridization (GISH) and Fluorescent *in situ* hybridization (FISH) in the condensed mitotic metaphase chromosomes generate detailed information due to their optimum size and presence of characteristic chromomere patterns and secondly, only half the number of chromosomes are visible as compared to mitotic cells. Pachytene karyotypes were developed with the view to identifying synapsing homologous chromosomes in interspecific hybrids of pigeonpea with its wild relatives. Reddy (1981a, b, c) was the first to identify pachytene chromosomes of pigeonpea as they paired with those of wild species on the basis of relative length, arm length, nucleolar association, and the amount and distribution of heterochromatin by preparing ten well spread cells.

Genetic diversity and its utilization

Collection, maintenance and utilization of genetic diversity to enrich the gene pool of pigeonpea is an important activity in breeding. International crops Research Institute for Semi-Arid and Tropics, Patancheru, Hyderabad and National Bureau of Plant genetic Resource, New Delhi in collaboration of State Agricultural Universities have collected usefuil germplasm of pigeonpea from different locations. These germplasm are being maintained by these institutions. For incorporation of beneficial exotic alleles of different desired traits into cultivated varieties, along with diversification of extremely narrow genetic base, distant hybridization is one of the viable option in pigeonpea. In terms of trait-introgression, inter-specific hybridization led to the recovery of remarkably distinct phenotypes in pigeonpea.Total available germplasm for utilization is characterized in different gene pool. Harlan and de Wet (1971) proposed a systematic means of grouping the germplasm of a crop species and their wild relatives. A total of 31 species of pigeonpea are distributed across primary (only one, *C. cajan*), secondary (10 species) and tertiary (20 species) gene pools (Ramanadam, 1990). Wild species have been categorized into different gene pools mainly on the basis of morphological features and ease of crossing (Table 1) (Mallikarjuna, 2011).

Table 1. *Cajanus* species grouped into different gene pools

Primary gene pool	Secondary gene pool	Tertiary Gene Pool	Quaternary gene Pool
C. cajan and its land races	*C. cajanifolius* *C. lineatus* *C. lanceolatus* *C. laticepalus* *C. albicans* *C. reticulatus* *C. sericeus* *C. scarabaeoides* *C. trinervius* *C. acutifolius*	*C. goensis, C. heynei, C. kerstingi, C. mollis,* *C. rugosus, C. volubilis, C. platycarpus, C. niveus,* *C. gandiflorusC. crassicaulis, C. rugosus,* *C. elongates, C. villosus, C. confertiflorus,* *C. visidus, C. aromaticus, C. crassicaulis* *C. lanuginosus, C. pubescens, C. cinereus* *C. marmoratus, C. mareebensis, C. lanuginosus* and *C. pubescens*	*Flemingia* *Rhynchosia* *Dunbaria* *Erisema* *Paracalyx* *Adenodolichos* *Bolusafra* *Carissoa* *Chrysoscias* *Baukea*

Several instances of natural out crossing leading to the development of viable hybrids have been documented in interspecific hybridization of pigeonpea (Saxena and Kumar, 2010). The maintenance of purity of seeds in the pigeonpea varieties becomes difficult due to insect aided out-crossing (Saxena et al. 2016).

Although there are higher levels of meiotic abnormaities due to genetic differences between pigeonpea and its wild relatives and differential affinity between the chromosomes of species, numerous evidences are available for the successful introgression of useful genes/traits from secondary gene pool through conventional hybridization methods. Various techniques of pollination, tissue culture and embryo rescue techniques have facilitated the transfer of desirable traits Such as the development of unique cytoplasmic nuclear male sterile systems (CMS), extra-early flowering and maturity, photoperiod insensitivity, prolific flowering and higher number of pods per plant, high harvest index, annuality and rapid seedling growth, high protein lines, cleistogamous lines, dwarf plant stature, disease and pest-resistance, drought and salinity tolerance from wild relatives into culticated background. (Rao et al. 2003; Bohra et al. 2010).

Pundir and Singh (1987) reported incompatibility in hybridization between parents from primary gene pool (*C. cajanus*) and tertiary gene pool (in particular *C. platycarpus*), frequent abortion of hybridized embryos was common in these crosses. *Cajanus platycarpus*, a wild species in the tertiary gene pool of pigeonpea, has been successfully crossed with cultivated pigeonpea by hormone aided pollinations and the aborting hybrid embryos rescued in vitro (Mallikarjuna et al. 2006). To achieve further breakthrough in enhancing yield of pigeon pea, diverse sources of genes needs to be identified and utilized for its improvement. Developing early maturity genotypes resistant to insect pest, *Helicoverpa armigera* in particular, should be prioritized in breeding programme.

Pigeonpea improvement prior to initiation of AICRP on pulses

Agriculture research in India goes back to as early as 1910, when Imperial Agricultural Research Institute, Pusa (Bihar) was established. It included crop breeding which was limit ed to collection and evaluation of local genotypes and their identification for high yield with disease resistance. Pal (1934) emphasized on wilt resistance breeding in pigeonpea. He reported the multiple gene control of resistance against *Fusarium* wilt.

In mid 20th century (around 1950 to 1956) purification of heterogeneous local cultivars/landraces was done at Kanpur in Uttar Pradesh, Nagpur the then Central Province and Berar and few more research centers. Evaluation of local germplasm and selection against pod shattering, seed dormancy, photo-thermo sensitivity, uniformity in flowering, maturity and seed color along with wilt resistance etc. were main objectives. NP (WR) 15 and C11 are the stable sources of resistance identified from the local germplasm. The resistance however, varied in different regions most probably due to evolution of physiological races of the pathogen investigated during later years. It resulted in recognition of large number of populations and local materials as location specific improved varieties. Selected materials were hardly exposed to testing across the region in country in absence of a effective mechanism for testing. The ‘T’ series of varieties was named for ‘types’ evolved at Kanpur. Similarly ‘C’

series possibly named for 'cultures' developed at Nagpur. The long standing and popular varieties like, UPAS120, Gwalior3, T-17, C-11 still exist in cultivation. C-11 is one of the local cultures from Sangareddy (Telangana) which was collected, evaluated and released in 1956 from Nagpur center by the then Economic Botanist. Some of these long standing varieties were registered and notified after 1978 (under Seed Act, 1966) when quality seed availability was considered for better agricultural production, while other vanished in due course.

All India Coordinated Research Project (AICRP) on pulses

The sites for evaluation of promising cultivars or varieties developed by different breeders across the country were available after 1967, when ICAR established All India Coordinated Research Project on Pulses. Several centers spread throughout the country were identified with their head quarter at Indian Agricultural Research Institute (IARI), New Delhi. Professor S. Ramanujam was the first Project Coordinator for pulse program. Interdisciplinary research on individual crop was emphasized as a major objective of the project. It helped in development of production technology including plant protection measures for new varieties bred in due course of time. During VIIIth five year plan proposal, AICRP on Pulses was divided into three independent projects in 1995, one of which had a major responsibility of pigeonpea. Other one was AICRP on chickpea and third had combined responsibility of 6 other pulses *viz*., mungbean, urdbean, lentil, lathyrus, rajmash and pea, which was named as AICRP on MULLaRP at Kanpur in the campus of Indian Institute of Pulses research.

Conventional breeding

Under All India Coordinated Pulses Improvement Project, selection and recombination breeding in pigeonpea was undertaken at different centers. Considering diverse agro-ecological and other climatic factors, the country has been divided into different zones based on local priorities. States of Punjab, Haryana, Delhi, North West Rajasthan and western Uttar Pradesh including part of Uttarakhand (North West Plain Zone) concentrated on early/short duration *arahar* varieties maturing in less than 130-140 days to suit double cropping. The centers in Eastern UP, Bihar, Jhakhand, West Bengal (North Eastern Plain Zone) worked for long duration pigeonpea of more than 210 days to save the crop from severe winter during December-January. Central and South zones comprised of the regions where majority of traditional pigeonpea of medium maturity group (165 to 200 days) existed. Hence, the centers in central and south worked in this maturity group. The breeding of short duration varieties was also considered in other zones for selecting genotypes for different cropping patterns.

Initially, the improvement was strategically concentrated on the selection from available germplasm. Later on, it was shifted to recombination breeding. During 1990s exploitation of heterosis through F_1 hybrids was planned at IARI, Ludhiana, IIPR, Faizabad, SK Nagar, Akola, Bangluru, Coimbtore based on genetic male sterility discovered at ICRISAT. Later on, the emphasis was given on hybrid based on cytoplasmic genic male sterility. Mutation breeding had been undertaken at very few centers. It was resorted to overcome the small drawbacks from established varieties.

More than 120 varieties of pigeonpea from early (120 to 140 days), medium (150 to 170 days), midlate (170 to 200 days) to late maturity (more than 200 days) were made available to Indian farmers under diverse cropping systems by AICRP (Singh 2014).

Selection from local germplasm including farmers' established varieties and landraces was performed and promising genotypes were identified through multilocation testing. AL15 (Punjab); BR60, BR 65, BR 183, Basant, Bahar and Birasa *Arahar* (Bihar, Jharkhand and Eastern UP); UPAS 120, T7 and T17 (Uttar Pradesh); Khargone-2, JA9-19 (Madhya Pradesh); No. 148, Hyderabad-185, C11, BDN1 and BDN2 (Maharashtra); GT1 and T15-15 (Gujarat); Hy1, Hy2, Hy3A, Hy3C, Hy5, ST1, LRG36 and PDM 1 (Andhra Pradesh); GS1, TTB7 and Maruti/ ICP8863 (Karnataka); CO-1, CO4 and SA-1 (Tamil Nadu) and many more exist in the list of such selections released and/or identified at national or state level.

Prior to launching of AICRP on pulses, very few age old varieties were evolved through hybridization. T 21 evolved from a cross T1 x T190 in early 1960s, which was released in 1980s is one of them. The breeders meticulously attempted recombination breeding after 1970 and resorted to the pedigree selection in segregating generations of the crosses attempted with specific objectives. In early 1970s, Indian Agricultural Reasearch Institute, New Delhi (IARI) developed Sharda, Mukta and Pusa Ageti from such program. It is interesting to note that Brazil 1-1

is one of the parents in the pedigree of these varieties. Brazil-1-1 is an early determinate genotype, similar to Prabhat. It is expected that Prabhat reached Brazil from Indian sub-continent in a form of germplasm and it had back journey to Indian breeding program to have the new recombination. Thereafter, similar program was successfully executed at many centers to release of many varieties (Table 2).

ICPL95 x H80-110 having diverse parentage.

Mutation breeding has been in practice at very few centers. The Bhabha Atomic Research Center worked on early types to improve the seed size. TAT10 (115 to 125 days maturity), TT5 and T Vishakha-1 (135 to 145 days maturity) were developed as stable genotypes with better seed size over existing one.

Table 2. List of varieties, place of origin and year of release/notification

Varieties	Institute/place of release	Notification date/release	Varieties	Institute/place of release	Notification date/ release
Pusa 33	IARI, New Delhi	1988	GT 100	SKNagar, Gujarat	1992
Pusa 84	IARI, New Delhi	1985	Laxmi/ICPL85063	Andhra Pradesh	1997
Pusa 9	IARI, New Delhi	2003	WRP1	Gulberga	2002
Pusa 992	IARI, New Delhi	2004	AKT 8811,	Akola, Maharashtra	
AL 201	PAU, Ludhiana, Punjab	1995	PKV Tara	Akola, Maharashtra	2013
PAU 881	PAU, Ludhiana, Punjab	2007	BSMR 736,	Badnapur, Maharashtra	1996
Sagar	Hissar, Haryana	-	BSMR 853,	Badnapur, Maharashtra	2001
Manak		1985	Amol (BDN708),	Badnapur, Maharashtra	2004
Paras		1997	BDN 711,	Badnapur, Maharashtra	2012
Azad	CSAUT, Kanpur, Uttar Pradesh (U.P.)	1997	BDN 716/ BDN2002-8	Badnapur, Maharashtra	
IPA 203	IIPR, Kanpur (U.P.)		Vipula,	Rahuri, Maharashtra	2006
NDA 99-6	Faizabad (U.P.)	-	Rajeswari/PT12	Rahuri, Maharashtra	2013
DA 11	Dholi, Bihar	-	WRG65	Warangal, Andhra Pradesh);	-
WB 20	West Bengal	-	ICPL87,	ICRISAT, Hyderabad	1986
JA 3	Khargone, Madhya Pradesh (M.P.)	1979	ICPL151,	ICRISAT, Hyderabad	1989
JA 4	Khargone (M. P.)	1991	ICPL161,	ICRISAT, Hyderabad	-
JKM 7	Khargone (M.P.)	1996	Asha/ ICPL87119	ICRISAT, Hyderabad	1993
JKM 189	Khargone (M.P)	2006	Vamban-1,	Vamban, Tamil Nadu	1993
TJT 501	Khargone (M. P.)	2009	Vamban-2	Vamban, Tamil Nadu	1999

Papilionaceous corolla and partial cleiogamy reported in few cases has been mistaken at some instances to treat these pigeonpea varieties as pure lines. However, pigeonpea varieties with evidential mechanism of cross pollination, as high as 70 per cent (Saxena et al. 1990) are blessed with abundant variability, diversity and heterotic expressions. It would be more appropriate to consider them as populations at equilibrium. Variety like AKT8811 provided such evidence of population derived by mass selection from a bulk segregants from four heterotic crosses, namely, ICPL6 x DA6, ICPL6 x AL57, ICPL 84008 x AL57and

Tamil Nadu Agricultural Universiyu, Coimbatore developed two cultivars, CO3, CO6 through mutations.

Post rainy season (PRS) or pre-*rabi* pigeonpea

In North Plane Eastern Zone pre-*rabi*/post rainy season pigeonpea sowing during first fortnight of September was advocated by RoySharma et al. (1981). In Bihar, PRS pigeonpea suffers severe yield losses due to *Alternaria* leaf blight. Resistant variety, DA11 (Sharad) was one of the preferred option. Other varieties recommended for cultivation were, Bahar, WB20 (105),

AS71-31 and Pusa-9. When the regular *monsoon* crop could not be sown or failed in the event of inadequate or excess soil moisture depending on the rainfall, contingency crop planning for the vacant fields was possible through the concept of PRS pigeonpea in central India. The trials proved that the existing medium duration varieties like Asha (ICPL 87119) and BSMR 736 are useful in this context.

Genetic improvement for enhancing yield potential

Development of short duration pigeonpea

After 1970, the efforts were made to breed varieties for non-conventional cropping patterns emerging with the change due to adoption of short duration varieties of millets and cereals. Centers in North India worked for pigeonpea-wheat rotation and ended with many short duration varieties like Prabhat, AL15, UPAS120, Pusa74, Al201and Manak etc. However, these varieties have tendency of extended maturity with late monsoon rains due to which wheat planting is also delayed. Pusa 992 however, ensures maturity by early November (Masood Ali and Shiv Kumar, 2005).

BARC mutants with improved seed size from T21 *viz*., TT5 and T Vishakha-1(TT6) maturing within 135 to 140 days with good stability for high yield were released around 1985. Extra early genotypes like Prabhat, UPAS120 and others having110 to 125 days maturity with seed index of 6.9 to 7.4 g per 100 seeds were not acceptable to the farmers for no preference for their marketing. Therefore, it was necessary to improve the seed size in this maturity group. Variety TAT 10 was developed from a cross (T8 x T2) involving two mutants of T21. The early types hold promise in upland area of east Madhya Pradesh (Rewa, Satana, Umaria districts), Jharkhand, Bihar and eastern U.P. to escape the sufferings from frost or cool temperature injury in December and early January. The short duration pigeonpea (120-133 days) were found to suit in peninsular and central India under sole cropping and multiple harvesting system, where medium duration varieties suffer due to terminal drought in October-November under mono-cropping on medium shallow soils. T Vishakha-1, TAT10 with indeterminate growth habit and ICPL 87 (Pragati) characterized by determinate bushy growth habit were popular in Gujarat, Maharashtra and Karnataka during 1990s. Later, ICPL87 survived mostly in the adjoining western Maharashtra and south Gujarat for marketing green pods as vegetable in big cities including Mumbai.

Heterosis breeding

Heterosis breeding is considered as modern system rather a conventional breeding. However, be clear that the parental lines for this system are bred through conventional breeding methods although biometrical analyses applied to test heterosis and combining ability may be non-conventional are useful in selection of the parents. Often cross pollinated behavior in pigeonpea could be exploited for hybrid breeding, when stable genetic male sterility (Reddy et al. 1978) was discovered at ICRISAT and heterotic yield advantage to the tune of more than 60 per cent was recorded in various experimental hybrids (Srivastava 1997). Through conventional, Back Cross Method, the male sterility has been diversified in the background of various locally established varieties. These new male sterile lines were useful in the hybrid pigeonpea program intensified with special project financed by ICAR at selected centers in India during 1988 to 1997. ICPH8 (ms Prabhat x ICPL161) was the first GMS based hybrid, released for cultivation in central zone in 1991 (Saxena et al. 1992). It was followed by development of region specific hybrids *viz*., PPH4 (ms Prabhat x ICPL 81) in Punjab; IPH 732 (msT21 x ICPL 87109) named as CoH1 and CoH2 (msCo5 x ICPL 83027) in Tamil Nadu, AKPH4101 (AKms4 x AK 101) and AKPH 2022 (AKms2 x AK22). In spite of yield superiority of the hybrids over respective popular straight varieties (checks), they were not popular due to constraint of large scale seed production. Seed growers could not effectively remove 50% fertile segregates from male sterile parent at flower initiation stage. This labor intensive operation posed a major drawback/hinderace in the success of hybrid breeding. Another major constraint was identified as damage due to pod borer and pod fly with minimum load of chemical pesticide as the pollinator vector is important for hybrid seed setting (Niranjan et al. 1998).

Many interspecific crosses have been attempted by pigeonpea breeders to develop five cytoplasmic male sterility (CMS) systems. Cytopasm in A_1 male sterile line was transferred from *C. sericeus* (Ariyanayagam et al. 1995); A_2 cytoplasm derived from *C. scarabaeoides* (Tikka et al. 1997; Saxena and Kumar 2003); A_3 cytoplasm from *C. volubilis* (Wanjari et al. 2001); A_4 cytoplasm has been derived from *C. cajanifolius* (Saxena et al. 2005) while A_5 from *C. acutifolius* (Mallikarjuna and Saxena 2005). Tikka et al. (1997) developed a stable CMS line cmsGT288 with A_2 cytoplasm, which has been used for the development of early duration hybrid GTH-1

(cmsGT288 x GTR 11) for central zone. Saxena and Kumar (2003) also utilized the same source to develop a hybrid. Medium duration hybrid AKPHM 11303 (Akms11 x AKPR 303) based on A_2 cytoplasm was promising with 25 to 39 per cent standard heterosis (Wanjari and Rathod 2012). Hybrids with A_4 cytoplasm gave 119 per cent of heterosis in early and 52 per cent in medium maturity group (Saxena et al. 2006). Medium duration hybrids, ICPH 2671 and ICPH 2047 based on A_4 cytoplasm are reported to have high heterosis (Saxena et al. 2013, 2014). It is expected that the spread of these hybrids may lead to quantum jump in stagnated productivity.

In view of the successful development of hybrids, thrust was shifted to cytoplasmic male sterility (CMS) where three parental lines *viz*., male sterile (ms) (A) line, maintainer (B line) and a fertility restorer (R line) are essentially required for breeding of fertile hybrid. Deliberate search for cytoplasmic male sterility succeeded in identification of five cytoplasmic sources (A_1 to A_5) of male sterility (Saxena et al. 2009). Two of them *viz.,* A_2 (*C. scarabaeoides*) and A_4 (*C. cjanifolius*) were more useful for development of hybrids. For diversification of hybrids, their parental lines (A, B and R) should be bred for improvement with respect to different traits. In this quest several male sterile and fertility restorer lines have been developed in the national program at IARI, SK Nagar, Akola, IIPR and few other centers, along with an independent program at ICRISAT through conventional approaches like pedigree and back cross breeding.

Ideotype breeding in pigeonpea

The ideal plant type targeted for better yield per unit area/time will vary under different cropping systems where pigeonpea is cultivated. For planting in *pre-monsoon* period in northern states under pigeonpea-wheat rotation, 130-150 days of crop duration is suitable. In central and southern regions, the crop duration need to be restricted to 125 to 135 days for planting in regular *monsoon* season in absence of irrigation. In addition to, short duration, photoperiod insensitive and deep root system as in traditional cultivars, determinate growth habit, short statured with faster growth rate and elevated harvest index combined in a genotype may be a suitable ideotype of pigeonpea for above described situations (Singh et al. 2005).

Under predominant intercropping with cotton, soybean etc. in central and south India the medium to mid-late varieties of 165 to 210 days are grown in such a way that the grand growth period of the companion crop does not occur at same time. In case of pigeonpea-soybean intercropping, the growth of pigeonpea is initially for 90 to 100 days is very much restricted, until the pod development stage of soybean, while it is flourished thereafter to complete the maturity by 165 to 175 days. In case of cotton-pigeonpea intercropping with pigeonpea varieties maturing in 180 to 200 are more suitable, to avoid competition with cotton.

For sole cropping under rainfed condition, early types are suitable in central and south zones where the crop escape terminal drought in October, frost or cool temperature injuries occurring in late December or January. In that case determinate flowering to terminate the crop life within the scheduled period is very desirable. The variety, ICPL87 (Pragati) released for south zone in 1986 was better adopted in central zone particularly in medium shallow soils in the area receiving <450 mm annual rainfall terminating in mid-August.

Breeding for disease resistance

Fusarium wilt, sterility mosaic disease (SMD) and *Phytopthora* blight are major diseases of monsoon planted pigeonpea. Breeding for resistance against these diseases has been more difficult due to existing pathogenic variability. Gupta et al. (1988) reported seven strains while Gaur and Sharma (1989) reported eleven strains causing wilt disease. Reddy et al. (1996) observed five predominant strains of *Fusarium* in India based on the differential host genotypes. Misra and Vishwa Dhar (2003) reported three variants from adjoining area of Kanpur in Uttar Pradesh. For SMD four variants of the isolates have been reported by Vishwa Dhar et al. (2005) while a single strain from Nepal was found to be different from that from Patancheru, India (Chaurasia 1993). ICAR-ICRISAT collaborative research done during 1987-1990 indicated the prevalence of five variants in sterility mosaic agent in pigeonpea growing area in India (Reddy et al. 1993) *Alternaria* leaf spot caused by *Alternaria alternata* and *A. tenuissima* is a minor disease in *kharif* but causes more economic losses in post rainy season (pre-*rabi*) crop planted in August-September.

During 1972 to 2005, a good understanding was developed about management of wilt and sterility mosaic diseases especially through host resistance (Vishwa Dhar et al. 2005). More stable multiple resistance against SMD and wilt are bred in the form

of varieties such as Asha, BSMR 736 and BSMR 853 (Vishwa Dhar and Chaudhary 2001). Germplasm Several varieties have been improved with resistance against individual strains of wilt or SM disease includes BDN1, BDN2, ICP8863 (Maruti), Birsa Arahar-1, TS3 etc against *Fusarium* wilt and Bahar, BSMR175, ICPL 87051 against SMD. Pusa-9 and Sharad (DA11) popular varieties of Bihar and eastern UP are reported to be resistant against SMD and *Alternaria* leaf spot. Lava Kumar et al (2005) reported that many of the wild *Cajanus* species show resistance to all the isolates of the SMD virus, and its inheritance was worked out to be recessive monogenic by Kulkarni (2002). *C. scarabaeoides*, possesses multiple disease resistance (Kulkarni et al. 2003; Upadhyaya 2006) and has been used to introgress resistance against sterility mosaic disease at ICRISAT and on testing the progeny many of the plants were found to be disease-free and were classified as resistant.

Resistance to pod borer and other insect pests

Around 1990-1993, pigeonpea growing areas in central and south zone suffered frequent epidemics of *Helicoverpa* pod borer. It is difficult to breed for host resistance against *Helicoverpa* being a polyphagous pest feeding on tender leaves, buds, flowers, pods and grains on wide range of hosts. However, tolerance was located in a germplasm line ICP1903 at ICRISAT. The selection, ICPL332 named as Abhaya was released in Karnataka State in 1989 which proved worthy in the epidemic years. Wild relatives of pigeonpea are useful sources of resistance against different insect pests. *Cajanus scarabaeoides, C. sericeus, C. acutifolius, C. albicans, Rhynchosia aurea, R. bracteata* and *Flemingia bracteata* are reported to be highly resistant to *H. armigera*. Some of the other wild relatives of pigeonpea also exhibits resistance to pod fly (*Melanagromy zaobtusa*) and pod wasp (*Tanaostigmodes cajaninae*) (Sharma et al. 2003). Advanced generation population from cross involving *C. acutifolius* as the pollen parent has shown resistance to pod borer (Mallikarjuna et al. 2007). Sujana et al (2008) reported *Cajanus scarabaeoides, C. acutifolius, C. sericeus* and *C. albicans* as the outstanding donors for resistance to pod borer.

Breeding for other useful traits

High seed protein lines been developed from *C. albicans, C. sericeus*, and *C. scarabaeoides*. ICPL 87162, developed by crossing *C. cajan* with *C. scarabaeoides* (Reddy et al. 1997) is one such example with protein content ranging from 30 to 34% compared to 23% in general. HPL 2, HPL 7, HPL 40 and HPL 51 are some of the high protein and high seed weight lines derived from wild species (Saxena et al. 1987) at ICRISAT, Hyderabad.

Partially cleistogamous flowers showing very low level of cross-pollination (<1%) were also recovered from another inter-specific cross i.e. *C. cajan* × *C. lineatus* (Saxena et al. 1998). A partially cleistogamous line, which was governed by a single recessive gene (Saxena et al. 1992) developed from the above cross that can be utilized in pigeonpea to obtain pure seeds from genetic stocks.

Challenges ahead

Presently, pigeonpea is being considered as a premier crop for better prices fetched in the market and the non-conventional areas are being brought under its cultivation. For better productivity pre-*monsoon* planting is becoming popular in Maharashtra and Karnataka. The irrigated area in sugarcane belt of Maharashtra is non-conventional for pigeonpea, where it is entering in the crop rotation. Drip irrigation used for cotton, is attracting pigeonpea as a good alternative and remunerative option in black cotton soils in central and southern regions. The new area is likely to come with new problems to be resolved through breeding; because responsive genotype to the changing environment is always a convenient option to the farmers. Restructuring of pigeonpea plant with early maturity, determinate growth habit and reduced height.Thus, conventional breeding has no disadvantage and should continue to resolve challenges in near future. Modern tools are to be judiciously used to exploit wild relatives for introgressing useful genes into suitable genetic backgrounds.

Declaration

The authors declare no conflict of interest.

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