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Pigeon pea Genetic Resources and Its Utilization in India, Current Status and Future Prospects

Review Article

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Abstract

Pigeon pea (*Cajanus cajan* (L.) Millspaugh) is an important grain legume crop of the semi-arid regions and is also recognized as the second most important pulse crop in India. Realizing the significance of genetic resources, large number of germplasm lines have been collected, conserved, characterized and evaluated for various morpho-agronomical traits using the minimal descriptors by the National Bureau of Plant Genetic Resources New Delhi, India. Genetic resources of Pigeon pea have also been screened for resistance to several biotic stresses like *Fusarium* wilt, *Phytophthora* blight and sterility mosaic disease and resistant lines have been identified. A core collection comprising 1290 accessions and mini core set of 146 accessions developed at ICRISAT, India showed wide spectrum of variation for grain yield and its important component traits, which may facilitate their utilization in breeding programmes. Narrow genetic base of cultivated Pigeon pea varieties and yield losses caused by several biotic and abiotic stresses still remain the major concerns. Introduction of useful traits from the wild relatives of Pigeon pea like, *C. platycarpus, C. scarbaeaides, C. acutifolius and C. lineatus* and use of biotechnological tools, wherever necessary, have been suggested to broaden the genetic base of commercial cultivars. Useful variants were also identified using mutation breeding that resulted in the release of five mutant cultivars for commercial cultivation in India. About 65 Pigeon pea varieties have been released in India and 57 selections provided by ICRISAT to various Pigeon pea growing countries for their commercial cultivation. Genomic resources and genome sequence analysis predicted about 48,680 genes which may be exploited for further improvement of Pigeon pea.

Key words: Characterization; Genetic resources; Documentation; Pre- breeding; Utilization

Introduction

Pigeon pea (*Cajanus cajan* (L.) Millspaugh.) is one of the major grain legume crops in the tropical and subtropical regions of the world. India is the primary centre of origin and diversification for pigeon pea [1,2]. It is also cultivated in Kenya, Uganda, Malawi, China, Myanmar and Nepal [3]. It is an important source of protein and vitamin B [4]. Pigeon pea seeds have 20-22% protein and are used as green peas, whole grain or split peas [4]. Its seed husks and leaves are used as nutritious animal feed, while the stem is used as fuel and also for making baskets, thatching, fencing and huts. Pigeon pea fixes nitrogen in the soil and also reduces soil erosion [5]. The species is diploid (2n=2x=22) with a genome size of 858 Mbp [6]. It is a hardy, widely adapted and drought tolerant crop with a large temporal variation (97-299 days) for grain maturity [7]. These traits allow its cultivation in a wide range of environments and different cropping systems. Globally Pigeon pea is cultivated on 4.64 mha with an annual production of 3.43 mt. The average productivity of 780 kg ha^{-1} (http://faostat.fao.org/2010) indicates further need for improving its genetic potential. India is the largest Pigeon pea growing country in the world, accounting for 3.53 mha area with the production of 2.51 mt (http://faostat.fao.org/2010) followed by Myanmar (0.58 mha), Kenya (0.17 mha), Malwai (0.12 mha), Tanzania (0.09 mha), Uganda (0.08 mha) and Nepal (0.03 mha) (http://faostat.fao.org/2010) [8]. The relatively low crop yields may be attributed to a lack of genetically superior varieties, low use of gene bank collections, poor crop husbandry and exposure to several biotic (diseases and insect pests) and abiotic (drought, salinity and water logging) stresses [9]. Plant genetic resources are an invaluable source of genes and gene complexes for yield and several biotic and abiotic factors and provide raw materials for further genetic improvement. Therefore, the collection of Pigeon pea germplasm and its proper characterization and evaluation, conservation and utilization in improvement programmes assume great significance especially in view of climate change.

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Historical Overview

As compared to other Pigeon pea growing countries, the research and development activities in India are extensive with the first scientific Pigeon pea breeding effort initiated by Shaw in 1933 [10], who studied morphological and agronomic traits of 86 elite indigenous Pigeon pea germplasm accessions. Some of the accessions were found to have high level of resistance to *Fusarium* wilt. Identical efforts were also made by [11], who reported some agronomically superior, early and late maturing high yielding lines of Pigeon pea. Considering the high significance of Pigeon pea in India, the Indian Council of Agricultural Research (ICAR) started an All India Co-ordinated Pigeon pea Improvement Project in 1965. Under its umbrella, genetic improvement programmes were started simultaneously at 30 research centres located in various agro-climatic zones of the country [12]. The prime objectives of this programme were to collect Pigeon pea germplasm, identify stable sources of resistance to various diseases and insects and develop high yielding varieties in different maturity groups. Further, plant exploration and collection programme was initiated in a systematic manner with the establishment of a central agency for this purpose i.e. National Bureau of Plant Genetic Resources (NBPGR) Pusa New Delhi, India. During 1960-70, special efforts were made under the collaborative scheme between ICAR and the USDA to collect Pigeon pea germplasm from different parts of the country.

Diversity distribution

The prime areas of variability for Pigeon pea species are in the states of Uttar Pradesh, Madhya Pradesh, Maharashtra, Karnataka, Gujarat, Andhra Pradesh and Bihar. These areas display tremendous variability for both cultivated types and related wild species of primary and secondary gene pools [3]. Shaw et al. [9] distinguished 86 different indigenous collections from all over the country. These reports were followed by many other studies which indicate that considerable variation exists for morphological, reproductive, nutrient content and biotic and abiotic stress tolerance related traits. Seed colour pattern in Pigeon pea can be plain, mottled, speckled, mottled or speckled and ringed. Seed coat colour may be white, cream, orange, light brown, reddish-brown, light grey, grey, purple, dark purple or dark grey. The growth habit varies from erect and compact to semi-spreading and spreading. Flowering can be determinate, semi-determinate or indeterminate. Days to flowering can vary from 55-237 days, days to maturity from 97-299 days, plant height from 39-385 cm, number of primary branches from 2-66, number of secondary branches from 1-145, number of racemes from 6-915. Number of seeds/pod vary from 1.6-7.6, 100-seed weight from 2.8-25.8 g, harvest index from 1.0-63%, shelling ratio from 5.7-87.5% and seed protein content from 12.4-29.5% [7]. Vegetable types also found in tribal areas of Karnataka and Maharashtra and have very long pods upto 7 to 8 seeds/pod, whereas short duration annuals are bushy with synchronous maturity and medium to small pods [13]. Several biochemical markers have been used to detect polymorphism in the genus *Cajanus*. Krishna & Reddy [14] used esterase isozymes to study species affinity between Pigeon pea and some of its wild relatives, revealing the relationships between C. *scarabaeoides*, *C. albicans*, *C. sericeus* and *C. volubilis* and especially between C. *albicans* and *C. scarabaeoides*. Similarly, an analysis of seed albumins and globulins of 11 *Cajanus* species along with cultivated species revealed that *C. cajan* shares homology with *C. cajanifolius* and also with *C. scarabaeoides*, *C. albicans* and *C. s*ericeus [15]. The phylogenetic relationships among 12 species (four genera) were explored by Nadimpalli et al. [16] using RFLP markers. This study concluded that two closely related *Cajanus species* (C. *scarabaeoides* and *C. cajanifolius)* showed a close relationship with each other. C. *albicans*, *C. sericeus* and *C. lineatus* (all of Indian origin) were shown by Ratnaparkhe et al. [17] to be closer to *C. cajan* than to *C. acutifolius*, *C. grandifolius* and *C. reticulata* (Australian species), while Parani et al. [18] suggested that *C. scarabaeoides* is more closely related to *C. cajan* than is *C. cajanifolius*. The merger of the genera *Cajanus* and *Atylosia* is supported by their common chromosome number [19-21]. According to Pundir & Singh [22], *C. cajanifolius* is the likely progenitor species of *C. cajan* as their interspecific hybrid showed high pollen fertility and seed set. Upadhyaya et al. [23] were able to separate wild and cultivated types in two classes based on SSR genotyping. AFLP analysis has however suggested that cultivated Pigeon pea is not genetically diverse [24], a conclusion supported by the SSR-based analysis conducted by Odeny et al. [25] who showed that the cultivated species was less polymorphic than the wild relatives.

Germplasm exploration and collection

The areas surveyed under the National Agricultural Technology Project (NATP) from 1999 to 2005 included central and eastern Rajasthan, eastern Gujarat, lower hills and eastern part of Uttar Pradesh and adjoining Bihar, central Bihar, eastern Madhya Pradesh, Orissa, Maharashtra, Andhra Pradesh, southern Karnataka, Tamil Nadu and adjoining parts of Kerala. Several explorations were undertaken under the collaborative research project between the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad and NBPGR. These resulted in a collection of 5,244 cultivated germplasm accessions. Of these, 5,136 were collected from India and 108 from 16 other Pigeon pea growing countries. Later on, many explorations were also conducted within India under the PL480 scheme from Andhra Pradesh, Madhya Pradesh, Tamil Nadu and Orissa. NBPGR has also in its collection about 288 accessions of wild and related species such as *Rhynchosia, Cajanus trinervius, C. lineatus, C. albicans and C. scarabaeoides* from Western Ghats of Maharashtra India. The Bureau in collaboration with ICRISAT collected another 420 Pigeon pea accessions from various parts of Maharashtra and Rajasthan.

Germplasm introduction and conservation

The National Bureau of Plant Genetic Resources has introduced Pigeon pea germplasm from different countries. Since the inception of NBPGR in 1976, a total of 4432 samples have been introduced from more than 25 countries including some wild species from France and Australia. Some trait specific germplasm has also been introduced for short plant height, early maturity, bold seededness and resistance to pod borer, stem blight and *Fusarium* wilt. So far, a total of 11,221 accessions are being conserved in the National Gene Bank of NBPGR for long term storage as base collections. The Bureau has also introduced some promising accessions of cultivated Pigeon pea including an early type with high yields from Australia (EC284065), early with medium type selections from Malawi (EC215296) and

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landrace with desirable agronomic traits from Kenya (EC577961-79). At ICRISAT, about 9759 accessions were acquired mainly by donations from various institutes of different countries and 3,873 accessions only through 99 Pigeon pea germplasm collecting missions in 33 countries [26]. The ICRISAT global gene bank holds 13,632 accessions from 74 countries (www.icrisat.org/genebank). of these, 13,077 accessions belong to the primary gene pool and 555 accessions of wild relatives, which represent six genera and 57 species [27]. For conservation, accessions are assigned a national identity number *i.e.* indigenous collection number, dried to seed moisture of around 5±2% and stored at -18 °C. The accessions meeting international standards *i.e.* seed viability of more than 85% and quantity of about 4000 seeds transferred in the long-term storage of National Gene Bank. (http://www.nbpgr.ernet.in) [28].

Evaluation and maintenance

The International Crops Research Institute for Semi-Arid Tropics and National Bureau of Plant Genetic Resources have conducted studies on systematic characterization and evaluation of Pigeon pea germplasm either independently or in collaboration. All Pigeon pea germplasm accessions have been evaluated using Pigeon pea descriptors [29]. A majority of Pigeon pea germplasm accessions have been evaluated for various morpho-agronomic traits and a multi-disciplinary approach has also been followed to evaluate germplasm for various biotic and abiotic stresses. The maturity groups are broadly classified into 4 classes, viz, extra early, early, medium and late maturity types. Germplasm accessions from the central, peninsular and northern plains exhibit good variability for earliness. Perennial Pigeon pea varieties viz; JP-6 and Richa 2000 have also been reported from India [30]. Majumder et al. [31] characterized 43 Pigeon pea commercial varieties for 14 traits under distinctness, uniformity and stability (DUS) testing at Indian Institute of Pulses Research, Kanpur India regularly for three years. Anthocyanin pigmentation of the hypocotyl is the most stable, uniform and distinguishable trait to distinguish Pigeon pea varieties at seedling stage. Likewise, other traits like growth habit, stem colour, petal colour and pubescence on lower surface of leaf are the most stable traits for the identification of Pigeon pea varieties at real field levels.

Screening of germplasm against various biotic and abiotic stresses at ICRISAT and in other Indian crop based institutes have led to the identification of accessions tolerant to major diseases such as wilt (*Fusarium udum*) and *Phytophthora* blight (*Phytophthora drechsleri*) as well as important insect pests viz, pod borers (*Helicoverpa armigera and Maruca vitrata*) and pod fly (*Melanagromyza obtuse)* presented in Table 1. Among major diseases, over 210 pathogens have been reported in Pigeon pea [32-34]. Pathogenic variability and physiological races of *Fusarium udum* have been reported from Uttar Pradesh [35]. Sivaramakrishnan et al. [36] characterized isolates of *Fusarium udum* using random amplified polymorphic DNAs (RAPD) and amplified fragment length polymorphism (AFLP) techniques and the results revealed variability in the isolates of *Fusarium udum.* Information on physiological specialization of sterility mosaic is limited in literature [33]. Kooner & Cheema [37] also evaluated 89 Pigeon pea accessions consecutively for four years and identified sources of resistance to pod borers. Evaluation of wild species had also resulted in the identification of genes for resistance to blight and mosaic, high protein content, tolerance to soil salinity and drought [38-40] and root knot nematode resistance [41]. Germplasm lines from various parts of India have contributed dwarfing genes with recessive mode of gene action [42]. Sharma & Green [43] summarized that the important agronomic traits are controlled by genes with additive effects but non-additive effects were also detected for grain yield, plant height and protein content. Saxena et al. [44] concluded that inheritance of yield and other associated characters is confounded with pleiotropic effects of genes influencing phenology of Pigeon pea.

Frankel & Brown [45] suggested that greater use of genetic resources in crop improvement is possible if a small collection representing most of the diversity is made available to researchers. Frankel [46] coined the term "core collection" for this representative variability from the entire collection. A core collection contains

Table 1: List of some promising accessions identified for resistance to major diseases and insect-pests.

Sr. No.	Disease/Pest	Accession
1.	Wilt	ICP4769 (IC306520), ICP7118, (IC306497), ICP7182, ICP9168, ICP10958, ICP11299, ICP9145, Birsa Arhar, Pragati (IC306505), Maruti (ICP8863), NP(WR) 15, Asha (ICPL87119)
2.	*Phytophthora* stem blight	METH12, UC2515/2, UC796/1, UC2113/1, UC2568/1, Pant A83-14, Pant A3, ICPL161, Comp 1ESR6, ICP4726-8, ICP113 (IC306508), ICP580 (IC306495
3.	Sterility mosaic	Sehore367, DPPA84-61-3, DPPA84-8-3, ICP786 (IC306500),ICP8327, DA12, DA13, DA51, DA11, MA97, Rampur, Bahar, Bageshwari, Pant A3, Pant A104, Pant A8505
4.	Pod borer	ICP332 (IC306517), ICP1903 (IC306514), ICPL84060, ICPL84660, ICPX77303, ICPL87088, ICPL87089
5.	Pod fly	MA2, MA3, Gwalior 3, PICX82062, ICP332 (IC306517), ICP11964, ICP1053 (IC306509), ICP1053E,
6.	*Fusarium* wilt, sterility mosaic and *Phytophthora* stem blight resistance	ICP7035 (IC306496), ICP1348, BSMR1, ICP7336 (IC306499), ICP8862, Purple 1, ICP74360
7.	*Fusarium* wilt and sterility mosaic	ICPL87119, ICP88046, ICPL88047, ICPL87104, ICP8860, ICPL83027, ICPL83024, ICP85047.
8.	*Fusarium* wilt and nematode resistance	ICPL89044, ICP8094, ICPL86005, ICPL88023, ICPL88025, Pusa 23, GAUT87-2
9.	*M. javanica*	AK8811, BSMR203, DA11, H82-1, 86-1, ICPH8, ICP87 (IC306505), ICP227 (IC306515), 331M, ICP87104, ICP88026, ICP88040, IPH732, MTH9, Type 9, UG218
10.	Pod fly and pod borer	ICP11964, ICP10531

Source: Singh *et al*., 2009

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approximately 10% accessions from the entire collection that captures most of the available diversity in the species (BROWN 1989). The Pigeon pea core collection, comprising of 1290 accessions sampled from 12,153 germplasm accessions from 53 countries, was developed at ICRISAT [47]. Subsequently, a mini core collection, comprising 146 accessions, was constituted by evaluating a collection of 1290 Pigeon pea accessions for important morpho-agronomic, biotic and abiotic traits [48]. However, allelic diversity data of a composite collection of Pigeon pea, a reference set of 300 diverse germplasm was selected representing diversity of the entire collections validated with DNA (Simple Sequence Repeats) markers for the trait of interest to identify accessions for their enhanced and effective utilization in Pigeon pea breeding and genomics as well [49].

Enhancement of Pigeon pea germplasm through wide crosses

Moose & Mumm [50] suggested that genetic variation can be generated from segregating populations, use of unadapted exotic germplasm, transgenic events and distant interspecific crosses for widening the genetic base of commercial cultivars. In Pigeon pea, existing variability among cultivated varieties has been exploited to reach to a desirable level of productivity today. Wild species of Pigeon pea have contributed traits for high protein content, cleistogamy, dwarfing habit and cytoplasmic male sterility [51]. Five unique cytoplasmic male sterile (CMS) systems have been derived from wild *Cajanus* species [52-56]. Four wild relatives of Pigeon pea have been successfully utilized in developing cytoplasmic genetic male sterile (CGMS) lines [57-60].

Rigorous efforts have also been made to transfer resistance to *Helicoverpa armigera* from *Cajanus scarabaeoides*, *C. acutifolius* and *C. platycarpus* to the cultivated gene pool for widening the genetic base of Pigeon pea. Saxena et al. [61] reported a partially cleistogamous line which showed less than one percent cross pollination. They purified breeding population of a cross between *C. cajan x C. lineatus* and registered three (ICPL 87018, ICPL87047 and ICPL 87154) germplasm lines with this trait. Likewise, high protein content lines ICPL 87162 and ICPL 88075 were developed from the cross of *C. cajan* x *C. scarabaeoides* [62]. Other important traits found in wild species are root knot nematode resistance [63] and salinity resistance [64]. Information is also available on the transfer of pod borer resistance from *Cajanus scarabaeoides and platycarpus* species [65,66]. Mallikarjuna et al. [67] and Mallikarjuna & Moss [68] utilized *Cajanus platycarpus* with the help of hormone aided pollinations and embryo rescue approaches to transfer *Phytophthora* blight resistance and that was further confirmed by Reddy et al. [69].

Induced variation through mutation

Mutagenesis has produced eight commercial Pigeon pea varieties. Ethyl methane sulphonate (EMS) treatment (0.6% solution) was found effective for producing high-yielding variety CO3, while 16 kr of gamma rays resulted in the development of another high yielding variety CO5. Using fast neutrons, two other high performing varieties, TT 5 and TT 6, were developed for rainfed areas of central zone in India [70]. The cultivar TT 6 has 25% larger seeds and higher yield than its parental cultivar T2. Another important Pigeon pea variety TAT10 has been developed by mating two mutant inbreds derived from fast neutrons. TAT10 has high yielding ability and it matures one month earlier than the control [71]. Induced mutation studies in Pigeon pea have been mostly targeted to detect effective doses of several mutagens and to study their influence on inducing genetic variation for agronomically desirable traits [72]. Potdukhe & Narkhede [73] studied the effect of various mutagens (gamma rays, ethyl methane sulphonate and sodium azide) on survival of plants in different generations and reported that the reduction in survival was more pronounced in M_1 generation as compared to M_2 and M_3 generations. Chintapalli et al. [74] investigated somaclonal variation from regenerated cotyledon explants and they observed a wide spectrum of variation in floral morphology, seed size, seed colour and plant height. Line ICPL 99073 has been rated as superior to the control in respect of seed size, colour and plant height [75].

Registration of Pigeon pea germplasm and utilization

Germplasm registration is considered an essential component for systematic and effective utilization in Pigeon pea improvement. The National Bureau of Plant Genetic Resources, India has been designated as nodal institute for registering of crop germplasm. Some Pigeon pea germplasm lines have been registered for unique traits by various crop based institutes and are presented in Table 2. In fact Pigeon pea genetic improvement began quite early in India in the 1920s [76]. Some varieties have been developed through hybridization followed by selection and several cultivars grown are landraces or selections from the traditional extant cultivars [77]. Several commercial varieties like UPAS120, BR65, Gwalior 3, Hy3C, C11, B517 and BDN10 have been developed through direct selection from landraces. An exotic introduction, Brazil 1-1 has proved as a good source of earliness in the development of early maturing varieties namely, Mukta, Sharda and Pusa Ageti. Some traits have also been introduced from its wild relatives to exploit the hybrid vigour. A genetic male sterile (GMS) line carrying gene ms2 was used for the production of first Pigeon pea hybrid (ICPH8) in grain legumes. Some of the high yielding varieties of Pigeon pea developed in India are presented in Table 3. ICRISAT has also released 57 Pigeon pea selections based on improved performance in various countries for their commercial cultivation including Asia (38), Africa (13), Australia (3) and USA (3).

Genomic resources

DNA markers are important tools to study the geographical distribution, cultivar identification, genetic diversity and linkage analysis, gene tagging, marker assisted selection and association mapping. Pigeon pea genomic initiative has focussed mainly on the development of robust set of molecular markers including microsatellites, single nucleotide polymorphisms (SNPs) and diversity array technology markers [78]. Dubey et al. [79] developed large number of microsatellite markers from BAC-end sequences and microsatellite enriched libraries. They have generated about 496,705 sequence reads and 10,000 Sanger ESTs from *Fusarium* wilt (FW) and sterility mosaic (SM) samples that resulted into 4,557 unigenes. Similarly, Ganesha et al. [80] developed the intra-specific genetic maps and identified QTLs for SMD resistance. Yang et al. [81] used DArT analysis for cultivar identification and differentiation between

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Table 2: Some promising Pigeon pea germplasm registered for unique traits.

National identity	Pedigree	Unique features
IC296750	3383A x Acc 3072) x Acc 3072	GMS mutant
IC296772	*C. scarabaeoides* x *C. cajan*	First stable cytoplasmic genetic male sterile line
IC296794	Segregating material from ICRISAT	Long duration and multiple disease resistance
IC296804	(*C. scarabaeoides* x *C. cajan*) x GT100	Stable cytoplasmic genetic male sterile line
IC296805	SKNP-9902	Fertility restorer line of stable CMS line GT288A
IC296802	SKNP-99813	Fertility restorer line of stable CGMS line, GT288A
IC296807	*C. scarabaeoides* x *C. cajan*, back-crossing with ICPL87119	Fertility restorer line of stable CGMS line, GT288A
IC296808	*C. scarabaeoides* x *C. cajan*, back-crossing with GUT88-9	Fertility restorer line of stable CGMS line, GT288A
IC296809	*C. scarabaeoides* x *C. cajan*, back-crossing with QMS-2	Fertility restorer line of stable CGMS line, GT288A
IC296582	(*C. scarabaeoides* x *C. cajan*) x F2 x Pusa33	Indeterminate stable CGMS line and early maturity
IC296584	(*C. scarabaeoides* x *C. cajan*) x F2 x Pusa33	Determinate stable CGMS line and early maturity
IC296588	ICP-9260	Indeterminate, restorer line of GCMS, GT 288A
IC296589	GT-100	Determinate, restorer line of GCMS GT, 288A
IC296624	CMS67A x ICPL84023	CMS in early maturity and multiple disease resistance
IC296622	*C.sericeus* x ICPL850) x Mutant	CMS with cytoplasm of *Cajanus sericeus*
IC537352	Mutant in ICPL88039	Extra early (100 days) and dwarf type (1m)
IC548343	GT288Ax UPAS120	Thermo-insensitive
IC555902	*C. scarabaeoides* x *C. cajan*, F1-F2 x ICPL8	Stable CGMS line with red medium seeded
IC555904	*C. scarabaeoides* x *C. cajan*, F1-F2 x BDN2	Stable CGMS line with creamy white bold seeded
IC555909	*C. scarabaeoides* x *C. cajan*, F1-F2xICPL84	Stable CGMS line with red medium seeded
IC555911	*C. scarabaeoides* x *C. cajan* x ICPL87	Stable CGMS line, early in maturity (148 days)
IC557430	CMS288A x H28B	Late maturing (255 days) and resistant to sterility mosaic

Source : (http://www.nbpgr.ernet.in)

Table 3: List of some important Pigeon pea released varieties and their salient features.

Name of variety	Pedigree	Area of adoption	Salient features
NP (WR)	selection	North eastern plain zone and central zone	Wilt resistant and late maturity (275 days), seed yield 20-25q/ha
Pusa Ageti	Brazil-1 x NP69	Throughout country	Dwarf, compact, determinate type, seed yield 12-15 q /ha
Sharda	Brazil-1 x NP15	Central zone	Medium tall indeterminate type, seed yield 15-18 q /ha
Mukta	Brazil-1 x NP15	Northern zone	Maturity 180-200 days, resistant to wilt, seed yield 15-18 q/ha
Pusa 74	Khargone 2 x Pusa Ageti	Central India	Medium tall semi determinate, seed yield 18-20 q /ha
Pusa 84	Pusa Ageti x T21	North western zone	Medium tall indeterminate type, seed yield 20-25 q /ha
Pusa 33	C11 x UPAS 120	North west and central zone	Tall, erect, early maturity (130-140 days), seed yield 20-25 q /ha
Pusa 85	No. 148 x UPAS 120	North west region	Tall, maturity (150 days), bold seeded, seed yield 20-25 q/ha
Pusa 855	Mutant of T21	North west region	Medium tall, maturity (140-160days), seed yield 20-25 q/ha
Pusa 9	UPAS 130 x 3673	North eastern region for pre- winter	Tall, erect, resistant to *Alternaria* leaf blight, seed yield 25-30 q/ha
Pusa 992	selection	North western plain zone	Medium tall, bold seed, maturity (140-145 days),seed yield16q /ha
Pusa 991	GL81 x ICPL 383	Central zone	Medium tall, maturity (140-142 days), seed yield 16-18 q /ha
Pusa 2001	No- 148 x UPAS 120	Central zone	Medium tall, maturity (140-150 days), seed yield 18-20 q /ha
Azad	Bahar x KPBA 80-1	North zone	Medium tall, maturity (140-145 days) seed yield 18-20 q/ha
CO6	Mutant of SA-1	Central zone	Dwarf type, medium seed size, seed yield, 15-18 q/ha
ICPL 87119	C11 x ICPL6	North western plain zone	Tall, indeterminate growth habit, maturity (145-150 days), seed yield 19-20 q/ha
T-15-15	Selection from landrace	North plain zone	Indeterminate growth habit, maturity (150-155 days), seed yield 20-22 q/ha
CO5	Mutant from CO-1	Central zone	Determinate growth habit, medium seed size, seed yield 20-22 q/ha
Manak	T-21 x UPAS 120	North western plain zone	Tall, maturity (150-152 days), seed yield 20-22 q/ha

Source: Singh *et al*., 2006; Singh *et al*., 2009

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regions and place of origins. They observed morphological variation in cultivated germplasm was much higher than that at molecular level and the wild related species revealed substantial molecular diversity than that observed at morphological level. Varshney et al. [6] have published the draft sequence of Pigeon pea and predicted 48,680 genes and their potential role in unravelling drought tolerance, domestication of Pigeon pea and the evolution of its ancestors [82].

Future Perspectives

Based on current knowledge, the following issues need specified attention in future research with respect to genetic and genomic resources of Pigeon pea.

1. The exploration and collection process of Pigeon pea germplasm including wild relatives should continue and must be given top priority for those areas that are yet to be explored thoroughly like, the Eastern Ghats covering Tamil Nadu and Orissa and North-Eastern region of India.
2. Fundamental genetic studies on the heritable components of desirable agronomic traits should be given emphasis for their effective utilization in breeding programmes.
3. Pre-breeding and genetic enhancement efforts should be taken up on priority basis for broadening the genetic base and introduction of useful biotic (pod borer, *Fusarium* wilt, sterility mosaic disease and *Phytophthora* blight), abiotic (drought, soil salinity and water logging) and morpho-agronomic traits (earliness, dwarfness) from secondary and tertiary gene pools.
4. Special efforts need to be made for screening of germplasm for high protein content and their response to major biotic and abiotic stresses to identify desirable donors for future breeding programmes.
5. Development of genomic resources and genome-wide markers for opening up of new avenues for molecular marker–assisted gene intorgression and breeding.

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