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REVIEW ARTICLE

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Origin of early maturing pigeonpea germplasm and its impact on adaptation and cropping systems

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Abstract

Pigeonpea breeding activities started about a century ago and for decades only late maturing cultivars dominated the global cultivation. Historically, no early maturing cultivar was available for a very long time and breeding of such varieties started in the third quarter of 20th century but at a low key. From these efforts, some pigeonpea varieties maturing in 90–150 days were bred. Information gathered from various sources revealed that the first few early maturing genotypes originated through spontaneous mutations in the late maturing field-grown landraces. In other cases, transgressive segregation and induced mutations also produced early maturing varieties. At present, the high yielding early maturing cultivars are contributing significantly towards widening the adaption barriers and in the diversification of some age-old cropping systems. In this paper, the authors, besides discussing the importance of early maturing cultivars in present agricultural systems, also summarize information related to the origin of primary sources of earliness.

KEYWORDS

Cajanus cajan, early maturity, mutation, transgressive segregation

1 | INTRODUCTION

Earliness in crop plants fascinates equally to both researchers and farmers. Pigeonpea (*Cajanus cajan* [L.] Millspaugh), also known as red gram, is an important pulse crop of tropical and subtropical regions of Asia, Africa, and the Caribbean. In most areas, its late maturing (6–9 months) varieties and landraces are in cultivation for centuries. Such cultivars constitute a major component of subsistence agriculture involving intercropping or mixed cropping with different short-aged cereals, legumes or oil seed crops (Saxena, Choudhary, Saxena, & Varshney, 2018). For a long time, the domination of late maturing pigeonpea cultivars in rain-fed agriculture was total and the early maturing genotypes were non-existent.

Information related to the origin of early maturing pigeonpea germplasm is not properly documented in literature; but it seems that earliness in this crop was first discovered around middle of the 20th century as a natural mutant in a farmer's field. This development triggered agronomy and breeding research to assess the potential role of the new (early maturing) genotypes in agriculture. The organized breeding programmes to develop high yielding early maturing cultivars were launched in the third quarter of the 20th century. Since then, dozens of early maturing cultivars have been bred in different parts of the world. In this paper, an effort has been made to throw some light on the evolution of early maturing pigeonpea genotypes through back-tracking the literature. Besides this, the authors also discuss the utility and impact of early maturing pigeonpea cultivars in the context of various agricultural systems.

2 | FLOWERING VERSUS MATURITY

So far, there is no information on the existence or length of the juvenile phase in pigeonpea. However, it is evident that the process of floral bud initiation in pigeonpea plants starts when they enter in the short photoperiod regime. The formation of floral buds and subsequent opening of flowers are influenced by both temperature and photoperiod (Turnbull, Whiteman, & Byth, 1980; Wallace, Yourstone, Masaya, & Zobel, 1993). In Kenya, Silim, Gwata, Coeb, and Omanga (2007) demonstrated that the flower initiation in pigeonpea was delayed when the day length was extended beyond 13 hr. They also reported that the optimum mean temperature for flowering in pigeonpea was 24.7°C for extra-early, 23.1°C for early, 22.2°C for medium and 18.3°C for late maturing genotypes.

Pigeonpea germplasm is blessed with a vast genetic variability for flowering (<50 to >160 days) and maturity (85–270 days). Broadly, the genetic materials maturing up to 120–160 days are considered early; and within this group, three popular maturity groups—extra early, early and mid-early are recognized (Table 1). However, for the sake of greater precision, breeders created five classes within the broad early maturity group; and these were evolved over the time. The latest group being 'super early', which flowers and matures, respectively, in 45 and <90 days. Thus, in pigeonpea, at present 12 breeders' maturity groups are in existence (Green et al., 1981; Saxena, 2008; Srivastava et al., 2012). Since this classification was done at Patancheru (17°N), the flowering and maturity of the reference genotypes may change slightly at other latitudes, but their relative rankings are likely to remain more or less the same.

Interestingly, the pigeonpea breeders working for a long time on this crop realized that in pigeonpea the number of days taken from sowing to maturing did not always give the correct information about their maturity. This happened due to large canopy of the plants and asynchrony in pod maturity. These two factors always made it difficult to record the maturity data with precision. Therefore, for all practical purposes, data on days to 50% flowering (i.e. when about 50% of the plants under observation have at least one open flower) were considered as better indicator of maturity in pigeonpea breeding research (Green et al., 1981). It was also observed that within the super early group the determinate genotypes generally flowered 3–5 days ahead of non-determinates and produced small biomass and yield, and therefore required high density sowings for economical yields. Vales et al. (2012) reported that super early group did not perform well at lower latitudes, but at higher latitudes/altitudes they produced 1,000–1,200 kg/ha grain in around 100 days. At present, a pigeonpea improvement programme is in progress at ICRISAT to increase their 100-seed mass from 6 to 10 g. This will enhance their acceptability both as dry grain (for preparing marketable decorticated splits) and off-season fresh vegetable.

Srivastava et al. (2012) observed that within a set of super early inbred lines, which flowered more or less at the same time, significant variation was present for the time taken from flowering to maturity. The re-examination of this data set revealed that the inbred lines could be discriminated clearly into two groups (Table 2). The first group involved those which, on the average, took 31 days from flowering to maturity; while in the second group, this period was extended by over two weeks to 48.6 days. Such differences may appear due to the presence of different genetic regulatory mechanisms which control photoperiod reaction (Y. S. Chauhan; pers. Comm.). Such genes induce indeterminateness in pigeonpea plants and extend their reproductive phase, resulting in significant delays in pod setting and maturity. Pazhamala et al. (2016) using an RNA sequence also revealed the presence of some differentially expressed genes in pigeonpea, and these genes remain functional only during the period of flowering to pod setting. The presence of such genes in a random population will generate significant genetic variability for the time taken from flowering to pod maturity. It is possible that the selection of individual plants with pods maturing earlier than the rest (Table 2, Type 1 progenies) may help in developing pigeonpea cultivars with synchronous maturity.

3 | ORIGIN OF EARLY MATURING GERMPLASM

Various taxonomical, cytological and genomics evidences related to the origin of pigeonpea have confirmed that the cultivated form of pigeonpea originated in central India from a wild species known as *Cajanus cajanifolius* through various natural mutational and selection events (Pundir & Singh, 1985; van der Maesen, 1980; Varshney et al., 2017). This wild species is non-determinate and photosensitive which flowers in about 120 days and matures in 170–180 days (Remanandan, Sastry, & Mengesha, 1988). The data available from ICRISAT Gene Bank also revealed that the landraces present around the centre of origin have flowering/maturity durations more or less similar to that of *C. cajanifolius*. These late maturing landraces spread in all the directions and their cultivation continued for centuries until around the middle of 20th century, when breeding of early maturity cultivars commenced in India.

Natural gene flow from the wild relatives to cultivated species is considered an important channel for creating new genetic variability (Darwin, 1859). A perusal of flowering and hybridization record of the wild relatives of pigeonpea revealed that with the exception of *C. platycarpus*, none of the wild relatives of pigeonpea had early maturing accessions (Remanandan et al., 1988).

TABLE 1 Variation for flowering time within early maturity group in pigeonpea

Popular group	Breeders' group	Days to flower	Reference cultivar
Super early	00	<50	MN 5
Extra early	0	50–60	ICPL 88039
	I	61–65	Prabhat
Early	II	66–70	UPAS 120
	III	71–80	T- 21

Source. Vales et al. (2012).

TABLE 2 Genotypic differences for seed filling and maturation in six extra early maturing inbred lines

Genotype	Time (days) flower	mature	Difference	Seeds/pod	100-seed wt (g)
Type I progenies					
4–8	54	82	28	3.7	5.9
5–11	56	89	33	3.7	6.7
9–1	50	82	32	3.6	6.8
Mean	53.3	84.3	31.0	3.67	6.47
Type II progenies					
4–1	51	100	49	2.9	8.0
8–13	50	100	50	3.6	8.3
9–6	50	100	47	3.9	6.2
Mean	50.3	100.0	48.6	3.47	7.50

Source. Srivastava et al. (2012).

This wild species cannot be crossed to the cultivated types due to various hybridization and post-zygotic barriers (Dundas, 1984; Mallikarjuna & Moss, 1995; Pundir & Singh, 1985). Based on these two observations, it can be inferred that, in the past, there was no possibility of any direct flow of early maturity gene(s) from any wild species to the cultivated type. Hence, it can be assumed that for the emergence of new variability with respect to earliness, there may be only two possible avenues—mutation or transgressive segregation. The authors, in the following text, examine the possibilities of such events using a thorough literature search.

4 | EARLINESS THROUGH SPONTANEOUS MUTATIONS

Role of spontaneous mutations in the evolution of species is well documented (Darwin, 1859) and understood; the frequency of useful mutations, however, is low. In case of pigeonpea, within a field-grown crop of late maturing cultivar, any early flowering odd plant (mutant) can be detected easily. Ramanujam and Singh (1981) stated that from 1920 onwards, some early flowering individual plants were observed in pigeonpea fields from time to time; but these did not receive any attention from breeders because during that era only late maturing types were considered suitable for cultivation.

It was in 1953, when within a late maturing landrace grown in a farmer's field in Gorakhpur district of Uttar Pradesh (India), an early maturing mutant was identified and preserved as new germplasm. This spontaneous mutant, designated as 'T-1', was used in hybridization with a late maturing genotype 'T-190' and it led to the development of the first early maturing cultivar 'T-21' at Kanpur in 1961 (Pathak & Singh, 1961). At about the same time, another early maturing line Brazil 1-1 was also crossed to 'T-190' at Pusa and cv. 'Pusa Ageti' was developed. These two new cultivars matured in 150–160 days, about 100–120 days ahead of the conventional late maturing types. However, due to its determinate and compact growth habit and high pod borer damage, 'Pusa Ageti' was not accepted by farmers. On the other hand, 'T-21', being a non-determinate type with spreading growth habit, was adopted for cultivation in rotation with wheat (Ramanujam and Singh, 1981). Soon, it was observed that under high moisture situations, the maturity of 'T-21' was extended and it resulted in significant delays in the sowing of the following wheat crop. At this point, a pressing need was felt to breed pigeonpea varieties maturing earlier than 'T-21' and to achieve this, breeding programmes were launched at a few research centres.

The first extra early maturing (120–130 days) variety 'Co-1' was developed in 1970 from a spontaneously mutation that occurred within a late maturing local landrace grown at Perambalur in Tamil Nadu (Veeraswamy & Rathnaswamy, 1972). At the same time, another early maturing variety 'Prabhat' was also bred at Kanpur from the selection of a spontaneous mutation that originated from cv. 'T-21' (Lal & Sinha, 1972). In 1974, the most popular early maturing high yielding variety 'UPAS 120' was developed at Pantnagar University from a spontaneous mutant found in a germplasm line 'P-4758' (Singh, Gupta, & Singh, 1974). Later, three extra early maturing cultivars 'Pant A-1', 'Pant A-2' and 'Pant A-3' were also bred at Pantnagar through the selection of spontaneous mutants for earliness within the population of 'UPAS 120' (Anonymous, 1976). Subsequently, a few more extra early maturing cultivars including 'Co-2' from 'PB-4278', 'Hy 2' from 'PI 4628', 'Hy 4' from 'PI 4839', 'Hy 5' from 'PI 3701', 'Co-4' from 'S-80', 'AL-15' from '8-9', 'Pusa-855' from 'T-21', 'Pusa-992' from 'ICPL 90306', 'AKP-1' from 'ICPL 87101' and 'CORG (RG)-7' from 'PB-9825' were also developed through the selection of spontaneous mutants (Table 3).

Some extra early maturing lines such as '3D 8111' and '3D 8113' were also bred at the International Institute of Tropical Agriculture (IITA), Nigeria. Their parental materials originated from a late maturing germplasm in Puerto Rico and it reached IITA through Uganda (Rachie et al., 1975).

5 | EARLINESS THROUGH INDUCED MUTATIONS

Various physical and chemical mutagens are known to create novel heritable variations in crop plants. In pigeonpea, there are numerous

TABLE 3 Early maturing pigeonpea varieties developed through selection of natural and induced mutations

Year	Variety	Source
Natural mutants		
1953	T-1	Landrace
1970	Co-1	Perambalur
1972	Prabhat	T-21
1973	3D 8111	UC 5543-1
1973	3D 8127	UC 1381
1973	3D 8104	UC 5103
1974	UPAS 120	P 4758
1976	Pant A-1, -2, -3	UPAS 120
1977	Co-2	No. 4278
1981	Co-4	S-80
1982	AL 15	P 8-9
1993	Pusa 855	T- 21
1999	APK 1	87101
2002	Pusa 992	90306
2004	Co (RG) 7	PB 9825
Induced mutants		
1977	Co-3	Co-1
1985	Co-5	Co-1
1984	TAT- 5	T-21
1993	Pusa 855	T-21
1993	Co 6	SA-1
1976	Vishakha 1 (TT 6)	T-21

reports where early flowering mutants have been identified following various mutagen treatments. But most of them were found unproductive due to various side effects associated with the treatments. The mutagens such as EMS @ 0.6%, fast neutrons and 16 Kr of gamma rays were effective in creating a useful genetic variation for earliness in pigeonpea (Pawar, Thakre, Reddy, & Bhatia, 1990). Nevertheless, six popular pigeonpea cultivars also originated through mutagenesis (Table 3).

6 | EARLINESS THROUGH TRANSGRESSIVE SEGREGATION

Transgressive (extreme) segregation is a natural breeding phenomenon where some of the recombinants out-perform both the parents with respect to any specific trait. Such results could be in either a positive or negative direction. In most cases, such transgressed products are created when two parents possessing different alleles are crossed; and in the segregating population some unique recombinants emerge. Such transgressive genotypes could arise due to (a) additive effects—combining different beneficial alleles from the two parents; (b) epistasis—genes from one parent interacting with non-homologous loci from the other parent and give additional positive results; or (c) complementation—a defective gene from one parent is compensated by its functional homologue from the other parent; (d) chromosomal rearrangements, mobilization of transposable elements; or (e) DNA methylation (Liu & Wendel, 2000; Michalak, 2009; Rieseberg, Archer, & Wayne, 1999).

In pigeonpea, Srivastava et al. (2012) demonstrated the presence of transgressive segregation for extreme early (super early) maturing types (Table 4) within the segregating populations of crosses involving early flowering parents. These "super early" selections flowered significantly earlier than either of the parents. One of the super early non-determinate inbred lines had significantly high grain yield with 34% advantage over the control cv. 'ICPL 88039'. In the present study, the exact reason behind this genetic phenomenon was not determined. It may, however, be possible that additive effects, the most common factors associated with transgressive segregation, may have played a role in the emergence of super early genotypes. These super early inbred lines are the earliest maturing genotypes ever reported in genus *Cajanus*.

TABLE 4 Super early pigeonpea genotypes bred through transgressive segregation

Parent 1		Parent 2		Mid-parent value (d)	Transgressive segregants	
Name	Flowering (d)	Name	Flowering(d)		Name	Flowering (d)
Pant A-2	61	ICP 7035	130	95.5	MN 1	55
Pant A-2	61	ICP 7035	130	95.5	MN 8	56
ICPL 161	71	C-11	122	96.5	ICPL 88039	55
MN 1	55	AL 1518-2	65	60.0	#06016-8-1	48
MN 1	55	AL 1621	66	60.5	#06017-12-20	50
MN 5	56	AL1621	66	61.0	#06027-4-6	50
MN 8	56	AL 1518-2	65	60.5	#06036-3-2	48
AL1518-2	65	MN 8	56	60.5	#06036-4-8	49

Note. Data source: Pigeonpea Breeding, ICRISAT# S. Em ±0.1; CV% = 2.7; Srivastava et al. (2012).

7 | EARLY MATURING CULTIVARS BRED THROUGH HYBRIDIZATION AND SELECTION

Apart from the selection of spontaneous mutants and transgressive segregation, hybridization-based breeding methods have also resulted in development and release of a number of early maturing varieties for cultivation in diverse agro-ecologies in India (Singh, Bohra, & Singh, 2016). The noteworthy examples include TAT 10 (1984), Jagriti (1985), Pragati (1986), Vamban 1 (1993), AL 201 (1993), Sarita (1994), Durga (1995), Paras (1998), VBN (Rg) 3 (2005), PAU 881 (2007), PA 291 (2009), AL 882 (2017), PDAT 16 (2018) and so on. Breeding of early maturing pigeonpea was also undertaken in Uganda, Nigeria and the Caribbean and a few early maturing germplasms such as 3D 8103, UWI-17 and Royes were bred (Ariyanayagam, 1981; Rachie et al., 1975).

8 | MOLECULAR VALIDATION INVOLVING WHOLE-GENOME RESEQUENCING

In the last decade, significant developments have been made in generating and deployment of genomics resources for the improvement of pigeonpea. At present, thousands of simple sequence repeat (SSR) markers, millions of single nucleotide polymorphism (SNP), several cost-effective genotyping platforms, a number of dense genetic maps, draft genomes and resequencing data for several hundred to thousand genomes have been developed (Saxena, Thudi, & Varshney, 2016). A number of trait-associated markers have also been developed and these are being used in developing improved lines through genomics-assisted breeding (GAB). With respect to earliness in pigeonpea, some initial molecular leads have been generated from sequenced data. Such as the mutations identified in genes responsible for early flowering and photoperiod responses (Varshney et al., 2017). Such mutations in pigeonpea need to be validated through various reverse/forward genetic approaches to establish links between the genotypes and phenotypes.

In the earlier discussion, it has been concluded that the spontaneous mutations have played a key role in the evolution of early and extra early maturing pigeonpea cultivars. This hypothesis was validated in a recent study involving whole-genome resequencing (WGRS) of 292 *Cajanus* accessions including 117 breeding lines, 166 landraces, and seven accessions from three wild relative species namely *C. cajanifolius*, *C. scarabaeoides* and *C. platycarpus*. According to Varshney et al. (2017), the detailed analysis of WGRS data revealed two different haplotypes of gene '*C.cajan_22378*', a homolog of *EARLY FLOWERING3* (*ELF3*) gene, located on CcLG09. Further, three missense mutations were also identified in *ELF3* gene within the cultivated pool; whereas in the wild species *ELF3* gene has been identified responsible for photoperiod-dependent flowering and normal circadian regulation in plants; and the mutations in *ELF3* gene have produced early flowering plants (Boden et al., 2014). From these observations, it can also be inferred that the maturity in pigeonpea was controlled by a few dominant genes, and recessive mutation occurring spontaneously in each such gene substantially reduced the maturity period.

9 | IMPACT OF EARLY PIGEONPEA IN PRESENT-DAY AGRICULTURE

The onset of reproductive stage in pigeonpea plants puts partial brakes in the growth and development of canopy. These changes are more striking in the early group of plants as compared to late types. The most obvious changes occur in the canopy parameters and its related component traits. The early flowering pigeonpea genotypes produce reduced canopy, less number of branches and pods/plant. Therefore, to harvest economic yields, the early types need to be sown with high plant density (25–30 cm × 15–20 cm). Hence, the early maturing cultivars are invariably grown as a sole crop which also allows various mechanized field operations (Wallis, Byth, & Saxena, 1981).

In India, so far over three dozen of early and extra early maturing cultivars have been released for cultivation. The adaptation of these cultivars under diverse soil and climatic conditions has encouraged scientists to explore the possibility of growing them in the niches where pigeonpea was never cultivated earlier. According to the estimates provided by the Directorate of Economics and Statistics, the adoption of this genetic material in such niches has added over 100,000 ha of pigeonpea area in India (DES, 2017).

10 | EARLINESS—A TOOL FOR WIDENING PIGEONPEA ADAPTATION

To extend the use of pigeonpea in crop diversification programmes in different countries, it is important that the varieties should be able to flower and mature within a defined period. According to Wallis et al. (1981) and Wallace et al. (1993), the adaptation of pigeonpea can be enhanced beyond 35° latitudes only if photoperiod insensitive cultivars are developed. This can be achieved by breeding early or super early cultivars because in pigeonpea earliness is directly related to photoinsensitive (Turnbull et al., 1980; Wallis et al., 1981). Saxena (1981) also demonstrated that the responses to photoperiod and flowering time in pigeonpea were strongly linked and controlled by the same genetic system.

In order to take pigeonpea crop to new areas, a range of high yielding extra early maturing cultivars were developed under the aegis of both Indian Council of Agricultural Research (ICAR) and ICRISAT.To test their adaptation, the promising lines were evaluated at locations ranging from 7 to 46°N latitudes in an International Nursery in five countries. The data from these assessments (Table 5) showed that extra early genotypes such as 'ICPL 83015' and 'ICPL 85010' produced over 2 t/ha of grain even at 46°N.

TABLE 5 Seed yield (t/ha-) of early maturing lines at different latitudes

ICPL No	7°N	17°N	29°N	32°N	46°N
83015	2.32	2.35	1.06	3.73	2.06
83019	2.21	1.46	1.00	3.58	1.76
84023	2.34	1.42	1.37	2.99	1.59
85010	2.79	1.59	1.17	3.16	2.15
83006	3.09	2.22	1.28	3.38	1.43
Mean	2.17	1.65	1.16	3.19	1.77
SE	± 0.28	± 0.15	± 0.10	± 0.04	NA
CV%	22.8	14.5	12.9	17.1	NA

Note. NA = Not available, non-replicated experiment. *Source*. Table adapted from Saxena et al. (2018).

11 | PIGEONPEA FOR DIVERSIFICATION OF CEREAL-BASED CROPPING SYSTEMS

A broad-based assessment carried out by Khoury et al. (2014) revealed that in the last 50 years the crop diversity in Indian agriculture has narrowed down significantly; and in certain cases, it has also eliminated some regionally important varieties/crops from the traditional farming systems. Such losses have also adversely affected the all important diversity of diet and nutrition. They further mentioned that out of more than 20 cropping systems prevailing in India, the rice-wheat rotation is the most widely spread and important from the points of view of income generation and production of calorie-rich food. According to Bhatt and Yadav (2016), this system is labour, water, capital and energy intensive, and its profitability is directly related to the availability of these inputs.

This crop rotation has undoubtedly brought food security through the famous 'green revolution'; but it also played a major role in displacing the soil-rejuvenating high-protein grain legumes from the farming systems. The persistence of cereal-cereal cultivation over decades is now showing its ill effects on soil health in terms of soil compaction, poor drainage, increase in soil salinity and poor response to added fertilizers and declined productivity per se (Dahiya et al., 2002; Kataki, 2002). Overall, this rotation is becoming unsustainable and more research with respect to crop diversification is warranted. In this context, pigeonpea-wheat rotation, wherein deep-rooted pigeonpea replaced the water-sucking paddy, was found ideal with respect to both profitability and sustainability.

Initially, in this rotation, early variety 'T-21' was tried but it often delayed the sowings of valued wheat crop. Soon this variety was replaced by an earlier maturing cultivar 'UPAS 120'. Even this variety was often found to delay wheat sowings due to extended maturity caused by early winter rains and poor drainage (Dahiya et al., 2002). Therefore, need of a variety which could mature earlier than 'UPAS 120' was felt. In this context, the development of extra early maturing pigeonpea cultivars such as Manak, ICPL 88039 and a few more was significant because it allowed a normal sowing of wheat crop after the harvest of pigeonpea.

The use of new extra early pigeonpea cultivars has not only helped in stabilizing the pigeonpea-wheat rotation but also resulted in its large-scale adoption in the states of Punjab, Haryana and Uttar Pradesh. In this cropping sequence, the wheat also benefitted by the preceding pigeonpea crop by recording additional yield of around 1,000 kg/ha. Such yield increases were attributed to the timely sowing of wheat and various beneficial residual effects of pigeonpea including incorporation of nutrient-rich organic matter to the soil through heavy leaf fall and extensive root biomass (Dahiya et al., 2002).

The other rice–rice cropping system, prevalent in the southern parts India and subtropical areas of eastern Gangetic plains, is continuously suffering from low productivity (Mangal Deep, Kumar, Saha, & Singh, 2018) and also rapidly deteriorating the soil health and human dietary pool (Dwivedi et al., 2017). In order to overcome such limitations, the diversification of cropping system is the key; and this can be achieved by introducing a deep-rooted legume such as extra early pigeonpea, especially in the upland fields (Kataki, 2002).

12 | PIGEONPEA IN SOME UNEXPLORED NICHES

Besides being a part of cereal-based cropping systems, the extra early maturing pigeonpea has also shown promise in some unexplored new niches. The first such initiative, where early pigeonpea has made an impact, is the rain-fed hilly region of Uttarakhand state of the country. In general, the slopping hill agriculture repeatedly suffers from a heavy top-soil erosion and post-rainy season drought, resulting in poor (300–400 kg/ha) crop productivity. The introduction of extra early pigeonpea cultivar 'ICPL 88039' (VL Arhar 1) has provided an answer to this age-old issue due to its ability to curtail erosion and tolerate both the intermittent as well as terminal droughts (Saxena et al., 2011). The on-farm trials conducted using the pigeonpea variety 'ICPL 88039' showed that it could be grown successfully at the elevations up to 1,580 m with grain productivity of 1,250–1,878 kg/ha (Saxena et al., 2011). This variety is also being grown successfully even in the rocky terrains, where no food crop can produce economic yield.

The other situation where the extra early pigeonpea has been introduced successfully is the low (about 300 mm) rainfall areas of Rajasthan and Madhya Pradesh. In these areas, frequent drought is a regular feature, and only coarse cereals are grown with low productivity. The introduction of pigeonpea not only provides protein-rich grains to farming families, but also farmers get good economic returns with yields up to 1,500 kg/ha (S. J. Singh; pers. com.).

13 | CONSTRAINTS IN PROMOTING EARLY MATURING PIGEONPEA

In promoting pigeonpea in the new niches, farmers generally encounter some kick-off issues, and these need to be addressed appropriately. The severe most constraint to pigeonpea production is

TABLE 6 Summary information on global distribution of early maturing pigeonpea germplasm based on seed supply record of ICRISAT and different publications

Exporting country	Recipient countries
India/ICRISAT	Australia, Bangladesh, Belize, Bhutan, Cambodia, Cameroon, China, Fiji, Kenya, Malaysia, Malawi, Nepal, New Zealand, Niger, Nigeria, Pakistan, Papua New Guinea, Philippines, Puerto Rico, Sri Lanka, South Korea, South Africa, Surinam, Taiwan. Tanzania, Thailand, Tobago, Trinidad, USA, Uganda, Vietnam, Zambia, Zimbabwe
Australia	Fiji, Indonesia, Thailand, S. Africa
Trinidad	Australia, Belize, Dominican Republic, Guyana, Haiti, India, Jamaica, Panama, Sri Lanka
Nigeria	India/ICRISAT

Source. ICRISAT Pigeonpea Breeding Reports and different publications.

insect damage caused by pod borers (*Helicoverpa armigera*, *Maruca vitrata*) and blister beetle (*Mylabris pustulata*) (Choudhary, Raje, Datta, Sultans, & Ontagodi, 2013). Among these, blister beetle is the most damaging. The large size beetles attack flowers, and within no time they chew petals, stigma and anthers of the flowers. This damage, however, reduces as the crop area increases. The pod borer damages can be controlled by timely spray of systemic insecticides such as indoxacarb and spinosad.

14 | GLOBAL MOVEMENT OF EARLY MATURING PIGEONPEA GERMPLASM

The efforts made under All India Co-ordinated Pulses Improvement Project (AICPIP) jointly by ICAR and ICRISAT resulted in the generation of a number of early maturing pigeonpea germplasm in India. Besides these, some early maturing germplasm were also bred in Australia, Trinidad and Nigeria.

The early maturing inbred lines and cultivars were shared with a number of countries in Asia, Africa and Americas. Bulk of this material was supplied by ICRISAT as a part of its International Pigeonpea Observation Nurseries. Besides this, the early maturing germplasm was also supplied from ICRISAT to Australia, Sri Lanka, China and Myanmar under bilateral research and development programmes. Some early maturing genotypes, initially supplied by ICRISAT to Australia, were sent from there to South Africa, Fiji and Papua New Guinea for adaptation studies. Some early breeding lines were also supplied by IITA, Nigeria to ICRISAT. A summary of the seed movements is given in Table 6. The information about the present status of the supplied germplasm to different recipient countries is, however, not available.

15 | NEW TECHNOLOGIES FOR BREEDING EARLY MATURING CULTIVARS

Despite significant improvement in the duration and productivity, the early maturing cultivars could never occupy >20% of the pigeonpea area (Choudhary & Nadarajan, 2011). This has impeded diversification of rice-wheat cropping system, and there is a need to breed new high yielding cultivars with traits such adaptation, productivity and tolerance to key stresses. During the past decade, some new breeding and genomics technologies have been evolved to develop new pigeonpea cultivars more efficiently. For the same, brief description presented here as following:

15.1 | Hybrid breeding

Breeding hybrids is a new concept in pigeonpea and it has potential to bring about quantum jumps in productivity. The three-parent hybrid breeding technology is based on a cytoplasmic-nuclear male sterility and insect-aided natural cross-pollination. A number of early maturing hybrids, developed by ICAR-IIPR and ICRISAT have been tested over the last few years, and some of these hybrids are under advanced stages of evaluation. A few recently developed early maturing hybrids have shown great promise with 30%–50% yield advantage over pure line cultivar (Table 7). Moreover, these early maturing hybrids and their parental materials have recently been shared with the interested public and private seed companies for further testing, promotion and adoption of hybrids. The technology details related to hybrid breeding, commercial seed production and adoption have been discussed in length by Saxena, Sharma, and Vales (2018).

15.2 | Rapid generation advancement

Pure line breeding is a resource intensive activity and it takes 10 years or more to develop a new variety. Saxena, Saxena, and Varshney (2017) showed that in early maturity group four seed-to-seed generations can be taken within in a year. This technology is

TABLE 7 Mean yield of early maturing hybrids in multi-location trials conducted in 25 environments

Hybrid	Mean maturity (days)	Mean yield (kg/ha)	Gain (%) over check
ICPH 2433	114	2,306	54
ICPH 2438	115	2,127	42
ICPH 2363	115	2,048	36
ICPH 2429	114	1,946	30
UPAS 120	120	1,502	(check)

Source. Saxena and Tikle (2015).

based on the germination of immature (35 days) seeds and single seed descent method of generation advancement. This scheme ensures conservation of genetic variability, generation-after-generation and brings homozygosity in the breeding populations in a short period of only 2 years, and thus, considerably reduce the time required to breed early maturing cultivars. Moreover, early generation screening based on molecular markers will help in selecting preferable progenies (with homozygosity and desired traits) to be advanced and in turn reduce the load of advancing large populations.

16 | CONCLUSIONS

Although pigeonpea is under cultivation for centuries, but the early maturing germplasm is of recent origin. The information on the origin of this genetic material is scattered in literature with no firm conclusions. In this research paper, the authors have compiled information on the origin of early maturing germplasm through back-tracking the literature. They concluded that this group of germplasm originated in the past mainly through spontaneous mutations. The other sources identified were transgressive segregation and induced mutations. The early maturing pigeonpea cultivars have played a significant role in the diversification of cereal-based cropping systems.Recent success in breeding super early maturing (<90 days) genotypes and advances in genomics have further enhanced the scope for diversifying agriculture in new niches where pigeonpea was never tried and development of suitable varieties. This will help in the horizontal expansion of the crop and contribute to the national production of protein-rich pulses to meet nutritional sustainability of farming community.

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CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

AUTHOR CONTRIBUTION

KBS and AKC conceived the concept. KBS, RKS, AKC, RKSr and AB developed the manuscript. RKV provided inputs on the draft MS. KBS is the primary corresponding Author. On behalf of KBS and other Authors, RKS handled the correspondences with Journal.

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