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SHORT COMMUNICATION

# The earliest maturing pigeonpea [*Cajanus cajan* (L.) Millspaugh] germplasm bred at ICRISAT

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**Abstract** Adaptation of pigeonpea [*Cajanus cajan* (L.) Millspaugh], a short-day species, is restricted due to its sensitivity to photo-period. Earliness in this crop is reported to be linearly associated with photo-insensitivity; and this provides an opportunity to breed widely adapted cultivars through the selection for earliness. This research note reports breeding of the earliest maturing pigeonpea germplasm at ICRISAT. This germplasm, nicknamed as 'super early' and bred through the selection of transgressive segregants matured in < 90 days. It can be used as a source material in breeding early maturing cultivars and also can be introduced for cultivation in new production niches.

**Keywords** Pigeonpea · Early germplasm · Super-early · *Cajanus* · Breeding · Transgressive segregation

## Introduction

Pigeonpea [*Cajanus cajan* (L.) Millspaugh] is a popular pulse crop in a number of Asian, African, and the Caribbean countries. Taxonomically, it is classified into tribe *Phaseoleae*, sub-tribe *Cajaninae*, family *Leguminosae*, genus *Cajanus*, and species *cajan*. According to van der Maesen (1980), the cultivated form of this crop originated in the hilly forests of central India about 3500 years ago from a wild species identified as *Cajanus cajanifolius* (Hains) Maesen. The gene banks at ICRISAT (13,632 accessions), National Bureau of Plant Genetic Resources of India (11,229 accessions), United States Department of Agriculture (4116 accessions), and Ministry of Agriculture, Kenya (1288 accessions) hold huge germplasm of genus *Cajanus* (Singh et al. 2013; Upadhyaya et al. 2007). These include landraces, advanced breeding lines of the primary gene pool and various wild species representing secondary and tertiary gene pools. This germplasm collection has tremendous variability for most qualitative and quantitative traits including maturity (Singh et al. 2013; Remanandan et al. 1988). However, for a long time, only late maturing landraces and cultivars dominated the agricultural scenario (Saxena et al. 2018).

Considering the present-day shortage of high protein food among the masses and various sustainability issues, the diversification of agriculture has become a necessity; and to achieve this goal the legume crops are considered the best bet. Among these, pigeonpea is rated high because of its proven role in soil rejuvenation and sustainability of cropping systems (Saxena 2008). Therefore, for the diversification of cropping systems, breeding of cultivars with new plant types to suit various production niches has

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been emphasized (Saxena et al. 2018). In this context, the photo-insensitive early maturing pigeonpea cultivars can play a significant role (Byth et al. 1981; Dahiya et al. 2002).

Since the early maturing germplasm was not available in the past, a programme was designed to breed such unique genotypes. The first early maturing spontaneous mutant was detected by breeders in 1953 in a farmer's field. This triggered the breeding for earliness, and by the turn of the century, pigeonpea cultivars varying in maturity periods were bred (Saxena et al. 2019). Traditionally, the early maturing pigeonpea germplasm is classified into three broad groups including mid-early (150–160 days to mature), early (130–140 days to mature), and extra-early (110–120 days to mature). This research note reports breeding of the earliest maturing (< 90 days) pigeonpea germplasm and its potential uses.

## Materials and methods

In order to bring together the diverse and scattered alleles imparting earliness through breeding, 11 early maturing cultivars were acquired from different institutions. These included MN1, MN5, MN8 from the USA; ICPL 85010, ICPL 88039 from ICRISAT; ICP 6972, ICP 6973, ICP 6974 and UPAS 120 from Agricultural University, Pantnagar (India) and AL 1518 and AL 1621 from Agricultural University, Ludhiana (India). These genotypes were sown at Patancheru in 2006 rainy season and crosses were made manually in a diallel mating design.

In 2007 season, all the $F_1$ hybrids were grown inside an insect-proof net to produce self-pollinated $F_2$ seeds. In the subsequent season (2008) about 1000 $F_2$ plants were raised in each cross. An early cultivar ICPL 88039 was sown after every 10 rows as a control. Each plant was tagged for the days to first flower opening. This activity continued till all the plants in ICPL 88039 flowered (63 days); and those which flowered later were rouged. All the early maturing tagged plants were harvested manually and the selections with small seed size (< 6 g/100 seeds) and fewer seeds (< 10 g/plant) were discarded. In 2009, the selected $F_3$ progenies were grown and all the segregants flowering in < 50 days were selected; and again the small seeded and less productive types were rejected. These selections were multiplied in the off-season at Patancheru and progeny bulks were harvested without any selection. In 2010 rainy season, 29 non-determinate promising $F_5$ progeny bulks were evaluated in a preliminary trial using a randomized complete block design with two replications at Patancheru. The crop was partially damaged with *Phytophthora* blight disease and this did not permit recording yield data. However, data on other key traits were recorded.

In each season the sowings were done on ridges, 60 cm apart, with plant-to-plant pacing of 10 cm. A basal fertilizer dose of di-ammonium phosphate was applied @100 kg/ha. The crop was irrigated as and when required. Just before flower initiation, the entire plot was covered with insect-proof nylon net to protect the crop from *Maruca vitrata* (Geyer) and *Helicoverpa armigera* (Hübner), the two major pod-boring insects.

## Results and discussion

Significant gains were achieved in breeding genotypes which matured much earlier than the extra early maturing (102 days) control cultivar ICPL 88039. These genotypes, as a group, were classified as "super early" types. Within this group, however, a little variation (48–51 days) was observed for 50% flowering, but all of them matured in < 90 days (Table 1) and six of them maturing in only 82 days. This is the earliest maturing pigeonpea germplasm presently available anywhere in the world. In comparison to the control ICPL 88039, these lines gained 20 days as far as their maturity was concerned. The best super early line was ICPX 060016-10-8-1 and it was derived from a cross involving two very diverse parents, MN 1 (bred in Minnesota, USA) and AL 1581 (bred at Ludhiana, India). This line flowered in 48 days and its maturity was achieved in 82 days. Its pod size (4.5 seeds/pod) and seed size (8.9 g/100 seeds) were also within the acceptable range. The short stature (88 cm height) of this line will allow easy mechanized field operations such as inter-cultivation, spraying, and combine harvesting. A series of agronomy experiments conducted by Wallis et al. (1981) in Australia and Chauhan (1990) in India revealed that in pigeonpea, the biomass production was positively associated with productivity. Since these super early genotypes produce relatively small amount of biomass on single plot basis, one needs to grow them at high plant

**Table 1** Some key traits of selected brown seeded super early $F_5$ lines, rainy season 2010

| Cross | Pedigree ICPX | Days to flower | Maturity (days) | | Plant height (cm) | Seeds/pod | g/100 seeds |
|---|---|---|---|---|---|---|---|
| | | | Duration | Time gain over control | | | |
| MN 5 × AL 1621 | 060027-3-4-18 | 51 | 82 | 20 | 108 | 3.4 | 7.9 |
| MN1 × AL 1518 | 060016-10-8-1 | 48 | 82 | 20 | 88 | 4.5 | 8.9 |
| AL 1518 × MN8 | 060063-8-9-4 | 50 | 82 | 20 | 98 | 3.5 | 8.0 |
| AL 1518 × MN8 | 060063-11-6-6 | 50 | 82 | 20 | 102 | 4.0 | 5.9 |
| AL 1621 × MN5 | 060077-6-6-4 | 51 | 82 | 20 | 102 | 4.4 | 6.8 |
| MN1 × AL 1621 | 060017-2-1-1 | 50 | 82 | 20 | 95 | 3.4 | 7.2 |
| AL1621 × MN5 | 060077-6-5-16 | 50 | 84 | 18 | 98 | 3.5 | 8.4 |
| MN8 × AL 1812 | 060036-15-15-1 | 50 | 85 | 17 | 85 | 4.0 | 6.6 |
| AL1621 × MN5 | 060017-12-12-20 | 50 | 85 | 17 | 102 | 4.1 | 9.6 |
| AL 1518 × MN8 | 060063-8-9-11 | 51 | 85 | 17 | 98 | 4.1 | 7.7 |
| MN 5 × AL 1621 | 060027-12-12-12 | 50 | 85 | 17 | 100 | 3.6 | 7.2 |
| AL 1518 × MN8 | 060063-11-9-12 | 50 | 85 | 17 | 95 | 3.8 | 6.5 |
| AL 1518 × MN 5 | 060066-16-14-9 | 49 | 85 | 17 | 95 | 4.1 | 6.6 |
| AL 1518 × MN8 | 060063-8-9-12 | 50 | 86 | 16 | 98 | 3.5 | 7.1 |
| MN8 × AL 1812 | 060036-5-8-9 | 50 | 86 | 16 | 105 | 3.1 | 8.1 |
| MN8 × AL 1812 | 060036-12-3-2 | 48 | 86 | 16 | 102 | 4.5 | 6.6 |
| ICPL 88039 | Control | 58 | 102 | – | 115 | 3.9 | 8.3 |
| Mean (n = 30) | – | 50.7 | 88.1 | – | 99.4 | 3.9 | 8.3 |
| SEm ± | – | 1.2 | 2.5 | – | 2.6 | 0.1 | 0.5 |
| CV % | – | 3.3 | 4.0 | – | 3.7 | 2.5 | 9.1 |

population (200,000–300,000 plants/ha) as against the normal population density of about 66,000 plants/ha.

Wallis et al. (1981) demonstrated that earliness in pigeonpea was associated with insensitivity to day length; and therefore breeding for extreme earliness can help in achieving the objective of wide adaptation. In the present breeding exercise, the super early recombinants flowered and matured earlier than both the parents. The emergence of such extreme (transgressive) segregants in breeding populations may be attributed to the unique recombination events where the diverse desirable alleles from the two parents combined together in a single individual. Theoretically, in most cases, such genotypes arise due to the presence of additive, epistatic or complementary gene action. Also, sometimes chromosomal re-arrangements, mobilization of transposable elements, or DNA-methylation can also produce such recombinants (Rieseberg et al. 1999; Liu and Wendel 2000; Michalak 2009).

Building on the work of Srivastava et al. (2012), Vales et al. (2012) evaluated some super early selections at three very diverse locations including Patancheru (17°N, 78°E, altitude 545 m), Ludhiana (30°N, 75°E, altitude 247 m) and Almora (29°N, 79°E, altitude 1250 m). At Patancheru three super early lines (ICPLs 20325, 20326, 20327) recorded yield as good as the control (1612 kg/ha). ICPL 20329 performed well both at Ludhiana (2213 kg/ha) and Almora (2083 kg/ha) with productivity similar to that of the control cultivar ICPL 88039. Besides high yield, these lines also had acceptable phenology and seed traits.

The new super early germplasm is unique and adds to the useful genetic variability to the existing diversity of pigeonpea germplasm. Such genotypes can be used as an elite source of earliness in breeding programs. Besides this, these can also be used directly as cultivars in the arid areas where the annual rainfall is $< 300$ mm and often the rainy seasons are limited to a few weeks. This will also provide an opportunity to the farmers to include a legume component in the existing cropping systems if a short window available for cultivation. Besides this, it can also find a place in new niches where pigeonpea was never cultivated due to its lateness and photo-sensitivity (Saxena et al. 2014). The cultivation of pigeonpea crop always contributes towards the improvement of soil structure and fertility through its deep penetrating roots, nitrogen fixation, the release of soil-bound phosphorous and extensive dry leaf fall (Saxena 2008). This new germplasm is available with the pigeonpea breeding unit of ICRISAT.

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**Compliance with ethical standards**

**Conflict of interest** The authors declare that they have no conflict of interest directly or indirectly and informed consent to publish this study and that the manuscript complies with the ethical standards of the journal.

## References

Byth DE, Wallis ES, Saxena KB (1981) Adaptation and breeding strategies for pigeonpea. In: Nene YL, Kumble V (eds) Proceedings of the international workshop on pigeonpeas, vol 1. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, pp 450–465

Chauhan YS (1990) Optimum agronomic management. In: Nene YL, Hall SD, Sheila VK (eds) The pigeonpea. CAB International, Wallingford, pp 257–278

Dahiya SS, Chauhan YS, Johansen C, Waldia RS, Sekhon HS, Nandal JK (2002) Extra short duration pigeonpea for diversifying wheat based cropping systems in sub-tropics. Exp Agric 38:1–11

Liu B, Wendel GF (2000) Retrotransposon activation followed by rapid repression in introgressed rice plants. Genome 43:874–880

Michalak P (2009) Epigenetic transposones and small RNA determinants of hybrid dysfunctions. Heredity 102:45–50

Remanandan P, Sastry DVSSR, Mengesha MH (1988) ICRISAT pigeonpea germplasm catalog. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru

Rieseberg LH, Archer MA, Wayne RK (1999) Transgressive segregation, adaptation, and speciation. Heredity 83:363–372

Saxena KB (2008) Genetic improvement of pigeonpea—a review. Trop Plant Biol 1:159–178

Saxena KB, Singh IS, Kumar RV, Hingane AJ, Mula MG, Patil SB, Sameerkumar CV (2014) Challenges and opportunities of breeding early maturing pigeonpea hybrids. J Food Legumes 27(1):1–8

Saxena KB, Choudhary AK, Saxena RK, Varshney RK (2018) Breeding pigeonpea cultivars for intercropping—synthesis and strategies. Breed Sci. https://doi.org/10.1270/jsbbs.17105

Saxena KB, Choudhary AK, Srivastava RK, Bohra A, Saxena RK, Varshney RK (2019) Origin of early maturing pigeonpea germplasm and its impact on adaptation and cropping systems. Plant Breed (accepted)

Singh N, Tyagi RK, Pandey C (2013) Genetic resources of pigeonpea: conservation for use. Institute document. National Bureau of Plant Genetic Resources (NBPGR), New Delhi

Srivastava RK, Vales MI, Sultana R, Saxena KB, Kumar RV, Thanki HP, Sandhu JS, Choudhary KN (2012) Development of super early pigeonpea with good yield potential from early × early crosses. J SAT Agric Res 10:1–6

Upadhyaya HD, Reddy KN, Gowda CLL, Singh S (2007) Phenotypic diversity in the pigeonpea (*Cajanus cajan*) core collection. Genet Resour Crop Evol 54:1167–1184

Vales MI, Srivastava RK, Sultana R, Singh S, Singh I, Singh G, Patil SB, Saxena KB (2012) Breeding for earliness in pigeonpea: development of new determinate and non-determinate lines. Crop Sci 52:2507–2516

Van der Maesen LJG (1980) India is the native home of pigeonpea. In: de Wit HCD (ed) Liber Grantulatorius innonerem. Agriculture University Wageningen, Wageningen, pp 257–262

Wallis ES, Byth DE, Saxena KB (1981) Flowering responses of thirty-seven early maturing lines of pigeonpea. In: Nene YL, Kumble V (ed) Proceedings of the international workshop on pigeonpeas, vol 2, International Crops Research Institute for the Semi-arid Tropics (ICRISAT), Patancheru, pp 143–159