



## DG(RG) 55- High yielding short duration dwarf line of pigeonpea

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### ABSTRACT

Pigeonpea (*Cajanus cajan*), the essential vegetarian protein diet of India is yielding lesser than as potential. The major constraints for productivity of pigeonpea are inadequate availability of seeds of high yielding short duration improved varieties, biotic and abiotic stress and poor crop management. To utilize the genomic resources for yield improvement it is necessary to evaluate the pigeonpea germplasm for yield traits and biotic and abiotic stress tolerance. The present investigation led to the identification of better performing lines based on yield. A total collection of 2000 accessions were subjected to initial evaluation. From these 2000 accessions better performing lines were selected for crossing and generation of mapping populations. Initial data was evaluated to identify better performing accessions over the check varieties used in evaluation. Based on days to first flowering, days to 50 per cent flowering and days to maturity parental lines for crossing were identified. Among selected accessions IC33671 and Palamedu local were found to have short stature and early maturing independently. These selected accessions were crossed and progenies were evaluated to identify high yielding individuals. The resultant high yielding determinant short duration crop DG (RG) 55 has been evaluated for its performance under multiple locations and identified to yield up to 15 per cent more than the better performing check varieties Asha and APK1.

**Keywords:** abiotic stress, biotic stress, dwarf, high yielding pigeonpea, legumes



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### INTRODUCTION

Pulses are grown under rainfed conditions in marginal, less fertile lands with meagre pest and nutrient management. Pigeonpea is a perennial legume belonging to the family Leguminaceae (Fabaceae). Since its domestication in India at least 3,500 years ago, pigeonpea has become a common pulse and dal of Asia, Africa, and Latin America (Singh, 2012). India requires about 38 million tonnes of pulses by 2017–18 to meet the World Health Organization recommendation of 80 g protein/capita/ day to avoid protein malnutrition. To meet this demand a total of 6,557,712 tonnes worth 368 crore US\$ pulses were imported from December 2016 to November 2017 (<http://commerce.gov.in/>). Only SMART agriculture can fill the

gap between demand and supply towards which development of new germplasm resources are needed (Ramya et al. 2013). Among these pulses, India contributes to 90% of the total global production of red gram/ pigeonpea (*Cajanus cajan* L.). The present area under pigeonpea is approximately 3.5 mha, 2.57 mt production with an average productivity of 600-800 kg/ha. The major constraints for productivity of pigeonpea are inadequate availability of seeds of improved varieties, biotic and abiotic stress and poor crop management. The National Gene Bank (NGB) houses over four million accessions of different crops including a large collection of pigeonpea. However, to exploit the full potential of the genetic diversity of conserved pigeonpea germplasm it is important that a targeted screening of all the germplasm for identification of useful/superior material is required.

To utilize the genomic resources for yield improvement it is necessary to evaluate the pigeonpea germplasm for yield traits, biotic and abiotic stress tolerance. Pigeonpea genome sequencing (Singh et al., 2012) is a major milestone for genetic improvement of this important pulse crop. The existing varieties or the so called ruling varieties failed to make a major change in increasing productivity. We have identified stress tolerance mechanisms of pigeonpea (Singh et al., 2012, Mishra et al., 2016) and hence, the direct approach will be to identify better performing lines based on yield. The AICRP on

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pigeonpea has developed some high yielding and resistant varieties which are already in the seed chain. These varieties may also be utilized for developing Essentially Derived Varieties (EDVs) having a few more desired characters. The main resources to be utilized for the present investigation, are the germplasm conserved and explored. A large scale evaluation programme is envisaged keeping in mind the need of the hour in the present investigation. An extra-early pigeonpea accession was identified by germplasm evaluation and evaluated. In many crops where hybrid development and multiplication is a problem, cross derivatives offer a better tool to overcome the yield barriers. The higher seed input cost and problems in producing hybrid seeds force the breeders to go for derivatives in enhancing crop productivity. In majority of the instances F<sub>1</sub>s outperform the parental lines. Hybrids yield 25 per cent more in pigeonpea (Bajpai *et al.*, 2003). Hence, with an objective of selecting a high yielding line from the cross derivatives the present investigation was carried out.

## MATERIALS AND METHODS

### *Germplasm Evaluation*

A total collection of 2000 accessions were subjected to initial evaluation. From these 2000 accessions better performing lines were selected for crossing and generation of mapping populations.

### *Hybridisation and selection*

From F<sub>1</sub> of selected crosses between short and race collected from Maharashtra by NGB (National Gene Bank, ICAR-NBPGR), India, during 1979 (IC33671) and a determinate pigeonpea material collected from Tamil Nadu during 2014 (Palamedu local), the progenies were forwarded upto F<sub>4</sub> and selection process from each stage targeted short duration determinate high yielding accession. Field trials at farmers' locations were conducted at multi locations to confirm the trait.

### *Multilocation evaluation*

Using MOD (You *et al.*, 2013), a type 2 modified augmented design data analysis, initial data was evaluated to identify better performing accessions over the check varieties used in evaluation. Based on days to first flowering, 50 days to flowering and days to maturity parental lines for crossing were identified. These selected accessions were crossed and progenies were evaluated to identify high yielding individuals. Selections were evaluated at multiple locations including farmers' fields to assess the yield performance under OFT.

For this purpose ten cultures were raised in recommended 45X15 cm spacing in a plot size of 3.375 sq meter area in RBD.

## RESULTS AND DISCUSSION

From F<sub>2</sub> high yielding lines segregated for earliness and plant height Selection was initiated and forwarded in plant to row method. Further selections in F<sub>3</sub> and F<sub>4</sub> were carried out based on single plant yield. Selected high yielding line is illustrated in Fig. 1. The resultant high yielding determinant short duration crop has been evaluated for its performance under



**Fig. 1:** High yielding short duration pigeonpea at first flowering stage

multiple locations and identified to yield up to 15 per cent more than the better performing check varieties Asha and APK1 under evaluated conditions.

The tested line DG (Rg) 55 is a selection from the F<sub>4</sub> population proved to be better performing line under the tested multi locations. The yield advantage is promising (Fig. 2).

Pigeonpea a member of legume family is a close relative of the already sequenced soybean but lacks suitable varieties (Varshney *et al.*, 2012). An international genomics initiative was started by ICAR with US collaboration and was successfully completed (Singh *et al.*, 2012 and Varshney *et al.*, 2012). However, the effective utilization of large scale phenotyping for various traits is required. Hence, the present investigation was set with an objective of evaluating diverse accessions to identify a better parental line to incorporate in breeding. An estimated 545000 tonnes of redgram produce was damaged by pest and disease incidence. Under these conditions a short duration crop can escape from biotic and abiotic stress conditions. Being a perennial crop by nature exploring short duration lines is a difficult task. Hence, a large set of germplasm accessions were identified for initial evaluation and selection of parental lines were done based on its performance. IC33671 was identified to be a short plant growing upto 150cm under fertile conditions which was selected as a male parent and palamedu local was used as a female parent to make crosses. Traits were found to segregate in their progenies and rigorous selection for plant type and yield linked traits yielded a high yielding line.

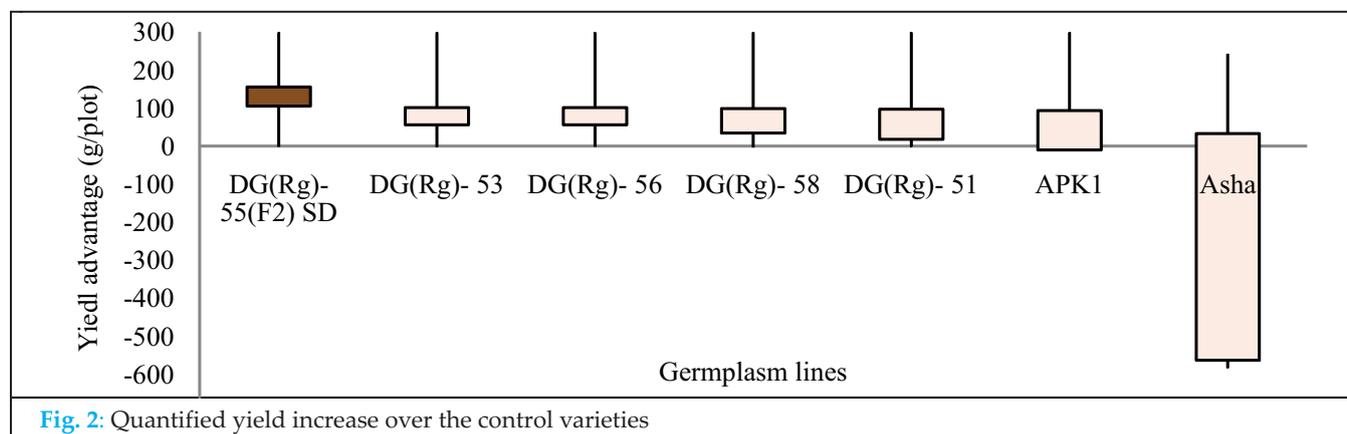


Fig. 2: Quantified yield increase over the control varieties

The identified material may be utilized directly for increasing the crop productivity and may also be suitably modified by application of traditional as well modern approaches for its further utilization. Recently the decoding of pigeonpea genome (Singh *et al.*, 2012 and Varshney *et al.*, 2012) and development of molecular markers (Varshney *et al.*, 2010)

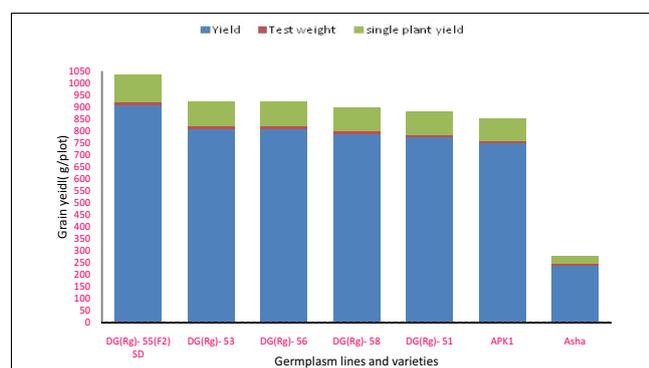


Fig. 3: Yield potential of tested lines over the control varieties

provides useful resources for improvement of pigeonpea. In the present proposal it is proposed to augment diversity in red

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gram from various sources and its evaluation (field and molecular) for identification and development of new genotypes for increasing productivity in red gram using the following strategies.

## CONCLUSION

DG (Rg) 55 is highly suitable for compact and high density planting. At maturity stage the plant reaches a maximum height of 80cm under fertile soil conditions which is highly suitable for inter-cultural operations. DG (Rg) 55 is a short duration crop and can be grown under Bihar, Maharashtra and Tamil Nadu conditions as a solitary crop, bund crop or as intercrop. Application of basal fertilizer indicated lack of nodule formation, hence basal dose of fertilizer application is to be avoided. Foliar spray of DAP and micro nutrient mixture indicated better response in pod setting and prevention of flower shedding. Under Delhi, Tamil Nadu and Haryana conditions pod borer incidence was not observed.

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