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RESEARCH ARTICLE

Genetic diversity and characterization of pigeonpea germplasm

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Abstract

The study is planned to study variability, genetic divergence and characterization of pigeonpea germplasm at Regional Agricultural Research Station, Palem. Two genotypes i.e. RG-183 and RG-189 recorded white colour and the same genotypes are identified as high yielder too. While other genotypes are light, reddish or dark brown in colour These traits can be used for identifying individual germplasm. Ten genotypes were grouped into two major clusters. Five genotypes grouped under I^st^ cluster and the another five genotypes grouped under II^nd^ cluster. RG-189,185,192,190 and 193 falls under first cluster while RG-183,191,186,187 and 184 falls under another cluster. Based on *per se* performance genotype *viz.*, RG-185 RG-183, RG-189 and RG-192 recorded highest yield per hector and medium duration genotype recorded as RG-187 and 190. Hence, it can be considered that high yielding genotypes are grouped under I^st^ cluster while in second cluster medium yielding genotypes are grouped representing high genetic diversity among the germplasm.

Key words: Pigeonpea, germplasm, genetic diversity, yield.

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millspaugh) ($2n = 22$) is the second most important pulse crop of India after chickpea, commonly known as arhar, redgram and tur. Pigeonpea/redgram is a grain legume belonging to the Cajaninae sub-tribe of the economically important leguminous tribe Phaseoleae. Based on the natural genetic variability in local germplasm and the presence of numerous wild relatives, Van der Maesen (1990) concluded that India is probably primary centre of origin. Pigeonpea is an important pulse crop that performs well in semi-arid tropics where moisture availability is unreliable or inadequate (Reddy *et al.*, 1993). India is the largest producer of pigeonpea in the world sharing approximately 70% of the production and covering 74% of the area. Pigeonpea has a unique place in Indian farming and India accounts for about 90% of the global production. It is the second most important pulse crop next to chickpea, covering an area of around 4.42 m ha (occupying about 14.5% of area under pulses) and production of 2.86 mt (contributing to 16% of total pulse production) and productivity of about 707 kg/ha (FAOSTAT, 2011). Although India leads the world both in area and production of pigeonpea, its productivity is lower than the world average. One of the factors responsible for the poor productivity of pigeonpea is the lack of improved cultivars. Research for genetic improvement of this crop is required to raise yield levels effectively through widening genetic base. Information on genetic divergence among the plant materials is vital to a plant breeder for an efficient choice of parents for hybridization. It is an established fact that genetically diverse parents are likely to contribute desirable segregants and or to produce high heterotic crosses. Hence, this study is planned to study variability, genetic divergence and characterization of redgram germplasm at Regional Agricultural Research Station, Palem.

Materials and method

The experiments for the present study were conducted in the Regional Agricultural Research Station, Palem, PJTSAU, India during *Kharif* 2013. The experimental material comprised of 10 pigeonpea germplasm. The experiment was laid out in Randomised Block Design with two replications. Observations were recorded for eight quantitative traits. They are days to maturity (DM), plant height (PH) measured in cm, number of branches per plant (NBP), number of pods per plant (NBP), and seed yield kg per hector (YPH). The morphological character i.e. colour of the seed coat was noted to distinguish the genotypes from each other. R version 3.1.3 package 'gplots' was used to draw heat map for diversity study. Hierarchical clustering and heatmap analysis were performed for mean-centered and standardized data in R. The 'hclust' function was used for hierarchical clustering. Heatmap.2 function used to draw 'heatmap' for given genotypes and traits analysed.

Results and discussion

In India medium duration genotypes are mostly preferred among the pigeonpea growing farmers. The genotype which matures within the range of 150-160 days is considered as medium duration genotype. The different variability parameters like mean, minimum, maximum is presented in table 1.

Table: 1. The mean performance of the genotype along with the Colour of the seed coat trait

Genotype	PH (cm)	NBP	DM	NPP	YPH (kg/ha)	Seed coat color
RG-183	149	22	169	238	1498	White
RG-184	119	14	125	251	915	Light brown
RG-185	161	19	165	357	1523	Dark brown
RG-186	154	18	168	272	1081	Reddish Brown
RG-187	142	17	158	281	1185	Light brown
RG-189	159	19	172	384	1448	White
RG-190	112	16	158	387	1432	Reddish brown
RG-191	158	20	185	285	943	Light brown
RG-192	149	17	178	363	1388	Light brown
RG-193	109	16	165	342	1232	Reddish brown
Mean	141	17	164	316	1264.5	
Max.	161	22	185	387	1523	
Min.	109	14	125	238	915	

Days to maturity (DM), plant height (PH) measured in cm, number of branches per plant (NBP), number of pods per plant (NBP), and seed yield kg per hector (YPH)

For plant height the range was recorded from 109 cm to 161 cm, for number of branches it is varying from 14 to 22. In case of days to maturity it is 125 days to 185 days which means great variation among genotype like short duration RG 184 and RG-191 long duration is present It is interesting to note that the average mean of genotype falls under medium duration. Two genotypes RG-190 and RG-187 falls under medium duration category in present study. The range for yield for hector is 915 to1523 kg/ha. Wide range for seed yield per hector is recorded among the genotypes. The highest yield was recorded for genotype RG-185 followed byRG-

183, RG-189 and RG-192 respectively. These genotypes proved good yielder than the others and can be utilized in future breeding programme. Only two genotypes i.e. RG-183 and RG-189 recorded white colour and the same genotypes are identified as high yielder too. While other genotypes are light, reddish or dark brown in colour. Similar results were being reported by Upadhyaya *et al.,* (2007) and *Manyasa et al.,* (2008) for growth habit, base flower color, pattern of streaks, pod colour, pod form and seed color pattern. These traits can be used for identifying individual germplasm. Other objective of the present study was to identify the high yielding and medium duration genotypes through cluster analysis. Hierarchical clustering of genotypes based on the Euclidian distances for the eight traits is represented. Heat map approach gives an opportunity to visualize the expression of the each trait in particular the environments. Heat map and dendrogram displaying relatedness of genotypes and traits under study based on their Euclidean distances. Red and yellow correspond to low and high diversity for expressed traits. White colour represents median levels of expression. The color key indicates the correlation between diversity and colors. The histogram represents a distribution of each value under observation for particular trait. Based on the Ward's clusters analysis (Squared Euclidean distance) .The dendrogram of 10 genotypes of Pigeonpea is presented in Fig.1. Ten genotypes were grouped into two major clusters. Five genotypes grouped under Ist cluster and the another five genotypes grouped under IInd cluster.

RG-189,185,192,190 and 193 falls under first cluster while RG-183,191,186,187 and 184 falls under another cluster. Based on per se performance genotype *viz*., RG-185 RG-183, RG-189 and RG-192 recorded highest yield per hector and medium duration genotype recorded as RG-187 and 190. Hence, it can be considered that high yielding genotypes are grouped under Ist cluster while in second cluster medium yielding genotypes are grouped representing high genetic diversity among the germplasm. Earlier in pigeonpea Thombre *et al.,* (2000), Rekha *et al.,* (2011), Praveen Pandey *et al.,* (2013) and Rupika and Bapu (2014) studied genetic divergence either in among working germplasm and identified most divergent genotypes for the yield and yield attributing traits in redgram. Use of diverse parents in hybridization programme can serve the purpose of combining desirable genes or to obtain recombination. Crosses between divergent parents usually produce greater heterosis than those between closely related ones hence, identified genotypes can be utilised for the development of high yielding and medium duration varieties in pigeonpea.

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Fig.1: The dendrogram of ten pigeonpea germplasm showing diversity among the pigeonpea genotypes