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Sandeep Kumar Yadav

Department of Genetics and Plant Breeding, Ranchi Agriculture College, Birsa Agricultural University, Kanke, Ranchi, Jharkhand, India

Niraj Kumar

Department of Genetics and Plant Breeding, Ranchi Agriculture College, Birsa Agricultural University, Kanke, Ranchi, Jharkhand, India

Krishna Prasad

Department of Genetics and Plant Breeding, Ranchi Agriculture College, Birsa Agricultural University, Kanke, Ranchi, Jharkhand, India

CS Mahto

Department of Genetics and Plant Breeding, Ranchi Agriculture College, Birsa Agricultural University, Kanke, Ranchi, Jharkhand, India

HC Lal

Department of Genetics and Plant Breeding, Ranchi Agriculture College, Birsa Agricultural University, Kanke, Ranchi, Jharkhand, India

Anuj Kumar Choudhary

Department of Genetics and Plant Breeding, Ranchi Agriculture College, Birsa Agricultural University, Kanke, Ranchi, Jharkhand, India

Shreya Sen

Department of Genetics and Plant Breeding, Ranchi Agriculture College, Birsa Agricultural University, Kanke, Ranchi, Jharkhand, India

Corresponding Author:

Sandeep Kumar Yadav Department of Genetics and Plant Breeding, Ranchi Agriculture College, Birsa Agricultural University, Kanke, Ranchi, Jharkhand, India

Morphological characterization of pigeonpea [Cajanus cajan (L.) Millsp] germplasm for selection of elite genotypes

Sandeep Kumar Yadav, Niraj Kumar, Krishna Prasad, CS Mahto, HC Lal, Anuj Kumar Choudhary and Shreya Sen

Abstract

Altogether 104 genotypes of pigeonpea along with 4 checks *viz*; Asha, BA-1, Bahar and ICPB 2078 were evaluated in Augmented Block Design-II. Characterization and grouping of genotypes for yield and other traits was carried out with the help of descriptor of pigeonpea. All these data were recorded on 1 to 9 scales as per descriptor. The knowledge of nature and extent of genetic variation are available in the pigeonpea genotypes. Collection, conservation and characterization of genetype is the backbone of any crop improvement programme which in turn depends on the extent of genetic diversity in gene pool. Diversity in plant genotypes provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics, which include both preferred traits *viz*. earliness and yield attributing traits.

Keywords: Characterization, pigeonpea, genotypes, collection, conservation, diversity

Introduction

Pigeon pea is highly proteinaceous crop whose seed can be prepared into various meals and can also be served as a substitute for Cowpea. It contains 62.78 g. carbohydrates, 1.49 g. fats and 21.7 g. proteins per 100 grams. Generally, the Protein content ranges from 18-29 % which is about three times the value found in cereals (Techale *et al.* 2013) ^[11]. It has been recognized as a good source of vegetarian protein particularly in the developing countries where majority of the population depends on the low priced vegetarian foods. In India, Pigeonpea is second most important pulse crop after Chickpea (Vijayalakshmi *et al.* 2013) ^[13]. India is the world's largest pigeon pea producer accounting for 90 per cent of the world production (Rangare *et al.* 2013) ^[8]. The major pigeonpea producing areas in the world are India, Eastern Africa, Central and South America, the Caribbean and West Indies (Vijayalakshmi *et al.* 2013) ^[13]. It is widely grown in india. Pigeonpea is grown in the area, production and productivity having 5.13 (million ha), 4.23 (million tonnes) and 824 kg/ha respectively (Anonymous, 2016-17) ^[2].

The major pigeonpea growing state in India are Maharastra, Karnataka, Madhaya Pradesh, Uttar Pradesh, Gujarat, Andhra Pradesh and Jharkhand which contribute about 32 %, 17%, 15%, 11%, 10%, 8% and 6% respectively. Pigeonpea is an important kharif pulse crop of Jharkhand.

The knowledge of nature and extent of genetic variation are available in the Pigeonpea genotypes which is the prerequisite for any plant breeding experiment. Collection, conservation and characterization of genotype is the backbone of any crop improvement programme which in turn depends on the extent of genetic diversity present in gene pool. Diversity in plant genotypes provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics. From the very beginning of agriculture, natural genetic variability has been exploited within crop species to meet subsistence food requirement, and now it is being focused to surplus food production in order to fulfill the requirements of increasing populations. Hence the present investigation was undertaken to characterized and grouping one hundred four genotypes along with four checks of pigeonpea [*Cajanus cajan* (L.) Millsp] for isolation of desirable line which can be used as a parent in further breeding programme.

Materials and Methods

Altogether 104 genotypes of pigeonpea along with 4 checks *viz*; Asha, BA-1, Bahar and ICPB 2078 were evaluated in Augmented Block Design-II with the spacing 4 x 0.2 m during *kharif* season 2016-17 at experimental area of pigeonpea, BAU Research farm (Dryland Section),

Kanke, Ranchi. The characterization and grouping of the genotypes for yield and other traits was carried out with the help of descriptor of pigeonpea. All these data were recorded on 1 to 9 scales as per descriptor. All these traits have been classified into seven groups according to the formula given by Sturgis's (1926).

$$K = 1 + 3.332 \log_{10}(N)$$

Where,

K = No of Class N = No. of observed data

W Highest – Lowest

Where, W=Breath of class interval

Result and Discussion

Characterization based on days to 50% flowering ranged from 87.75 (BRG15-1) to 121.00 days (GJP1401) with mean 102.10. Maximum variability were found in second group (Medium), which comprised of 105 germplasm out of 108 which indicated that maximum number of germplasm confined only one group. While, the first group (Early) comprised of only three genotypes *viz*; BSMR 243, BRG 15-1 and CRG 2012-30 which were found to be most promising for earliness in pigeonpea (Table- 1 & 2). Therefore it may be

used as donor parent in future breeding programme for earliness. Similar finding was corroborated by Upadhaya *et al.* (2011) ^[12] and Nethravathi and Patil (2014) ^[7]. The important character Days to maturity ranged from 181.00 days (WRG286) to 247 days (BAHAR(C)) with mean 194.01. All the genotypes are categorized into two groups. One hundred two genotypes falls under medium group whereas six genotypes were found late in second group.

Pod size ranged from 0.03 cm (RVSA12) to 6.76 cm (GJP1406) with a mean value of 5.42. All these genotypes were categorized into three groups namely Long (>5 cm), Medium (4.1-5 cm) and small (<4 cm) (Table- 1 & 2). ninety nine genotypes falls under third group having longer pods whereas, eight and only one genotypes comes under second and first groups having medium and smaller pods respectively. It may be suggested that third group genotypes may be used in further breeding progamme where, long size of pods is desirable. Similar result was reported by Singh and Kumar (2004), Manyasa *et al.* (2007), and Moharand and Narinder (2014) ^[9, 5, 6].

Yield is an important trait for any breeding programme and its characterization revealed that maximum number of genotypes (sixty seven) comes under fourth whereas, only one genotype (WRG 204) was present in seventh group which showed highest value of grain yield (Table -1 & 2). The yield ranged from 18.94 kg/ha (RVSA12) to 1813.04 kg/ha (WRG204) with a mean value of 893.29. It indicates that this line may be used as a parent in further breeding programme. These result was in accordance with the studies of Upadhayaya *et al.* (2011) ^[12].

Table 1: Mean (Adjusted) performance of Pigeonpea genotypes of three quantitative traits

Sl. No.	Genotypes	Days to 50 % flowering	Pod size (cm)	Yield (kg/ha)
1	AKTE 12-20	90.75	4.96	681.54
2	AKTM 1-2	88.75	5.46	1051.54
3	BRG 15-1	87.75	6.16	985.54
4	BSMR 579	94.75	5.86	1225.54
5	BAUPP13-1	98.75	5.46	795.54
6	BSMR 736	92.75	5.36	955.54
7	BAUPP13-2	96.75	5.56	768.54
8	BRG 5	91.75	5.86	968.54
9	BRG 1	94.75	5.86	951.54
10	BSMR 853	104.75	5.16	695.54
11	BDN 2008	99.75	5.36	851.54
12	BSMR 511	97.75	5.26	835.54
13	BRG 4	96.75	5.36	635.54
14	BSMR 846	98.75	6.46	901.54
15	BRG 15-2	96.75	5.46	718.54
16	BSMR 243	88.75	5.66	735.54
17	IIPR-09-06	94.75	5.16	885.54
18	IIPR-09-09	104.75	5.56	791.54
19	CRG 82	102.75	5.46	665.54
20	CORG 2012 -25	98.75	4.66	768.54
21	CORG 9701	91.75	5.36	828.54
22	CRG 2010-9	96.75	5.36	708.54
23	CRG 2012-30	89.75	5.46	735.54
24	C-11	96.75	4.96	868.54
25	GJP 1406	97.75	6.76	751.54
26	GJP 1207	99.75	5.46	835.54
27	GRG2013	101.75	4.93	799.46
28	GRG 1310	111.00	5.43	765.46
29	GJP 1401	121.00	4.43	699.46
30	GRG 2009-1	100.00	5.23	815.46
31	GRG 160	101.00	4.83	732.46
32	WRG 102	101.00	5.63	797.46
33	WRG 244	98.00	5.33	1032.46
34	ICP 2376	99.00	5.83	732.46

25	ICD 0174	106.00	5 72	000.46
33	ICF 91/4	100.00	5.73	999.40
36	ICP 8863	100.00	5.33	932.46
37	ICP 7035	99.00	6.23	865.46
38	ICP 87119	101.00	5.13	899.46
39	ICPB 2051	101.00	5 13	1099.46
40	ICDD 2076	00.00	5.02	722.46
40	ICPB 2076	99.00	5.83	/32.46
41	BSMR 2	109.00	5.53	799.46
42	BDN 02	101.00	4.83	765.46
43	GIP 1205	103.00	5.43	815.46
44	IKM 180	110.00	5.13	1022.46
44	JKW 169	110.00	5.45	1032.40
45	KBA 32-3	111.00	5.73	805.46
46	LRG 105	116.00	5.33	969.46
47	LRG 151	109.00	5.83	965.46
/18	L RG 107	113.00	5.13	832.46
40		100.00	5.15	000.46
49	LAXMI	109.00	5.73	999.46
50	LRG 117	106.00	5.63	732.46
51	LRG 170	101.00	5.13	715.46
52	L RG 133	108.00	5 53	832.46
52	LING 155	102.00	5.55	941.04
53	LKG 104	103.00	6.03	841.94
54	MAL 38	111.00	6.13	985.94
55	NTL 624	110.00	5.13	<u>9</u> 78.94
56	NTPL 769	109.00	5.33	808.94
57	PT 0012	112.00	5 /3	958.04
51		112.00	5.45	20.74
58	KVKT 260	107.25	5.23	895.94
59	RPS 2007-10	99.25	5.53	978.94
60	RVSA 07-10	103.25	5.13	861.94
61	RVSA 12	100.25	0.03	18.94
61	DVCA 07 21	106.25	5.00	929.04
62	KVSA 07-31	106.25	5.33	838.94
63	RVSA 07-12	99.25	5.23	801.94
64	RVSA -9	106.25	5.53	928.94
65	RVSA 2014-2	109.25	5 13	785 94
66	DVSA 2014	105.25	5.13	1051.04
00	KVSA2014	103.23	5.45	1031.94
67	VIPULA	102.25	5.13	1085.94
68	RVSA 7-15	100.25	5.53	885.94
69	WRG 278	106.25	5.33	785.94
70	WPG 283	107.25	5 73	818.94
70	WKU 263	107.25	5.13	010.94
/1	WRGE 248	100.25	5.43	851.94
72	WRG 220	102.25	5.33	1285.94
73	WRG 197	104.25	6.03	1368.94
74	WRG 260	105.25	5.63	885 94
75	WDC 200	105.25	5.03	051.04
73	WKG 222	100.23	5.25	931.94
76	WRG 285	109.25	5.33	985.94
77	WRG 293	106.25	5.33	1318.94
78	WRG 292	104.25	5.73	1335.94
70	WPG 204	102.00	5.46	1813.04
19	WKO 204	102.00	5.40	1813.04
80	WRG252	107.00	6.06	973.04
81	WRG 297	106.00	5.46	1220.04
82	WRG 97	101.00	5.46	880.04
83	WRG 289	105.00	5.56	1113.04
84	WRGE 256	103.00	5 56	073.04
04	WDC 47	103.00	5.50	973.04
85	WKG 65	100.00	6.06	863.04
86	WRG 248	99.00	5.36	830.04
87	WRG 282	100.00	5.66	1113.04
88	WRG 286	102.00	5 96	967.04
00	DVET 207	102.00	5.70	700.04
07	KVK1 29/	100.00	5.00	/ 60.04
90	GRG 107	105.00	5.46	880.04
91	WRG 242	102.00	5.46	747.04
92	WRG 223	105.00	5.66	853.04
93	WRG 232	103.00	5 36	960.04
75	WDC 200	104.00	5.50	012.04
94	WKG 288	104.00	5.90	913.04
95	WRG 281	100.00	5.66	963.04
96	WRG 246	102.00	5.76	1007.04
97	TS-3R	99.00	5.16	827.04
00	TDDC 170	104.00	5.10	852.04
90		104.00	5.00	033.04
99	TRG 78	102.00	5.86	777.04
100	TDRG 107	98.00	4.86	1117.04
101	WRGE 140	100.00	4.96	837.04
102	TRG 50	102.00	5 66	880.04
102	1 KU JY	102.00	5.00	000.04
103	TDRG 33	104.00	5.76	823.04

104	TJT 50	100.00	5.16	873.04
105	ASHA	99.50	5.07	908.25
106	BA-1	99.00	5.30	888.25
107	BAHAR	111.50	5.35	896.00
108	ICPB 2078	99.00	4.82	780.67
	C.D.95%			
	Ci-Cj	12.38	0.45	159.52
	BiVi-BiVj	24.76	0.90	319.04
	BiVi-BjVj	27.69	1.01	356.70
	Ci-Vi	21.89	0.80	281.99

Sl. No.	Characteristics	Group No	State	Frequency	Percentage
1	Dave to 50% flowering	1	Early (61-90 days)	3	3
1.	Days to 50% nowening	2	Medium (91-130)	105	97
		1	Small (<4 cm)	1	1
2.	Pod size	2	Medium (4.1-5 cm)	8	7
		3	Long (>5 cm)	99	99
		1	18-278	1	1
Sl. No. Characteristics G 1. Days to 50% flowering	2	278-538	0	0	
	Yield (kg/ha)	3	538-798	28	26
		4	798-1058	67	62
		5	1058-1318	8	7
		6	1318-1578	3	3
		7	1578-1838	1	1

Fable 2: Grou	uping based	on three c	uantitative	traits
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Conclusion

More number of pods plant⁻¹ were observed for the early genotype namely ICPB 2051, WRG 204, WRG 197 and BSMR 243. These genotypes can be used for hybridization programme for disease resistance. Low incidence of wilt and Sterility Mosaic Disease was recorded for the entries, WRG 260, WRG283 and RVSA-9. These genotypes will be further tested in wilt sick plot for future use. The genotypes WRG 204, WRG260, WRG220, WRG197 and BSMR 243 were identified as good performer for most of the yield attributing traits and hence may be used as a parent for further breeding programme.

References

- 1. Anonymous. Guidlines for the conduct of test for distinctiveness, uniformity and stability on Pigeonpea (*Cajannus cajan* (L.) Millsp.), PPV & FRA, Govt. of India 2007, 1(1).
- 2. Anonymous. All India area, production and yield of total pulses 2016-17. Ministry of Agriculture, Govt. of India 2016-17, 11349.
- 3. Anonymous. Jharkhand, area, production and productivity of Pigeonpea. Indian Institute of Pulse Res. Kanpur, UP 2016-17.
- 4. Federer WT. Augmented designs. Hawiian Planters Records 1956;55:191-207.
- Manyasa EO, Silim SN, Githiri SM, Christiansen JL. Diversity in Tanzanian pigeonpea [*Cajanus cajan* (L.) Millsp.] landraces and their response to environments, Genet Resour Crop Evol 2007;55:379-387.
- 6. Moharand S, Narinder KG. Pigeonpea Genetic Resources and Its Utilization in India, Current Status and Future Prospects. J of Plant Sci & Res 2014;1(2):107.
- 7. Nethravathi KH, Patil BR. Character association and path coefficient analysis for yield and its components in pigeonpea. Kar. J of Agric Sci 2014;27(2):225-226.
- Rangare NR, Reddy GE, Kumar SR. Study of heritability, genetic advance and variability for yield contributing characters in pigeonpea (*Cajanus cajan L.* Millspaugh). Trends in Biosciences 2013;6(5):660-662.

- 9. Singh N, Kumar S. Chickpea germplasm catalogue. Indian Institute of Pulses Res 2004, 106.
- 10. Sturgis H. The Choice of Class Interval. J. of the American Statistical Association 1926;21(153):65-66.
- Techale, Birhan Habtamu, Zeleke Amsalu, Ayana Tilahun A, Chemeda A. Genetic variability, heritability and genetic advance in early maturing pigeon pea (*Cajanus cajan* L.) genotypes. World J of Agric Sci 2013;1(7):241-247.
- Upadhyaya HD, Reddy KN, Shivali Sharma, Varshney RK, Bhattacharjee R, Sube Singh *et al.* Pigeonpea composite collection and identification of germplasm for use in crop improvement programmes. Plant Genetic Resources 2011;9:97-108.
- Vijayalakshmi P, Anuradha CH, Pavan Kumar D, Sreelaxmi A, Anuradha G. Path Coefficient and Correlation response for Yield Attributes in Pigeon Pea (*Cajanas cajan* L.). International J. of Scientific and Res 2013;3(4):2250-3153.