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Short Communication

Assessment of morphological variation for different qualitative characters in pigeonpea [*Cajanus cajan* (L.) Millsp.] germplasm

SANDEEP KUMAR YADAV, NIRAJ KUMAR, HC LAL, KRISHNA PRASAD, CS MAHTO, SHREYA SEN and BINAY KUMAR

Birsa Agricultural University, Kanke, Ranchi; E-mail: nirajsri224@rediffmail.com

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ABSTRACT

The present study was conducted at the Birsa Agricultural University, Research Farm (Dryland Section), Kanke, Ranchi during *Kharif* season 2016-17 utilizing 104 genotypes of pigeonpea along with 4 checks *viz.,* ASHA, BA 1, BAHAR and ICPB 2078 evaluated in a augmented block design II with 4 blocks having spacing 1.5 m × 20 cm. Observation were recorded from each plants and checks for thirteen qualitative characters *viz.,* plant branching pattern, plant growth habit, flower colour, flower streaks, stem colour, pod colour, pod pubescence, pod surface stickiness, pod waxiness, pod constriction, seed shape, seed colour and seed colour pattern. Branching pattern was found to be either erect, semi-spreading or spreading while growth habit was either determinate or indeterminate. The characters like flower streaks, pod pubescence, pod stickiness and pod waxiness was categorized on the basis of presence or absence of the following characters. Stem colour was found either green or purple while flower colour was either yellow or purple. For pod colour five different categories were observed namely green, green with brown streaks, green with purple streaks, purple and dark purple. Hence the characterization of several qualitative traits will help in selection of suitable parent in formulating sound breeding programme.

Key words: Determinate, Indeterminate, Semi spreading, Spreading, Streak and qualitative traits

Pigeonpea [*Cajanus cajan* (L.) Millsp.] also known as Arhar, Red gram, Tur, Angole and Aahar etc. is often cross pollinated (20-70%) out crosses crop with 2n=2x=22 diploid chromosome number belongs to the family Leguminoseae. India is considered as the native of pigeonpea (Van der Maesen, 1980) because of its natural genetic variability available in the local germplasm and the presence of its wild relatives in the country. It is a deep rooted and drought-tolerant leguminous food crop and can grow tropical and sub-tropical regions.

Pigeonpea contains 62.78 g carbohydrates, 1.49 g fats and 21.7 g proteins per 100 grams. In India, pigeonpea is second most important pulse crop after chickpea (Sodavadiya *et al.* 2009 and Vijayalakshmi *et al.* 2013). It is widely grown in India accounting for 90 per cent of the world production (Rangare *et al.* 2013). Pigeonpea is grown in the area 5.13 mha with the production 4.23 mt and 824 kg/ha productivity respectively (Anon, 2016-17).

The good genotypes with broad genetic base have capability to perform good in adverse climatic situation and is most suitable for the region that faces moisture stress. Being a pulse, pigeonpea enriches soil through symbiotic nitrogen fixation, release soil–bound phosphorus, recycles the soil nutrients and add organic matter and other nutrients that make pigeonpea an ideal crop for sustainable agriculture. It is chiefly grown for its seed which are consumed either as dry splits (dal) or as a green vegetable.

It is also used on a limited scale as a fodder crop while its stem provides a good source of fuel. A flourishing plant breeding programme heavily relies upon existence of genetic variability present in the base population for various traits and information on genetic control of concerned trait is useful for effective execution of any breeding programme. Systematic study and characterization of germplasm is not only important for utilizing the appropriate attribute based donors, but also essential in the present era for protecting the unique pigeonpea genotypes.

The present study was conducted at the Birsa Agricultural University Research Farm (Dryland Section), Kanke, Ranchi during *Kharif* season 2016-17. A total of 104 genotypes (Table 1) of pigeonpea along with 4 checks *viz.,* ASHA, BA 1, BAHAR and ICPB 2078 were evaluated in a augmented block design II with 4 blocks. The spacing was 1.5 m X 20 cm observation were recorded from each plants and checks for thirteen qualitative characters *viz.,* plant branching pattern, plant growth habit, flower colour, flower streaks, stem colour, pod colour, pod pubescence, pod surface stickiness, pod waxiness, pod constriction seed shape, seed colour and seed colour pattern given in descriptor *i.e.* 1 to 9 scale (Table 3).

The collection, conservation and characterization of genotype 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. The progress of breeding programme depends mainly upon the magnitude of variability present in the breeding materials.

In pigeonpea, plant branching pattern type is important qualitative characters which was classified into three groups i.e. erect, semi-spreading and spreading (Table

2 & fig. 1). Seventy three genotypes had erect plant type whereas, twenty three and twelve genotypes had semi-spreading and spreading type respectively while semi-spreading genotypes (BAUPP 13-1, BRG 1, BSMR 243 and GRG 160) can be used as a donor parent in future breeding programme. This work supported by Katiyar *et al. (*2005), Manyasa *et al*. (2007) and Upadhayaya *et al* . (2011).

Branching pattern

Fig 1. Pie chart of branching pattern

Plant growth habit *i.e.* determinate and indeterminate (Fig 2), ninety two genotypes were found indeterminate type and sixteen genotypes were determinates type. Similar findings were obtained by the results of Manyasa *et al*. (2007), Neelam *et al*. (2014) and Kalihal *et al*. (2016).

Growth habbit

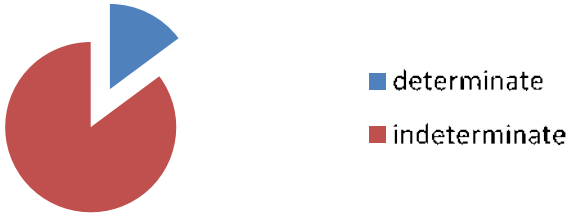

Fig 2. Pie chart representing growth habbit

In present investigation flower colour (Table 2) of eighty genotypes were found yellow whereas, twenty eight genotypes had purple. Similar results were shown by Manyasa *et al*. (2007), Provazi *et al.* (2007) and Neelam *et al*. (2014).

Flower streak (Table 2) in fifty two genotypes were absent while, twenty five genotypes had sparse, nineteen genotypes medium and twelve genotypes had dense streak. Manyasa *et al. (*2007), Kalihal *et al*. (2016) also characterized the pigeonpea flower streaks.

Sixty one genotypes had purple coloured stem while forty seven genotypes had green coloured stem (Table 2). The findings of Neelam *et al*. (2014) was in accordance with the result. Five different types of pod colour i.e. green, green with brown streaks, green with purple streaks, purple and dark purple (Table 2) was seen. Out of which, forty genotypes had green with brown streaks, twenty genotypes had green with purple streaks, twenty five genotypes had green, thirteen genotypes had purple and ten genotypes were founded dark purple coloured. Similar characterization of pod colour was done by Manyasa *et al*. (2007), Provazi *et al. (*2007) and Kalihal *et al*. (2016).

On the basis of presence and absence of pod pubescence (Table 2 and Fig 3), the genotypes were classified into two groups Fifty nine genotypes having pod pubescence whereas, forty nine genotypes does not have pod pubescence, which was supported by Manyasa *et al.* (2007) and Kalihal *et al.* (2016).

Seventy genotypes had stickiness on pod surface whereas, thirty eighty genotypes stickiness (Table 2 & Fig 3) was totally absent. This work supported by Manyasa *et al*. (2007) and Kalihal *et al. (*2016) in pigeonpea crops.

In terms of presence or absence of waxiness (Table 2 & Fig 3), sixty eight genotypes had pod waxiness while in forty genotypes waxiness was absent. Similar findings were obtained by Manyasa *et al.* (2007) and Kalihal *et al*. (2016) in pigeonpea crops.

Pod constriction was classified into two groups i.e. slight and prominent (Table 2). Sixty two genotypes had slight pod constriction while forty six genotypes falls in prominent pod constriction category. Similar characterization of pod constriction was done by Manyasa *et al*. (2007) and Kalihal *et al*. (2016) in pigeonpea crops.

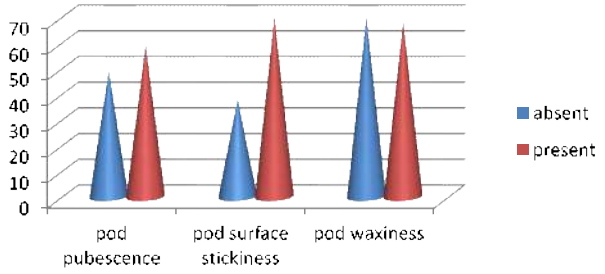

Fig 3. Graph showing different pod characters

Three different types of seed shape *i.e.* oval. Elongated and Globular (Table 2) were found. Out of total fifty two had oval genotypes, while fifty one genotypes had elongated and five genotypes had globular seed shape. This characterization was supported by Manyasa *et al*. (2007) and Provazi *et al*. (2007) in pigeonpea crop.

Seed colour was classified into five groups *i.e.* cream, brown, dark brown, grey and purple (Table 2). The seed colour in forty four genotypes was creamy while forty four genotypes had brown colour seventeen genotypes were dark brown, two genotypes was grey and the remaining one genotype was purple coloured. Similar characterization was revealed by the work of Manyasa *et al.* (2007), Provazi *et al*. (2007), Upadhayaya *et al*. (2011), Neelam *et al*. (2014) and Kalihal *et al*. (2016).

Two different seed colour patterns was obtained *i.e.* uniform and mottled (Table 2). fifty seven genotypes showed uniform pattern, while fifty one genotypes were mottled that was in accordance with the studies of Manyasa

Table 1. Details of test entries and checks

S.No.	Genotypes	S.No.	Genotypes	S.No.	Genotypes
1	AKTE 12-20	38	ICP 87119	75	WRG 222
2	AKTM 1-2	39	ICPB 2051	76	WRG 285
3	BRG 15-1	40	ICPB 2076	77	WRG 293
4	BSMR 579	41	BSMR 2	78	WRG 292
5	BAUPP13-1	42	BDN 02	79	WRG 204
6	BSMR 736	43	GJP 1205	80	WRG 252
7	BAUPP13-2	44	JKM 189	81	WRG 297
8	BRG 5	45	KBA 32-3	82	WRG 97
9	BRG 1	46	LRG 105	83	WRG 289
10	BSMR 853	47	LRG 151	84	WRGE 256
11	BDN 2008	48	LRG 107	85	WRG 65
12	BSMR 511	49	LAXMI	86	WRG 248
13	BRG 4	50	LRG 117	87	WRG 282
14	BSMR 846	51	LRG 170	88	WRG 286
15	BRG 15-2	52	LRG 133	89	RVKT 297
16	BSMR 243	53	LRG 104	90	GRG 107
17	IIPR-09-06	54	MAL 38	91	WRG 242
18	IIPR-09-09	55	NTL 624	92	WRG 223
19	CRG 82	56	NTPL 769	93	WRG 232
20	CORG2012-25	57	PT 0012	94	WRG 288
21	CORG 9701	58	RVKT 260	95	WRG 281
22	CRG 2010-9	59	RPS 2007-10	96	WRG 246
23	CRG 2012-30	60	RVSA 07-10	97	TS-3R
24	C-11	61	RVSA 12	98	TDRG 179
25	GJP 1406	62	RVSA 07-31	99	TRG 78
26	GJP 1207	63	RVSA 07-12	100	TDRG 107
27	GRG2013	64	RVSA -9	101	WRGE 140
28	GRG 1310	65	RVSA 2014-2	102	TRG 59
29	GJP 1401	66	RVSA 2014	103	TDRG 33
30	PBRG 2009-1	67	VIPULA	104	TJT 50
31	GRG 160	68	RVSA 7-15	105	ASHA (C)
32	WRG 102	69	WRG 278	106	BA-1 (C)
33	WRG 244	70	WRG 283	107	BAHAR(C)
34	ICP 2376	71	WRGE 248	108	ICPB 2078(C)
35	ICP 9174	72	WRG 220		
36	ICP 8863	73	WRG 197		
37	ICP 7035	74	WRG 260		

*Hyd. = Hyderabad

Table 2. Grouping of genotypes on the basis of character

S. No.	Characters	Grouping				
1.	Branching pattern	Erect (73)	Semi spreading (23)	Spreading (12)		
2.	Growth habbit	Determinate (16)	Indeterminate (92)			
3.	Flower colour	Yellow (80)	Purple (28)			
4.	Stem colour	Green (47)	Purple (61)			
5.	Flower streak	Absent (52)	Sparse (25)	Medium (19)	Dense (12)	
6.	Pod colour	Green (23)	Green with brown streak (40)	Green with purple streak (20)	Purple (13)	Dark purple (10)
7.	Pod pubescence	Absent (49)	Present (59)			
8.	Pod surface stickiness	Absent (38)	Present (70)			
9.	Pod waxiness	Absent (70)	Present (68)			
10.	Pod constriction	Slight (62)	Prominent (46)			
11.	Seed shape	Oval (52)	Elongated (51)	Globular (5)		
12.	Seed colour	Cream (44)	Brown (44)	Dark brown (17)		
13.	Seed colour type	Uniform (57)	Mottled (51)			

et al. (2007), Upadhayaya *et al.* (2011) and Kalihal *et al.* (2016).

The knowledge of variability for various qualitative characters will provide an estimate in formulating sound breeding programme and will also help breeder in selection of suitable parent for future breeding programme. Most of the qualitative characters are governed by monogene or oligogenes, thus can be easily transferred in progenies. This information used to studies. Phenotypically the characteristics of genotypes will also give opportunity for molecular screening of the genotype utilizing markers linked with the trait of interest. Seed colour, seed colur pattern and seed shape determines the usability of crop either in the form of vegetables or pulses. The characters like pod pubescence, waxiness and stickiness of pod and pod colour can be used to study the pod characters that may either

Table 3. Descriptors of different qualitative traits

Score	Qualitative traits (No. of Score)												
	PBP(3)	**PGH(2)**	**FC(5)**	**FS(5)**	**St.C(2)**	**PC(5)**	**PP(2)**	**PSS(2)**	**PW(2)**	**P. Con.(2)**	**SS(3)**	**SC(5)**	**SCP(2)**
1	-	Deter-minate	Light yellow	Absent	Green	Green	Absent	Absent	Absent		Oval	Cream	Uniform
2	-	Indeter-minate	yellow	-	Purple	Green with brown streaks	Present	Present	-	Slight	Elongated	Brown	Mottled
3	Erect (<30˚)	-	Orange yellow	Sparse	-	Green with purple streaks	-	-	-	-	Globular	Dark brown	-
4	-	-	Purple	-	-	Purple	-	-	-	-	-	Grey	-
5	Semi spreading (30-60˚)	-	Red	Medium	-	Dark purple	-	-	-	-	-	Purple	-
6	-	-	-	-	-	-	-	-	-	-	-	-	-
7	Spreading (>60˚)	-	-	Dense	-	-	-	-	-	Prominent	-	-	-
8	-	-	-	-	-	-	-	-	-	-	-	-	-
9	-	-	-	Mosaic	-	-	-	-	Present	-	-	-	-

PBP= Plant Branching Pattern, PGH=Plant Growth Habit, FC=Flower Colour, FS=Flower Streaks, StC=Stem Colour, PC=Pod Colour, PP=Pod Pubescence, PSS=Pod Surface Stickiness, PW=Pod Waxiness, P.Con.= Pod Constriction, SS=Seed shape, SC=Seed Colour, SCP=Seed Colour Pattern

favour or inhibit insect growth and development. Stem colour and flower streak can be used as an important morphological marker. The results also suggested about the genotype which could use as a parent for development of determinate variety along with the suitable branching pattern.

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