

Original Research Article

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Genetic Diversity for Quality Traits and Seed Yield in Pigeonpea [*Cajanus cajan* (L.) Millsp.]

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ABSTRACT

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A set of 75 pigeonpea genotypes were evaluated during *kharif* 2017-18, to determine the genetic divergence among these genotypes for 17 seed yield and quality characters and to identify divergent parents. UPGMA method of Hierarchical Cluster analysis used with City Block distances grouped these genotypes into ten distinct clusters comprising of one to twenty genotypes. Maximum inter cluster distance was observed between cluster II and VIII followed by cluster II and VI and cluster II and IX. Genotype of cluster II showed highest mean values for plant height, methionine content and tryptophan content whereas, genotypes in cluster VIII showed highest mean values for number of pods, number of seeds and biological yield. Hybridization between the genotypes belonging to these distinct clusters is expected to produce desirable transgressive segregants. Genotypes AL 1404, AL 1356-04, ICPL 89011-1, AL 668 and AH 09-38 were found promising for both yield and quality traits and also belonged to distant clusters hence can be utilized for future pigeonpea improvement programmes.

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is the fourth most important pulse crop of the world and second most important of India which is its largest grower and producer sharing about 80% of its area and production. It is a diploid ($2n=22$) often cross pollinated (20-70%) major grain legume crop and generally known as *arhar*, *red gram* and *tur*. It is a widely adapted, drought tolerant multiple use pulse crop cultivated throughout the semi arid tropics and subtropics (Saxena *et al.*, 2010). It is of considerable importance in areas of

South Asia (mainly on the Indian-subcontinent), Africa, the Caribbean and Latin America, where it is a prominent source of protein in the human diet (Vijayalakshmi *et al.*, 2013), as well as wood for fuel and light duty structural applications such as thatch for roofing. It is a promising source for protein, water soluble vitamins especially thiamine, riboflavin, niacin and choline (Sinha, 1977), carbohydrates 53.23% (Aruna and Devindra, 2016), crude fiber, fat, trace elements (Saxena *et al.*, 2010) and some minerals such as potassium, phosphorus, calcium and magnesium (Nwokolo, 1986). Among amino

acids, lysine concentration is high (7.79 g/16gN) in pigeonpea seed, but it is deficient in the sulphur containing amino acids cystine and methionine (0.24 and 0.16 g/100g protein, respectively) as per reports of Saxena *et al.*, (2008).

In India, though pigeonpea occupies second place among pulses after chickpea yet its productivity is stagnant since almost two decades due to many reasons major being different biotic and abiotic stresses and narrow genetic base which may be because of the frequent use of the same parents and their derivatives in breeding programmes (Kumar *et al.*, 2004). Pigeonpea germplasm represents a diverse set of landraces and heterogeneous feral forms that are adapted to various agro-ecological settings (Saxena, 2008). Despite extensive phenotypic diversity, molecular evidence from Simple Sequence Repeats (Odeny *et al.*, 2007) and Diversity Array Technology (Yang *et al.*, 2006) suggests very low genetic diversity within cultivated pigeonpea when compared to its wild relatives. Hence the search for new, diverse and useful genetic stocks and their precise evaluation for improvement programmes is never ending. The magnitude of genetic variability and diversity can determine the pace and quantum of genetic improvement through selection or hybridization followed by selection. The assessment of genetic diversity is important not only for crop improvements programmes but also efficient management and conservation of germplasm resources. Detailed evaluation of germplasm for good agronomy and quality and tolerance to biotic and abiotic stresses helps in the identification of superior genetic stocks and subsequently for their utilization in breeding programmes (Rana *et al.*, 2016). Further inclusion of all the component traits in selection scheme for intricate characters like yield and quality is impractical because of apparent reasons, knowledge of association of

various traits is fundamental in formulating efficient breeding programme.

Materials and Methods

The field experiment was conducted at research area of Pulses Section and the biochemical analysis of seed samples were carried out in Quality Lab of Oilseed Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. Seventy five pigeonpea genotypes of diverse origin (Table 1) were sown in Randomized Block Design with three replications during *kharif* season 2017-18. Each entry was sown in single row of 4 m length with 60 x 15 cm spacing. From every genotype, five competitive plants were randomly selected for recording of data for 17 seed yield and quality characters *viz.* Days to 50% flowering, Days to maturity, Plant height (cm), Number of branches per plant, Number of pods per plant, Biological yield per plant (g), Seed yield per plant (g), Harvest index (%), 100 seed weight (g), Number of seeds per pod, Crude protein (%), Ash content (%), Fat content (%), Crude fiber content (%), Methionine content (mg/g of protein), Tryptophan content (mg/g of protein) and Tannin content (mg/g). Unweighted Pair Group Method using Arithmetic Averages (UPGMA) method of Hierarchical Cluster analysis was used with City Block distances to classify the genotypes for their genetic diversity on the basis of 17 yield and quality variables.

Results and Discussion

The germplasm is the reservoir of genetic diversity, which is exploited to meet the changing needs for developing improved varieties of a crop. It is also important that considerable variability for economic traits must exist in the germplasm for profitable exploitation following recombination during selection. The need of parental diversity in

optimum magnitude to obtain superior genotypes for recovering transgressive segregants has also been repeatedly emphasized. Earlier workers considered distance in place of origin as index of genetic diversity and used it for selection of parents for hybridization. However, the genetic diversity of selected parents is not always based on factors such as geographic diversity or place of release or ploidy level (Durga *et al.*, 2005; Dwevedi and Gaibriyal, 2009; Sreelakshmi *et al.*, 2010 and Yadav *et al.*, 2010). Thus, for characterization of germplasm for genetic divergence and selection for suitable diverse genotypes should be based on sound statistical procedures, such as hierarchical cluster analysis. These procedures characterize genetic divergence using the criteria of similarity or dissimilarity based on the aggregate effect of a number of agronomically important characters. Unweighted Pair Group Method Using Arithmetic Averages (UPGMA) method of hierarchical cluster analysis was used with City Block distances to classify the 75 pigeonpea genotypes for their genetic diversity on the basis of 17 yield and quality variables.

The hierarchical cluster analysis grouped the 75 pigeonpea genotypes into ten distinct clusters (Table 2 and Fig. 1). The discrimination of germplasm lines into so many discrete clusters indicated presence of substantial amount of diversity in the material evaluated. Maximum number of genotypes were grouped in cluster I (20 genotypes) followed by cluster IV (18 genotypes), cluster VI (12 genotypes), cluster VIII and IX (six genotypes each), cluster III and V (five genotypes each) and cluster II, VII and X (one genotype each). Earlier workers have also reported existence of high degree of genetic diversity in pigeonpea material (Reddy *et al.*,

2015, Sreelakshmi *et al.*, 2011, Birhan *et al.*, 2013, Pandey *et al.*, 2013 and Rao *et al.*, 2013). Presence of substantial genetic divergence among the germplasm line screened in present investigation suggested that this material might serve as good source for selection of diverse parents for hybridization programme aimed at isolating desirable combination for seed yield as well as other characters.

In the present study, the maximum intra cluster distance was shown by cluster I followed by cluster IV and cluster VI, while, maximum inter cluster distance were showed between cluster II and cluster VIII followed by cluster II and cluster VI and cluster II and IX (Table 3) The estimates of average intra and inter cluster distances for ten clusters revealed that the genotypes of the same cluster have little genetic divergence from each other with respect to aggregate effects of 17 characters under study while much more genetic diversity was observed between the genotypes of different clusters. Since high or optimum genetic divergence is required between the parents of hybridization plan for obtaining high frequency of desirable recombinants with favourable chances of obtaining good segregants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances. The above findings are broadly in agreement with report of (Sreelakshmi *et al.*, 2011; Birhan *et al.*, 2013; Pandey *et al.*, 2013; Rao *et al.*, 2013; Shweta and Srivastava, 2013; Reddy *et al.*, 2015; Navneet *et al.*, 2017).

The cluster means for the 17 quantitative traits studied in genotypes of pigeonpea revealed considerable differences among all the clusters (Table 4). Cluster wise means for the characters studied were presented.

Table.1 List of genotypes included in the study

Sr. No.	Genotype	Sr. No.	Genotype	Sr. No.	Genotype
1	AH06-4	26	AH06-9	51	AL1356-04
2	H01-22	27	AL1577	52	Pusa855-2
3	AH06-5	28	AL1581	53	CORG9701
4	AL442	29	AL1590	54	EKD-12
5	H03-41	30	AL1508	55	AH09-8
6	AL601	31	ICPL87	56	AH09-13
7	Pusa2008-2	32	H05-15	57	ICPL91039
8	AL668	33	AH09-44	58	Pusa945
9	AL1685	34	AL1455	59	AH09-247
10	AH06-2	35	Vmbn-1	60	A293-4
11	AL1313	36	AL1484	61	ICPL91021
12	AL1389	37	AH10-27	62	ICPL92040
13	AL1401	38	H93-22	63	Scl-285
14	AL1404	39	H01-8	64	ICPL89011-1
15	AL1416	40	AH10-13	65	ICPL91008
16	AL1417	41	H04-21	66	AL1354-2-2
17	AL1419	42	AL609	67	H05-06
18	AL1421	43	AH10-08	68	AH09-18
19	AL1425	44	ICPL28323	69	B-17200
20	AL1431	45	Harsana	70	AH05-65
21	AL1434	46	D36	71	AH09-38
22	AL1439	47	H9343	72	UPAS120
23	AL1444	48	PA421	73	Manak
24	AL1452	49	AH09-06	74	Paras
25	AL1453	50	AL1366-1	75	PAU881

Table.2 Cluster membership and number of genotypes in each cluster of pigeonpea

Cluster No.	Name of Genotypes	No. of Genotypes
I	AH06-4 , AH06-5, AL1685, AL1439, AL1444, AL1452, AH 10-27, AH 10-13, HARSANA, D-36, AL 1366-1, AL 1356-04, PUSA 855-2, CORG 9701, AH09-8, AH 09-13, PUSA 945, ICPL 92040, ICPL 89011-1, MANAK	20
II	H01-22	1
III	AL 442, AL1577, H05-15, AH09-18, B-17200	5
IV	H03-41, AL 668, AL 1401, AL 1417, AL 1434, AL 1453, AL 609, ICPL 28323, AH09-06, AH09-247, A293-4, ICPL 91021, SCL-285, AL1354-2-2, AH05-65, UPAS 120, PARAS, PAU 881	18
V	AL 601, AL 1419, AL 1421, AH 06-9, EKD-12	5
VI	PUSA2008-2, AH06-2, AL1313, AL1581, ICPL 87, AH09-44, AL 1455, VMBN-1, AL 1484, H01-8, AH 10-08, ICPL 91008	12
VII	AL 1389	1
VIII	AL 1404, AL 1431, AL 1508, H93-22, H93-43, AH09-38	6
IX	AL 1416, AL 1590, H04-21, PA 421, ICPL 91039, H05-06	6
X	AL 1425	1
Total		75

Table.3 Inter and intra – cluster distances in pigeonpea

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X
I	59.73									
II	91.828	-								
III	128.458	183.262	47.782							
IV	136.886	196.792	99.17	58.191						
V	98.164	160.872	86.456	82.011	51.003					
VI	196.48	254.636	103.677	94.296	135.072	57.269				
VII	143.433	167.963	181.608	117.733	142.642	131.927	-			
VIII	242.836	305.746	145.505	139.129	178.281	84.229	156.12	45.88		
IX	179.27	245.287	134.239	87.489	121.263	82.856	108.198	104.285	48.66	
X	106.776	116.831	116.885	142.556	106.235	187.812	214.784	231.516	184.354	-

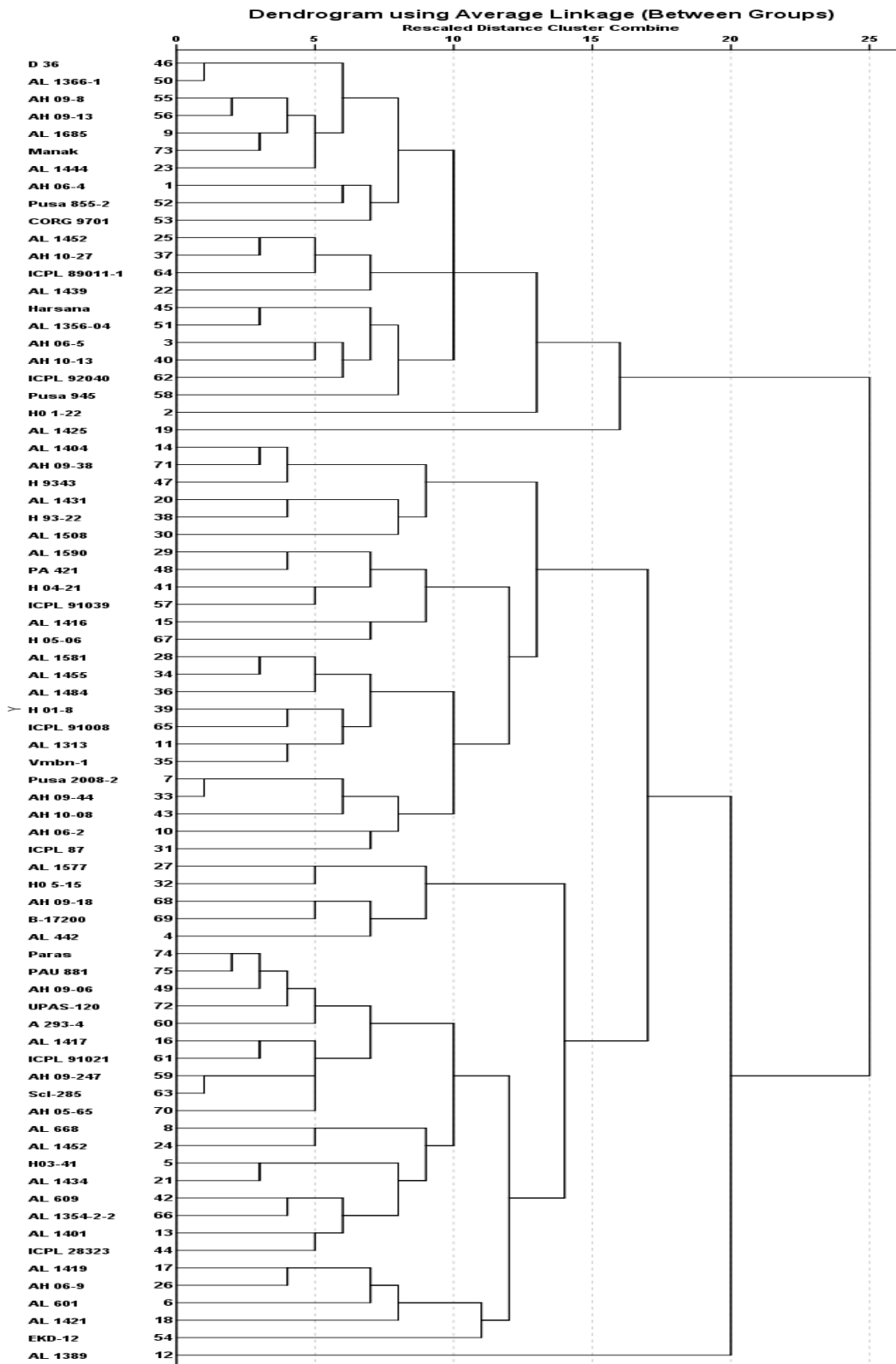
Diagonal- Intra-cluster distances, Off-diagonal- Inter-cluster distances

Table.4 Cluster means for different characters in pigeonpea

Characters	DF	DM	PH	NB	NP	BIOL	SY	SW	NS	HI	Ash	Fat	CF	CP	Met	Try	Tan
I	86.2	131.5	254.0	12.9	165.6	172.1	24.7	6.5	3.8	14.5	3.7	5.1	5.7	20.5	0.9	0.015	0.518
II	87.3	132.3	265.2	13.9	138.4	149.3	21.4	6.4	3.0	14.4	5.3	2.2	5.5	19.7	1.8	0.027	2.000
III	86.8	132.1	257.2	14.9	233.7	196.5	29.2	6.4	4.0	14.9	3.8	5.8	5.3	20.4	1.0	0.022	0.900
IV	86.4	132.6	253.8	15.0	205.8	232.5	29.6	6.3	3.9	12.8	3.9	5.0	5.7	20.9	0.9	0.017	0.746
V	87.2	129.6	248.0	13.3	198.0	202.6	28.7	6.7	3.9	14.2	4.5	4.7	6.1	20.0	1.1	0.022	0.590
VI	86.3	131.9	258.7	16.2	236.6	256.0	35.2	6.2	4.4	13.9	3.9	7.0	5.5	21.3	1.1	0.017	0.677
VII	86.0	132.3	258.1	15.7	153.7	257.7	39.3	6.1	4.3	15.3	5.5	2.2	7.0	21.4	1.2	0.019	0.050
VIII	87.1	130.9	255.0	16.3	264.4	272.8	40.0	6.5	4.6	14.6	4.0	6.1	6.0	20.8	0.9	0.016	0.796
IX	87.9	131.9	252.6	16.4	208.4	268.7	31.8	6.4	4.1	11.9	3.9	7.3	6.0	19.9	0.9	0.018	0.500
X	88.3	128.0	251.2	10.9	212.1	143.9	22.4	5.7	3.7	15.6	5.4	2.3	4.7	21.4	1.2	0.015	0.325
General Mean	86.9	131.3	255.4	14.5	201.7	215.2	30.2	6.3	4.0	14.2	4.4	4.8	5.8	20.6	1.1	0.019	0.710

DF: Days to flowering, DM: Days to maturity, PH: Plant height (cm), NB: Number of branches per plant, NP: Number of pods per plant, BIOL: Biological yield per plant (g), HI: Harvest index (%), SW: 100-seeds weight (g), NS: Number of seeds per pod, CP: Crude protein (%), CF: Crude fiber (%), Met: Methionine (mg per g of protein), Try: Tryptophan (mg per g of protein), Tan: Tannin (mg per g), SY: Seed yield per plant (g).

Fig.1



From the study, it was evident that genotypes under cluster X showed highest mean values for days to 50% flowering, harvest index and crude protein content and lowest for days to maturity, number of branches per plant, biological yield per plant, 100 seed weight, crude fibre and tryptophan content. Genotypes of cluster IX showed highest mean value for number of branches per plant and fat content and lowest for harvest index and methionine content. Genotypes under cluster VIII showed highest mean value for number of pods per plant, biological yield per plant, seed yield per plant and number of seed per pod and lowest for methionine content. Genotype of cluster VII showed highest mean value for ash, crude fibre and crude protein content and lowest for days to 50% flowering and tannin content. Genotypes under cluster V showed highest mean value for 100 seed weight and lowest for plant height. Genotypes of cluster IV showed highest mean value for days to maturity and lowest for methionine content. Genotype of cluster II showed highest mean value for plant height, methionine, tryptophan and tannin content and lowest for number of pods per plant, seed yield per plant, number of seed per pod, fat content and crude protein content.

Based on yield and quality traits studied, the genotypes *viz.*, AL1404, AL1356-04, ICPL 89011-1, H 93-43, AH 09-38, AL1389, AL 668, ICPL 91039, AH 06-4 and AL 609 were found genetically diverse and superior. The present study was intended to examine the genetic diversity for yield and quality traits, will be of great use and will serve as a stepping stone in formulation and effective execution of future breeding programmes in pigeonpea. To initiate a systematic breeding programme and to develop pigeonpea varieties with combination of high seed yield and quality the above specified genotypes should be used in pigeonpea breeding programmes for further improvement.

From the findings of present investigation, it could be concluded that the 75 pigeonpea genotypes differed significantly for all yield and quality traits. The maximum inter cluster distance was observed between cluster II (H 01-22) and cluster VIII (AL 1404, AL 1431, AL 1508, H 93-22, H 93-43 and AH 09-38) followed by between cluster II and cluster VI and cluster II and cluster IX. Based on yield and quality traits studied, the genotypes *viz.*, AL 1404, AL 1356-04, ICPL 89011-1, H 93-43, AH 09-38, AL 1389, AL 668, ICPL 91039, AH 06-4 and AL 609 showed sufficient genetic diversity and contrasting characters and these can be used in pigeonpea breeding programmes for further improvement.

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