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Agro-Morphological Characterization of Pigeonpea (*Cajanus cajan* (L.) Millsp.) germplasm

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ABSTRACT: Genetic variability is prerequisite for any crop improvement programme and phenotypic characterization of crop genetic resources generates important information for plant breeders, therefore the present investigation was undertaken in which three hundred five pigeonpea accessions were evaluated and morphological characterization was carried out during *kharif* 2021 at Pulses Research Station, SDAU Sardarkrushinagar (Gujarat) under Consortium Research Platform on Agro-biodiversity. Out of three hundred five accession one accessions did not germinate. Majority of the accessions showed very good early plant vigour (212 acc.), semi spreading plant growth habit (292 acc.), indeterminate plant type (304 acc.), yellow flower colour (275acc.), green stem colour (300 acc.), glabrous leaf pubescence (304acc.), sparse streak (198 acc.), glabrous pod pubescence (304 acc.), cylindrical pod shape (304 acc.), green and purple pod colour (293 acc.), very large seeded (19 acc.), plain seed colour pattern (283acc.), medium seed eye width (40 acc.), orange base seed colour (96acc.), globular seed shape (38 acc.) and very low biotic stress susceptibility (4 acc.). Wide range of variability was observed for days to flowering, primary branches, days to maturity and 100 seed weight (9.0-14.0g). Considering the wide range of variability for qualitative and quantitative characters, germplasm has high potential which can be utilized in future pigeonpea improvement programmes. This study thus provides a foundation for the selection of parental material for genetic improvement.

Keywords: Pigeonpea, Agro-biodiversity, Characterization, Germplasm.

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is the second most important pulse crop of India after chickpea, commonly known as arhar, red gram and tur.It is an important crop for millions of people living in dry regions of the world as it is a multipurpose crop that integrates crop and livestock production, thus contributing to food security (Ayenan, 2017). It is a rich source of protein, carbohydrate, vitamins, lipids and certain minerals. Compared to other food legumes, breeding in pigeonpea has been more challenging due to various crop specific traits and highly sensitive nature to biotic and abiotic stresses. Germplasm is vital resource in generating new plant types having desired traits that help in increasing crop production with quality and thus improve the level of human nutrition. The search for diversity in a germplasm collection is a way of identifying desirable genes for future utilization in breeding, where the diversity in crop species usually depends on mutation, recombination, selection and genetic drift (Bhandari *et al.*, 2017). Germplasm characterization and documentation are important activities in plant genetic resources management and it eases the data retrieval and short listing of accessions for the genetic improvement. Germplasm utilization is increased if detailed characterization of data is obtained for individual accessions, which should include qualitative and quantitative phenotypic traits, genotypic data and responses to biotic and abiotic stresses. Detailed characterization of data is lacking in pigeonpea collections, which emphasizes the need for further data collection and characterization which are the pre-requisite for the utilization of available diversity in the pigeonpea improvement programme. Plant genetic resources are invaluable source of genes and gene complexes for yield and several biotic and abiotic factors and provide raw materials for further genetic improvement (Patel *et al*., 2021). Therefore, the collection of pigeon pea germplasm and its proper characterization, evaluation, conservation and utilization in improvement programmes assume great significance, especially in view of climate change. Genetic diversity in a crop species can be studied using different methods including morphological and/or phenotypic, biochemical and molecular markers (Mehmood *et al*., 2007). In the past, morphological traits, both qualitative and quantitative have been successfully used to study genetic diversity in pigeonpea (Kallihal *et al*., 2016; Navneet *et al*., 2017; Zavinon *et al*., 2019). A positive association between two desirable traits makes the job of the plant breeder easy for improving both traits at a time. The present investigation was carried out to analyze the genetic divergence existing in the crop. This information is highly useful for breeders in the selection of parents and breeding material for the development of high yielding varieties of pigeonpea. Hence, the present study was under taken at Pulses Research Station, Sardarkrushinagar Dantiwada Agriculture University, Sardarkrushinagar through the All India Coordinated Research Project on Pigeonpea under Consortium Research Platform on Agro biodiversity to characterize 305 accessions of pigeonpea germplasm (Table 1) during *kharif* 2021.This study aims to assess the morphological diversity in a collection of pigeon pea accessions with the objective of evaluating the phenotypic variations.

Table 1: List of pigeonpea accessions.

Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes
1.	IC261336	64.	IC397573	127.	IC468349	190.	IC468414	253.	IC468479
2.	IC261337	65.	IC407511	128.	IC468350	191.	IC468415	254.	IC468480
3.	IC261338	66.	IC407517	129.	IC468351	192.	IC468416	255.	IC468481
4.	IC261341	67.	IC407531	130.	IC468352	193.	IC468417	256.	IC468482
5.	IC261346	68.	IC407537	131.	IC468353	194.	IC468418	257.	IC468483
6.	IC261348	69.	IC407543	132.	IC468354	195.	IC468419	258.	IC468484
7.	IC261354	70.	IC407565	133.	IC468355	196.	IC468420	259.	IC468485
8.	IC261357	71.	IC407572	134.	IC468356	197.	IC468421	260.	IC468486
9.	IC261370	72.	IC407587	135.	IC468357	198.	IC468422	261.	IC468488
10.	IC261372	73.	IC407589	136.	IC468358	199.	IC468423	262.	IC468489
11.	IC261377	74.	IC407592	137.	IC468359	200.	IC468424	263.	IC468491
12.	IC261378	75.	IC407600	138.	IC468360	201.	IC468425	264.	IC468493
13.	IC261381	76.	IC407644	139.	IC468362	202.	IC468426	265.	IC468494
14.	IC261383	77.	IC407650	140.	IC468363	203.	IC468427	266.	IC468495
15.	IC298607	78.	IC407661	141.	IC468364	204.	IC468428	267.	IC468498
16.	IC298609	79.	IC407669	142.	IC468365	205.	IC468429	268.	IC468499
17.	IC298963	80.	IC407678	143.	IC468366	206.	IC468430	269.	IC468500
18.	IC323225	81.	IC407689	144.	IC468367	207.	IC468431	270.	IC489681
19.	IC323233	82.	IC407710	145.	IC468368	208.	IC468432	271.	IC489694
20.	IC323237	83.	IC407720	146.	IC468369	209.	IC468433	272.	IC489720
21.	IC323242	84.	IC407722	147.	IC468370	210.	IC468434	273.	IC489884
22.	IC323245	85.	IC407732	148.	IC468371	211.	IC468435	274.	IC489886
23.	IC323246	86.	IC407751	149.	IC468372	212.	IC468436	275.	IC489889
24.	IC323252	87.	IC407755	150.	IC468373	213.	IC468437	276.	IC489915
25.	IC323254	88.	IC407761	151.	IC468374	214.	IC468438	277.	IC489945
26.	IC323257	89.	IC407768	152.	IC468375	215.	IC468439	278.	IC489948
27.	IC323264	90.	IC407769	153.	IC468376	216.	IC468440	279.	IC490167
28.	IC323283	91.	IC407770	154.	IC468377	217.	IC468441	280.	IC523484
29.	IC323303	92.	IC407771	155.	IC468378	218.	IC468442	281.	IC523485
30.	IC323308	93.	IC407772	156.	IC468379	219.	IC468443	282.	IC523516
31.	IC328727	94.	IC407801	157.	IC468380	220.	IC468444	283.	IC523517
32.	IC333158	95.	IC407823	158.	IC468381	221.	IC468445	284.	IC523519
33.	IC338829	96.	IC407852	159.	IC468382	222.	IC468446	285.	IC523521
34.	IC339041	97.	IC417485	160.	IC468383	223.	IC468447	286.	IC523546
35.	IC339044	98.	IC421058	161.	IC468384	224.	IC468448	287.	IC523569
36.	IC339045	99.	IC442233	162.	IC468385	225.	IC468449	288.	IC523576
37.	IC343908	100.	IC446483	163.	IC468386	226.	IC468451	289.	IC523622
38.	IC343916	101.	IC468002	164.	IC468387	227.	IC468452	290.	IC523623
39.	IC343956	102.	IC468003	165.	IC468388	228.	IC468453	291.	IC523630
40.	IC343966	103.	IC468038	166.	IC468389	229.	IC468454	292.	IC523639
41.	IC369028	104.	IC468055	167.	IC468390	230.	IC468455	293.	IC523645
42.	IC369035	105.	IC468059	168.	IC468391	231.	IC468456	294.	IC523647
43.	IC369049	106.	IC468073	169.	IC468392	232.	IC468457	295.	IC523648
44.	IC369052	107.	IC468079	170.	IC468393	233.	IC468458	296.	IC525286
45.	IC369054	108.	IC468082	171.	IC468394	234.	IC468459	297.	IC525293
46.	IC369057	109.	IC468083	172.	IC468395	235.	IC468460	298.	IC525298
47.	IC369060	110.	IC468085	173.	IC468396	236.	IC468461	299.	IC525299
48.	IC369064	111.	IC468086	174.	IC468397	237.	IC468462	300.	IC525303
49.	IC369067	112.	IC468092	175.	IC468398	238.	IC468463	301.	IC109901
50.	IC369068	113.	IC468094	176.	IC468399	239.	IC468464	302.	IC525757
51.	IC369111	114.	IC468099	177.	IC468400	240.	IC468466	303.	IC245484
52.	IC369118	115.	IC468100	178.	IC468401	241.	IC468467	304.	IC407467
53.	IC369575	116.	IC468105	179.	IC468402	242.	IC468468	305.	IC527696
54.	IC369681	117.	IC468108	180.	IC468403	243.	IC468469		
55.	IC382850	118.	IC468122	181.	IC468404	244.	IC468470		
56.	IC396078	119.	IC468156	182.	IC468406	245.	IC468471		
57.	IC396813	120.	IC468342	183.	IC468407	246.	IC468472		
58.	IC396817	121.	IC468343	184.	IC468408	247.	IC468473		
59.	IC397213	122.	IC468344	185.	IC468409	248.	IC468474		
60.	IC397312	123.	IC468345	186.	IC468410	249.	IC468475		
61.	IC397359	124.	IC468346	187.	IC468411	250.	IC468476		
62.	IC397475	125.	IC468347	188.	IC468412	251.	IC468477		
63.	IC397493	126.	IC468348	189.	IC468413	252.	IC468478		

MATERIAL AND METHODS

The trial was conducted in Augmented Block Design (ABD) during *Kharif* 2021 at Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat which is located at 72.12 º E longitude, 24.9 º latitude and 154.5 m altitude above MSL. These accessions were divided into eight blocks and each block consisted of 50 accessions with two check varieties *viz*., BDN 711 and GT 101. The soil of the field was sandy loam in texture with pH value of 7.7 to 8.00 having good physical and chemical properties (Organic Carbon = 0.07, K_2O = 234.0 kg/ha and P_2O_5 = 56.0 kg/ha).

The experimental unit was a two-row plot of 4.0 m long, spaced at 0.60 m apart. Fertilizer dose of 25:50:00 (NPK) were applied as basal. Plots were thinned down after two weeks of crop emergence and plant-to-plant distance of 0.20 m was maintained. The experimental year showed different temperature regimes, humidity, rainfall and sunshine hours during the crop duration (Table 2). All the other recommended agronomical packages and practices were followed to raise a good crop. Data was collected based on the minimal descriptors released by NBPGR, New Delhi (Mahajan *et al*., 2000) and the list of pigeonpea descriptor released(Anonymous,2020). Five representative plants in each accession were tagged for recording the qualitative and quantitative traits (Anonymous, 2020). Plant protection measures were taken as and when required to raise a good crop.

Table 2: Weather data of experimental location: Sardarkrushunagar (*Kharif* 2021).

Sr. No.	Week No.	Temperature (°C)		Humidity (%)		Wind speed (km/h)	Rain fall (mm)	Rainy Days
		Maximum	Minimum	0830 Hr	1730 Hrs			
1.	26	37.2	25.6	79	65	7.9	9.0	1
2.	27	38.0	26.8	76	65	11.1	0.0	0
3.	28	39.1	26.0	81	63	6.7	47.0	2
4.	29	36.1	26.2	82	75	7.4	8.0	1
5.	30	31.6	24.8	85	90	10.2	65.5	3
6.	31	29.0	24.3	84	85	8.6	17.5	2
7.	32	33.5	25.9	80	74	5.4	0.0	0
8.	33	36.5	25.7	73	68	5.9	0.0	0
9.	34	36.9	26.0	76	67	4.9	2.0	0
10.	35	35.6	24.7	82	66	5.3	36.5	2
11.	36	34.4	24.9	88	83	5.7	41.0	3
12.	37	32.9	24.2	85	83	3.3	109.5	5
13.	38	33.5	23.6	80	77	4.7	6.0	1
14.	39	33.1	24.9	81	77	5.1	87.5	2
15.	40	34.7	25.0	78	70	3.9	0.0	0
16.	41	37.4	25.8	77	62	2.1	0.0	0
17.	42	36.9	21.1	69	62	2.2	0.0	0
18.	43	36.2	18.0	66	59	4.7	0.0	0
19.	44	33.3	15.9	69	50	2.3	0.0	0
20.	45	34.3	14.8	65	41	2.8	0.0	0
21.	46	32.4	13.6	71	51	2.7	0.0	0
22.	47	28.9	17.5	77	55	2.6	31.0	2
23.	48	31.6	15.4	74	47	2.6	0.0	0
24.	49	28.1	13.6	70	35	2.9	0.0	0
25.	50	26.5	10.6	70	32	2.7	0.0	0
26.	51	25.2	7.6	70	30	3.3	0.0	0
27.	52	27.1	11.7	76	41	2.8	3.0	1

RESULT AND DISCUSSION

Genetic diversity analysis in pigeonpea is crucial for effective breeding and germplasm conservation. Previous studies examined the genetic diversity of the crop using morphological and agronomic traits (Manyasa *et al*., 2008). The preliminary characterization of 305 accessions of pigeonpea germplasm were worked out for 20 agro-morphological characters *viz*., early plant vigour, plant growth habit, plant habit, days to flowering, base flower colour, stem colour, leaf pubescence, streaks pattern, pod pubescence, pod shape, pod colour, days to 80% maturity, 100 seed weight (g), seed colour pattern, seed eye width, base seed colour, seed shape, biotic stress susceptibility, plant height and pod size. Wide range of variability in both quantitative and qualitative characters was observed (Patel *et al*., 2020). The range of variability and frequency observed in qualitative characters are given in Table 3. Majority of the accessions showed very good early plant vigour (212 acc.), semi spreading plant growth habit (292 acc.), indeterminate plant habit (304 acc.), medium days to flowering (69 acc.), late days to flowering (228 acc.), yellow flower colour (275acc.), green stem colour (300 acc.), glabrous leaf pubescence (304acc.), sparse streak (198 acc.), uniform streak pattern (20 acc.), glabrous pod pubescence (304 acc.), cylindrical pod shape (304 acc.), green and purple pod colour (293 acc.), mid early maturing (30 acc.), medium maturity (119 acc.), very large seed (19 acc.), plain seed colour pattern (283 acc.), medium seed eye width (40 acc.), orange base seed colour (96acc.), globular seed shape (38acc.) and very low biotic stress susceptibility (300 acc.), such germplasm with resistance or tolerance to biotic stress can be an asset to plant breeder in developing resistant cultivar.

The wide range of variation was observed for early plant vigour (Good to Very good), plant growth habit (Erect & compact to semi spreading), plant habit (Indeterminate), plant height (199-226 cm), days to flowering (125-168 days), base flower colour (Yellow to orange yellow), primary branches (7.0-10.0), days to maturity (175-218 days), stem colour (Green), leaf pubescence (Glabrous), streak pattern (Sparse streak to uniform coverage of second colour), pod pubescence (Glabrous), pod shape (Cylindrical), pod colour (Green to green & purple), pod size (Short to long), 100 seed weight (9.0-14.0g), seed colour pattern (Plain to Speckled), seed eye width (Narrow), base seed colour (White to dark purple), seed shape (Oval to elongate), pods per plant (84-178), pod length (4.0-6.0 cm) and seeds per pod (4.0-5.0) showed wider ranges. The preliminary characterization and descriptive statistics revealed that seed yield, plant height, 100 seed weight, pod length, days to 50% flowering and seeds per pod were the most variable characters. Earlier reports by Kimaro *et al*. (2021); Ramesh (2017); Sahu *et al*. (2018); Rupika and Kannan (2014); Upadhyaya *et al*. (2007); Upadhyaya *et al*. (2005) have also exhibited the presence of variation for different characters in pigeonpea germplasm accessions.

Mean data revealed that some of the accessions showed outstanding performance for different agro-morphological traits *viz*., plant height IC525757 (162.0 cm) and IC527696 (255.0 cm), primary branches per plant IC261341 (5.2) and IC468389 (13), pods per plant IC525303 (31.4) and IC298609 (225), pod length IC498473 (2.92 cm) and IC525757 (6.54 cm), seeds per pod IC468472 (3.2) and bold seed IC343916. These accessions with potential for different agro-morphological traits may be utilized in crop improvement program through hybridization and selection for developing superior genotypes for yield as well as for biotic and abiotic resistance.

Table 3: Frequency distribution of morphological characters in pigeonpea.

Sr. No.	Characters	Score				
1.	Early Plant Vigour	1: Poor (9)	2: Good (83)	3: Very good (212)	99: Others (0)	
2.	Plant growth habit	1: Erect & Compact (12)	2: Semispreading (292)	3: Spreading (0)	4: Trailing(0)	99: Others(0)
3.	Plant habit	1: Determinate (0)	2:Semideterminate (0)	3: Indeterminate (304)	99: Others (0)	
4.	Days to flowering	3: Early 61-90 days (02)	5: Medium 91-130 days (69)	7: late131-160 days(228)	9: Very late >160 days (5)	
5.	Base flower colour	1: Ivory(0)	2: Light yellow(0)	3: yellow (275)	4: Orange yellow(29)	99: Others (0)
6.	Stem colour	1: Green (300)	2: Sunred (0)	3: Purple (4)	4: Dark purple (0)	99: Others (0)
7.	Leaf pubescence	1: Glabrous (304)	2: Pubescent (0)	99: Others (0)		
8.	Streaks pattern	3: Sparse streaks (198)	5: Medium streaks (60)	7: Dense streaks (26)	9: Uniform coverage of second colour (20)	99: Others (0)
9.	Pod pubescence	1: Glabrous (304)	2: Pubescent (0)	99: Others (0)		
10.	Pod shape	1: Flat (0)	2: Cylindrical (304)	99: Others (0)		
11.	Pod colour	1: Green (05)	2:Purple (05)	3: Green &Purple (293)	4: Dark purple (1)	99: Others (0)
12.	Days to 80% maturity	1: Very Early <130 days (1)	2: Early 131-150 days(4)	3: Mid early 151-165 days (30)	4: Medium 166-185 days (119)	5: Late 186-200 days (123) 6: Very late >200 (27)
13.	100 seed weight(g)	3: small <7 (7)	5: medium7-9 (203)	7: Large>9-11 (75)	9: Very large>11 (19)	
14.	Seed colour pattern	1: Plain (283)	2: Mottled (8)	3: Speckled (11)	4: Mottled & Speckled (2)	99: Others (0)
15.	Seed eye width	3: Narrow (264)	5: Medium (40)	7: Wide (0)	99: Others (0)	
16.	Base seed colour	1: white (41) 2: cream(135)	3: Orange (96) 4. Light brown(06)	7. Grey(03) 8: Purple(01) 9: Dark purple (03)	99: Others (19)	
17.	Seed shape	1: Oval (183)	2: Globular (38)	3: Square (77)	4: Elongate (5)	99: Others (1)
18.	Biotic stress susceptibility	1: Very low(300)	3: Low (4)	5: Intermediate(0)	7: High (0)	9: Very high (0)
19.	Plant height	1: Short (0)	2: Medium(0)	3: Tall(304)		
20.	Pod size	1: Short (118)	2: Medium(177)	3: Long(09)		

CONCLUSION

Information on genetic variability among the existing pigeonpea genotypes will increase the efficiency of crop genetic improvement. The present study affirmed that characterization and evaluation of 305 accessions of pigeonpea for agronomic traits are important in discerning genetic variability that can be exploited in plant breeding. The phenotypic traits therefore provide a useful measure of genetic distances among the pigeonpea genotypes and will enable the identification of potential parental materials for future breeding efforts especially in identifying donors for economic traits.

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Conflict of Interest. None.

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