Short Note [Nota Corta]

MORPHOLOGICAL CHARACTERIZATION OF PIGEON PEA [*Cajanus cajan* (L.) Millspaugh] ACCESSIONS FOR AGRONOMIC TRAITS IN ASSOSA DISTRICT, NORTHWESTERN ETHIOPIA †

[CARACTERIZACIÓN MORFOLÓGICA DE ACCESIONES DEL GANDUL [*Cajanus cajan* (L.) Millspaugh] POR RASGOS AGRONÓMICOS, EN EL DISTRITO DE ASSOSA, NOROESTE DE ETIOPÍA]

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SUMMARY

Background: Pigeon pea is a tropical grain legume being cultivated as important pulses for human food, feed and soil fertility improvement. Pigeon pea research in terms of crop improvement is still at a low level in Ethiopia. **Objective:** To estimate the Genetic variability of pigeon pea accessions with respect to important qualitative and quantitative traits and select high yielding grain and promising traits for variety development. **Methodology**: Treatments consisted in twenty two pigeon pea accessions (MPG1, MPG2, MPG3, MPG4, MPG5, MPG6, MPG7, MPG8, MPG9, MPG10, MPG11, MPG12, MPG13, MPG14, MPG15, MPG16, MPG17, MPG18, MPG19, MPG20, MPG21 and MPG22) collected from Assosa area. Treatments were laid out in a Randomized Complete Block Design with three replications. **Results:** Qualitative characteristics recorded for accessions showed different modalities and frequencies at vegetative growth stage with the qualitative traits dominated were semi-spreading growth habit 65 %, leaflet shape with lanceolate 70 %, color about 44 % of the accessions exhibited yellow, seed size where 55 % accounted large sized, seed color pattern: 52% of accessions showed plain, pod color where 56 % genotypes had purple, seed with red dominated was 50 % and 71 % of accessions had totally pigmented pod. With respect to quantitative traits, genotypes accessions MPG11 and MPG15 had relatively higher grain yield (> 4000 kg/ ha) with the highest grain yield recorded for genotype MPG18. **Implications:** The investigation of the present study for morphological evaluation of genotype Pigeon pea exhibited genetic variability among accession. **Conclusion**: Agronomic traits such as plant height, branches per plant, pods per plant, seeds per pod, pod length, pod width, hundred seed weight and grain yield for accessions were exhibited significant differences which suggest high yielding accessions could be directly recommended for production while others could be utilized effectively to develop high yielding varieties through hybridization followed by selection.

Key words: Genetic variability; Food; Hybridization; Legume Pulses; Variety.

RESUMEN

Antecedentes: El gandul es una leguminosa de grano tropical que se cultiva para la alimentación humana, los piensos y la mejora de la fertilidad del suelo. La investigación sobre el gandul en términos de mejora de cultivos todavía se encuentra en un nivel bajo en Etiopía. **Objetivo:** Estimar la variabilidad genética de las accesiones de gandul con respecto a rasgos cualitativos y cuantitativos importantes y seleccionar granos de alto rendimiento y rasgos prometedores para el desarrollo varietal. **Metodología**: Los tratamientos consistieron en veintidós accesiones de gandul (MPG1, MPG2, MPG3, MPG4, MPG5, MPG6, MPG7, MPG8, MPG9, MPG10, MPG11, MPG12, MPG13, MPG14, MPG15, MPG16, MPG17, MPG18, MPG19, MPG20, MPG21 y MPG22) recolectado en el área de Assosa. Los tratamientos se dispusieron en un Diseño de Bloques Completos Al Azar con tres repeticiones. **Resultados:** Las características cualitativas registradas para las accesiones mostraron diferentes modalidades y frecuencias en la etapa de crecimiento vegetativo con los rasgos cualitativos que dominaron fueron hábito de crecimiento semi-extendido 65 %, forma de folíolos lanceolados 70 %, alrededor del 44 % de las accesiones exhibieron amarillo, tamaño de semilla donde el 55 % representaron un tamaño grande, el 52 % de las muestras mostraron vaina liso, el 56 % de los genotipos tenían color púrpura, el color de semilla con predominio rojo

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† *Submitted June 11, 2024 – Accepted October 1, 2024. http://doi.org/10.56369/tsaes.5681*

ISSN: 1870-0462.

representó el 50 % y en la vaina el 71 % de las muestras estaban totalmente pigmentados. Con respecto a los rasgos cuantitativos, los genotipos. Las accesiones MPG11 y MPG15 tuvieron un rendimiento de grano relativamente mayor (> 4000 kg/ha) y el rendimiento de grano más alto se registró para el genotipo MPG18. **Implicaciones:** La investigación del presente estudio para la evaluación morfológica del genotipo del gandul exhibió variabilidad genética entre las accesiones. **Conclusión:** Los rasgos agronómicos: altura de la planta, ramas por planta, vainas por planta, semillas por vaina, longitud de vaina, ancho de vaina, peso de cien semillas y rendimiento de grano para las accesiones mostraron diferencias significativas que sugieren que las accesiones de mayor rendimiento podrían recomendarse directamente para la producción mientras otros podrían utilizarse eficazmente para desarrollar variedades de alto rendimiento mediante hibridación seguida de selección.

Palabras clave: Variabilidad genética; Alimento; Hibridación; legumbres; legumbres; Variedad.

INTRODUCTION

Pigeon pea (*Cajanus cajan* (L.) Millspaugh) is a shrub, which plays an important role in food security, nutritional balance and poverty alleviation in sub-Saharan Africa, developing countries of tropical and subtropical environments (Géofroy *et al.*, 2020). It is often cross pollinated crop with 2n=2x=22 diploid chromosome number which belongs to the family *Leguminoseae*. As a crop, pigeon pea is capable of growing in dry seasons exceeding six months or rainfall less than 300mm but performs best to areas with 600-1,000 mm average annual rainfall (Cook *et al*., 2005), which plays an important role in food security, nutritional balance and poverty alleviation in Sub-Saharan Africa (Rao *et al*., 2002). It is predominantly cultivated in the developing countries of tropical and subtropical environments (Suman *et al*., 2017). Africa, with 19.03 % of the world's total production represents the second producer followed by Americas 3.15 % and behind Asia 77.82 % (Anon, 2017a). Various parts of pigeon pea plant are used for food consumption, as medicine for cure diseases. Leaves are used in traditional medicine to cure diseases such as malaria and fever, in Benin (Dansi *et al*., 2012; Ayenan *et al*., 2017; Zavinon *et al.*, 2018), in Nigeria (Aiyéloja and Bello, 2006; Oladunmoye *et al*., 2011) and in South Africa (Mander *et al.*, 1996). In most African countries, seeds are used in human nutrition as food in combination with cereals and in commercialization (Odeny, 2007). It has been produced high quality fodder and can be integrated to crop livestock farming system as feed supplements (Rao *et al.,* 2003).The crude protein content in pigeon pea seed ranges between 8-22 % (Saxena, *et al.*, 2006) and whereas, the crude protein of pigeon pea leaf ranges between 10-18 % (Denbela *et al*., 2018). Its dry matter yield ranges from 20-40 t / ha dry matter (DM) of fodder and stalks have been reported in Sahel (FAO, 2016) and whereas, up to 40 t/ ha of DM could be expected under optimal conditions (ILRI, 2013). The integration of well-adapted protein bank legumes to supplement poor quality feeds in animal production systems has the potential to improve forage quality exclusively in the dry seasons and this strategy is being adopted much more widely by smallholders in many countries (Olayeki *et al.*, 2009). Accordingly, Beef cattle In the USA, yearling cattle intensively grazing pigeon pea in late-summer achieved an average daily weight gain close to 1.0 kg/ d (Rao and Northup, 2012) in Nigeria, fresh pigeon pea was found to be preferred by sheep among 8 browse species (Omokanye *et al.*, 2000). In Zimbabwe, fresh pigeon pea included at 30 % DM as a protein source to supplement a poor quality maize Stover diet increased total voluntary dry matter intake by 20 % and total diet organic matter (OM) digestibility from 52 to 61 % (Masama *et al*., 1997). Unlike other legume crops, pigeon pea is highly regarded for its multiple uses. Its grains are rich in minerals, vitamins and protein is also of excellent quality, being high in lysine (Njung'e *et al*., 2016). Apart from the use of grain, farmers make use of pigeon pea in various ways depending on their ethnic groups and locality. Medicinal uses of pigeon pea encompasses to treat ailments such as dizziness, snake bite, measles are determined by farmers' location and ethnic group (Tariku *et al*., 2022).

Various a biotic and biotic stresses, as well as lack of quality seeds and poor crop husbandry, comprise the main factors contributing to the low grain yield of pigeon peas (Shende and Raut, 2013; Cheboi *et al.*, 2016). Successful breeding and release of new cultivars mainly rely on the availability of a wider genetic base. On the other hand, pigeon pea research in terms of crop improvement is still at a low level in Ethiopia. Therefore, characterization and quantification of the genetic diversity and information on the genetic diversity within and among closely related pigeon pea genotypes is paramount essential for a rational use of plant genetic resources. Hence, this study was initiated with objective to evaluate the variability of pigeon pea accessions with respect to important qualitative and quantitative traits.

MATERIALS AND METHODS

Description of the study area

Afield experiment was conducted during 2022/2023 rain fed cropping season (April 2022 to January 2023) at Nebare Comoshe testing site of Asossa zone in northwestern Ethiopia. The approximate geographical coordinates of the site are 10º 5. 25’’ N latitude and 34º 33. 50’’ E longitude having an altitude of 1553 meters above sea level. The area is characterized by a uni-modal rainfall pattern that starts at the end of April and extends to mid-November where maximum rainfall occurs from June to October. The average annual rainfall of the area is 1375 mm with minimum and maximum temperatures of 16 and 32ºC respectively. The soil type of experimental area is nitosols with soil pH 5.5 which was slightly acidic.

Treatments and Experimental Design

Treatments consisted in 22 pigeon pea accessions (MPG1, MPG2, MPG3, MPG4, MPG5, MPG6, MPG7, MPG8, MPG9, MPG10, MPG11, MPG12, MPG13, MPG14, MPG15, MPG16, MPG17, MPG18, MPG19, MPG20, MPG21 and MPG22) were collected from Assosa zone. The list of collected accession and its district site are indicated on Table 1. The treatments were laid out in a randomized complete block design (RCBD) with three replications. The plot size was 7.2 m wide and 6.0 m long with total gross area of 43.20 m^2. Before planting, the experimental area was plowed, pulverized and leveled in order toget smooth seedbed for planting.Seeds were hand planted by placing two seeds per hill at inter and intra row spacing of 120 and 50 cm, respectively. Fertilizer rate of 100 kg/ ha NPS were used, the source from Benishangul Region Agricultural office. Seeding reduced a few numbers per row after 12-15 days of germination. Thinning was made after emergence to maintain the proposed plant density per unit area. Crop management activities such as fertilization, hoeing and weeding were carried out during crop growing season. Diseases and pest events were visually monitored in the field. Although there couldn’t be any prevalence of pest and disease had occurred in the field from sowing up to harvesting, due to proper time of sowing.

Data collection

All quantitative data were measured by taking the mean value of five plants, which were tagged randomly before the time of data collection. Descriptors for Pigeon pea (*Cajanus cajan* (L.) Millspaugh) developed each accession both for quantitative and qualitative characters.

Table 1. Pigean pea (*Cajanus cajan* (L.) Millspaugh) accessions and their area of collection.

No	Accessions	Region	Woreda	District site	latitude	Longitude
1	MPG1	Beneshagul	Menge	Kulo	10º33. 25’’ N	34º 23. 50’’E
2	MPD2	Beneshagul	Homesha	Bloha	10º33. 27’’ N	34º 23. 60’’E
3	MPG3	Beneshagul	Homesha	Ashula	10º33. 25’’ N	34º 23. 50’’E
4	MPG4	Beneshagul	Homesha	Alemetema	10º33. 15’’N	34º 23. 50’’E
5	MPG5	Beneshagul	Homesha	Dungaheromela	10º30. 28’’N	34º 22. 43’’E
6	MPG6	Beneshagul	Homesha	Shula	10º34. 55’’ N	34º 28. 59’’E
7	MPG7	Beneshagul	Homesha	Molomengele	10º35. 25’’ N	34º 27. 50’’E
8	MPG8	Beneshagul	Menge	kashafi	10º38. 55’’ N	34º 20. 45’’E
9	MPG9	Beneshagul	Assosa	Amba 6	10º5. 66’’ N	34º 33. 55’’E
10	MPG10	Beneshagul	Assosa	Amba 7	10º5. 59’’ N	34º 33. 48’’E
11	MPG11	Beneshagul	Sherkole	Dizene	10º39. 59’’ N	34º 19. 48’’E
12	MPG12	Beneshagul	Sherkole	Tyba	10º38. 57’’ N	34º 18. 41’’E
13	MPG13	Beneshagul	Assosa	Mengele 29	10º5. 76’’ N	34º 33. 32’’E
14	MPG14	Beneshagul	Assosa	Amba 12	10º4. 56’’ N	34º 23. 38’’E
15	MPG15	Beneshagul	Assosa	Amba 5	10º5. 43’’ N	34º 35. 44’’E
16	MPG16	Beneshagul	Assosa	Gambela	10º5. 46’’ N	34º 37. 41’’E
17	MPG17	Beneshagul	Assosa	Amba4	10º5. 44’’ N	34º 36. 48’’E
18	MPG18	Beneshagul	Assosa	Amba 14	10º4. 56’’ N	34°42. 22″ E
19	MPG19	Beneshagul	Bambasi	Sonka	9°45. 42″ N	34°47. 32″ E
20	MPG20	Beneshagul	Bambasi	Sonka	9°45. 44″ N	34°47. 23″ E
21	MPG21	Beneshangul	Ura	Amba 24	10º 3. 77’’ N	34°43. 20″E
22	MPG22	Benshangul	Ura	Amba 8	10º3. 67’’ N	34°42. 27″ E

Table 2. List of qualitative morphological characters of Pigean pea (*Cajanus cajan* (L.) Millspaugh) accessions with respective code and character code.

Character	Code	Character code
Growth habit	Gh	Semi spreading (1) Erect (2) Spreading type (3)
Leaf let shape	LLS	Lanceolate (1) Oblong Lenceolete (2)
Seed size	SS	Large (1), Small (2), Medium (3)
Seed color pattern	SCP	Plain (1), Mottled (2)
Base flower color	BFC	Yellow (1), Light Yellow (2) , Orange Yellow (3)
Pod color	PC	Purple (1), Green (2), Mixed (3)
Seed shape	SSH	Oval (1), Globular (2), Square (3)
Pod form	PF	Flat (1), Curve (2)
Seed color	SC	Red (1),Cream (2), Light Red (3), Blackish (3), Brown (4)
Pod color pattern	PCP	Total pigmentation (1), Pigmentation (2), Spots or bands dark rose (3)

Table 3. List of quantitative morphological characters of Pigean pea (*Cajanus cajan* (L.) Millspaugh) accessions with respective code and description.

Traits	Code	Description
Days to 50 % flowering (count)	DF	Number of days from emergence to when 50 % of plants have started flowering in a plot.
Days to maturity	DM	Number of the day from emergence to maturity.
Plant height (cm)	PH	It was measured for five randomly selected plants per plot at physiological maturity from the ground level to tip of a plant.
Leaf per plant (count)	LN	Count of total number of leaves per plant main stem in randomly selected five plants.
Branches per plant	BPP	Counting total number of branches per main stem in randomly selected 5 plants in each plot.
Podper plant	FPP	Number of Pod per plant mean from five representative plants in each plot.
Podlength	FL	Measuring fruit length per plant mean from five representative plants in each plot.
Hundred seed weight (g)	HSW	Weight of 100 seed counts at 12 % moisture content.
Seeds per pod	SPP	Number of Seed per Pod Mean from five representative plants in each plot.
Grain yield	GY	It was manually harvested from plot t area, seed weight were exposed to driedon sun light and converted to kg/ ha after adjusting the moisture content at 10 %.

Crop phenology and growth traits

Days to 50 % flowering, days to 90 % maturity of pods, branches per plant, plant height (cm), pod length (mm) and pod width (mm).

Yield and yield component

Pods per plant, Seed per pod, hundred seed weight (HSW) and Grain yield (kg/ ha) was taken from randomly selected five plants in representative areas. Similarly, morphological traits recorded were plant growth habit, leaf let shape, base flower color, seed size, seed color pattern, pod color, pod form and pod color pattern.

Statistical analysis

Data were subjected to analysis of variance (ANOVA) appropriate to factorial experiment in RCBD according to the General Linear Model (GLM) of GenStat15th edition (Gen Stat, 2020) and interpretations were made following the procedure described by Gomez and Gomez (1984). Whenever the effects of the treatments were found to be significant, the means were compared using the Least Significant Differences (LSD) test at 5% probability level.

The estimation of genetic parameters was done to identify and ascertain the genetic variability among the accessions and determine the extents of environmental effect on various characters. Variance components due to phenotype (σ^2p), genotype (σ^2g) and the environment ($\sigma^2 e$) were calculated by adopting the following formula suggested by name of author Burton and Devane (1953).

$$Genotypic\ variance\ (\sigma\ 2g) = \frac{MSg - MSe}{r}$$

$$Phenotypic\ variance\ (\sigma 2p)\ =\ \sigma 2g\ + \sigma 2e$$

$$Environmental\ variance\ (\sigma 2e) = Error\ mean\ square$$

Where,
Msg = Mean squares due to genotypes
Mse = mean squares due to error
r = number of replications

The phenotypic and genotypic coefficients of variances were expressed as (Singh, 2001).

$$PCV = \frac{\sqrt{Phenotypic\ variance}}{Population\ mean\ for\ trait}$$

$$or$$

$$PCV\ =\ \frac{\sigma 2P}{X} x\ 100$$

Where,
PCV = phenotypic coefficient of variation

$$GCV\ =\ \frac{\sqrt{Genotypic\ variance}}{Population\ mean\ for\ trait}$$

$$or$$

$$GCV\ =\ \frac{\sigma 2g}{x}\ x\ 100$$

Where,
GCV = Genotypic coefficient of variation
X = the grand mean of a character

Heritability in a broad sense was calculated for each trait by using the formula (Allard, 1960)

$$H^2\ (\%) = \frac{\sigma 2g}{\sigma 2p}\ x 100$$

Where,
H = Heritability in broad sense
σ^2g = genotypic variance
σ^2_p = Phenotypic variance

Genetic advance (GA) under selection, assuming the selection intensity of 5% was calculated according to Johnson *et al*. (1955):

$$GA = K\sqrt{\sigma 2p}.\frac{\sigma 2g}{\sigma 2p} = K.H^*\sqrt{\sigma 2p}$$

Where,
GA = Expected genetic advance
K = the selection differential (K= 2.06 at 5 % selection intensity)

Genetic advance as a percent of the mean was calculated to compare the extent of predicted advances of different traits under selection using the formula (Falconer and Macky, 1996).

$$GAM = \frac{GA}{x} X\ 100$$

Where,
GAM = Genetic advance as percent of mean
GA = Genetic advance under selection
X = Mean value

RESULTS

Growth habit and degree of branching

The data for frequency of qualitative traits of pigeon pea accessions is depicted in Table 4. The growth habit of pigeon pea accessions was variable and categorized as erect types with 25 %, semi-spreading 65 % and spreading types with 10 % where the semi-spreading types dominated.

Seed color, seed size, leaf let shape and base flower color

With respect to leaflet shape lanceolate dominated accounting 70 % while 30 % accessions had oblong leaflet shape. About 44 % of accessions exhibited yellow, 36 % light yellow and 20 % orange yellow base flower color. Information recorded on seed size for accessions showed that large 55mm, small 34 mm and medium 11 mm sized. With respect to Seed color pattern, 52 % of accessions showed plain and 48 % mottled seed color pattern.

Pod color

Regarding the pod color, 56 % genotypes had purple, 30 % green and 14 % mixed color. Likewise, genotypes with red seed color dominated being accounted to be 50 % followed by cream amounted to be 32 %, light red 10 % and the remaining 5 % was with blackish seed color. Occurrence of pod color pattern varies across the pigeon pea germplasm with 71 % of accessions were with total pigmentation, 25 % pigmentation on surface and 4 % with spots or bands dark rose pattern of pod color. For 22 accessions of pigeon pea considered, the qualitative traits dominated were grow habit semi-spreading 65 %, leaflet shape with lanceolate 70 %, base flower color about 44 % of the accessions exhibited yellow, seed size where 55 % accounted large sized, seed color pattern 52 % of accessions showed plain, pod color where 56 % genotypes had purple, seed color dominated red accounted to be 50 % and occurrence of pod color pattern had the maximum amount with 71 % of accessions were totally pigmented. The results of this research agree with Kimaroa *et al*. (2021) that semi-spreading growth habit; plain seed color and yellow flower color dominated the genotypes. This result was in contrast to that of (Zavinon *et al.,* 2019) reported the dominance of compact and erect genotypes they characterized for qualitative traits. Thus, morphological characterization provides an understanding of the crop species based on the phenotype under field conditions but is greatly influenced by the environment (Abdi *et al*., 2002; Fufa *et al*., 2005).

Table 4. Frequencies of qualitative characters studied in 22 pigeon pea accessions.

Trait	Variable	Frequency (%)
Growth habit	Semi-spreading	65
	Erect	25
	Spreading	10
Leaf let shape	Lanceolate	70
	Oblong-lanceolate	30
Base flower color	Yellow	44
	Light yellow	36
	Orange yellow	20
Seed size	Large	55
	Small	34
	Medium	11
Seed color pattern	Plain	52
	Mottled	48
Pod color	Purple	56
	Green	30
	Mixed	14
Seed shape	Oval	73
	Globular	22
	Square	5
Pod form	Flat	64
	Curve	36
Seed color	Red	50
	Cream	32
	Light red	10
	Blackish	5
	Brown	3
Pod color pattern	Total pigmentation	71
	Pigmentation on surface	25
	Spots or bands dark rose	4

Crop phenology and growth trait

Days to flowering and maturity

Significant differences were detected for pigeon pea accessions with respect to days to flowering and maturity (Table 5). Generally, days to flowering varied from 109 to 195 and days to maturity from 169 to 239. Accession MPG10 took the longest days to flowering (195 d) and maturity (239 d). The shortest days to flowering (109 d) and maturity (169 d) were recorded accession MPG18.

Plant height and Branches per plant

Analysis of variance indicated that pigeon pea accessions were significantly differed for plant height and number of branches per plant (Table 5). Plant height for accessions ranged from 178.33 to 335 cm while number of branches per plant from 29.67 to 48.33. The tallest plant height (335 cm) was recorded for accession MPG21 and the greatest number of branches per plant (48.33) was recorded for accession MPG10. The shortest plant height (178.33 cm) was seen for accession MPG21 whereas the lowest number of branches per plant (29.67) for accession MPG11.

Pod length and Pod width

Pigeon pea accessions were significantly differed for pod length and pod width (Table 5). Pod length for accessions ranged from 34.33 to 75.33 mm while pod width from 3.19 to 6.80 mm. The longest pod length (75.33 mm) was obtained from accession MPG18 whereas the greatest pod width (6.80 mm) was achieved from accession MPG9. The shortest pod length (34.33 mm) was seen for accession MPG10 and the lowest pod width (3.19 mm) was achieved from accession MPG11.

Pods per plant and seeds per pod

Analysis of variance showed that accessions of pigeon pea were significantly differed for number of pods per plant and seeds per pod (Table 6). Number of pods per plant for accessions varied from 818 to 1957 and seeds per pod from 2 to 6. The highest number of pods per plant (1957) and seeds per pod (6) were obtained from accession MPG18. The lowest number of pods per plant (818) and seeds per pod (2) were achieved from accession MPG10.

Table 5. Mean performance of pigeon pea accessions for phonologic and growth traits.

Accession	Days to flowering	Days to maturity	Plant height (cm)	Branches per plant	Pod length (mm)	Pod width (mm)
MPG1	121.67hi	186.67gh	230.67e-h	35.00k	61.00cd	3.28h
MPG2	143.33fg	208.00c-e	194.67hi	38.00ij	53.00f	3.41h
MPG3	181.67a-c	207.67c-e	216.33g-i	41.67f-h	47.00h	4.99de
MPG4	177.67bc	229.00ab	283.33b-d	46.00a-d	41.67ij	5.23c-e
MPG5	162.33de	227.68ab	216.67g-i	41.00f-h	44.67hi	5.20c-e
MPG6	186.00a-c	230.00ab	217.67f-i	47.00ab	36.67kl	6.09a-c
MPG7	132.67gh	193.33fg	277.67b-d	34.67k	58.00de	3.35h
MPG8	182.00a-c	218.33b-d	180.67i	42.33e-g	47.00h	4.72d-f
MPG9	186.67a-c	220.67bc	258.00c-f	43.67c-f	41.00ij	6.80a
MPG10	194.67a	239.00a	218.00f-i	48.33a	34.33l	6.19ab
MPG11	114.33i	178.00hi	299.67ab	29.67l	66.67b	3.19h
MPG12	181.33bc	225.33ab	231.67f-h	43.33d-f	40.17jk	4.99de
MPG13	159.00e	206.33d-f	200.67hi	39.00hi	55.00ef	3.61gh
MPG14	182.67a-c	227.33ab	226.33f-h	46.33a-c	41.33ij	5.19de
MPG15	117.67i	185.67gh	295.00a-c	35.33jk	65.00bc	3.99f-h
MPG16	178.33bc	230.00ab	246.67d-g	44.67b-d	41.00ij	5.47b-d
MPG17	173.67cd	199.33e-g	194.67hi	41.67f-h	52.03fg	5.19c-e
MPG18	109.00i	169.00i	335.00a	31.00l	75.33a	3.82gh
MPG19	149.67ef	204.33ef	231.67f-h	36.00jk	51.67fg	3.72gh
MPG20	162.33de	223.00b	227.33f-h	39.67g-i	48.33gh	4.40e-g
MPG21	190.67ab	221.33bc	178.33i	45.67a-d	42.67ij	6.16ab
MPG22	141.33fg	187.00gh	260.00b-e	37.00i-k	55.67ef	3.56gh
LSD (5%)	13.16	13.85	40.74	2.85	4.09	0.89

Means labeled by different superscript letters in the columns are significantly different according to Turkey's Student Range Test (α = 0.05)

Hundred Seed Weight and Grain Yield

Pigeon pea accession exhibited significant difference for hundred seed weight (HSW) and varied from 5.73 to 13.40 g (Table 6). The highest HSW (13.40 g) was recorded for accession MPG18 followed by accession MPG11 with mean HSW of 13.09 g. The lowest HSW (5.73 g) was seen for accession MPG10. Similarly, grain yield showed significant variation among the pigeon pea accessions (Table 6). The grain yield of accessions varied from 445 to 5098 kg/ ha. Pigeon pea accessions with relatively low yielder (< 1000 kg/ ha) were MPG4, MPG6, MPG9, MPG10, MPG12, MPG14 and MPG16. Likewise, accessions with relatively intermediate yielders (1000-4000 kg/ ha) encompass MPG1, MPG2, MPG3, MPG5, MPG7, MPG8, MPG13, MAPG17, MPG19, MPG20, MPG21 and MPG22.

Variance Components

Phenotypic and Genotypic Variations

In this observation, phenotypic variance (б^{2}p) of pigeon pea accessions varied from 1.40 for number of seeds per pod to 19840 for grain yield. Higher phenotypic variance (≥ 100) was observed for days to flowering, days to maturity, plant height, pod length; pods per plant and grain yield (Table 7).

Broad sense heritability and genetic advance

Generally, heritability in broad sense (H^2) ranged from 70.63 % for plant height which was the lowest to 99.91 % for grain yield which was the highest value (Table 7). Grouped heritability estimates as low if < 30 %, moderate if 30-60 % and high if > 60 %. Based on this grouping, all measured traits fall in high H^2 estimate with no moderate low heritability values.

Correlation of Agronomic Traits

The data foe correlation coefficients of agronomic trait for pigeon pea accessions are presented in Table 8. In general, the correlation coefficient (r value) varied from -0.97 to 0.98. All agronomic traits were significantly correlated with grain yield where plant height (r = 0.60), pod length (r = 0.98), pods per plant (r = 0.94), seeds per pod (r = 0.98) and HSW (r = 0.97) were significantly positively correlated with grain yield. This is evidence that these traits are important to be used as criteria for direct selection in breeding for improving grain yield in pigeon pea. Conversely, days to flowering (r = -0.96), days to maturity (r = -0.97), branches per plant (r = -0.95) and pod width (r = -0.83) were significantly negatively correlated with grain yield.

DISCUSSION

According to the results of this study accession were collected from potential areas in representative region of five districts such as Menge, Homesha, Bambasi, Sherkole and Assosa located in northwestern part of Ethiopia. These characteristics can assist breeders in genotype selection dependent on phenotype in the genetic improvement in breeding scheme. Based on these morphological traits, it could be possible to identify elite genotypes for grain yield purposes within the genotype population.

Table 6. Mean performance of pigeon pea accessions for yield components and yield.

Accession	Pods per plant	Seeds per pod	HSW (g)	Grain yield (kg/ ha)
MPG1	1890.00a-c	4.47c	12.18cd	3720d
MPG2	1699.30c-f	3.49f-g	9.45e	2363h
MPG3	1519.0ef	3.14gh	8.93ef	1609j
MPG4	947.70i-j	2.59i-j	6.59jk	733no
MPG5	1215.00g	2.83h-j	7.76g-i	1139kl
MPG6	879.70jk	2.34j-m	6.97h-j	655op
MPG7	1826.30a-d	4.35cd	12.26b-d	3490e
MPG8	1168.00gh	2.77h-k	7.79gh	1265k
MPG9	879.00jk	2.25k-m	6.93ij	834m-o
MPG10	818.00k	2.00m	5.73k	445p
MPG11	1922.00ab	5.39b	13.09ab	4625b
MPG12	1129.30g-i	2.19lm	8.13fg	871mn
MPG13	1732.00b-e	3.83de	11.49d	2749g
MPG14	984.00h-k	2.29j-m	7.93g	809m-o
MPG15	1907.30a-c	5.04b	12.73a-c	4093c
MPG16	1094.30g--j	2.52i-m	7.00h-j	961lm
MPG17	1552.00ef	3.25f-h	9.14e	1800j
MPG18	1956.70a	6.25a	13.40a	5098a
MPG19	1674.30d-f	3.73ef	9.35e	2530h
MPG20	1502.70f	3.00g-i	8.60e-g	2067i
MPG21	1121.00g-i	2.32j-m	7.75g-i	1102kl
MPG22	1826.00a-d	3.92de	11.76d	3261f
LSD (5%)	215.44	0.54	0.86	215

Means labeled by different superscript letters in the columns are significantly different according to Turkey's Student Range Test (α = 0.05) and HSW; hundred seed weight.

Table7. Phenotypic and genotypic coefficient of variability, heritability and genetic advance for pigeon pea accessions.

Trait	σ^{2}p	б^{2}g	σ^{2}e	PCV	GCV	H^{2}	GA
				(%)	(%)	(%)	(%)
Days to flowering	791.26	727.46	63.80	17.54	16.82	91.99	33.33
Days to maturity	435.07	364.39	70.68	9.94	9.10	83.75	17.15
Plant height	2081.72	1470.29	611.43	19.23	16.16	70.63	6.40
Branches per plant	29.42	26.42	3.00	13.45	12.75	89.80	24.88
Pod length	114.94	108.75	6.19	21.46	20.87	94.61	41.81
Pod width	1.38	1.09	0.29	25.21	22.40	78.99	40.99
Pods per plant	15546.7	15373.67	1709	27.76	27.61	98.90	1.43
Seeds per pod	1.40	1.29	0.11	35.21	33.80	92.14	66.96
Hundred seed weight	5.82	5.54	0.28	25.88	25.25	95.19	50.75
Grain yield	19840.86	19823.75	17108	45.08	26.03	99.91	4.36

Table 8. Correlation of agronomic traits of Pigean pea accessions.

Trait	DF	DM	PH	BPP	PL	PW	PPP	SPP	HSW	GY
Days to flowering (DF)	-	0.89*	-0.63*	0.95*	-0.94*	0.85*	-0.89*	-0.95*	-0.92*	-0.96*
Days to maturity (DM)		-	-0.55*	0.92*	-0.96*	0.76*	-0.92*	-0.95*	-0.95*	-0.97*
Plant height (PH)			-	-0.55*	0.58*	-.0.32^{NS}	0.08^{NS}	0.01^{NS}	0.53*	0.60*
Branches per plant (BPP)				-	-0.94*	0.86*	-0.93*	-.0.94*	-0.93*	-0.95
Pod length (PL)					-	-0.80*	0.93*	0.98*	0.95*	0.98*
Pod width (PW)						-	-.0.90*	-0.78*	-0.85*	-0.83*
Pods per plant (PPP)							-	0.90*	0.94*	0.94*
Seeds per pod (SPP)								-	0.94*	0.98*
Hundred seed weight (HSW)									-	0.97*
Grain yield (GY)										-

No moderate genotypic $(\sigma 2g)$ variance (50-100) was observed for traits investigated. Lower phenotypic variance (< 50) was recorded for branches per plant, pod width, seeds per pod, environmental variance were observed for the traits days to flowering, days to maturity, pods per plant and grain yield and HSW. On the other hand, genotypic variance $(\sigma 2g)$ ranged from 1.29 to 19823.75 with the higher genotypic variance for days to flowering, days to maturity, plant height, pod length and grain yield. No moderate genotypic $(\sigma 2g)$ variance was seen for traits investigated. Lower genotypic variance $(\sigma 2g)$ was observed for ranches per plant, pod width, seeds per pod and HSW. In general phenotypic coefficient of variation (PCV) varied from 9.94 for days to maturity to 45.08 % for grain yield. Sivasubramanian and Madhavamenon (1973) categorized PCV as high if PCV > 20 %, moderate if PCV is 10-20 % and low if PCV is below 10 %. Based on this categorizing, traits pod length, pod width, pod per plant, seeds per pod, HSW and grain yield had higher PCV. Conversely, traits days to flowering, plant height and branches per plant exhibited moderate PCV whereas a trait only day to maturity showed lower PCV with PCV value below 10 %. This could be evidenced as the prominent influence of environment for the expression of these traits. In line with this, genotypic coefficient variance (GCV) varied from 910 to 33.80 % where traits pod length, pod width, pods per plant, seeds per pod, HSW and grain yield had high GCV and days to flowering, plant height and branches per plant showed moderate GCV value. A day to maturity was the only trait with low GCV value below 10 %. This result revealed that environment has low influence for the expression of the traits. Thus, selection could be effective in genotypes for these traits and the possibility of improving pigeon pea accessions through direct selection for grain yield and related traits. Genetic advance as a percent mean was ranged from 1.43 % for pods per plant to 66.96 % for seeds per pod. This result indicated that selecting the top 5 % of the accessions could result in an advance of 1.43 to 66.96 % over the respective population mean. (Sivasubramanian and Madhavamenon, 1973) classified genetic advance as percent of mean as low if < 10 %, moderate if 10-20 % and high if > 20 %. Based on this classification, days to flowering, branches per plant, pod length, pod width, seeds per pod and HSW exhibited high genetic advance whereas a trait days to maturity had moderate genetic advance. On the other hand, traits plant height, pods per plant and grain yield had low genetic advance. On the other hand, correlation of agronomic trait of pigean pea accessions considered as traits are important to be used as indirect selection criteria in breeding for yield improvement. Hailu (2021) reported the presence of positive and relatively strong correlations between grain yield and other traits and hence the improvement in grain yield could be achieved by direct or indirect selection for yield determining traits. Likewise, Mesay et al. (2022) showed that in Bambara groundnut higher correlation values were observed for plant height, pods per plant, seed per pod and HSW indicating that these traits are very important to be used in selection for the crop improvement. Thus, agronomic and morphological evaluations have provided accurate estimation of genetic diversity of the raw material of plant breeding.

CONCLUSION

Pigeon pea accessions exhibited variability for qualitative and quantitative traits recorded and measured due to their genetic variability. Grain yield showed significant variation among the pigeon pea accessions. The mean grain for accessions varied from 445 to 5098 kg/ ha. Pigeon pea accessions with relatively low yielder (< 1000 kg/ ha) were MPG4, MPG6, MPG9, MPG10, MPG12, MPG14 and MPG16. Likewise, accessions with relatively intermediate yields (1000-4000 kg/ ha) encompass MPG1, MPG2, MPG3, MPG5, MPG7, MPG8, MPG13, MPG17, MPG19, MPG20, MPG21 and

MPG22. Pigeon pea accessions with relatively low yielder (< 1000 kg/ ha) were MPG4, MPG6, MPG9, MPG10, MPG12, MPG14 and MPG16. Likewise, accessions with relatively intermediate yielders (1000-4000 kg/ ha) encompass MPG1, MPG2, MPG3, MPG5, MPG7, MPG8, MPG13, MPG17, MPG19, MPG20, MPG21 and MPG22. Accessions MPG11, MPG15 and MAPG18 had relatively higher (> 4000 kg/ha) grain yield over others. Generally, substantial variability in the considered traits among the pigeon pea accessions was observed and this might be used for direct recommendations high yielding accessions for production and as important inputs for the future breeding program.

Acknowledgments
I acknowledge Assosa Biodiversity Center, Biodiversity Director Dereje Mosissa for valuable in financial support and data collection.

Funding. This work was funded in Assosa Biodiversity Center for characterizing of some important horticulture species for crop improvement program.

Conflict of interest. The author declares no conflict of interest.

Compliance with ethical standards. Does not apply.

Data availability. The data used to support the findings of this study are available from corresponding authormesi.and.paul.66@gmail.com.

Author contribution statement (CRediT): M. Paulos–Conceptualization; Data curation; Formal analysis; Investigation; Methodology; Writing original draft; Writing-review & editing.

REFERENCES

Aiyéloja, A.A. and Bello, O.A. 2006. Ethnobotanical potentials of common herbs in Nigeria: A case study of Enugu state. *Educational Research and Review*, 1, pp.16-22

Allard, W., 1960. Principle of plant breeding, John Willey and Sons, Inc. New York.

Ayenan,T., Danquah, A., Ahoton, E. and Ofri, K.., 2017. Utilizationand farmers' knowledge on Pigeon pea diversity in Benin, West Africa. *Journal of Ethnobiology and Ethnomedicine*, 37, pp.13-20. https://doi.org/10.1186/s13002-017-0164-9

Burton, G., W. and Devane, E., H., 1953. Estimating heritability in tall fescue from replicate clonally material. *Agronomy Journal*, 45, pp. 478-481. https://doi.org/10.2134/agronj1953.00021962004500100005x

Chattopadhyay, K. and Dhiman, R., 2006. Characterization, variability, diversity and path coefficient analysis of Pigeon pea genotypes. *Indian Journal of Genetics*, 34, pp.56-63.https://arccarticles.s3.amazonaws.com/webArticle/articles/lr282016.pdf

Chebo, J., Kinyua, G., Kimurto, K., Kiplagat, K., Towett, K., Kirui, C. and Gangarao, R., 2016. Yield potential and adaptability of medium duration Pigeon pea (*Cajanus cajan* (L.) Millsp.) genotypes in dry parts of North Rift Valley, Kenya. http://www.innspub.net

Cook, B.G., Pengelly, B.C., Brown, S.D., Donnelly, J.L., Eagles, D.A., Franco, M.A., Hanson, J., Mullen, B.F., Partridge, I.J., Peters, M. and Schultze-Kraft, R., 2005. Tropical Forages. An interactive selection tool. Web Tool. CSIRO, DPI & F (Qld), CIAT and ILRI, Brisbane, Australia. https://hdl.handle.net/10568/49/49072/

Dahat, V., Deshmukh, B. and Patil, V., 2006. Genetic variability and character association in pigeon pea grown as sole and intercrop in pearl millet. *Indian Journal of Agriculture and Research*, 34, pp. 413-420.

Dansi, A.,Vodouhè, R., Azokpota, P., Yedomonhan, H., Assogba, P., Adjatin, A., Loko, Y.L. and Dossou-Aminon, I., Akpagana, K., 2012. Diversity of the neglected and underutilized crop species of importance in Benin. *Scientific World Journal*, 2012, pp. 1-19. https://doi.org/10.1100/2012/932947

Denbela, H., Adugna, T. and Ajebu, N., 2018. Effect of lablab and Pigean Pea leaf meal supplementation on performance of goats fed Abasal diet of haricot bean haulms. *Tropical Animal Health and Production*, 50(3), pp. 1-9. https://doi.org/10.1111/jpn.13119/

Falconer, D.S. and Mackay, F.C., 1996. Introduction to Quantitative Genetics. 4th edition, Longman group Ltd, England.

FAO, 2016. Grassland Index. A searchable catalogue of grass and forage legumes. FAO, Rome, Italy.

Géofroy, K., Gustave, D., Laura, L., Relique, A., Saxena, K., Varshney, K. and Alexandre, D., 2020. Agro-morphological characterization of Pigeon pea (*Cajanus cajan* (L.) Millspaugh) landraces grown in Benin: Implications for breeding and conservation. *Journal of Plant Breeding and Crop Science*, 12 (1), pp. 34-49. https://doi.org/10.5897/JPBCS2019.0836

Hailu, G., 2021. Genetic Variability and Trait Associations among Sorghum [*Sorghum bicolor* (L.) Moench] Genotypes for Yield and Yield Related Traits in West Hararghe, Ethiopia. A thesis submitted to the School of Plant Sciences, Postgraduate Program Directorate Haramaya University, Dire dawa, Ethiopia.

ILRI (International Livestock Research Institute), 2013. Lablab (*Lablab purpureum* cultivar Rongai) for livestock feed on small-scale farms (English Version). ILRI, Nairobi, Kenya. https://hdl.handle.net/10568/1815

Johnson, W., Robinnson, F. and Comstock, E., 1955. Estimate of genetic and environmental variability in soybean, *Agronomy Journal*, 43, pp.477-483. https://doi.org/10.2134/agronj1955.00021962004700070009x

Kimara, D., Melisa, R., Sibiyaa, J. and Hussein, S., 2021. Agro-morphological characterization of pigeon pea (*Cajanus cajan* (L.) Millsp.): Basis to Breeding, *Agriculture and Natural Resource*, 55, pp. 23-32. http://dx.doi.org/10.34044/j.anres.2021.55.1.04

Masama, E., J. H, Topps, N. T, Ngongoni, B.V. and Maasdorp., 1997. Effects of Supplementation with foliage from the tree legumes *Acacia angustissima*, *cajanus cajan*, *collianda calotyrsus* and *leucaena leucocephala* on feed intake, digestibility and nitrogen metabolism of sheep given maize stover ad libitun. *Animal Feed Science Technology*, 69 (3), pp. 233-240. https://doi.org/10.1016/S0377-8401(97)81638-0

Mesay, P., Gobeze, L. and Mesfin, K., 2022. Characterization and Evaluation of Bambara Groundnut (*Vignasubterranea* (L.) Verdc.) for Yield and Related Traits in Asosa Zone, Northwestern Ethiopia. *Applied and Environmental Soil Science*, 2022, pp. 1-7.https://doi.org/10.1155/2022/8533233

Njoroge, M., Matumba, L., Kanenga, K., Siambi, M., Waliyar, F., Maruwo, J. and Monyo, S., 2016. A case for regular aflatoxin monitoring in peanut butter in sub-Saharan Africa: lessons from a 3-year survey in Zambia, *Journal of Food Protection*, 79(5), pp. 795-800. https://doi.org/10.4315/0362-028X.JFP-15-542

Odeny, D.A., 2007. The potential of pigeon pea (*Cajanus cajan* (L.) Millsp.) in Africa. *Natural Resources Forum* 31, pp. 297-305. https://doi.org/10.111

Oladunmoye, M. K. and Kehinde, F.Y., 2011. Ethno-botanical survey of medicinal plants used in treating viral infections among Yoruba tribe of South Western Nigeria. *African Journal of Microbiology Research*, 5, pp.2991-3004. https://doi.org/10.5897/AJMR10.004

Olayeki, L.A. I., Olatunij-Bello, A.O., oladoye, O.R., Jimoh, O., G. and Ighodalo, M., 2009. Effects of aqueous leaf extracts of *Cajanus cajan* on litter size and Serum Progesterone in Pregnant rats. *Journal of Pharmacognosy, Phytotherapy*, 1(2), pp. 21-24.

Omokanye, A.T., Balogun, R.O., Onifade., O.S., Afolayan, O.R, and Olayemi, M.E., 2001. Assessment of Preference and intake of browse species by yankasa sheep at Shika Nigeria. *Small Ruminants Research*, 42(3), pp. 201-208. https://doi.org/10.1016/S0921-4488(01)00250-4

Saxena, K.B., 2006. Seed Production systems in Pigeonpea. Patancheru, 502 324 Andra Pradesh, India: International Crops research institute for semi-Arid Tropics. 76 pp. https://citeseerx.ist.psu.edu/document?repid=rep1&type=pdf&doi=64d41186fd57dca3f1f3f5007e4a8aeb2b1ddac3

Shende, S. and Raut, A., 2013. Analysis of genetic diversity in pigeon pea (*Cajanus cajan*) by using PCR based molecular marker. *Recent Research in Science and Technology*, 5 (2), pp. 20-23.

https://updatepublishing.com/journal/index.php/rrst/article/view/1017

Shahzad, A., Din, U., Sahi, Khan., M., Ehsanullah, M. and Ahmad, M., 2007. Effect of sowing date and seed treatment on grain yield and quality of wheat. *Pakistan Journalof Agricultural Science*, 44 (4), pp.581-583. https://api.pakjas.com.pk/downloadPaper/254.pdf

Sivasubramanian, S. and Madhavamenon, P., 1973. Combining ability in rice. *Madras Agricultural Journal*, 60, pp. 419-421.

Suman, S., Mula, M.G., Panwar, G., Kumar, S. and Ghosh, M. 2017. Weed Management Strategies in Pigeon pea under Alfisol and Vertisol. *International Journal of Pure and Applied Bioscience*, 5 (6), pp.138-143. https://dx.doi.org/10.18782/2320-7051.5353

Rao, S.c., Phillips, W.A., Mayeux, H.S. and Phatak, S.C., 2003. Forage and grazing lands. Potential Grain and Forage Production of Early Maturing Pigeon Pea in the Southern Great Plains, *Crop Science Society of America*, 43, pp. 2212-2217. https://doi.org/10.2135/cropsci2003.2212

Rao, S.C. and Northup, B. k., 2012. Pigeon pea Potential for summer growing in the Southern Great Plains. *Agronomy journal*, 104 (1), pp.199-203. https://doi.org/10.2134/agronj2011.0260

Tariku, S., Dembele, E. and Asnake, F., 2022. Performance Evaluation of Pigeon Pea (*Cajanus cajan* (L.) Millsp.) Variety for Registration in the Lowland Areas of Ethiopia. *Advances in Agriculture*, 2022, pp.1-7. http://dx.doi.org/10.1155/2022/7013602

Zavinon, F., Adoukonou-Sagbadja, H., Ahoton, L., Vodouhê, R. and Ahanhanzo, C., 2018. Quantitative Analysis, Distribution and traditional management of pigeon pea [*Cajanus cajan* (L.) Millsp.] Landraces' diversity in Southern Benin. *European Scientific Journal* 14(9), pp. 184-211.https://hdl.handle.net/10568/96897