

Diversity of Agronomic Characters of Pigeon Pea (*Cajanus cajan* (L.) Millsp.) Genetic Resources

Keragaman Karakter Agronomi Plasma Nutfah Kacang Gude (*Cajanus cajan* (L.) Millsp.)

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ABSTRACT

Germplasm has an important role in breeding activities. Characterization is needed to classify germplasm collections base on the specific characters such as maturity age, number of pods per plant, and yield. The purpose of this test was to classify 60 pigeon pea accessions from germplasm collection of Indonesian Legumes Instrument Standard Testing Institute (ILISTI). The classification was undertaken by using principal component analysis and cluster analysis. The sixty pigeon pea accessions were planted at Muneng station, East Java during dry season 2018. Each accession was planted in a 2 m × 4 m plot with plant spacing of 100 cm interrow and 20 cm intra row spacing in between the plants. The observation was carried out on 13 quantitative characters or variables. Total variance of the observed variables was 75.3% as it was explained by four principle components. Among these four components, the first component dominantly influenced with 40.4% of variability that consisted of the characters of flowering age, maturity age, plant height, pod bearing length, number of main branches, and number of pods per plant. Sixty pigeon pea accessions could be divided into four groups: group 1, 2, 3 and 4 with 29, 7, 8, and 16 accessions, respectively. Group 2 was potential to be developed because of its good plant performance as characterized by long stem segment that produce pods, large seed size, and high seed yield.

Keywords: *cajanus cajan*, characterization, cluster analysis, principal component analysis

ABSTRAK

Plasma Nutfah memiliki peranan penting dalam kegiatan pemuliaan. Karakterisasi diperlukan untuk mengklasifikasi koleksi plasma nutfah berdasarkan karakter tertentu seperti umur masak, jumlah polong per tanaman, dan hasil. Tujuan pengujian ini adalah untuk mengelompokkan 60 aksesori plasma nutfah kacang gude koleksi Balai Pengujian Standar Instrumen (BPSI) Tanaman Aneka Kacang menggunakan analisis komponen utama dan analisis kluster. Enam puluh aksesori kacang gude ditanam di Kebun Pengujian Muneng Jawa Timur pada musim kemarau tahun 2018. Setiap aksesori ditanam dalam plot berukuran 2 m × 4 m, jarak tanam 100 cm × 20 cm. Pengamatan dilakukan pada 13

karakter kuantitatif. Total ragam dari variabel pengamatan adalah 75,3% yang dijelaskan oleh empat komponen utama. Komponen yang paling berpengaruh adalah komponen pertama yang menjelaskan 40,4% keragaman dan terdiri dari karakter umur berbunga, umur masak, tinggi tanaman, kedudukan polong, jumlah cabang utama, dan jumlah polong per tanaman. Enam puluh aksesori kacang gude koleksi plasma nutfah BPSI Tanaman Aneka Kacang dapat dibagi menjadi empat kelompok, masing-masing terdiri dari 29, 7, 8, dan 16 aksesori. Kelompok 2 berpotensi untuk dikembangkan karena memiliki keragaman tanaman yang baik yang dicirikan oleh kedudukan polong panjang, berbiji besar, dan hasil biji tinggi.

Kata kunci: analisis kluster, analisis komponen utama, *cajanus cajan*, karakterisasi

INTRODUCTION

Pigeon pea (*Cajanus cajan* (L.) Millsp.) is a perennial crop. The plants are woody with upright erect type with trifoliate and oval leaves. Flowers are located on branches or at the tip of branches with yellow, stripped red, or red color of the dorsal petal. The plants have flat oval pods with or without purple streaks on young pods. Primary seed colors are grey, cream, brown, orange, purple, or black with various color patterns. The leaves are source of natural antioxidants, and the local communities use as traditional medicine for malaria, measles, typhoid, headache, fever, and constipation. Instead of as traditional medicine function, about 55% of farmers in Benin Africa use pigeon pea leaves as fertilizer, while 40% of farmers use as herbicide. The centers of production and diversity of pigeon pea in the world are India, Africa, and Australia (Sahu *et al.* 2018; Zavinon and Sagbadja 2019; Adegboyegun *et al.* 2020; Patel *et al.* 2020; Ranjani and Jayamani 2021).

Pigeon pea in Indonesia is known as *kacang kaju* (Java), *kacang hiris* (Sunda), and *kekace* or *undis* (Bali). Several studies have explored the potency

of pigeon pea seeds as soybean substitution in soy sauce production (Andriana 2014), vegetable broth (Utami *et al.* 2015), and “tempe” (Dewi *et al.* 2014). Augustyn *et al.* (2017) reported that pigeon pea seeds contain 0.68% ash, 21.48% protein, 3.64% fat, 64.92% carbohydrate, and 2.47% crude fiber. The development and utilization of pigeon pea in Indonesia faces some problems such as the absence of improved variety, lack of product processing technology, and less promotion (Maintang *et al.* 2015).

Indonesian Legumes Instrument Standard Testing Institute (ILISTI) collected 72 accessions of pigeon pea including one Indonesia variety named Mega. Until recently, the utilization of pigeon pea germplasm in breeding activities and food processing is still limiting. Mega variety is the only variety released by The Minister of Agriculture in 1987. This variety was introduced from Australia as an Australian variety namely QPL-Hunt. The average seed yield of Mega variety is 1.2 t/ha with seed size of 9-10 g per 100 seeds. The seed color is light brown, days to flowering is 55 days, while days to maturity is 95 days. The seed of Mega variety contains 20% protein and 1,8% fat. The plant is tolerant to sterile mosaic virus (Balitkabi 2016).

Characterization and evaluation are very important in breeding activities. These activities help breeders to recognize the character of the collection, facilitate the grouping and forming of core collection, as well as find out the potency of collections for breeding activities. Plant characterization by morphological, physiological and agronomical traits has long been used in selective breeding (Kinhogbe *et al.* 2020; Lutatenekwa *et al.* 2020). The results of character identification can be used to classify germplasm collections and to clearly outline/map the superior characters (Asadi *et al.* 2016).

Cluster analysis is a method of grouping some object data base on their differences or similarities. So that, the members of a group have similar character but different from other groups. This analysis is useful for identifying genotypes that potential to be used as parents as well as reducing the time required to screen large populations (Hemavathy *et al.* 2017). The germplasm characterization data are usually large with various units so that a technique is needed to overcome this problem before grouping. Principal component analysis (PCA) is a popular method to reduce the dimensions of the data without reducing the characteristics. Principal component analysis based on morphological and physiological traits under stress conditions could be an excellent tool to classify the

genotypes (Sivakumar *et al.* 2020). The objective of this study was to classify 60 pigeon pea accessions as the genetic resources collection of ILISTI.

MATERIALS AND METHODS

The 60 pigeon pea accessions of ILISTI collection were planted at Muneng station in dry season of 2018. Each accession was planted in a 2 m × 4 m plot size with 100 cm interrow and 20 cm of intra row spacings. The plants were fertilized with 300 kg/ha of composite fertilizer (15 N-15 P₂O₅-15 K₂O) and 100 kg/ha of phosphate fertilizer (36% P₂O₅), where all fertilizers were broadcasted just after planting. Irrigation was applied three times i.e. after planting, at flowering stage, and at pod filling stage. Plant protection was undertaken by applying chemical pesticides such as 200 g imidacloprid/L water for controlling insect pests at juvenile stage, 50 g fipronil/L water for controlling *Bemisia tabaci* at vegetative stage, and the mixture of 100 g klorantraniliprol/L + 200 g tiametoksam /L for *Maruca* that attacked the plants at generative stage. Observations on 13 quantitative traits were carried out following the descriptor of pigeon pea (IBPGR 1993). Number of pods per plant was observed from three sample plants. The collected data were analysed using descriptive statistics analysis, principal component analysis and cluster analysis, and these analyses were run by using a Minitab 21 program.

RESULTS AND DISCUSSION

Morpho-agronomical Characters

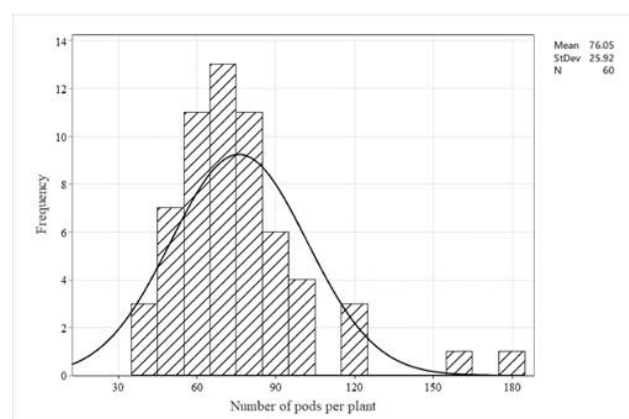
Descriptive analysis was conducted on 13 quantitative traits i.e. flowering and maturity days, plant height, pod yield and yield components. The highest diversity was shown in the number of pods per plant with value ranged from 42 pods up to 180 pods (Table 1). More than 50% of accessions had lower number of pods per plant than the average (76.05 pods) (Figure 1). Moreover, Kinhogbe *et al.* (2020) reported the highest variation from 134.6-1956 pods per plant. Meanwhile, Yohane *et al.* (2022) and Patel *et al.* (2020) stated the range of 14.6-208.2 and 0-400 pods per plant, respectively.

In the current study, plant height of the accessions hugely varied where the shortest was 71.2 cm and the tallest was 151.8 cm height (Table 1). This result was in line with the research of Hemavathy *et al.* (2017), Ranjani and Jayamani (2021), also Patel *et al.* (2020). Meanwhile, Adegbayegun *et al.* (2020) stated that plant height had a medium variance with coefficient of variation of 23.46%.

Table 1. Descriptive analysis of 13 quantitative characters from 60 accessions of pigeon pea. Muneng station, dry season 2018

	Minimum	Maximum	Mean	StDev ¹⁾	Variance
Days to flowering (days)	58.00	69.00	61.77	2.53	6.42
Days to maturity (days)	86.00	119.00	98.52	6.13	37.61
Plant height (cm)	71.20	151.80	122.17	19.45	378.38
Pod bearing length (cm)	18.40	79.60	52.55	12.48	155.64
Number of main branches	3.80	12.40	8.10	2.02	4.08
Number of secondary branches	0.00	5.00	0.53	1.08	1.17
Number of flowers per cluster	7.70	15.00	11.56	1.57	2.46
Pod length (cm)	5.05	6.81	5.92	0.46	0.21
Number of seeds per pod	3.80	5.10	4.35	0.27	0.08
Number of pods per plant	42.00	179.60	76.05	25.92	671.76
100-seeds weight (g)	8.39	12.55	10.02	0.88	0.77
Seed weight per plot (kg)	0.68	2.31	1.43	0.33	0.11
Seed yield (t/ha)	0.85	2.89	1.79	0.42	0.17

Notes: ¹⁾ StDev: standard deviation

**Figure 1.** Number of pods per plant of 60 pigeon pea accessions. Muneng station, dry season 2018

Most of the accessions had more than 120 cm height and these values were higher than the average value (Figure 2a). The shortest pigeon pea plant by 44.7 cm height had been reported, despite this species is potentially can reach 300 cm height (Adegboyegun *et al.* 2020; Patel *et al.* 2020; Ranjani and Jayamani 2021; Yohane *et al.* 2022). Meanwhile in Indonesia, the height of pigeon pea plant ranged from 101-200 cm (Yuniastuti *et al.* 2020).

The pod bearing length represents to the pod position or the length of stem segment that produce pods. The maximum pod bearing length was 79.6 cm with an average of 52.6 cm (Table 1). Pod bearing length had the third largest variation in this study, similar to that reported by Hemavathy *et al.* (2017). Characters with high variability values can provide a high level of segregation in a breeding line population (Suman *et al.* 2019). The length of the stem segment that produces the pods can determine the production of pigeon pea plants.

The flowering day of pigeon pea accessions was 61.8 days in average, while the earliest and latest flowering days of the accessions were 58 days and 69 days, respectively. The shortest maturity was 86 days, while the longest was 119 days with an average of 98.5 days. The earliest flowering accessions generally will have the earliest maturity. This condition also occurred in this study, where ICPL 89021 which had the shortest days for flowering, became the earliest in maturity. But, QPL 42 which had the longest days for flowering was mature at 109 days, which was earlier than the latest. Days to flowering and maturity in this study, however, were earlier than the flowering and maturity days of pigeon pea in subtropical countries (Patel *et al.* 2020; Yohane *et al.* 2022). Patel *et al.* (2020) grouped the days to flowering as early (61-90 days), medium (91-130 days), late (131-160 days), and very late (>160 days).

The maximum pod length was 6.8 cm with an average of 5.9 cm. Each pod has 4-5 seeds. The number of productive pods per plant ranged from 42-180 pods with an average of 76 pods (Table 1). This result was similar to that obtained by Kinhogbe *et al.* (2020), Patel *et al.* (2020), and Ranjani and Jayamani (2021).

The seed size was expressed by the weight of 100 seeds, and the value ranged from 8.4-12.6 g with an average of 10 g. Seed size was grouped into four categories i.e. small seeds (<7 g/100-seed weight), medium seed (7-9 g/100-seed weight), large seed (9-11 g/100-seed weight), and very large seed (>11 g/100-seed weight) (Patel *et al.* 2020). Seed size of the materials in this study was classified as medium and very large size (Table 1).

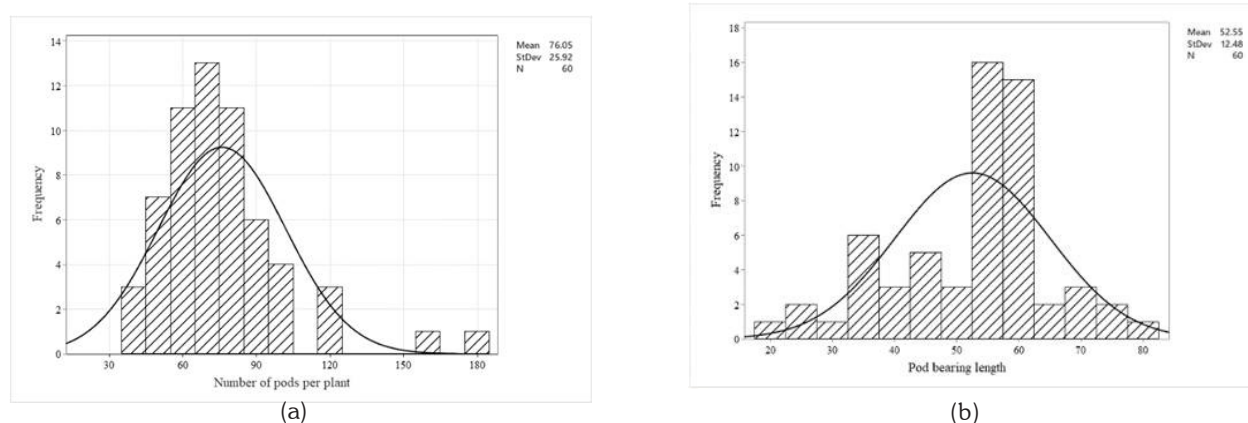


Figure 2. Plant height (a) and pod bearing length (b) of 60 pigeon pea accessions. Muneng station, dry season 2018

Seed yield per plot was converted to the seed yield per hectare. The seed yields of 60 accessions were from 0.85 t to 2.89 t/ha with an average yield of 1.79 t/ha (Table 1). The higher seed yield was obtained by accessions with longer maturity days and taller plants. A 2.93 m tall pigeon pea produced 3.73 t/ha of seed weight in average (Kinhoegbe *et al* 2020). In this study, however, the taller and latest mature accession ICPL 92060 did not produce the highest seed yield as this accession only yielded 2.08 t/ha of seeds. Meanwhile, the highest seed production by 2.89 t/ha of seeds was produced by ICPL 92038.

Ranking the accessions base on quantitative character was complicated because there was no single accession could reach the best performance for all characters. The ranking base on early maturity character obtained the accessions with low to medium seed yield. Furthermore, ranking the accession base on late maturity character resulted in accessions which produce higher seed yield.

Later, the accessions were ranked base on days to flowering, days to maturity, 100 seed weight, and seed yield (per ha). The average values from each of those characters were used as limiting factor. Ten

accessions with the value of those four characters close to their average values were categorized as the best ten accessions (Table 2). The general mean of 60 pigeon pea accessions for days to flowering was 61-62 days, days to maturity was 98-99 days, 100 seed weight was 10 g, and seed yield was 1.79 t/ha.

Table 2 pointed out the characters of 10 selected accessions i.e. 60-63 days to flowering, 95-101 days to maturity, 9.1-12.1 g of 100 seeds weight, and 2.12-2.89 t/ha of seed yield. ICPL – 92040 needed 101 days to mature and obtained high seed yield of 2.46 t/ha. Similarly, QPL – 87 C had 101 days to flowering but with slightly lower seed yield (2.25 t/ha) compared to that of ICPL – 92040. These two accessions were merit to be materials in breeding program by improving the flowering or maturity dates so that produce early flowering or maturity varieties with high seed yields.

Correlation among the Quantitative Characters

The perfect correlation was shown between seed yield per hectare and seed yield per plot ($r=1^{**}$). The lower coefficient correlation was between plant

Table 2. The best ten pigeon pea accessions based on days to flowering, days to maturity, 100-seed weight, and seed yield. Muneng station, dry season 2018.

No.	Accessions	Days to flowering (days)	Days to maturity (days)	100-seed weight (g)	Seed yield (t/ha)
1.	ICPL - 92038	63	99	12.1	2.89
2.	ICPL - 92040	62	101	9.9	2.46
3.	ICPL - 91053	63	98	10.2	2.43
4.	ICPL - 91021	60	95	10.2	2.42
5.	ICPL - 83015	63	98	9.1	2.35
6.	LO - 3-44	62	98	10.3	2.31
7.	ICPL - 92055	62	98	10.0	2.30
8.	QPL - 87 C	60	101	9.9	2.25
9.	ICPL - 91040	62	99	10.1	2.22
10.	ICPL - 88023	60	97	9.4	2.12

height and pod bearing length ($r=0.84^{**}$), days to maturity and days to flowering also plant height and days to maturity ($r=0.73^{**}$). Hemavathy *et al.* (2017) and Kinhoegbe *et al.* (2020) stated that plant height correlated with single plant yield. In the current study, plant height was positively correlated with seed yield ($r=0.64^{**}$) (Table 3).

Sarwono (2006) categorized the correlation as follows: no correlation ($r=0$); very weak ($r=0-0.25$); medium ($r=0.26-0.50$); strong ($r=0.51-0.75$); very strong ($r=0.76-0.99$); and perfect correlation ($r=1$). According to Table 3, seed yield per ha perfectly correlated with seed yield per plot ($r=1$), strong correlated with plant height ($r=0.64$) and pod bearing length ($r=0.52$), medium correlated with days to flowering ($r=0.47$), days to maturity ($r=0.33$), number of main branches ($r=0.30$), and number of pods per plant ($r=0.41$). Days to flowering and days to maturity correlated with single plant yield was reported by Hemavathy *et al.* (2020).

On the other hand, Kinhoegbe *et al.* (2020) and Patel *et al.* (2020) mentioned the negative correlation between days to flowering with grain yield, and days to maturity with grain yield.

Principal Component Analysis

Principal component analysis was carried out to simplify the large number of characters data in making group among accessions. Principal component analysis is very useful for breeding purpose. It is a technique to identify the most contributive plant traits within a group of genotypes (Suman *et al.* 2019) and to discriminate potential crop genotypes (Fouz Abo Elenen *et al.* 2019; Sivakumar *et al.* 2020). The results showed that diversity of the data was 75.3% as explained by 4 main components that had eigenvalue >1 (Table 4).

The first component (PC1) had eigenvalue of 5.25 and consisted of 6 characters i.e. days to

Table 3. Correlation among 13 quantitative characters of 60 pigeon pea accessions. Muneng station, dry season 2018.

Variable	1	2	3	4	5	6	7	8	9	10	11	12	13
1. Days to flowering													
2. Days to maturity	0.73 ^{**}												
3. Plant height	0.64 ^{**}	0.73 ^{**}											
4. Pod bearing length	0.46 ^{**}	0.53 ^{**}	0.84 ^{**}										
5. No. main branches	0.63 ^{**}	0.68 ^{**}	0.60 ^{**}	0.41 ^{**}									
6. No. secondary branches	0.62 ^{**}	0.56 ^{**}	0.33 ^{**}	0.24 ^{ns}	0.46 ^{**}								
7. No. flowers per cluster	0.16 ^{ns}	-0.05 ^{ns}	-0.18 ^{ns}	-0.22 ^{ns}	-0.15 ^{ns}	0.06 ^{ns}							
8. Pod length	-0.09 ^{ns}	-0.14 ^{ns}	-0.08 ^{ns}	-0.09 ^{ns}	-0.20 ^{ns}	-0.20 ^{ns}	0.13 ^{ns}						
9. No. seeds per pod	-0.10 ^{ns}	-0.18 ^{ns}	-0.13 ^{ns}	-0.07 ^{ns}	-0.13 ^{ns}	-0.24 ^{ns}	-0.13 ^{ns}	0.51 ^{**}					
10. No. pods per plant	0.70 ^{**}	0.59 ^{**}	0.55 ^{**}	0.39 ^{**}	0.54 ^{**}	0.70 ^{**}	0.07 ^{ns}	-0.17 ^{ns}	-0.22 ^{ns}				
11. 100-seed weight	0.01 ^{ns}	0.16 ^{ns}	0.04 ^{ns}	0.04 ^{ns}	-0.02 ^{ns}	-0.12 ^{ns}	0.03 ^{ns}	0.03 ^{ns}	-0.16 ^{ns}	0.03 ^{ns}			
12. Seed weight per plot	0.47 ^{**}	0.33 ^{**}	0.64 ^{**}	0.52 ^{**}	0.30 ^{**}	0.09 ^{ns}	-0.11 ^{ns}	0.06 ^{ns}	-0.11 ^{ns}	0.41 ^{**}	0.19 ^{ns}		
13. Seed yield per ha	0.47 ^{**}	0.33 ^{**}	0.64 ^{**}	0.52 ^{**}	0.30 ^{**}	0.09 ^{ns}	-0.11 ^{ns}	0.06 ^{ns}	-0.11 ^{ns}	0.41 ^{**}	0.19 ^{ns}	1.00	

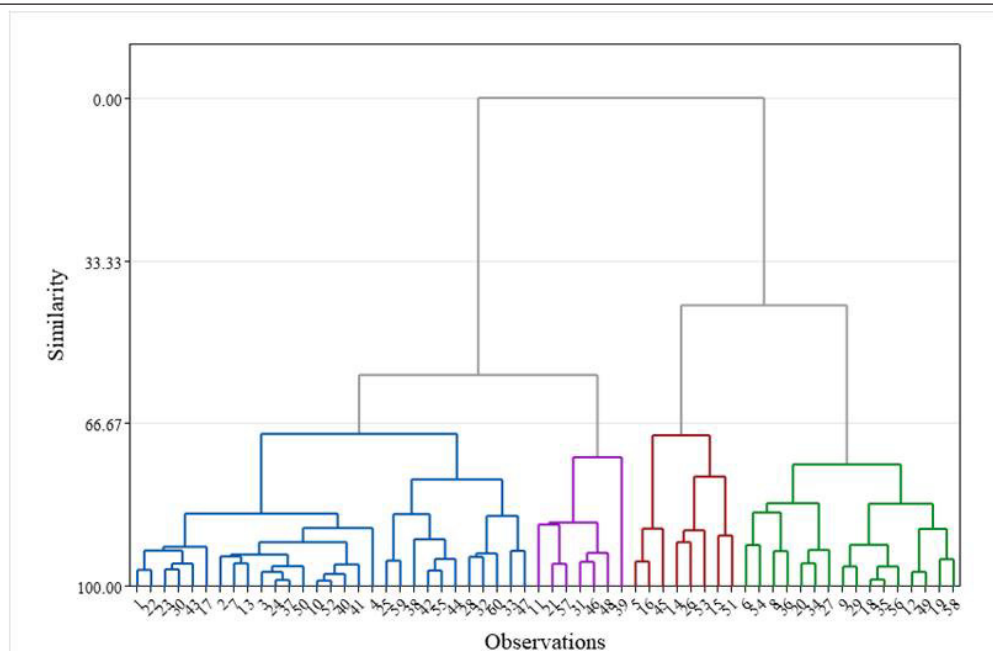
Table 4. Main components of 60 pigeon pea accessions. Muneng station, dry season 2018

Variable	PC1	PC2	PC3	PC4
Days to flowering	0.365	0.134	-0.209	0.183
Days to maturity	0.357	0.150	-0.094	-0.032
Plant height	0.386	-0.157	-0.020	-0.157
Pod bearing length	0.317	-0.199	0.020	-0.237
Number of main branches	0.318	0.164	-0.113	-0.201
Number of secondary branches	0.261	0.423	-0.179	0.056
Number of flowers per cluster	-0.040	0.201	-0.119	0.725
Pod length	-0.080	-0.365	-0.537	0.286
Number of seeds per pod	-0.108	-0.289	-0.631	-0.144
Number of pods per plant	0.340	0.209	-0.096	0.158
100-seeds weight	0.046	-0.176	0.379	0.371
Seed weight per plot	0.303	-0.423	0.154	0.157
Seed yield	0.303	-0.423	0.154	0.157
Eigenvalue	5.254	1.907	1.373	1.258
Proportion (%)	40.4	14.7	10.6	9.7
Cumulative (%)	40.4	55.1	65.6	75.3

Note: PC = principal component

Table 5. Grouping of 60 accessions of pigeon pea of ILISTI collection

Mean	Group			
	1	2	3	4
Days to flowering (days)	59-69	60-68	58-61	59-62
Days to maturity (days)	95-112	99-119	86-98	92-102
Plant height (cm)	121-145.4	137.8-151.8	71.2-97	105.2-122.6
Pod bearing length (cm)	45.8-63.8	66.2-79.6	18.4-38.6	35.2-58.8
Number of main branches	5.4-12.4	5.2-11.6	3.8-9	5.2-10.2
Number of secondary branches	0-5	0-2	0-1	0-2
Number of flowers per cluster	7.7-15	8.7-13	9.7-14	9.3-15
Pod length (cm)	5.05-6.81	5.76-6.53	5.31-6.52	5.22-6.75
Number of seeds per pod	3.8-5.1	4.1-4.8	3.9-5	4-4.9
Number of pods per plant	42.6-179.6	64.2-98.6	42-70.4	47.2-95.6
100-seed weight (g)	8.42-11.48	8.81-12.07	8.39-11.12	9.06-12.55
Seed yield per plot (kg)	1.01-1.96	1.43-2.31	0.68-1.28	1.04-1.94
Seed yield (t/ha)	1.27-2.46	1.78-2.89	0.85-1.60	1.29-2.42
Member (accessions)	29	7	8	16kk

**Figure 4.** Grouping of 60 pigeon pea accessions of ILISTI collection

flowering (0.365), days to maturity (0.357), plant height (0.386), pod bearing length (0.317), number of main branches (0.318), and number of pods per plant (0.340). These six characters had the highest variance among the quantitative characters tested and these contributed 40.4% to the data variability. The six characters were primer measures of pigeon pea plant yield in this study.

The second component (PC2) explained 14.7% of the data variability and consisted of 4 characters and there were number of secondary branches (0.423), pod length (-0.365), seed weight per plot (-0.423), and seed yield (-0.423). Number of seeds per pod (-0.631) and 100-seed weight (0.379)

contributed 10.6% to the data variability and was in third component or PC3 (Table 4).

The fourth component (PC4) consisted of number of flowers per cluster (0.725) that explained 9.7% of the data variability. Even the PC4 consisted of a character with the highest eigenvalue of 0.725, and this character less contributed compare to the other characters in PC1, PC2 and PC3.

Cluster Analysis

The result of cluster analysis showed that 60 pigeon pea accessions were grouped into four clusters. Groups 1 and 2 had 60% degree of similarity, while groups 3 and 4 had 40% degree of similarity (Figure 4). The degree of similarity groups

1 and 2 was higher than that in groups 3 and 4. These conditions gave a meaning that the genetic distance between genotypes in groups 1 and 2 was closer than those in groups 3 and 4.

Cluster analysis is useful for selecting parents in breeding process base on genetic distance as the presence of genetic distance between parents can increase genetic diversity in breeding populations (Kinhoegbe et al. 2020). In this study, the diversity of breeding population from crosses between genotypes in group 1 and 3 would be higher than the crosses offspring between genotypes in groups 1 and 2.

The first group consisted of 29 accessions, which had many branches and pods per plant. The second group consisted of seven accessions. Characteristic of the second group was the latest days to flowering and maturity, also the highest seed yield per ha (Table 5).

Group 3 consisted of early maturity genotypes, while group 4 was characterized by its large seed size. Group 3 had shorter plant, early flowering and maturity days, but lower seed yield. Meanwhile, group 2 showed superiority in yield character, although the days to flowering and maturity was late. Breeding/crossing between genotypes in group 2 and 3 may produce the line which has early maturity and high seed yield.

CONCLUSION

Pigeon pea accessions showed diversity on quantitative characters observed. Total variance of the observed variables/characters was 75.3% as it was explained by four main principle components. Sixty accessions of pigeon pea of ILISTI collection could be classify into four groups that contained 29, 7, 8, and 16 accessions for group 1, 2, 3, and 4 respectively. Group 2 had the potential to be developed because of its good plant performance as described by long stem segment that produce pods, large seed size, and high seed yield.

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