



## **Genetic Variability and Diversity of the Agro-Morphological Traits of Torch Ginger (*Etlingera elatior*) Germplasm in Malaysia**

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### **Authors' contributions**

*This work was carried out in collaboration among all authors. Author MYR designed and supervised the study, while author NAI managed the study. Authors NAI and MYR performed the statistical analysis and wrote the first draft of the manuscript. Authors TMMM and MMH co supervised the study and made significant contributions to the editing and proofreading of the final manuscript. All authors read and approved the final manuscript.*

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### **ABSTRACT**

**Aims:** The main objective of this study is to quantify the genetic variability and relationship among the quantitative traits of the torch ginger germplasm collected across Peninsular Malaysia.

**Study design:** Initially, the experimental design was randomized complete block design (RCBD) but there were unequal number of replications due to limited planting materials.

**Place and Duration of Study:** The study was conducted at the Malaysian Agricultural Research and Development Institute (MARDI) Research Station, Jerangau, Terengganu, Malaysia on latitude 04°57.704'N and longitude 103°11.007'E. Data on agro-morphological characterization were collected for three years from June 2010 until May 2013.

**Methodology:** A total of 57 torch ginger accessions were collected from various wild/ cultivated

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sources from seven states of Peninsular Malaysia namely Terengganu (19), Perak (15), Kedah (7), Johor (6), Pahang (5), Kelantan (3) and Melaka (2). The collection was planted in 2009 and maintained as living collection. At three months old torch ginger plantlets were transplanted into 20 cm × 20 cm × 20 cm holes spaced at 100 cm diameter of culvert. The spacing of culvert between rows and within rows were 2 m respectively. Initially, the experimental design was randomized complete block design (RCBD) but there were unequal number of replications due to limited planting materials. Data on agro-morphological characterization were collected for three years from June 2010 until May 2013. All the 57 accessions were characterized according to descriptors list of genera under Zingiberaceae family with some modifications. A total of 6 qualitative and 16 quantitative descriptors were used. The mean values of each quantitative trait data were computed and subjected to statistical analysis to assess the amount of genetic variation using analysis of variance (ANOVA). The ANOVA was using PROC GLM of SAS 9.4 software (SAS Institute Inc., Cary, NC, USA). Genotypic coefficients of variation and error variance were estimated using PROC VARCOMP method Type I of SAS 9.4 software. Phenotypic coefficients of variation, heritability and genetic advance were calculated. Pearson correlation coefficient was determined using SAS 9.4 for comparing the relationship among the different traits. The morphological traits were analyzed by numerical taxonomic methods via cluster analysis and Principal Component Analysis (PCA) which was done using NTSYS-PC Version 2.1. PCA based on 16 quantitative and six qualitative traits was performed to determine the genetic variation in the torch ginger accessions. The cluster and PCA were performed to reveal clustering and grouping pattern of torch ginger accessions. Euclidean distance coefficients were estimated for all pairs of accessions, which was then used to present cluster analysis.

**Results:** Analysis of variance indicated that highly significant variation exists among the 57 accessions for most of the traits. The 57 accessions of torch ginger showed high variability for both qualitative and quantitative traits. Among the quantitative traits, the highest CV was observed from number of spikes with the value of 44.25%. The genetic coefficient of variation for 16 morphological traits ranged from 9.76 to 45.86%. Broad sense heritability estimates varied from low to high. Maximum estimates of broad sense heritability were recorded in bract length (80.16%), bud peduncle length (78.74%), number of leaves (75.66%), number of stems per clump (67.99%), inflorescence peduncle length (67.60%) and bud width (65.11%). The genetic advance (GA) in percent of mean was recorded from 11.82 to 67.97%. Besides that, positive correlation coefficient was obtained between some traits. Generally, the genotypes groups were related with morphological characteristics among the accessions.

**Conclusion:** Considering the distribution pattern, vegetative and yield performance of accessions, it is suggested that accessions from cluster VII (KAN022, KAN047 and KAN048) should be selected for future breeding program. These accessions possessed the highest peduncle length that could influence the yield in terms of bud size. Furthermore, the classification and divergence between torch ginger accessions analyzed in this study may assist in conserving plant materials both *in-situ* and *ex-situ*.

**Keywords:** *Etiligera elatior*; germplasm; variability; phenotypic characters.

## 1. INTRODUCTION

Torch ginger (*Etiligera elatior*), has long been known by Malaysians as a condiment, vegetable, traditional medicine and also for ornamental purposes. The vernacular names for torch ginger are Bunga Kantan (Malaysia), Bunga Siantan (Indonesia), Kaa Laa (Thailand) and Rosa-De-Porcelana (Brazil). It is a member of the Zingiberaceae family and native to Southeast Asia including Indonesia, Malaysia and South Thailand. Torch ginger is commonly propagated by rhizomes (asexually). It takes about 12 months after planting to start flowering but a

longer time is needed when seeds are used [1]. It is a perennial herb with closely grouped pseudo stems reaching 3 – 4 m high. The inflorescence is torch like, borne on erect stalks up to 1.5 m tall arising from fleshy underground rhizomes [2,3]. The development phase and growth of torch ginger are separated into two stages namely vegetative and reproductive. Predominantly, the vegetative stage includes the development of foliage and the emergence of leafy shoots. The reproductive stage begins when the inflorescence shoot grows out of the rhizome [1]. Generally, before the enlarging of inflorescence bud, it took around 30 days for an inflorescence

to grow out of the rhizome. The process of inflorescence development starts from the extension of the peduncle and the enlargement of the inflorescence bud [4]. During the flowering stage, it took another 30 days from tight-bud stage to reach full bloom where true flowers are borne. From the opening of the first ring of true flowers, it takes about 24 days for all true flowers to open ring by ring. At this stage, the inflorescence head turned brown and dried.

Torch ginger inflorescence varied from pink, red and white colors. The pink torch ginger is commonly cultivated in fields and house backyard. As an ornamental plant, torch ginger is widely commercialized in the floriculture industry. It is used as a cut flower and for garden landscapes in Brazil [5]. In Malaysia, the flower bud is usually used in culinary dishes such as curries, *nasi kerabu* and *nasi ulam* or cooked with mixed vegetables. It is also a compulsory ingredient as condiment for a popular local dish known as *Penang laksa*.

Torch ginger is a potential source of natural antioxidant and antibacterial in food and pharmaceutical industries. It has been identified to have high market demand among the 30 most popular herbs and new industrial crops in Malaysia. Torch ginger is considered as an important medicinal, aromatic and ornamental plant, which is cultivated for its flavor and as spice and medicinal aspects in many areas of the tropical regions. Besides, torch ginger was also reported to contain various classes of polyphenols, flavonoids and ascorbic acid, displaying different health-promoting properties, mainly from the antioxidant activities [6,7]. These properties make a significant contribution of torch ginger as a potential source of natural antioxidants for food and nutraceutical applications.

The studies on morphological characterization of gingers such as *Zingiber officinale* and *Curcuma longa* have been attempted, but none have been reported on torch ginger. Previous studies on ginger showed the existence of considerable variability among the genotypes [8-11] and a wide genetic variation in ginger populations [10,12,13]. Genetic analysis of morphological diversity is crucial for assessing, conserving and exploiting plant genetic resources. On the other hand, the investigation is essential for revealing the distinctness and distinctiveness of the genotypes. Besides, it will provide valuable information for genetic improvement [14].

Morphological characterization and evaluation are very important in the classification and utilization of germplasm. The process would permit the identification of the promising genotypes, which might be used in breeding programs or can be adopted for cultivation [15,16].

In Malaysia, torch ginger is mostly cultivated by small scale farmers with land race varieties. Hence, the fresh torch ginger flower production is low to fulfil the local demand. In addition, the quality is not consistent because of the unavailability of high yielding and superior quality varieties. This condition necessitates the need to conduct breeding programs after collection, evaluation and selection of torch ginger germplasm to develop superior variety. This program is important for high yielding and high-quality flowers production. The traits that contribute to high yielding variety can be identified through diverse germplasm evaluation and the relationship analysis among the yield and yield contributing traits [17]. The evaluation of plant genetic diversity such as breeding programs and crop improvement is considered as an advanced action for food and agriculture researchers [16,18]. Therefore, the data on genetic diversity such as the level and relationship between traits is essential for the utilization of plant genetic resources [19]. Furthermore, the identification of germplasm with superior trait must be isolated, and their performance in suitable environment be recorded [20].

The main objective of this study is to quantify the genetic variability and relationship among the quantitative traits of the torch ginger germplasm collected across Peninsular Malaysia. This study will be useful for plant breeders to perform effective selection for genetic improvement.

## 2. MATERIALS AND METHODS

### 2.1 Experiment Site and Plant Materials

The study was conducted at the Malaysian Agricultural Research and Development Institute (MARDI) Research Station, Jerangau, Terengganu. A total of 57 torch ginger accessions were collected from various wild/cultivated sources from seven states of Peninsular Malaysia namely Terengganu (19), Perak (15), Kedah (7), Johor (6), Pahang (5), Kelantan (3) and Melaka (2) (Table 1). The collection was planted in 2009 and maintained as living collection. Prior to cultivation the collected

torch ginger were propagated by rhizome at a rain shelter condition. At three months old torch ginger plantlets were transplanted into 20 cm × 20 cm × 20 cm holes spaced at 100 cm diameter of culvert. The spacing of culvert between rows and within rows were 2 m respectively. The crop was raised at optimum growing conditions. The experiment was maintained according to the recommended cultural practices [21]. Initially, the experimental design was randomized complete block design (RCBD) but there were unequal number of replications due to limited planting materials.

## 2.2 Agro-morphological Characterization

Data on agro-morphological characterization were collected for three years from June 2010 until May 2013. All the 57 accessions were characterized according to descriptors list of genera under Zingiberaceae family with some modifications depends on their characters. A total of 6 qualitative (Table 2) and 16 quantitative descriptors (Table 3) were used in the study. The qualitative traits included leaf shape, color of young leaf, leaflet surface, inflorescence shape, flower color and bract color. The color of leaf and flower were recorded by using a Munsell Color Charts for Plant Tissues. Meanwhile, quantitative traits recorded were plant height (m), number of plants, number of leaves, leaf length (cm), leaf width (cm), petiole length (cm), ligule length (cm), bud length (cm), bud width (cm), inflorescence length (cm), inflorescence width (cm), bud peduncle length (cm), inflorescence peduncle length (cm), corolla tube length (cm), bract length (cm) and number of spikes.

## 2.3 Data Analysis

The mean values of each quantitative trait data were computed and subjected to statistical analysis to assess the amount of genetic variation using analysis of variance (ANOVA). The ANOVA was using PROC GLM of SAS 9.4 software (SAS Institute Inc., Cary, NC, USA). Genotypic coefficients of variation and error variance were estimated using PROC VARCOMP method Type I of SAS 9.4 software. Phenotypic coefficients of variation, heritability and genetic advance were calculated as suggested by Burton and Devane [22] and Johnson *et al.* [23].

Phenotypic variance,  $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Genotypic coefficient of variation

$$(\text{GCV}\%) = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$$

Phenotypic coefficient of variation

$$(\text{PCV}\%) = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$$

Broad-sense heritability,  $h_B^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$

Genetic advance as % of mean,

$$\text{GA} = K \times \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times h_B^2 \times 100$$

**Table 1. List of torch ginger (*Etilingera elatior*) germplasms and their collection source**

Population	Accessions	Origin	
Perak	KAN002	Kg. Bongor, Grik	
	KAN003	Kg. Tersusun, Grik	
	KAN005	Kg. Pasang Api, Bagan Datoh, Hilir Perak	
	KAN006	Kg. Sg. Ular, Bagan Datoh, Hilir Perak	
	KAN008	Kg. Paya, Changkat Jering	
	KAN009	Kg. Jamuan Jenalik, Kuala Kangsar (A)	
	KAN010	Kg. Jamuan Jenalik, Kuala Kangsar (B)	
	KAN011	Kg. Seterus, Sauk, Kuala Kangsar	
	KAN012	Kg. Kerian, Batu Kurau	
	KAN013	Kg. Lalang, Grik	
	KAN031	Kg. Serentang, Bidor, Batang Padang	
	KAN045	Kg. Lempor Tengah, Kuala Kangsar	
	KAN046	Kg. Pecah Batu, Kuala Kangsar	
	KAN047	Lata Putih, Bukit Kulim, Larut Matang	
	Terengganu	KAN007	Kg. Telok, Kuala Nerus

Population	Accessions	Origin
	KAN014	Kg Tepus, Hulu Dungun
	KAN015	Kg. Pasir Raja, Hulu Dungun
	KAN017	Kg. Matang, Hulu Terengganu
	KAN018	Kg. Pasir Dula, Hulu Terengganu
	KAN019	Kg. Basong, Hulu Terengganu
	KAN020	Kg. Bahagia, Tok Kah, Kuala Abang, Dungun
	KAN021	Kg. Bemban, Dungun
	KAN022	Kg. Binjai, Kemaman
	KAN023	Kg. Che Long, Permaisuri, Setiu
	KAN024	Felda Selasih, Permaisuri, Setiu
	KAN025	Felda Selasih, Permaisuri, Setiu
	KAN026	Kg. Padang Bual, Pasir Akar, Jerteh
	KAN027	Kg. Pecah Rotan, Bt. Rakit, Kuala Terengganu
	KAN028	Mengabang Lekor, Bt. Rakit, Kuala Terengganu
	KAN029	Kg. Din Maras, Bt. Rakit, Kuala Terengganu
	KAN030	Chendering, Marang
	KAN059	Kg. Tebing Tembah, Paka, Dungun
	KAN083	Kg. Kuala Kubang, Jabi
Kedah	KAN004	Kg. Titi Terus, Yan
	KAN033	Kg. Tok Weng, Pulai, Baling
	KAN034	Kg. Telok Durian, Kupang, Baling
	KAN035	Kg. Bukit Iboi, Kupang, Baling
	KAN036	Kg. Parit Panjang, Kupang, Baling
	KAN039	Kg. Bt. 13.5, Kodiang, Jitra
	KAN041	Kg. Padang Gaung, Hulu Melaka, Pulau Langkawi
Johor	KAN052	Felda Ulu Dengar, Kluang
	KAN055	Compartmen 123, Hutan Simpan Labis, Segamat (A)
	KAN056	Compartmen 123, Hutan Simpan Labis, Segamat (B)
	KAN057	Hutan Rekreasi Gunung Arong, Mersing
	KAN058	Kg. Tenglu, Mersing
	KAN068	Kg. Sungai Mengkuang, Triang, Mersing
Pahang	KAN061	Kg. Peruas, Ulu Dong, Raub
	KAN062	Kg. Peruas, Ulu Dong, Raub
	KAN063	Kg. Peruas, Ulu Dong, Raub
	KAN064	Kg. Peruas, Ulu Dong, Raub
	KAN066	Taman Herba Jabatan Hutan Som, Ulu Cheka, Jerantut
Kelantan	KAN048	Kg. Jeli Dalam, Jeli
	KAN069	Kg. Kundur, Gua Musang
	KAN071	RPT Batu Mengkebang, Kuala Krai
Melaka	KAN080	Kg. Air Hitam Darat, Masjid Tanah
	KAN081	Kg. Permatang, Kuala Sungai Baru, Alor Gajah

**Table 2. Qualitative descriptors used to evaluate 57 accessions of torch ginger**

Qualitative traits	Observed phenotypic classes
Leaf shape	1- elliptical; 2- oblong elliptic
Color of young leaf	1- light green; 2- green; 3- dark green; 4- reddish green;
Leaflet surface	1- smooth; 2- smooth shiny; 3- rough
Inflorescence shape	1- spread to conical to apex; 2- rounded to conical to apex
Flower color	1- red; 2- dark red
Bract color	1- dark pink; 2- pink; 3- pale pink; 4- red

Where K is a constant which varies depending upon the selection intensity and, if the latter is 5%, stands at 2.06 [24].

$\frac{\sqrt{\sigma_p^2}}{x}$  is phenotypic standard deviation,  $h_B^2$  is heritability while X represents the mean of the trait being evaluated.

MSG = mean square of accessions

MSE = mean square of error

b = number of blocks

X = mean of the trait

Pearson correlation coefficient was determined using SAS 9.4 for comparing the relationship among the different traits. The morphological traits were analyzed by numerical taxonomic methods via cluster analysis and Principal Component Analysis (PCA) [25] which was done using NTSYS-PC Version 2.1 [26]. PCA based on 16 quantitative and six qualitative traits was performed to determine the genetic variation in the torch ginger accessions. The cluster and PCA were performed to reveal clustering and grouping pattern of torch ginger accessions. Euclidean distance coefficients were estimated for all pairs of accessions, which was then used to present cluster analysis.

**Table 3. Quantitative descriptors used to evaluate 57 accessions of torch ginger**

Quantitative traits	Descriptions
Plant height (m)	Height of each plant from soil surface to the tip was measured using measuring tape.
Number of plants	Average number of plants per clump.
Number of leaves	Average number of leaves per plant.
Leaf length (cm)	The length of leaf from base to the tip was measured with a digital caliper. The average value of six leaf length per plant was recorded.
Leaf width (cm)	The broadest part of leaf was measured with a digital caliper. The average value of six leaf width per plant was recorded.
Petiole length (cm)	The length of petiole was measured with a digital caliper. The average value of six petiole length per plant was recorded.
Ligule length (cm)	The length of ligule was measured with a digital caliper. The average value of six ligule length per plant was recorded.
Bud length (cm)	The length of bud from calyx to the tip was measured with a digital caliper. The average value of bud length was taken based on available bud per plant.
Bud width (cm)	The broadest part of bud was measured with a digital caliper. The average value of bud width was taken based on available bud per plant.
Inflorescence length (cm)	The length of inflorescence from the calyx to the tip was measured with a digital caliper. The average value of inflorescence length was taken based on available inflorescence per plant.
Inflorescence width (cm)	The broadest part of the inflorescence was measured with a digital caliper. The average value of inflorescence width was taken based on available inflorescence per plant.
Bud peduncle length (cm)	The length of bud peduncle was measured with a digital caliper. The average value of bud peduncle length was taken based on available bud peduncle per plant.
Inflorescence peduncle length (cm)	The length of the inflorescence peduncle was measured with a digital caliper. The average value of inflorescence peduncle length was taken based on available inflorescence peduncle per plant.
Corolla tube length (cm)	The length of the corolla tube was measured with a digital caliper. The average value of six corolla tube length per inflorescence was taken based on available inflorescence.
Bract length (cm)	The length of the bract was measured with a digital caliper. The average value of six bract length per inflorescence was taken based on available inflorescence.
Number of spikes	Total number of harvested spikes per year.

### 3. RESULTS

#### 3.1 Agro-morphological Variability based on Qualitative Traits

Observations on six qualitative traits were recorded for all the 57 accessions and the scores were analyzed (Table 4). The maximum number of accessions (53) was observed with elliptical leaf shape while four accessions namely KAN017, KAN046, KAN056 and KAN057 have oblong elliptic shape. The young leaves of two accessions (KAN053 and KAN064) were reddish green in color while others ranged from light green to dark green. In the case of leaflet surface, the maximum number of accessions (42) was found with smooth surface and other two characters were smooth shiny (2) and rough (13). Two groups for inflorescence shape namely spread to conical to apex and rounded to conical to apex were observed. Spread to conical to apex inflorescence was found in 54 accessions and three accessions were categorized as rounded to conical to apex. Among the accessions, three categories such as pale pink, pink and dark pink of bract were observed. Most accessions possessed pale pink bract (34), while pink and dark pink were found in 14 and 9 accessions, respectively. Only two categories of flower color (red and dark red) were identified. Red color was found in 43 accessions whereas dark red flower accounted for the other 14 accessions.

#### 3.2 Agro-morphological Variability based on Quantitative Traits

Agro-morphological traits were divided into two categories which includes vegetative and inflorescence traits (Table 5). The vegetative traits comprised of plant height, number of stems per clump, number of leaves, leaf length, leaf

width, petiole length and ligule length. The highest value for plant height was displayed by KAN063 with a value of 6.22 m, followed by KAN013 with 6.12 m while the lowest value for plant height was in accession KAN069 which is 1.60 m. Maximum number of plants (43) was recorded from KAN045 while the minimum number of plants (7) was found in accession KAN057. Among the vegetative traits, three traits (number of stems, ligule length and inflorescence width) showed coefficients of variation (CV) above 20% with the value of 21.87%, 24.95% and 22.99%, respectively. Other vegetative traits except number of spikes were found to have comparatively lower coefficient of variation.

Inflorescence traits were the components that are involved in contributing to the yield of torch ginger. These components comprised of bud length, inflorescence length, bud width, inflorescence width, bud peduncle length, peduncle length, corolla tube length, bract length and number of spikes. The longest bud of the torch ginger was 11.0 cm from accession KAN022, followed by KAN052 with bud length of 10.50 cm, while the shortest bud was 4.50 cm recorded from accession KAN063. For bud width, the highest value was 5.78 cm wide in KAN066 followed by 5.73 cm in KAN010. The lowest value of this trait was 1.56 cm which was observed in accession KAN007. The CV for these two traits was 14.46% and 18.18% with the standard deviation of 1.31 and 10.19, respectively.

Number of spikes is the total stalks of bud produced from each clump. The highest number of spikes was 124 recorded from accession KAN046, while KAN064 produced only two spikes per clump. Among the quantitative traits, the highest CV was observed from number of spikes with the value of 44.25%.

**Table 4. Distribution of phenotypic classes among qualitative traits**

Descriptor	Code	Category	Number of accessions	Frequency (%)
Leaf shape	1	Elliptical	53	93.0
	2	Oblong elliptic	4	7.0
Color of young leaf	1	Light green	46	80.7
	2	Green	7	12.3
	3	Dark green	2	3.5
	4	Reddish green	2	3.5
Leaflet surface	1	Smooth	42	73.7
	2	Smooth, shiny	2	3.5
	3	Rough	13	22.8
Inflorescence shape	1	Spread to conical to apex	54	94.7
	2	Rounded to conical to apex	3	5.3

Descriptor	Code	Category	Number of accessions	Frequency (%)
Flower color	1	Red	43	75.4
	2	Dark red	14	24.6
Bract color	1	Dark pink	9	15.8
	2	Pink	14	24.6
	3	Pale pink	34	59.6



Fig. 1. Different bract color of torch ginger. A: dark pink (KAN024); B: pink (KAN035); C: pale pink (KAN031)

Table 5. Coefficient of variation, standard deviation, minimum and maximum

	Traits	Mean	Minimum	Maximum	Std. Dev.	CV (%)
Vegetative traits	Plant height (m)	3.97	1.60	6.22	1.07	17.75
	Number of stems per clump	17.84	7.00	43.00	6.83	21.87
	Number of leaves	25.99	7.00	76.00	8.02	15.23
	Leaf length (cm)	63.18	36.50	94.50	13.46	16.81
	Leaf width (cm)	16.10	10.50	24.30	2.57	12.45
	Petiole length (cm)	2.77	1.00	4.70	0.82	19.78
	Ligule length (cm)	12.88	1.30	34.00	4.47	24.94
Inflorescence traits	Bud length (cm)	7.38	4.50	11.00	1.31	14.46
	Inflorescence length (cm)	9.03	5.50	14.00	1.66	12.94
	Bud width (cm)	33.36	15.61	57.78	10.19	18.18
	Inflorescence width (cm)	69.82	39.52	153.68	19.94	22.99
	Bud peduncle length (cm)	48.49	25.00	112.50	17.47	16.62
	Peduncle length (cm)	62.60	30.50	132.50	21.11	19.32
	Corolla tube length (cm)	4.10	2.80	5.65	0.54	8.93
	Bract length (cm)	6.82	3.50	9.60	1.22	7.96
	Number of spikes	35.89	2.00	124.00	22.93	44.25

**Table 6. Mean squares of quantitative traits of 57 torch ginger accessions**

Source of Variation	df	PH	NST	NLV	LFL	LFW	PTL	LGL	BDL
Blocks (B)	2	2.05	13.50	60.19	766.45	5.06	0.60	36.18	2.54
Accessions (G)	56	1.37**	59.10**	81.81**	184.64 <sup>ns</sup>	7.57 <sup>ns</sup>	0.82**	22.84*	1.88 <sup>ns</sup>
States (S)	(6)	1.13*	54.76*	76.57**	135.50 <sup>ns</sup>	4.69 <sup>ns</sup>	1.45**	80.18**	2.07 <sup>ns</sup>
G (S)	(50)	1.40**	59.62**	82.43**	190.53 <sup>ns</sup>	7.92*	0.74*	15.96 <sup>ns</sup>	1.86 <sup>ns</sup>
Error	20	0.39	15.22	15.67	112.81	4.02	0.30	10.33	1.14

Source of Variation	df	IFL	BDW	IFW	BPL	PDL	CTL	BRL	NSP
Blocks (B)	2	1.27	47.38	6.99	285.62	218.04	6.07x10 <sup>-3</sup>	1.26	633.05
Accessions (G)	56	3.32*	129.87**	461.74 <sup>ns</sup>	391.61**	560.39**	0.35*	1.91**	619.71*
States (S)	(6)	4.47*	192.55**	187.00 <sup>ns</sup>	235.39*	345.32 <sup>ns</sup>	0.28 <sup>ns</sup>	1.18**	1151.64**
G (S)	(50)	3.19*	122.35**	494.70 <sup>ns</sup>	410.35**	586.20**	0.36**	2.00**	555.88*
Error	20	1.37	36.77	257.64	64.97	146.25	0.13	0.29	252.20

Note: \*Significantly different at  $\leq 0.05$ ; \*\*Highly significantly different at  $\leq 0.01$ ; ns: Not significant at  $p > 0.05$ ; PH: Plant Height; NST: Number of stems/clump; NLV: Number of leaves; LFL: Leaf length; LFW: Leaf width; PTL: Petiole length; LGL: Ligule length; BDL: Bud length; IFL: Inflorescence length; BDW: Bud width; IFW: Inflorescence width; BPL: Bud peduncle length; PL: Inflorescence peduncle length; CTL: Corolla tube length; BRL: Bract length; NSP: Number of spikes

**Table 7. Mean comparison of seven states based on quantitative traits**

States	PH	NST	NLV	LFL	LFW	PTL	LGL	BDL
Perak	4.09ab	17.61b	26.91abc	63.24ab	16.14a	3.03ab	13.42b	7.48a
Terengganu	3.76ab	17.32b	23.76cd	64.72ab	15.64a	2.53bc	11.53b	7.61a
Kelantan	3.36b	27.67a	21.67d	52.07b	15.83a	3.53a	24.10a	7.43a
Kedah	3.85ab	18.25b	26.00bcd	60.53ab	16.04a	2.19c	10.89b	7.27ab
Johor	4.17a	15.67b	30.56ab	63.68ab	15.93a	2.61bc	12.79b	7.65a
Melaka	3.98ab	17.50b	31.00a	68.45a	16.65a	2.70bc	10.35b	6.03b
Pahang	4.39a	18.44b	25.56cd	63.19ab	17.48a	3.18ab	13.97b	6.54ab
LSD	0.78	4.89	4.96	13.32	2.51	0.69	4.03	1.34

States	IFL	BDW	IFW	BPL	PDL	CTL	BRL	NSP
Perak	9.21ab	34.34b	68.25a	49.58a	62.10a	3.98ab	6.99ab	44.44a
Terengganu	9.37a	31.63b	73.70a	51.76a	66.50a	4.14ab	6.83ab	40.60ab
Kelantan	8.96ab	28.31b	67.51a	51.51a	68.36a	4.28ab	7.45a	32.67abc
Kedah	8.71ab	31.18b	70.09a	48.54a	63.20a	3.88b	6.42b	30.88abc
Johor	9.54a	29.52b	64.74a	44.31a	58.89a	4.24ab	6.53b	26.89abc
Melaka	7.09c	32.28b	55.44a	26.88b	34.84b	3.99ab	5.58c	21.00bc
Pahang	7.88bc	43.37a	71.89a	44.32a	60.50a	4.36a	7.02ab	18.78c
LSD	0.78	4.89	4.96	13.32	2.51	0.69	4.03	1.34

Note: Means in the same column followed by different letters are significantly different at  $p < 0.05$ ; PH: Plant Height; NST: Number of stems/ clump; NLV: Number of leaves; LFL: Leaf length; LFW: Leaf width; PTL: Petiole length; LGL: Ligule length; BDL: Bud length; IFL: Inflorescence length; BDW: Bud width; IFW: Inflorescence width; BPL: Bud peduncle length; PL: Inflorescence peduncle length; CTL: Corolla tube length; BRL: Bract length; NSP: Number of spike

### 3.3 Genetic Diversity of Torch Ginger based on Agro-morphological Traits

A significant level of variation was discovered in different accessions for quantitative traits. Germplasm varied in many agro-morphological

traits comprising of plant height, number of stems, leaf width, petiole length, ligule length, bud length, inflorescence length, bud width, bud peduncle length, peduncle length, corolla tube length, bract length and number of spikes. Statistically, most of the quantitative traits

**Table 8. Estimation of variances, coefficient of variances and heritability in broad sense**

Traits	$\sigma_g^2$	$\sigma_p^2$	GCV%	PCV%	$h_B^2\%$	GA%
Plant height (m)	0.72	1.11	21.37	26.55	64.81	35.44
Number of stems	32.33	47.55	31.88	38.66	67.99	54.15
Number of leaves (cm)	48.73	64.40	26.86	30.88	75.66	48.13
Leaf length (cm)	52.92	165.74	11.51	20.38	31.93	13.40
Leaf width (cm)	2.62	6.64	10.05	16.00	39.42	13.00
Petiole length (cm)	0.38	0.68	22.36	29.85	56.12	34.51
Ligule length (cm)	9.21	19.55	23.56	34.31	47.13	33.32
Bud length (cm)	0.55	1.69	10.05	17.61	32.59	11.82
Inflorescence length (cm)	1.44	2.81	13.29	18.55	51.32	19.62
Bud width (cm)	68.60	105.37	24.83	30.77	65.11	41.27
Inflorescence width (cm)	150.39	408.03	17.56	28.93	36.86	21.96
Bud peduncle length (cm)	240.68	305.65	31.99	36.05	78.74	58.48
Inflorescence peduncle length (cm)	305.15	408.03	27.90	33.94	67.60	47.26
Corolla tube length (cm)	0.16	0.29	9.76	13.23	54.42	14.83
Bract length (cm)	1.19	1.48	16.00	17.87	80.16	29.51
Number of spikes	270.80	523.00	45.86	63.73	51.78	67.97

Note:  $\sigma_g^2$ : genotypic variance;  $\sigma_p^2$ : phenotypic variance; GCV%: genotypic coefficient of variation; PCV%: phenotypic coefficient of variation;  $h_B^2\%$ : Heritability; GA%: genetic advance

showed significant differences except leaf length, ligule length, bud length and inflorescence width which were not significant among the accessions within different locations (Table 6). Among them, eight traits (plant height, number of stems, number of leaves, petiole length, bud width, bud peduncle length, inflorescence peduncle length and bract length) showed highly significant difference from each other. Meanwhile, among the seven states six traits namely number of leaves, petiole length, ligule length, bud width, bract length and number of spikes displayed highly significantly different from each other. Comparing the collection source (states), almost all quantitative traits except four traits (number of spikes, ligule length, bud width, bud peduncle length and inflorescence peduncle length) showed no significant different among each other (Table 7). Accessions from Kelantan showed significantly different among other states for the number of spikes and ligule length. Meanwhile, Melaka displayed significantly different for the traits of bud peduncle length and inflorescence peduncle length among other states.

### 3.4 Heritability Analysis of Agro-morphological Traits

To compare the variation among various plant properties, estimation of variance components ( $\sigma_g^2, \sigma_p^2, \sigma_e^2$ ), phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV) and broad sense of heritability ( $h_B^2$ ) are given in Table 3.8. Phenotypic coefficients of variation ranged from 13.23 to 63.73% with the highest PCV obtained in number of spikes per clump and

the lowest in corolla tube length. In general, torch ginger germplasm inflorescence characteristics had low phenotypic coefficient of variations such as bud length, inflorescence length, corolla tube length and bract length. The genetic coefficient of variation for 16 morphological traits ranged from 9.76 to 45.86%. Broad sense heritability estimates varied from low to high. Maximum estimates of broad sense heritability were recorded in bract length (80.16%), bud peduncle length (78.74%), number of leaves (75.66%), number of stems per clump (67.99%), inflorescence peduncle length (67.60%) and bud width (65.11%). The genetic advance (GA) in percent of mean was recorded from 11.82 to 67.97% (Table 8).

### 3.5 Correlation Coefficients among 16 Quantitative Traits

Pearson correlation coefficient was employed among 16 agro-morphological traits (Table 9). Among the 120 inter correlation coefficients, 18 were significant. The highest significant positive correlation (0.91) was detected between bud length and inflorescence length and also between bud peduncle length and inflorescence peduncle length. Significant correlation among vegetative traits was observed between plant height with number of leaves (0.52), leaf length (0.70), leaf width (0.57) and petiole length (0.47); petiole length with leaf length (0.49) and leaf width (0.43); leaf length with number of leaves (0.42) and leaf width (0.71). For reproductive traits, bud length had a positive and significant association with inflorescence length (0.91), bud peduncle length (0.44) and inflorescence

peduncle length (0.40). A significant correlation between bract length with inflorescence width (0.45) and bud peduncle length (0.59) was also observed. In this study peduncle length appeared to be of prime importance as it directly influenced bud length as well as bract length.

### **3.6 Genetic Distance-based Analysis for Quantitative and Qualitative Traits of Torch Ginger**

#### **3.6.1 Cluster analysis based on quantitative traits**

Dendrogram based on Unweighted Pair Group Method with Arithmetic Mean (UPGMA) cluster analysis using Euclidean distance coefficients, grouped 57 accessions into seven clusters at 1.88 similarity coefficients for quantitative traits (Fig. 2). Cluster II was the biggest group consisted of 23 accessions followed by cluster III which comprised of 21 accessions (Table 10). Whereas, Cluster I had 6 accessions (KAN002, KAN007, KAN008, KAN080, KAN059, KAN045). Cluster IV and V1 consisted of 2 and 3 accessions, respectively. Two clusters (V and VII) were separated from other clusters, which are represented by one accession (KAN071 and KAN055, respectively). These genotypes were characterized by the highest number of leaves (KAN055) and least number of leaves (KAN071).

Quantitative and qualitative genetic distance between different pairs of accessions was obtained from the morphological data using Euclidean coefficient. Euclidean's distance coefficient indicated the quantitative genetic distance values for torch ginger accessions ranged from 0.49 to 3.72. The lowest genetic distance was obtained from accessions KAN035 and KAN083. The highest genetic distance was found in KAN046 and KAN066 (3.72) followed by KAN046 and KAN062 (3.65), KAN005 and KAN046 (3.55) and KAN030 and KAN046 (3.5).

#### **3.6.2 Principal component analysis (PCA) based on quantitative traits**

Sixteen quantitative traits were used for the principal component analysis of the 57 accessions of torch ginger. Two dimensional graphical illustrations (Fig. 3) showed that the

accessions were distributed with low distance revealed by eigen vector. The first dimension displayed the greatest distance to the left was found at eigen vector  $-1.46$  (KAN066) while at eigen vector  $1.91$  was found the farthest accession (KAN046) to the right on first dimension. The eigen vector of second dimension ranged from  $-1.69$  to  $1.36$  with the greatest distance accessions to the upper and lower are KAN057 and KAN047, respectively.

The range of eigen vectors in the accessions was very low. Thus, the two-dimensional graphical plot of PCA reveals that the dissimilarity exhibited in the torch ginger germplasm is very low. The first dimension of eigen vector ranged from  $-1.46$  to  $1.91$ , while  $-1.69$  to  $1.36$  was the ranged of second dimension eigen vector. The low values of the two dimensions indicate that the similarity between torch ginger accessions is very high.

#### **3.6.3 Cluster analysis based on qualitative traits**

For six qualitative traits the accessions were grouped into eight clusters at 1.11 distance coefficient (Fig. 4). Cluster II had the highest number of accessions (34) and was divided into two sub clusters A (15 accessions) and B (19 accessions). Cluster I, III, VI and VII consisted of 10, 4, 3 and 2 accessions, respectively (Table 11). Meanwhile cluster IV, V and VIII had one accession each. The 10 accessions from cluster I were characterized by the same flower color i.e., dark red. Four accessions which have the same character of pale pink bract color were placed together in cluster III. Cluster VI was characterized by the oblong elliptic of leaf shape, while two accessions in cluster VII contained the same inflorescence shape (rounded to conical to apex). Others cluster also contained the same characters of qualitative traits within the group.

For qualitative genetic distance, the distance values ranged from 0.00 to 3.02. About 119 pairs of accessions were similar to each other based on their qualitative traits. Between accessions 'KAN057 and KAN069', 'KAN026 and KAN046', 'KAN017 and KAN069', 'KAN056 and KAN069', and 'KAN026 and KAN057' exhibited the greatest genetic distance with the value of 3.02, 2.87, 2.82 and 2.80, respectively.

**Table 9. Correlation coefficient among 16 quantitative traits of torch ginger accessions**

	PH	NST	NLV	LFL	LFW	PTL	LGL	BDL	IFL	BDW	IFW	BPL	PDL	CTL	BRL
<b>NST</b>	0.00														
<b>NLV</b>	0.52**	-0.09													
<b>LFL</b>	0.70**	-0.12	0.42**												
<b>LFW</b>	0.57**	-0.12	0.32	0.71**											
<b>PTL</b>	0.47**	0.15	0.11	0.49**	0.43**										
<b>LGL</b>	0.14	0.13	-0.07	-0.12	0.05	0.30									
<b>BDL</b>	0.02	-0.14	-0.01	0.18	0.13	0.03	-0.09								
<b>IFL</b>	0.02	-0.20	0.09	0.14	0.13	-0.01	-0.06	0.91**							
<b>BDW</b>	0.16	0.16	-0.10	0.10	0.22	0.15	-0.13	0.12	0.00						
<b>IFW</b>	0.13	0.01	-0.12	0.14	0.21	0.09	-0.01	0.36**	0.23	0.45**					
<b>BPL</b>	0.11	0.02	0.03	0.05	0.09	0.05	-0.05	0.44**	0.43**	0.32	0.33				
<b>PDL</b>	0.21	-0.02	0.05	0.10	0.16	0.08	-0.06	0.40**	0.43**	0.34	0.30	0.91**			
<b>CTL</b>	0.04	0.00	-0.01	0.02	0.14	0.20	0.02	0.17	0.12	0.23	0.18	0.29	0.24		
<b>BRL</b>	0.11	0.06	-0.09	-0.07	0.06	0.24	0.11	0.31	0.26	0.26	0.45**	0.59**	0.56**	0.23	
<b>NSP</b>	0.09	-0.03	0.11	0.1	0.02	0.27	0.04	0.19	0.23	-0.1	0.0	0.2	0.2	0.0	0.21

Note: \*\*Significant at  $p \leq 0.01$ ; PH: Plant Height; NST: Number of stems / clump; NLV: Number of leaves; LFL: Leaf length; LFW: Leaf width; PTL: Petiole length; LGL: Ligule length; BDL: Bud length; IFL: Inflorescence length; BDW: Bud width; IFW: Inflorescence width; BPL: Bud peduncle length; PL: Inflorescence peduncle length; CTL: Corolla tube length; BRL: Bract length; NSP: Number of sp

**Table 10. Cluster number and their members based on quantitative traits of 57 torch ginger accessions**

Cluster	Number of accessions per cluster	Accession code
I	6	KAN002, KAN007, KAN008, KAN080, KAN059, KAN045
II	23	KAN003, KAN062, KAN004, KAN023, KAN058, KAN021, KAN030, KAN005, KAN052, KAN081, KAN066, KAN010, KAN050, KAN029, KAN063, KAN039, KAN015, KAN036, KAN068, KAN006, KAN011, KAN009, KAN056
III	21	KAN012, KAN025, KAN027, KAN031, KAN026, KAN064, KAN017, KAN035, KAN083, KAN019, KAN020, KAN033, KAN028, KAN014, KAN061, KAN034, KAN013, KAN018, KAN057, KAN041, KAN046
IV	2	KAN024, KAN069
V	1	KAN071
VI	3	KAN022, KAN047, KAN048
VII	1	KAN055

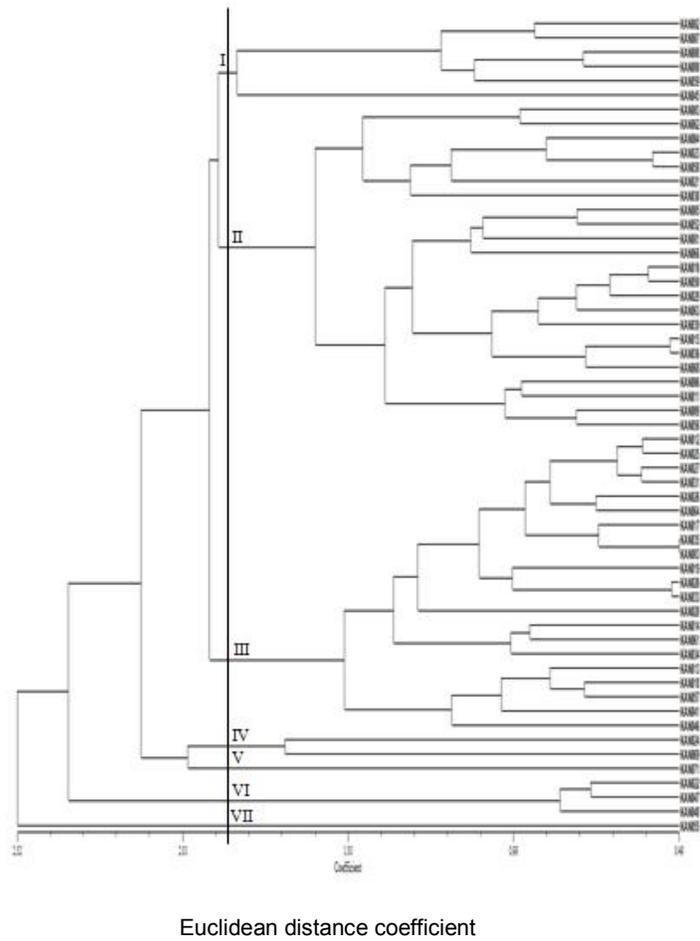
#### 3.6.4 Principal component analysis (PCA) based on qualitative traits

A two-dimensional graph and three-dimensional graph of principal component analysis were performed using all the qualitative traits. The cluster analysis was mostly confirmed by the PCA analysis. One distant accession such as KAN069 formed its individual cluster or group alone both in cluster (clusters VIII) and in PCA (GVIII) (Fig. 5). Two accessions, namely KAN026 and KAN059 formed one group (GVII), and KAN006 formed another group (GIII) with accessions KAN020, KAN068, and KAN071. Accessions KAN017, KAN050 and KAN057 formed one group (GVI), ten accessions formed another group (GI), and 38 accessions together formed GII. Another single group in PCA was observed in KAN009 (GIV) and KAN046 (GV), respectively. All the groups in PCA were in line with the grouping in the cluster analysis.

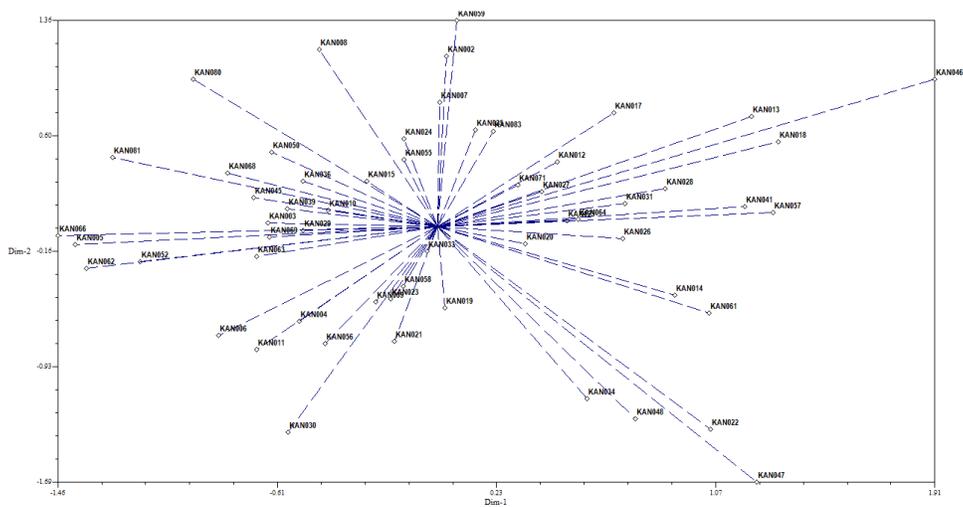
#### 3.6.5 Fitness of PCA for quantitative traits using eigen value

The PCA of 16 quantitative traits was estimated to access the degree of torch ginger variation (Table 12). Eigen values more than one were displayed by the four significant principal components (PCs). The PCA was accounting to 58.25% of the total variability among 57 torch ginger accessions. The first four principal components exhibited 21.28%, 16.32%, 10.55% and 10.11%, respectively of the total variation.

The characters associated with the first four components, their eigen values, variance percentage, cumulative proportion variances are given in Table 12. Seven traits (plant height, number of stems, number of leaves, leaf length, leaf width, petiole length and ligule length) associated positively to PC1. Meanwhile, five traits (bud length, inflorescence length, bud peduncle length, inflorescence peduncle length and bract length) were negatively associated with PC1. In PC1, maximum contribution was made by plant height (0.57) followed by leaf length and leaf width (0.49). The second principal component explained 16.32% and was positively related with the number of leaves, leaf length, leaf width, bud length and inflorescence length. However, number of stems and ligule length influenced in a negative direction. In PC2, leaf length contributed highest (0.52). The PC3 which contributed to the total variations of 10.55% positively contributed through bud width and inflorescence width. In the negative direction, it was associated with number of leaves, ligule length and inflorescence length. PC4 which exhibited 10.11% of total variation was positively associated with bud peduncle length, inflorescence peduncle length and number of spikes. Meanwhile, bud length and inflorescence length were related negatively in PC4. The most contributor traits for PC3 and PC4 were bud width (0.78) and number of spikes (0.45), respectively.



**Fig. 2. Dendrogram based on quantitative traits of 57 torch ginger accessions**



**Fig. 3. Principal component analysis showing the relationship among 57 torch ginger accessions in a two-dimensional graph**

**Table 11. Cluster number and their members based on qualitative traits of 57 torch ginger accessions**

Cluster	Number of accessions per cluster	Accession code
I	10	KAN002, KAN022, KAN048, KAN007, KAN018, KAN027, KAN033, KAN061, KAN013, KAN083
II	35	A - KAN003, KAN023, KAN036, KAN055, KAN058, KAN062, KAN080, KAN004, KAN008, KAN010, KAN012, KAN021, KAN035, KAN019, KAN050, KAN066, B - KAN005, KAN014, KAN015, KAN025, KAN029, KAN030, KAN031, KAN041, KAN045, KAN047, KAN063, KAN011, KAN024, KAN028, KAN034, KAN039, KAN052, KAN064, KAN081
III	4	KAN006, KAN020, KAN068, KAN071
IV	1	KAN009
V	1	KAN046
VI	3	KAN017, KAN056, KAN057
VII	2	KAN026, KAN059
VIII	1	KAN069

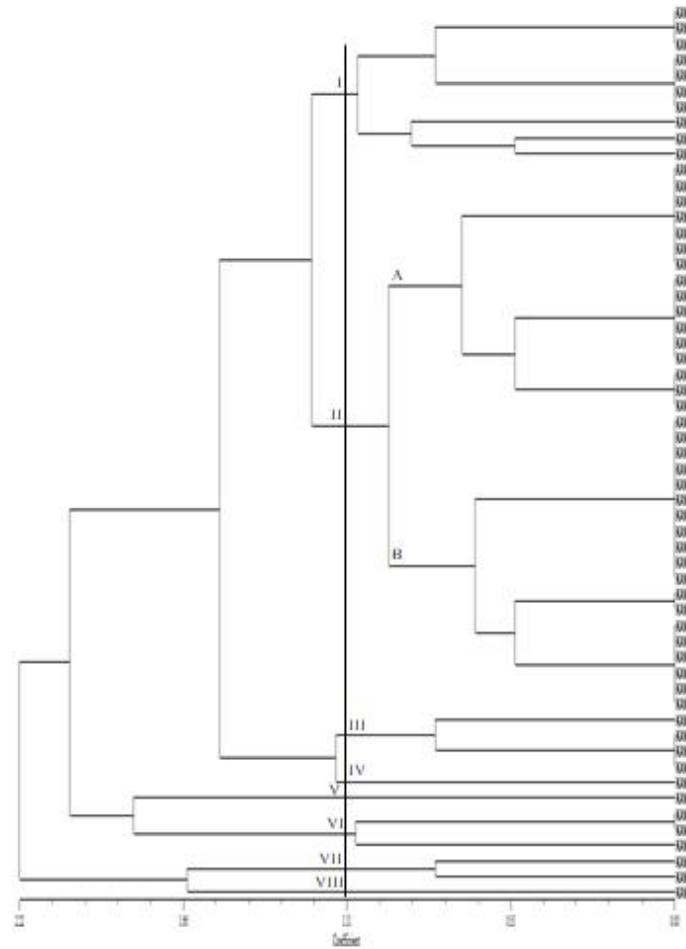
**Table 12. Principal components of the 16 quantitative traits in torch ginger accessions**

	PC1	PC2	PC3	PC4
Eigen value	2.60	1.99	1.29	1.23
Percent	21.28	16.32	10.55	10.11
Cumulative	20.60	37.60	48.15	58.25
Traits	Eigen vectors			
Plant height	0.57	0.23	0.01	0.20
Number of stems	0.20	-0.75	0.15	-0.22
Number of leaves	0.42	0.32	-0.33	0.17
Leaf length	0.49	0.52	0.008	0.03
Leaf width	0.49	0.38	0.17	-0.17
Petiole length	0.42	-0.18	-0.11	0.09
Ligule length	0.31	-0.67	-0.46	-0.26
Bud length	-0.57	0.31	-0.23	-0.46
Inflorescence length	-0.55	0.37	-0.31	-0.40
Bud width	-0.004	-0.04	0.78	-0.19
Inflorescence width	-0.12	0.008	0.27	-0.23
Bud peduncle length	-0.52	0.01	0.07	0.36
Inflorescence peduncle length	-0.43	0.08	0.14	0.37
Corolla tube length	-0.11	-0.20	0.05	0.008
Bract length	-0.39	-0.26	0.01	0.26
Number of spikes	-0.20	-0.14	-0.22	0.45

### 3.6.6 Fitness of PCA for qualitative traits using eigen value

Two significant principal components were identified and accounted for a cumulative variation of 54.49%. The first principal component accounted for 29.75% and second 24.74% of total variation (Table 13). Eigen vectors and principal components were estimated for all the qualitative traits (Table 13).

First principal component (PC1) was associated positively with leaf shape, leaflet surface and flower color. The color of young leaf and inflorescence shape were negatively related with PC1. PC2 which exhibited 24.74% of total variation was positively correlated with leaf shape and color of young leaf. The most contributor traits for PC1 and PC2 were leaflet surface (0.60) and leaf shape (0.55), respectively.



Euclidean distance coefficient

Fig. 4. Dendrogram based on six qualitative traits of 57 torch ginger accessions

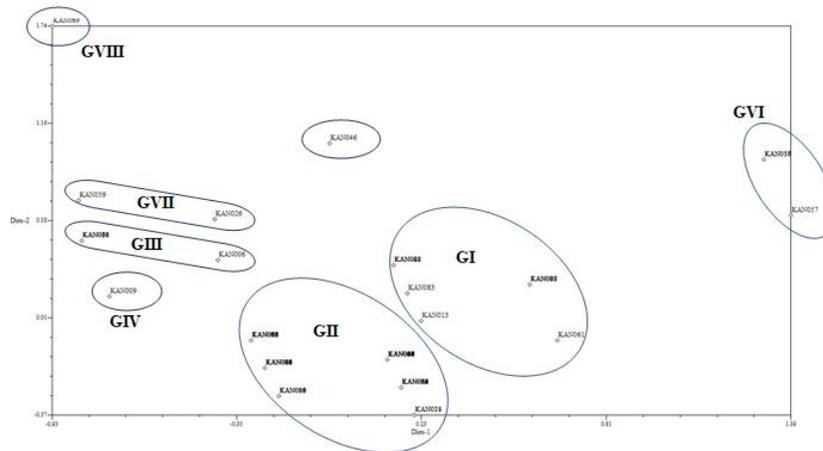


Fig. 5. PCA two-dimensional graph of 57 torch ginger accessions based on qualitative traits

**Table 13. Principal component of the 6 qualitative traits in torch ginger accessions**

	PC1	PC2
Eigen value	1.40	1.16
Percent	29.75	24.74
Cumulative	29.75	54.49
<b>Traits</b>	<b>Eigen vectors</b>	
Leaf shape	0.39	0.55
Color of young leaf	-0.64	0.43
Leaflet surface	0.60	-0.48
Inflorescence shape	-0.51	-0.20
Flower color	0.40	0.27
Bract color	-0.24	-0.57

#### 4. DISCUSSION

The broad genetic base of the germplasm and wide variability in characters provide a basis for sustainable utilization of germplasm in crop improvement, including vegetative propagated plant material. Characterization and studies of genetic diversity of multifunctional crops like torch ginger are crucial and will provide important information in planning meaningful breeding strategies.

To evaluate the degree of genetic diversity among 57 torch ginger accessions, 6 qualitative and 16 quantitative traits were studied. The qualitative characters are essential in describing a plant species. Primarily, it is influenced by the natural selection, socio-economic situation and consumer choices [11]. Several of the *Etilingera* species are completely characterized; however, some of the species are difficult to differentiate. Distinguished characters of torch ginger were the long peduncle size and the color of the bracts [27]. The significant differences among torch ginger accessions for most of the traits indicates existence of sufficient genetic variability amongst germplasm collections. This finding is in line with results of Nandkangre et al. [12], Ravishanker et al. [13] and Aragaw et al. [28] on ginger germplasm in Burkina Faso, India and Ethiopia, respectively.

The degree of genetic diversity in the agro-morphological traits is more reliable by doing an evaluation of the genotypic coefficient of variation (GCV) in relation to its phenotypic coefficient of variation (PCV). For all traits studied PCV value was greater than GCV indicating that the visible variance was not only due to the genotypes but also due to the environmental effect. This was similar with studies by Ravishanker et al. [13], Rajyalakshmi and Umajyothi [17] and Aragaw et al. [28] which evaluated the agro-morphological variability on ginger. A small difference between GCV and PCV was detected in plant height,

number of stems, number of leaves, leaf length, leaf width, petiole length, bud length, inflorescence length, bud width, inflorescence width, bud peduncle length, inflorescence peduncle length, corolla tube length, and bract length. It showed that variations among the genotypes were mostly due to genetic factor. It also revealed a high significant effect of genotype on phenotypic appearance with very little influence of the environment. Besides that, large differences between GCV and PCV were shown by ligule length and number of spikes. This may suggest the high environmental effect on the expression of these traits. Since it is an asexually propagated crop, hence, there seems to be higher influence of environment in governing some of the traits. The high magnitude between PCV and GCV indicates that these traits may be influenced by environmental effect [17,29]. On the other hand, some traits such as number of plants, number of leaves, petiole length, ligule length, bud width, bud peduncle length, inflorescence peduncle length and number of spikes displayed high GCV which indicates their high variability. Thus, further selection could be done to improve the genotypes for the targeted traits. However, low values of GCV shows that there is a limited scope for improvement of the traits through selection.

Heritability values indicated the effectiveness and efficiency in selection response of the traits in the population. Heritability estimates was categorized as low (5 - 10%), medium (11 - 30%) and high (> 30%) [30]. The broad sense heritability for most of the vegetative and yield traits is high except for leaf length and leaf width which had low heritability values. The effectiveness of selection is not only determined by heritability but also on genetic advance. High heritability supported by high genetic advance specifies that these traits are principally restricted by additive genes. The genotype for a trait is the

result of the type of gene action, which may be additive and non-additive. Heritability acts as an indicator of the type of gene action. Traits with high heritability are controlled by the additive gene action whereas those with low heritability by the non-additive gene action. The additive genetic effects are heritable and transferred directly from parents to offspring [31]. For the present study, plant height, number of stems, number of leaves, bud width, bud peduncle length and number of spikes are significant traits of torch ginger to be considered for selection. Hence, the selection of these traits might be effective for torch ginger improvement. High heritability coupled with genetic advance for several traits in ginger was also reported by Prajapati et al. [9] and Nandkangre et al. [12]. However, traits with high heritability and low genetic advance indicated the involvement of non-additive genes. Thus, the selection for these traits might not be rewarding because of the limited scope for improvement and further partitioning of the various through simple selection can be achieved.

Further, the association among various traits is crucial and important in identifying the traits that can potentially be focused on for future improvement [10]. Peduncle length showed significant and positive correlation with yield traits such as bud length and bract length. This condition suggests that the selection of peduncle length will influence and increase the size of flower bud.

Based on 16 quantitative traits, the 57 accessions of *E. elatior* were grouped into seven clusters. Five were real clusters and two were solitary. The solitary is also considered as a cluster, even if it consists of one accession [28]. According to the two-dimensional graphical illustration, it could be seen that some accessions are located at a very close distance to one another. Fifty-seven accessions which are grouped into seven clusters irrespective of which state were they collected from. These results are supported by Rana et al. [32] and Roy et al. [33] who evaluated common bean and lentil germplasm, respectively. The main factors namely genetic drift, selection pressure and environment could greater affect diversity than geographical distance [34].

Basically, PCA is performed to analyze variation coverage in the genotypes [35] and to identify the most relevant characters by explaining the total variation in the original set of variables [36]. As a

consequence of that, 58.25% of total variation was displayed by the first five principal components of quantitative traits and 54.49% from the first two principal components of qualitative traits. The traits with the largest impact on the components showed the highest rate of variation and hence can be used for grouping genotypes effectively. Besides that, the qualitative traits are also consisted of three solitary clusters from the total clusters. This indicates that the tested torch ginger germplasm was highly divergent.

Furthermore, the torch ginger accessions were grouped by the cluster analysis and PCA based on their relationship or morphology rather than by geographical origin. Generally, the genotype groups were related with morphological characteristics among the accessions. Phenotypically, most of the torch ginger genotypes have diverse traits. However, they were distributed into separate groups. Most hierarchical clustering showed that there was no relationship between the distribution of accessions and place of collection. This should be attributed to the origin of the materials that has remained with little genetic change and without exchange of genes among them because of the vegetative propagation [37]. The absence of any relationship between the distribution pattern and acquisition source observed in this study may likely exist as quantitative traits that vary when subjected to environmental changes [10].

## 5. CONCLUSION

This is the first study on torch ginger phenotypic variability in Malaysia. The study discovered the presence of significant genetic variability among the collected accessions for different traits. The 57 accessions of torch ginger showed high variability for both qualitative and quantitative traits. This finding suggests the opportunity to improve the traits through direct and indirect selection. Traits with high heritability and genetic advance are valuable traits which should be given more emphasis in order to generate a successful crop improvement. Considering the distribution pattern of vegetative and yield performance of accessions, it is suggested that accessions from cluster VII (KAN022, KAN047 and KAN048) should be selected for future crop improvement programs. These accessions possessed the highest peduncle length that could influence the yield in terms of bud size. Furthermore, the classification and divergence

between torch ginger accessions analyzed in this study may assist in conserving plant materials both *in-situ* and *ex-situ*. However, genotypic classification based on phenotypic character is not sufficient due to the influence of the environment. Therefore, molecular classification should be conducted to complement phenotypic classification.

## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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