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Genetic Divergence among On-farm Collections for Yield and Yield-related Traits in Ginger (*Zingiber officinale* R.)

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ABSTRACT

The present investigation was carried out at the farmer's field Neshwi village, Haveri District of Karnataka, India during *kharif* season (May, 2021 to January, 2022). The improvement of crop relies heavily on genetic diversity. The objective of the study was to assess the genetic divergence of 76 diverse genotypes of ginger collected from different parts of the Karnataka, India which including four checks. The genetic divergence of ginger genotypes was assessed using Mahalanobis D^2 statistics. Genetic divergence studies revealed considerable genetic diversity among 76 genotypes of ginger for a set of ten quantitative traits pertaining to the growth and yield characters viz., height of the shoot (cm), leaf area (cm^2), number of primary rhizomes, length of the primary rhizome (cm), girth of the primary rhizome (cm), number of secondary rhizomes, length of the secondary rhizome (cm), girth of the secondary rhizome (cm), crop duration (number of days) and rhizome yield $plant^{-1}$ (g). Analysed 76 ginger genotypes were clustered based on similarities between their D^2 values using Tocher's method, resulting in 14 distinct groups. Considerable diversity within and between 14 clusters was observed among the genotypes. The characteristics such as average rhizome yield $plant^{-1}$, girth of the primary rhizome and length of the primary rhizome were the main factors in differentiating the genotypes of ginger studied. Utilizing genotypes from clusters with high inter-cluster distances, such as clusters VI and XIII, VI and XIV and X and XIV can form potential pre-breeding material for the improvement of ginger crop.

KEYWORDS: Genetic divergence, inter-cluster distance, quantitative traits

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1. INTRODUCTION

The one of the oldest known spice ginger (*Zingiber officinale* Rosc.) is valued for its aroma and pungency (Sangwan et al., 2014). Ginger is a member of Zingiberaceae family grouped under the order Scitamineae (Thingbaijam and Huidrom, 2014). The somatic chromosome number of ginger 2n=22 was reported by Ramachandran (1969). Ginger is one of the key sources of foreign exchange (Shaikh et al., 2010, Thamang et al., 2022). Ginger rhizomes both fresh and dried are used as a spice all over the world (Mao et al., 2019), the fresh ginger is consumed locally while dried is traded internationally (Ravindran et al., 2016). It possesses several medicinal properties (Singh and Kumar, 2021), cures digestion related problems, have anticancer properties, prevents obesity, asthma, bronchitis, and nausea (Crichton et al., 2019). It is an integral component of homesteads in Kerala and coastal regions of Karnataka (Sudha et al., 2020, Ravi et al., 2022), it is used in flavouring and therapeutic ingredient in a variety of products (Camacho and Brescia, 2009, Rajyalakshmi and Umajoythi, 2014), valued for pleasant spicy aroma (Prasad and Tyagi, 2015) and has multifarious uses viz. confectionery (Saiah et al., 2018), ginger cordial and ginger candy, ginger wine and beer (Wei et al., 2017), pickles etc. (Ravi et al., 2017). The main constituents in the volatile oil of ginger include zingiberene, curcumene, and farnesene in addition to 1, 8- cineole, linalool, borneol, neral, and geraniol (Bhattarai et al., 2001, Sasidharan et al., 2012, Mahomoodally et al., 2021).

World ginger production is estimated to be 4.90 mt with an area of 0.45 mha and it is mainly distributed in India, Indonesia, China, Nigeria, Thailand, Bangladesh, Philippines, Nepal and Jamaica. The largest producer of ginger is India contributing to about 45.31%, followed by China, Nepal, Nigeria, Thailand and Bangladesh (Anonymous, 2021). In India, total area is 1.92 lakh hectares with production of 21.72 lakh tonnes and in India Madhya Pradesh is the largest producer followed by Karnataka (Anononymous, 2022a). In Karnataka the crop is grown in Hassan, Shivamogga, Mysore, Bidar, Chikkamagaluru, Kodagu, Haveri, Uttara Kannada, Mandya, Kalburgi, Dakshina Kannada, Bengaluru, Chamrajnagar, Belgaum, Davanagere, Udupi and Ramanagar Districts with an area of 30,000 hectares and production of 3.06 lakh tonnes (Anonymous, 2022a). Ginger is an asexually propagated crop with seldom formed flowers and no seed setting takes place. Because the crop lacks standard breeding approaches like as hybridization, selection is the simplest method of developing the crop other than mutation and polyploidy breeding (Dev and Sharma, 2022). As a result, most crop improvement efforts for this crop are focused on evaluating and selecting naturally occurring clonal variants. Unless germplasm is acquired from varied agro-ecological situations, the degree of genetic diversity in such species is minimal. Therefore, a key component of the ginger enhancement effort is the discovery of genetically distinct clones or genotypes using diversity analysis. To find the promising varied genotypes, genetic diversity information might be used. Considering these aspects and importance of ginger, the present study deals with the genetic divergence of ginger germplasm collected from different parts of the Karnataka state in order to create selection criteria for enhancing the rhizome production potential of ginger. A selection program based on genotypes identified through divergence analysis would be more promising (Singh et al., 2017, Singh et al., 2020, Tesfaye, 2022). Among the various methods available, Mahalanobis generalized distance estimated by D^2 statistic (Rao, 1952) is a unique method for disseminating populations that takes into account a set of parameters rather than interring from indices based on morphological similarities, eco-geographical diversity, and phylogenetic relationships.

2. MATERIALS AND METHODS

A total of 76 ginger genotypes which Includes 45 collections from various parts of Karnataka, India, 27 distinct genotypes selected from the different collections and four checks of ginger (IISR-Mahima, IISR-Varada, Rio-de-Jeneiro and Humnabad local) were utilized for the present study (Table 1). The genotypes were evaluated in a randomized block design with 2 replications during *kharif* (May, 2021 to January, 2022). The experimental field was located at an altitude of 602 m above MSL, 14°30´38" North latitude and 75°31´58" East-longitude in the north transition zone, farmer field, Neshwi village (Haveri Dist.), Karnataka, India. The land proposed for field investigation was brought to a fine tilth by repeated ploughing and harrowing. Raised beds (1.85×1.80 m^2) were laid out at the farmer's field. Seed rhizome units (having 2–3 buds weighing about 20–25 g) were taken, which constitute about 24 rhizome units from each genotype. Rhizomes were planted in the beds at 3.5 to 4.0 cm depth, 45 cm between rows and 30 cm apart, which constitute about 24 plants bed^{-1}. All agronomic practices were carried out in accordance with UHS, Bagalkot package of practises (Anonymous, 2022b), and required preventative plant protection measures were taken to protect the crop from pests and diseases. According to the accepted statistical practise, the mean data on yield and parameters that contribute to yield were treated to an analysis of variance using a randomised block design (Federer, 1956). The genetic divergence was assessed following Mahalanobis D^2 statistics (Mahalanobis, 1936).

Table 1: List of the ginger genotypes used in the study

Sl. No.	Name of genotypes	Source		Sl. No.	Name of genotypes	Source	
		Location	District			Location	District
1.	FBG-CTP	Chitgoppa	Bidar	28.	FBG-KRP-1	Krishnarajpete	Mandya
2.	FBG-HBD	Humnabad	Bidar	29.	FBG-KRP-2	Krishnarajpete	Mandya
3.	FBG-BDR-1	Bidar	Bidar	30.	FBG-MVL	Malavalli	Mandya
4.	FBG-BDR-2	Bidar	Bidar	31.	FBG-NML-1	Nagamangala	Mandya
5.	FBG-JWG	Jewargi	Kalburgi	32.	FBG-NML-2	Nagamangala	Mandya
6.	FBG-SMG-1	Shivamogga	Shivamogga	33.	FBG-CKM-1	Chickmagalur	Chickmagalur
7.	FBG-SMG-2	Shivamogga	Shivamogga	34.	FBG-CKM-2	Chickmagalur	Chickmagalur
8.	FBG-SKR-1	Shikaripur	Shivamogga	35.	FBG-MDG-1	Mudigere	Chickmagalur
9.	FBG-SKR-2	Shikaripur	Shivamogga	36.	FBG-MDG-2	Mudigere	Chickmagalur
10.	FBG-SRB-1	Soraba	Shivamogga	37.	FBG-HSR	Hunsur	Mysore
11.	FBG-SRB-2	Soraba	Shivamogga	38.	FBG-HDK-1	HD Kote	Mysore
12.	FBG-THL	Thirthahalli	Shivamogga	39.	FBG-HDK-2	HD Kote	Mysore
13.	FBG-RTL-1	Rattihalli	Haveri	40.	FBG-SWP-1	Somwarpet	Kodagu
14.	FBG-RTL-2	Rattihalli	Haveri	41.	FBG-SWP-2	Somawarpet	Kodagu
15.	FBG-HKR-1	Hirekerur	Haveri	42.	FBG-VJP-1	Virajpet	Kodagu
16.	FBG-HKR-2	Hirekerur	Haveri	43.	FBG-VJP-2	Virajpet	Kodagu
17.	FBG-RNR-1	Ranebennur	Haveri	44.	FBG-KNR	Khanapur	Belgaum
18.	FBG-RNR-2	Ranebennur	Haveri	45.	FBG-CKD	Chikkodi	Belgaum
19.	FBG-SRS-1	Sirsi	Uttarkannada	46.	FBG-CTP-1	Selection from FBG-CTP	
20.	FBG-SRS-2	Sirsi	Uttarkannada	47.	FBG-CTP-2	Selection from FBG-CTP	
21.	FBG-SRS-3	Sirsi	Uttarkannada	48.	FBG-HBD-1	Selection from FBG-HBD	
22.	FBG-MGD-1	Mundgod	Uttarkannada	49.	FBG-HBD-1	Selection from FBG-HBD	
23.	FBG-ARK-1	Arkalgudu	Hassan	50.	FBG-HBD-2	Selection from FBG-HBD	
24.	FBG-ARK-2	Arkalgudu	Hassan	51.	FBG-BDR-2-1	Selection from FBG-BDR-2	
25.	FBG-ALR-1	Alur	Hassan	52.	FBG-JWG-1	Selection from FBG-JWG	
26.	FBG-ALR-2	Alur	Hassan	53.	FBG-SMG-2-1	Selection from FBG-SMG-2	
27.	FBG-HNP	Holenarasipura	Hassan	54.	FBG-SKR-1-1	Selection from FBG-SKR-1	
55.	FBG-SKR-1-2	Selection from FBG-SKR-1		66.	FBG-SWP-2-1	Selection from FBG-SWP-2	
56.	FBG-SKR-2-1	Selection from FBG-SKR-2		67.	FBG-MDG-1-1	Selection from FBG-MDG-1	
57.	FBG-SRB-1-1	Selection from FBG-SRB-1		68.	FBG-MDG-1-2	Selection from FBG-MDG-1	
58.	FBG-RTL-1-1	Selection from FBG-RTL-1		69.	FBG-MDG-1-3	Selection from FBG-MDG-1	
59.	FBG-HKR-1-1	Selection from FBG-HKR-1		70.	FBG-CKD-1	Selection from FBG-CKD	
60.	FBG-HKR-2-1	Selection from FBG-HKR-2		71.	FBG-CKD-2	Selection from FBG-CKD	
61.	FBG-RNR-2-1	Selection from FBG-RNR-2		72.	FBG-CKD-3	Selection from FBG-CKD	
62.	FBG-SRS-2-1	Selection from FBG-SRS-2		73.	IISR-Mahima,	IISR, Calicut	
63.	FBG-SRS-3-1	Selection from FBG-SRS-3		74.	IISR-Varada,	IISR, Calicut	
64.	FBG-ARK-1-1	Selection from FBG-ARK-1		75.	Rio-de-Jeneiro	IISR, Calicut	
65.	FBG-CKM-1-1	Selection from FBG-CKM-1		76.	Humnabad local	IISR, Calicut	

Using Tocher's technique, as defined by Rao (1952), the genotypes of ginger were categorised based on minimum generalised distance. The Singh and Chaudhary (1977) formula was used to compute the average inter and intra-cluster distances and to calculate the contribution of various traits to genetic divergence.

3. RESULTS AND DISCUSSION

The ginger improvement program's core components include diversity analysis and the identification of genetically distant clones or genotypes. To find promising diverse genotypes, genetic diversity information might be employed. Given these factors and the significance of ginger, the current study explores the genetic diversity of ginger germplasm gathered from various regions of the state of Karnataka in order to create selection criteria for enhancing the rhizome production potentiality of ginger. A selection programme would be more successful if it focused on genotypes found by divergence analysis. In contrast to using indices based on morphological similarity, eco-geographical diversity, and phylogenetic relationships, the Mahalanobis generalised distance estimated by the D^2 statistic (Rao, 1952) is a special method for disseminating populations that takes a number of parameters into account. Ginger genotypes were divided into fourteen clusters using Tocher's method, which treated predicted D^2 values as the square of the generalised distance. Table 2 shows the distribution of entries into different clusters.

As shown in Table 2, of the fourteen clusters analysed, cluster I had the most genotypes (28), followed by cluster II (21), cluster III (13), cluster X (3), cluster VI (2), and I1V2, while the remaining clusters (V, VII, VIII, IX, XI, XII, XIII, and XIV) only had one genotype each. This indicated the tested ginger genotypes were highly divergent. In contrast to geographic distribution, genotypes did not cluster. This could be due to severe breeding efforts involving diverse genotypes leading to the segregants that have lost identity to their geographic origin. Desirable types can be chosen from the clusters based on the breeding programs objectives. Geographic diversity is typically evaluated to quantify genetic diversity. However, geographical diversity estimation is regarded as an inferential criterion, and it is probable that

Table 2: Classification of ginger genotypes into different clusters based on D^2 values

Clusters	No. of individuals	Individuals
Cluster-I	28	FBG-JWG, FBG-SMG-1, FBG-SMG-2, FBG-SRB-2, FBG-HKR-2, FBG-RNR-2, FBG-SRS-3, FBG-ARK-1, FBG-NML-1 FBG-CKM-1, FBG-MDG-1, FBG-MDG-2, FBG-HDK-1, FBG-VJP-2, FBG-KNR, FBG-CKD, FBG-JWG-1, FBG-SKR-1-1 FBG-SKR-1-2, FBG-SRB-1-1, FBG-SWP-2-1, FBG-MDG-1-1, FBG-MDG-1-3, FBG-CKD-1, FBG-CKD-2, FBG-CKD-3 IISR-Mahima and IISR-Varada
Cluster-II	21	FBG-BDR-2, FBG-SKR-1, FBG-RTL-2, FBG-ALR-2, FBG-HNP, FBG-KRP-1, FBG-KRP-2, FBG-MVL, FBG-NML-2, FBG-CKM-2, FBG-HSR, FBG-HDK-2, FBG-SWP-1, FBG-VJP-1, FBG-CTP-2, FBG-SKR-2-1, FBG-HKR-1-1, FBG-SRS-3-1, FBG-ARK-1-1, FBG-CKM-1-1 and Rio-de-Janeiro
Cluster-III	13	FBG-HBD, FBG-SKR-2, FBG-HKR-1, FBG-RNR-1, FBG-SRS-2, FBG-SWP-2, FBG-CTP-1, FBG-HBD-1, FBG-HBD-2, FBG-RTL-1-1, FBG-HKR-2-1, FBG-MDG-1-2 and Humnabad Local
Cluster-IV	1	FBG-SRS-1-1
Cluster-V	1	FBG-BDR-1
Cluster-VI	2	FBG-SRS-1 and FBG-SMG-2-1
Cluster-VII	1	FBG-RTL-1
Cluster-VIII	1	FBG-RNR-2-1
Cluster-IX	1	FBG-BDR-2-1
Cluster-X	3	FBG-CTP, FBG-SRB-1 and FBG-ARK-2
Cluster-XI	1	FBG-MVL-1
Cluster-XII	1	FBG-THL
Cluster-XIII	1	FBG-MGD
Cluster-XIV	1	FBG-ALR-1

it is ineffective in quantifying various populations (Gupta et al., 2015). The present pattern of genotypes grouping indicates that there is no parallelism between the genetic diversity and distribution of geographical diversity. The genotypes varied according to cluster formation. Although the genotypes were obtained from various locations of Karnataka, they were discovered to be dispersed in various clusters. As a result, the genotype clusters were not affected by their geographical locations. This is a natural population, and the heterogeneous grouping of all genotypes from the same geographical location could be attributable to genetics or mutational, random drift effects (Paw et al., 2020). It indicated that large variations are present among the ginger populations. This is in accordance with the results of Kizhakkayil and Sasikumar (2010), accessions of ginger were grouped into four clusters. At Tepi, ginger germplasm were grouped into seven cluster, whereas at Bahir Dar the germplasm were classified into 11 clusters (Aragaw et al., 2011). Sajeev et al. (2011) reported that cluster analysis of ginger clones identified five clusters, cluster I was the largest containing 33 clones distributed across all the six hypothetical populations. Cluster analysis for 12 accessions of ginger divided into two different clusters (Ashraf et al., 2014). Das et al., (2016) revealed that accessions were grouped into five clusters. Twenty ginger lines were grouped into five different clusters, the maximum number of genotypes were grouped in cluster IV and V (Islam et al., 2017). Paw et al., 2020 reported that 78 genotypes of black turmeric grouped into nine clusters according to their morphological traits. Within the panel of genotypes employed in the current investigation, there is no relationship between geographical distribution and genetic distance.

A perusal of data presented in Table 3, cluster X with three genotypes showed maximum intra-cluster diversity (D^2=21.71) followed by cluster III (D^2=19.35), cluster II (D^2=18.74), cluster I (D^2=16.32) and cluster VI (D^2=12.91). Cluster IV, V, VII, VIII, IX, XI, XII, XIII and XIV had only one genotype each and hence, the intra-cluster distance was zero. The maximum intra-cluster diversity revealed that the genotype included in cluster X is very diverse as compare to the other clusters. Those genetic stocks/genotypes found in clusters with the maximum inter-cluster distance are clearly more genetically varied. It implies that ginger breeders should include genotypes from these various clusters in future breeding programs (Gupta et al., 2015).

Table 3: Average intra-and inter-cluster D^2 values for 10 yield contributing traits formed by ginger genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	16.32	23.41	28.93	22.48	18.92	28.76	25.23	30.53	24.04	35.13	36.78	33.22	44.14	41.61
II		18.74	24.55	31.58	22.32	40.20	27.71	23.54	31.93	31.16	33.47	34.34	44.30	39.54
III			19.35	42.32	26.86	49.88	30.42	27.03	28.71	32.02	34.89	29.03	35.20	38.39
IV				0	27.53	17.78	31.37	37.5	36.75	44.72	41.44	44.06	57.79	49.87
V					0	29.78	35.06	22.99	24.79	23.28	44.71	40.45	50.69	51.05
VI						12.91	42.50	44.37	38.43	46.13	54.72	53.46	66.16	61.50
VII							0	37.57	29.44	46.57	16.88	17.13	30.15	20.64
VIII								0	33.41	20.75	38.82	39.91	52.03	49.64
IX									0	34.25	40.36	27.49	36.12	42.66
X										21.71	51.66	47.68	57.12	58.93
XI											0	20.19	32.95	18.74
XII												0	18.24	20.07
XIII													0	23.02
XIV														0

Based on the distance between clusters, *i.e.*, maximum divergence was seen between clusters VI and XIII (D^2=66.16), followed by clusters VI 15 and XIV (D^2=61.50), and clusters X and XIV (D^2=58.93) in terms of inter-cluster distances. Cluster VII had the least inter-cluster distance (D^2=16.88) with cluster XI. This showed that the genotypes found in clusters VI and XIII were closely related to one another. Average intra and inter-cluster distances showed that, generally, inter-cluster distances were substantially higher than those of intra-cluster distances, indicating that the genotypes inside and between the clusters, respectively, were homogeneous and heterogeneous. Similar results were previously supported by Aragaw et al. (2011) and revealed that at Tepi cluster II showed the maximum and significant

distance (1644.00) from cluster VI whereas cluster VI has maximum genetic distance (1145.00) from cluster XI at Bahir Dar in ginger. Cluster VI and Cluster VII had the higher inter-cluster distance (1020.64) in turmeric (Gupta et al., 2015). Islam et al. (2017) reported that higher intra-cluster distances were observed in cluster V and II (0.4157), maximum inter-cluster distance was found between cluster I and IV (48.71) in ginger. Black turmeric genotypes of clusters VIII and IX had the highest degree of divergence, with an intercluster distance of 50.04, while clusters III and IV had the lowest degree of divergence, with an intercluster distance of 4.66 (Paw et al., 2020).

Various characters contributions to the divergence have led to the formation of these clusters. Rhizome yield plant^{-1} contributed a maximum (27.86%) to the total genetic diversity among the genotypes followed by the girth of the primary rhizome (25.68%), length of the primary rhizome (20.70%), girth of the secondary rhizome (7.68%), length of the secondary rhizome (7.02%), number of secondary rhizomes (5.86%), crop duration (4.18%), rhizome yield plant^{-1} (0.95%), height of the shoot and leaf area (0.04%) (Table 4). Rhizome yield plant^{-1} contribution (25.99) to divergence is in accordance with Gupta et al. (2015) in turmeric.

The divergence was significantly influenced by rhizome yield plant^{-1}. According to the data in Table 5, cluster XI had the greatest cluster mean for rhizome yield plant^{-1}, followed by cluster V and cluster VII. For girth of the primary rhizome, cluster VI had the greatest cluster mean, which was followed by cluster IV and cluster I. Cluster XIV had the largest cluster mean for length of the primary rhizome, followed by cluster XI and cluster VII. Similar results were revealed by Islam et al. (2017). The study also showed that parameters that contribute significantly to genetic divergence in ginger, such as the number of primary rhizomes, their girth and

Table 4: Relative % contribution of different characters to the divergence in ginger

Sl. No.	Character or source	Times ranked first	% contribution
1.	Height of the shoot (cm)	1	0.04
2.	Leaf area (cm^2)	1	0.04
3.	No. of primary rhizomes	27	0.95
4.	length of the primary rhizome (cm)	590	20.70
5.	Girth of the primary rhizome (cm)	732	25.68
6.	No. of secondary rhizomes	167	5.86
7.	length of the secondary rhizome (cm)	200	7.02
8.	Girth of the secondary rhizome (cm)	219	7.68
9.	Rhizome yield plant^{-1} (g)	794	27.86
10.	Crop duration (No. of days)	119	4.18
Total			100

Table 5: Mean values of yield contributing traits for nine clusters in ginger

Sl. No.	Characters	Clusters						
		I	II	III	IV	V	VI	VII
1.	Height of the shoot (cm)	41.24	40.48	40.88	42.09	36.53	39.79	40.11
2.	Leaf area (cm^2)	5109.42	5364.91	5482.2	5387.63	5247.17	4875.6	4603.86
3.	Number of primary rhizomes	4.43	4.98	4.58	5.70	4.90	4.20	5.00
4.	length of the primary rhizome (cm)	4.34	4.11	3.78	5.01	3.57	4.35	5.57
5.	Girth of the primary rhizome (cm)	8.87	8.25	7.19	10.59	8.82	10.85	8.52
6.	Number of secondary rhizomes	11.45	12.27	12.56	14.40	15.30	9.25	9.00
7.	length of the secondary rhizome (cm)	5.59	5.83	5.76	5.55	5.75	5.39	7.39
8.	Girth of the secondary rhizome (cm)	7.53	6.82	5.97	7.95	7.21	8.48	7.27
9.	Crop duration (number of days)	232.75	237.36	233.58	239.50	231.00	234.00	241.50
10.	Rhizome yield plant^{-1} (g)	421.53	519.43	467.79	526.29	595.92	409.96	546.12

Table 5: Continue...

Sl. No.	Characters	Clusters						
		VIII	IX	X	XI	XII	XIII	XIV
1.	Height of the shoot (cm)	51.41	43.74	39.64	42.57	34.04	40.98	35.77
2.	Leaf area (cm^2)	5102.6	3884.48	4880.43	5314.03	4404.58	5160.29	3797
3.	Number of primary rhizomes	4.20	4.20	3.83	5.70	4.00	4.90	4.40
4.	length of the primary rhizome (cm)	3.29	4.03	2.45	6.07	5.22	5.35	6.14
5.	Girth of the primary rhizome (cm)	8.70	8.47	8.11	8.69	7.59	6.29	7.25
6.	Number of secondary rhizomes	13.60	10.80	9.60	12.9	8.40	11.40	10.00
7.	length of the secondary rhizome (cm)	7.75	8.73	7.19	9.19	8.56	8.24	8.18
8.	Girth of the secondary rhizome (cm)	4.81	7.12	5.33	6.08	5.97	6.99	7.23
9.	Crop duration (number of days)	241.50	230.00	231.83	241.50	233.50	231.00	236.50
10.	Rhizome yield $plant^{-1}$ (g)	407.66	395.68	374.91	747.56	345.33	481.02	384.52

length, can be exploited in the selection programme to develop high yielding varieties.

4. CONCLUSION

D^2 analysis classified all genotypes into fourteen clusters based on their morphological characteristics. It was found that the inter cluster distance is greater than the intra cluster distance, indicating that there is a high genetic diversity in ginger genotypes. The genotypes of clusters VI and XIII and clusters VI and XIV showed high genetic divergence between them and complimentary for the majority of traits may result in high genetic gain for selected characters and might be chosen for selection to create new varieties.

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