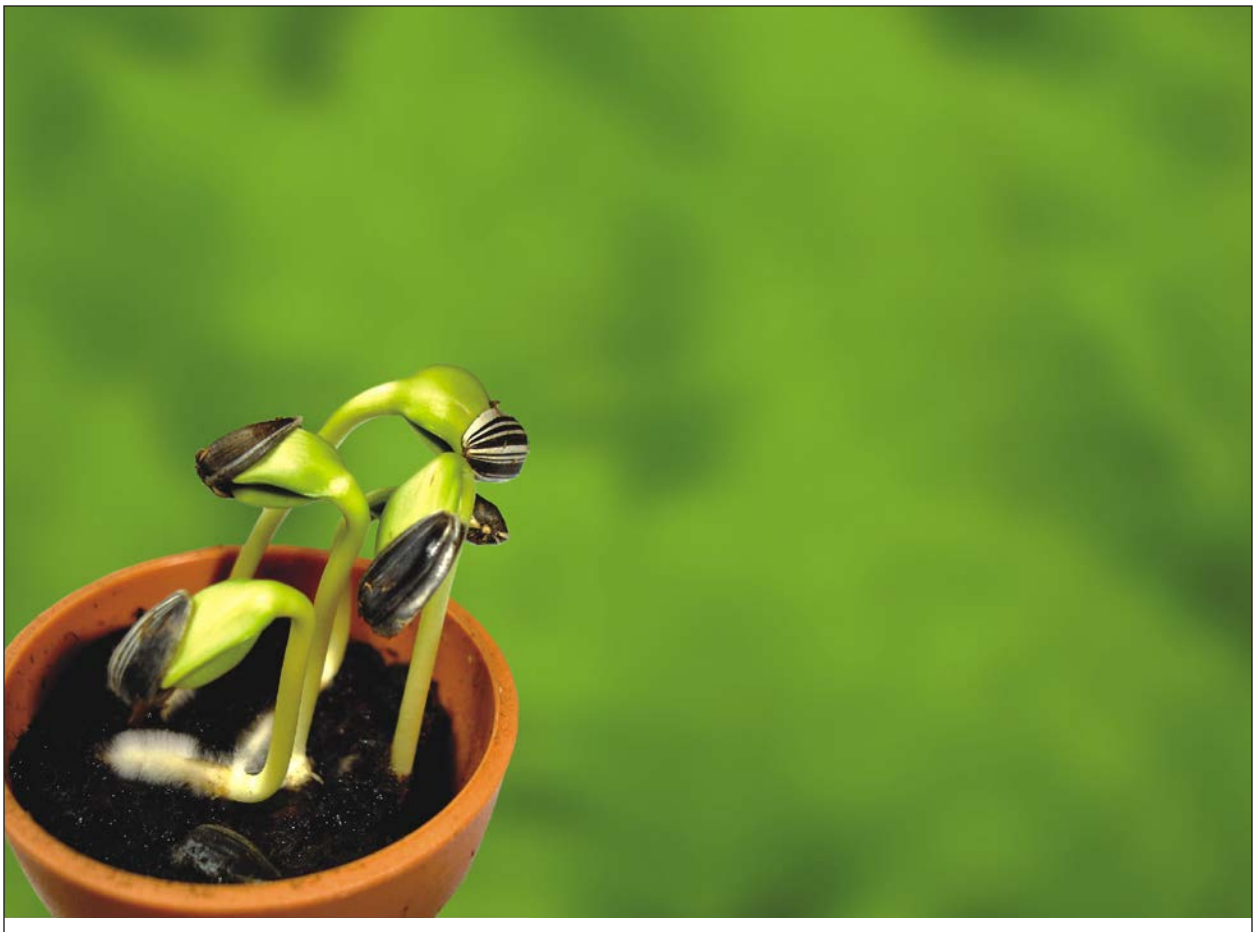

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Genetic Diversity Based on Cluster and Principal Component Analyses for Yield and Quality Attributes in Ginger (*Zingiber officinale* Roscoe)

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ABSTRACT

The present research work would be carried out to excavate diverse parents and determine selection parameters for Ginger. Therefore, present experiment was carried out to estimate genetic diversity by cluster and Principal Component (PC) analyses for thirteen yield and quality attributing traits in 25 ginger genotypes at main experiment station of N.D.U.A.T. Faizabad (U.P.) during Kharif season 2007-08 and 2008-09 under net house. Through cluster analysis, 25 genotypes are grouped into five main clusters. Maximum genetic divergence was observed among these clusters. Based on average cluster mean and difference of each cluster mean with total mean, first cluster represents higher yield potential and ascorbic acid content followed by second cluster. Moreover, rest of the clusters has poor yield potential. FZD-2 and NDG-8 genotypes were found extremely genetic diverse based on Euclidean distance. First six principal components (PC1, PC2, PC3, PC4, PC5 and PC6) having Eigen values greater than one accounted for 76.19% of total variability and account with values of 18.25, 16.65, 13.13, 11.49, 8.85, 7.81%, respectively. PC1 has positive association with plant height, number of primary and secondary fingers, TSS per cent, dry matter per cent and yield per fresh plant whereas negative association with days taken to harvest and acidity per cent. PC2 is positively associated with plant height, length and diameter of primary fingers, acidity percent and ascorbic acid content whereas negatively associated with oleoresin content.

Key words: PCA, cluster analysis, dendrogram, ginger, eigen value

INTRODUCTION

Ginger (*Zingiber officinale* Roscoe) is a cash crop of immense value having medicinal properties, pleasant pungent, spicy aroma and essential component of number of byproducts viz. confectionery, curry powder, ginger cordial, cocktail, ginger tonic, ginger candy, ginger brandy, ginger wine, beer,

flavoring pickles, sauces and preserves etc. Ginger rhizomes has several medicinal application to treat stomach upset, nausea and diarrhea and used as carminative, rubefacient, stimulant, gastritis, dyspepsia and flatulent (Langner *et al.*, 1997). Ginger is also treated as ayurvedic medicine and recommended for arthritis, morning sickness of pregnancy, motion sickness, as an anti-inflammatory, preventing blood clots and lower cholesterol and triglyceride levels (Sharma *et al.*, 1994; Bhandari *et al.*, 1998) and posses other traditional uses viz., colic, colds, fever, menstrual cramps and appetite stimulant (Backon, 1991).

Enormous breeding practices result reducing genetic diversity of elite ginger germplasm reveals problem associated with biotic stresses, abiotic stresses as well as adaptation (Rao and Hodgkin, 2002; Zhang *et al.*, 2005). Information on genetic diversity among elite germplasm is essential for identifying promising lines for trait of interest (Ali *et al.*, 2008) and estimating genetic distinctness among parents. Selection of genetically diverse parents is mandatory for exploitation of trangressive segregation (Joshi *et al.*, 2004). Vast genetic distance among parents is prerequisite for securing useful heterosis in progeny. Cluster analysis and Principal Component Analysis (PCA) are most frequent genetic diversity assessing methods while securing relative basic differences between them. The cluster analysis has open a new realm of assessing family relationships (Rogers, 1972). The major breeding objectives of present experiment is to screen out genetically diverse parents for developing high yielding ginger rhizome by using the tools i.e., cluster analysis and PCA especially to eastern part of India.

MATERIALS AND METHODS

Experimental site: The present investigation was carried out under net house at main experiment station of Department of Vegetable Science, Narendra Dev University of Agriculture and Technology, Kumarganj, Faizabad (U.P.), India during kharif season 2007-08 and 2008-09 which is located in between 24.47^0 and 26.56^0 N latitude and 82.12^0 and 83.98^0 E longitude having elevation of 113 m above the mean sea level in the Gangetic alluvial plains of eastern Uttar Pradesh which falls under humid sub-tropical climate. The experimental field had sandy loam, slightly alkaline soil (pH 8.0), low in organic carbon and nitrogen, medium in phosphorus and potassium. The soil composition constituted 64.4% sand, 27.8% silt and 11.3% clay.

Genotypes: Twenty-five ginger accessions were collected from different locations of Sultanpur, Deoria and Jaunpur districts of Uttar Pradesh, Kerala and rest were collected from Department of Vegetable Science, NDUA and T, Faizabad (Table 1).

Experimental design and crop management practices: The experiment was laid out in Randomized Block Design (RBD) with three replications. The experimental field was prepared by

Table 1: Collection of 25 indigenous ginger genotypes from selected areas of India

Accessations	Area of collection
DEO-1, DEO-2, DEO-3	Deoria district, U.P.
FZD-1, FZD-2, NDG-6, NDG-8, NDG-12, NDG-14, NDG-16, NDG-18, NDG-22, NDG-35, NDG-36, NDG-39, NDG-41, NDG-53	NDUA and T, Faizabad, U.P.
Suprabha, V2E5-2, PGS-8	Calicut district, Kerala
JNP-1, JNP-2, JNP-3	Jaunpur district, U.P.
Sultanpur-1, Sultanpur-2	Sultanpur district, U.P.

harrowing with hand hoeing followed by leveling whereas well decomposed manure F.Y.M @ 15 tonnes per hectare were applied at 30 days before sowing. Selected rhizomes of large shiny, free from spots or marks bud or eye injury were cut into bits of 3-5 cm in the length, 15- 20 g in weight and at least one sound bud treated with fungicide like carbendazim and mancozeb by dissolving 30 g of the chemicals in 15 L water as a safeguard against soft rot and to induce early sprouting. Single row of 1.40 m plot with the spacing of 40 cm row to row and 20 cm plant to plant was maintained. The bits of each genotype were sown on 18th may in 2007 and irrigation was done at weekly interval during summer as per requirement. The crop was fertilized with 120, 75 and 60 kg of N, P_2O_5 and K_2O per hectare, respectively. N, P_2O_5 and K_2O were supplied by urea, single super phosphate and muriate of potash, respectively. The whole amount of phosphorus and potassium were applied at the time of plantings. The nitrogen was applied in two equal split doses, half at the time of planting and remaining half at the time of earthing up. In order to make the net house free from weeds, three manual weeding done at 30, 45 and 60 days, respectively. The recommended cultural practices and plant protection measures were applied to raise a healthy crop.

Observations: The data were recorded from five randomly selected plants from each treatment in each replication and replication wise mean data was used for statistical analysis for thirteen diverse traitsviz. plant height (cm), girth of plant (cm), days taken to harvest, number of primary fingers, length of primary fingers (cm), diameter of primary fingers (cm), numbers of secondary fingers, TSS (%), acidity (%), ascorbic acid content (mg 100 g^{-1} of edible portion), dry rhizome recovery (%), oleoresin content (%) and fresh yield per plant (g).

Data analysis: Cluster analysis of 25 ginger genotypes based on 13 diverse traits to assess the magnitude of genetic variation was performed by using statistical software NTYSYSpc version 2.01 (Roulf, 2002) and a dendrogram was constructed (Fig. 1). Euclidean distance coefficient values were made for all paired genotypes which result euclidean dissimilarity coefficients. It is most frequently used to evaluate relationship among the entries with a cluster analysis. The statistical tool STATISTICA v.10 was utilized for principal component analysis. For first three principal components, explained variation among all the ginger genotypes was graphically represented in scattered plot (Fig. 2) (Jan *et al.*, 2012).

RESULTS

Genetic Divergence analysis: NTYSYSpc version 2.01 analysis results 5 distinct clusters in 25 ginger accessions, reveals the presence of wide genetic diversity among the experimental material (Table 2). The genetic distance (degree of dissimilarity) among 25 accessions is represented by dendrogram (cluster analysis tree chart) (Fig. 1). Euclidean genetic distance among 25 ginger genotypes represents total variability for 13 diverse traits (Table 3). Based on Euclidean distance,

Table 2: Clustering pattern of genotypes based on dendrogram (cluster analysis tree chart)

No. of Genotypes	Genotypes
5	NDG-8, NDG-22,Sultanpur-2, NDG-41 and FZD-2
5	NDG-18,Sultanpur-1, NDG-53, NDG-6 and NDG-35
3	DEO-1, DEO-2 and FZD-1
4	NDG-16, NDG- 14, JNP-2 and JNP-1
8	Suprabha, V2E5-2, DEO-3, JNP-3, PGS-8, NDG-39, NDG-36 and NDG-12

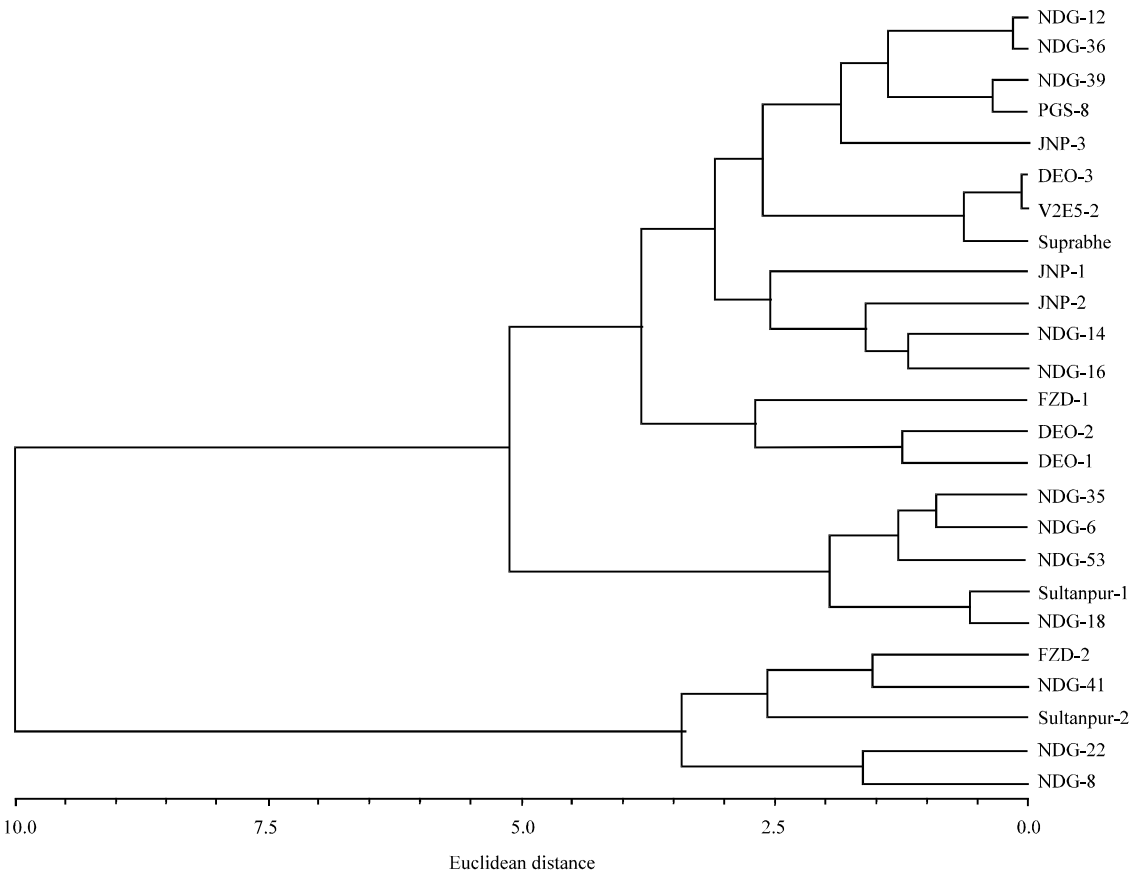

Fig. 1: Dendrogram (cluster analysis tree chart) showing the relationships among ginger genotypes using 13 diverse traits

paired genotypes (FZD-2 and NDG-8), (V2E5-2 and Suprabha) and (FZD-2 and Suprabha) were found extremely diverse while paired genotypes (DEO-2 and JNP-2) and (NDG-39 and NDG-35) exhibited closest genetic relationship (Table 3).

Genotypes of the first cluster: Five genotypes were categories under first cluster accounting for 20% of total genotypes (Table 2). The average value of genotypes in the cluster for , number of primary finger (4.41), length of primary finger (4.10 cm), diameter of primary finger (2.26 cm), number of secondary finger (4.70), ascorbic acid content (5.92 mg 100 g^{-1}) and yield per fresh plant (223.04 g) are above the mean of all genotypes representing high yield potential (Table 4) as similar reported by Khodadadi *et al.* (2011).

Genotypes of the second cluster: Five genotypes were categories under second cluster accounting for 20 % of total genotypes (Table 2). Cluster 2 represents second most prominent cluster having better genotypic mean value as comparison to mean value of all genotypes for traits viz., girth of plant (0.94 cm), diameter of primary fingers (2.18 cm), TSS (8.74%), oleoresin content (6.10%) and yield per fresh plant (173.20 g) (Table 4).

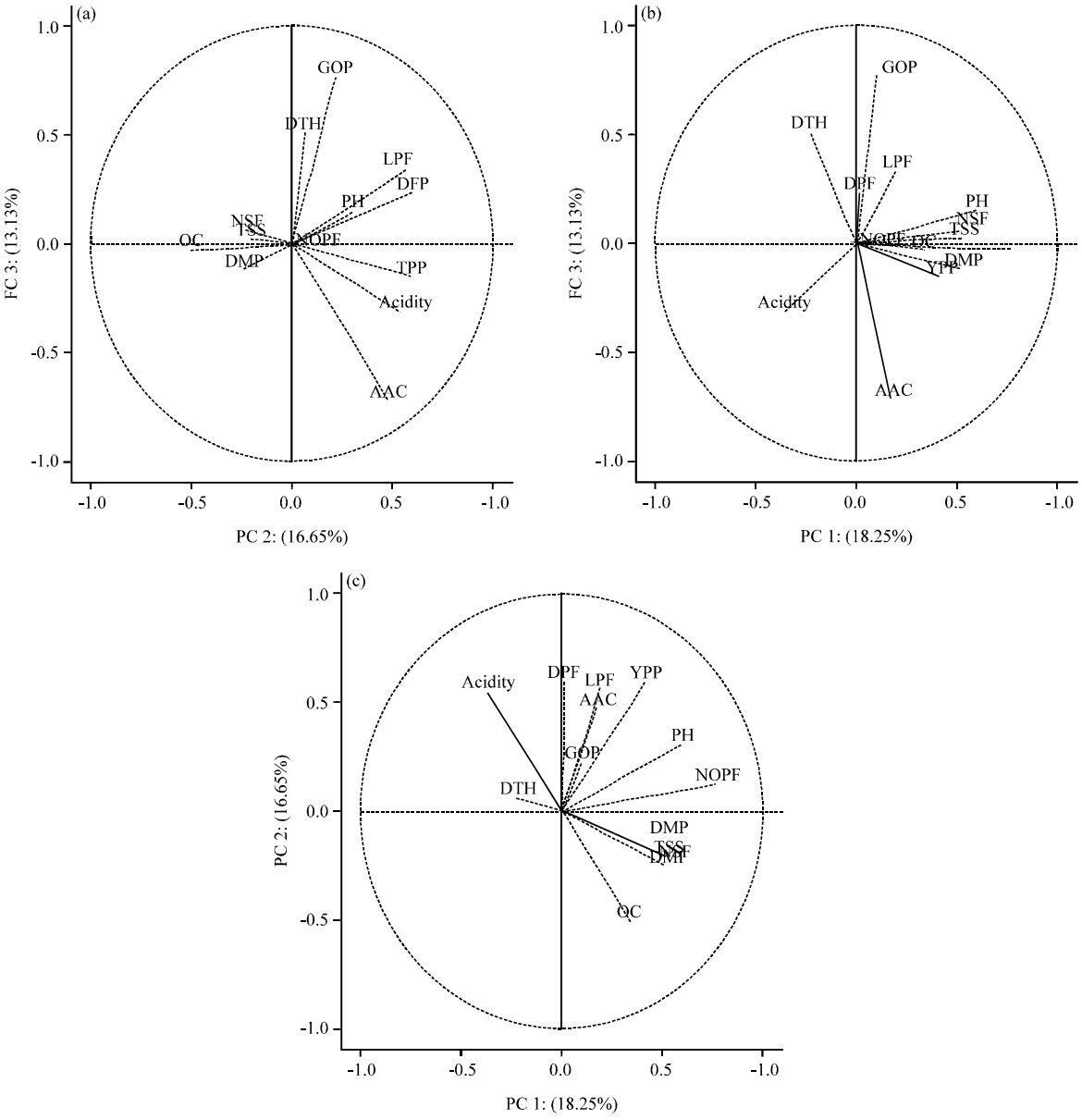

Fig. 2(a-c): Scattered diagram of first three principal components showing the contribution of 13 diverse traits in the separation of various Indian ginger genotypes

Genotypes of the third cluster: Three genotypes were categories under third cluster accounting for 12% of total genotypes (Table 2). The average value of genotypes in the cluster for TSS (10.16%), oleoresin content (7.91%) and number of secondary fingers (5.24) are above the mean of all genotypes (Table 4).

Genotypes of the fourth cluster: Four genotypes were categories under fourth cluster accounting for 16% of total genotypes (Table 2). The average value of genotypes in the cluster for acidity (0.56%) is above the mean of all genotypes. However, cluster 4

Table 3: Euclidean distance based on 13 diverse traits showing the variability among 25 ginger genotypes

Genotype	NDG-12	FZD-1	FZD-2	JNP-1	JNP-2	NDG-35	NDG-53	DEO-2	DEO-3	Suprabha	NDG-39	V2E5-2	NDG-41
NDG-12	0.0												
FZD-1	2.2	0.0											
FZD-2	8.4	1.8	0.0										
JNP-1	4.4	7.7	1.3	0.0									
JNP-2	9.5	5.8	1.4	3.6	0.0								
NDG-35	9.2	5.5	4.1	2.4	3.4	0.0							
NDG-53	5.1	4.7	5.5	1.8	2.8	2.5	0.0						
DEO-2	1.6	7.1	1.4	9.2	1.0	3.6	3.4	0.0					
DEO-3	7.0	2.1	8.6	1.1	1.1	1.6	1.7	8.4	0.0				
Suprabha	1.3	2.2	9.8	1.6	1.2	2.6	2.6	1.0	1.6	0.0			
NDG-39	2.2	2.1	7.9	7.4	9.7	1.0	9.0	1.1	1.5	5.3	0.0		
V2E5-2	8.7	2.5	8.2	1.5	1.3	1.7	1.8	1.2	4.8	10.0	2.4	0.0	
NDG-41	7.6	1.7	3.3	1.1	1.3	3.4	4.5	1.3	8.5	1.0	7.5	8.3	0.0
Sultanpur-1	1.5	6.1	3.4	3.3	4.0	5.1	1.0	3.5	1.2	1.8	1.0	1.1	3.4
NDG-6	7.5	5.1	4.3	2.3	3.0	1.8	2.8	3.3	1.1	1.9	6.9	1.2	3.8
DEO-1	8.6	7.5	1.2	4.9	5.0	2.8	2.4	2.5	4.5	6.1	5.4	6.6	1.2
NDG-14	7.4	1.8	1.1	8.8	4.4	2.6	2.0	1.9	8.8	9.1	7.1	8.7	1.1
NDG-16	1.1	1.0	1.3	8.3	2.7	3.5	2.9	1.1	7.4	6.0	8.4	7.9	1.3
NDG-18	1.4	6.4	3.1	3.3	4.0	2.9	7.1	4.0	1.5	2.3	1.2	1.5	2.9
Sultanpur-2	8.8	1.9	1.1	1.3	1.5	4.2	5.4	1.5	1.0	1.2	9.0	1.0	3.4
NDG-22	2.8	9.5	1.7	5.3	6.7	6.0	1.2	6.6	3.6	4.8	2.8	3.6	1.2
PGS-8	2.9	2.7	7.3	1.0	1.2	9.4	8.0	1.6	2.6	6.1	8.1	2.9	7.0
NDG-36	5.7	2.5	8.3	6.2	1.1	9.7	4.6	2.0	8.6	1.5	3.4	1.0	7.4
NDG-8	5.0	1.3	10.0	8.1	9.9	1.8	2.5	9.9	6.1	7.6	5.1	6.1	3.4
JNP-3	4.7	3.0	8.4	1.2	1.1	1.6	1.0	2.7	9.7	1.2	5.9	9.1	8.0

Genotype	Sultanpur-1	NDG-6	DEO-1	NDG-14	NDG-16	NDG-18	Sultanpur-2	NDG-22	PGS-8	NDG-36	NDG-8	JNP-3
Sultanpur-1	0.0											
NDG-6	2.9	0.0										
DEO-1	2.8	2.3	0.0									
NDG-14	2.8	1.9	9.4	0.0								
NDG-16	3.4	2.7	4.7	2.4	0.0							
NDG-18	1.2	1.8	3.1	2.8	3.6	0.0						
Sultanpur-2	4.7	5.0	1.3	1.3	1.5	4.1	0.0					
NDG-22	8.2	8.1	5.5	5.1	6.4	5.2	1.8	0.0				
PGS-8	9.2	5.0	8.5	5.7	8.8	1.0	8.7	2.6	0.0			
NDG-36	1.6	7.1	1.1	6.4	1.1	1.5	8.8	2.8	2.9	0.0		
NDG-8	2.1	2.2	8.6	7.9	9.6	1.6	7.0	3.6	4.7	4.9	0.0	
JNP-3	1.9	9.7	1.5	2.6	8.7	1.7	9.9	3.4	3.5	3.3	5.6	0.0

exhibits desirable lowest mean value for plant height (83.17 cm) as comparison to mean value of all genotypes as similar reported by Khodadadi *et al.* (2011) (Table 4).

Genotypes of the fifth cluster: Eight genotypes were categories under fifth cluster accounting for 32% of total genotypes (Table 2). The average value of genotypes in the cluster for girth of plant (1.05 cm) and dry matter content (18.65%) are above the mean of all genotypes. However, the cluster represents lowest days to harvest (257.09 days) i.e., desirable for early maturity (Table 4) as similar reported by Khodadadi *et al.* (2011).

Table 4: The average of traits for each cluster (above number) and the difference between each cluster mean with total mean (below number)

Clusters	Plant height (cm)	Girth of plant (cm)	Days taken to harvest	No. of primary fingers	Length of primary finger (cm)	Diameter of mary finger (cm)	No. of secondary finger	TSS (%)	Acidity (%)	Ascorbic acid content mg 100 g^{-1} of edible portion)	Dry matter (%)	Oleoresin content (%)	Yield per plant (fresh) g
Cluster 1	99.68	0.93	258.49	4.41	4.10	2.26	4.70	8.44	0.54	5.92	18.13	5.32	223.04
	6.70	-0.03	1.21	0.51	0.27	0.11	0.15	-0.15	0.04	1.35	0.39	-0.16	64.26
Cluster 2	94.13	0.94	258.40	3.65	3.67	2.18	4.55	8.74	0.51	4.05	17.63	6.10	173.20
	1.16	-0.02	1.13	-0.26	-0.15	0.03	0.00	0.16	0.01	-0.53	-0.12	0.62	14.42
Cluster 3	104.45	0.89	257.09	4.34	3.77	2.02	5.24	10.16	0.50	4.49	16.82	7.91	114.27
	11.48	-0.07	-0.18	0.44	-0.06	-0.13	0.69	1.58	-0.01	-0.09	-0.92	2.43	-44.51
Cluster 4	83.17	0.90	261.84	3.20	3.53	2.04	4.08	7.30	0.56	4.80	16.31	4.77	123.79
	-9.80	-0.06	4.56	-0.70	-0.30	-0.11	-0.47	-1.29	0.05	0.23	-1.44	-0.71	-34.99
Cluster 5	88.66	1.05	253.60	3.94	3.92	2.18	4.43	8.64	0.45	3.98	18.65	4.63	143.78
	-4.32	0.09	-3.68	0.03	0.10	0.02	-0.12	0.05	-0.05	-0.59	0.90	-0.84	-14.99

Table 5: Variation among ginger genotypes accounted for first eight principal components

Traits	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8
Eigen value	2.37	2.16	1.71	1.49	1.15	1.01	0.81	0.81
Cumulative Eigen value	2.37	4.54	6.25	7.74	8.89	9.9	10.72	11.52
Variance (%)	18.25	16.65	13.13	11.49	8.85	7.81	6.25	6.19
Cumulative variance (%)	18.25	34.91	48.04	59.53	68.38	76.19	82.44	88.64
Eigen vectors								
Plant Height	0.39	0.21	0.12	-0.23	0.50	-0.20	-0.15	0.08
Girth of plant (cm)	0.06	0.15	0.59	0.13	-0.12	-0.44	-0.11	-0.01
Days taken to harvest	-0.15	0.04	0.39	-0.46	-0.10	0.47	-0.16	-0.10
No. of primary fingers	0.50	0.08	-0.02	0.29	0.09	0.09	0.09	0.27
Length of primary finger (cm)	0.13	0.39	0.26	0.23	0.06	0.38	-0.27	0.22
Diameter of primary finger (cm)	0.01	0.41	0.18	-0.26	-0.22	-0.27	0.53	-0.26
No. of secondary finger	0.37	-0.16	0.05	-0.17	-0.21	0.24	0.58	0.38
TSS (%)	0.34	-0.14	0.02	-0.47	-0.24	-0.26	-0.38	0.14
Acidity (%)	-0.24	0.37	-0.24	-0.33	-0.18	0.13	-0.12	0.41
Ascorbic acid content (mg 100 g^{-1} of edible portion)	0.11	0.33	-0.55	-0.13	0.01	-0.21	-0.08	-0.03
Dry matter percentage	0.33	-0.17	-0.09	0.16	-0.63	0.04	-0.27	-0.22
Oleoresin content (%)	0.22	-0.35	-0.02	-0.32	0.36	0.16	0.02	-0.33
Yield per plant (fresh) g	0.27	0.41	-0.12	0.06	-0.03	0.32	0.01	-0.55

Principal components analysis (PCA): PCA reveals the major contributor of the total variation at each distinct point. Generally, the sum of Eigen values is equal to the number of variables. The Eigen value is often used to determine number of major principal components to be explained. The first six principal components (PCS) having Eigen values greater than one accounted for 76.19% of total variability amongst 25 ginger genotypes (Table 5) as similar reported by Hailegiorgis *et al.* (2011). The first principal component (PC1) contributed maximum towards variability (18.25%) followed by PC2 (16.65%), PC3 (13.13%), PC4 (11.49%), PC5 (8.85) and PC6 (7.81), respectively. PC1 has major positive association with number of primary (0.50), number of secondary fingers (0.37), TSS (0.34) and dry matter per cent (0.33) . PC2 has significant positive association with length of primary fingers (0.39), diameter of primary fingers (0.41), acidity per cent (0.37) ascorbic acid content (0.33) and yield per fresh plant (0.41) (Table 5). PC3 has significant positive association for single traits i.e. girth of plant (0.59). PC4 has positive association with number of primary finger (0.29) whereas desirable negative association with plant height (-0.23) and days

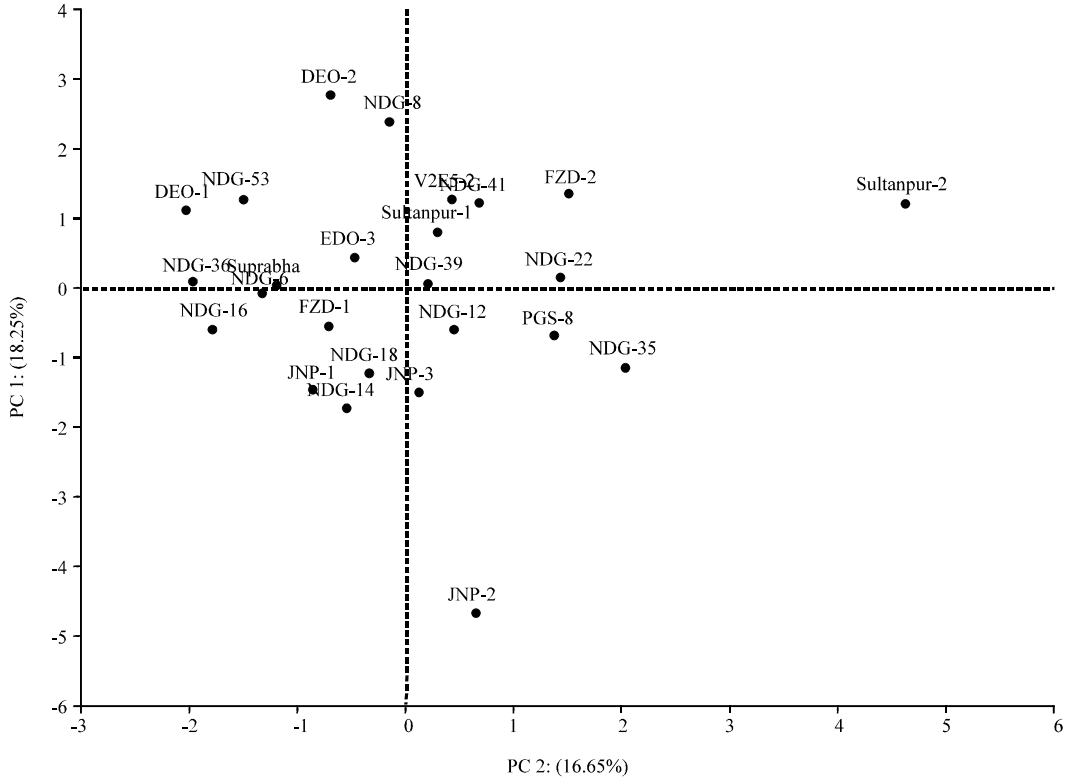

Fig. 3: Scattered diagram of first two principal components based on mean values of 13 diverse traits in 25 Indian ginger genotypes

taken to harvest (-0.46). PC5 has positive association with oleoresin content (0.36). PC6 has positive association with length of primary finger (0.38) and yield per plant (0.32). The first two PCS were plotted to observe the relationship between 25 genotypes of ginger (Fig. 3).

DISCUSSION

To analyze the degree of genetic diversity among ginger genotypes from India, twenty five genotypes were used as experimental material and were studied for thirteen yield and quality attributing traits. Maximum Euclidean distance was found between FZD-2 and NDG-8 genotypes than others (Table 3). The F1 originated from genotypes having maximum genetic distance resulted high yield and could be used in breeding programs for exploiting maximum heterosis (Rahim *et al*., 2010). The partitioning of total variance into its components facilitates the use of genetic resources in crop improvement programmes for distinct characters (Pecetti and Damania, 1996). Out of 25, 14 genotypes (56%) belong to Faizabad district (Table 1) (India). Observed morphological and agronomical data of the collected genotypes was found effective for identification and selection of best genotypes (Amanullah and Hatham, 2000). In this experiment, the PC analysis divided the total variability into 8 PCS out of which first 6 PCS contributing major amount of diversity i.e., 76.19% among the genotypes due to different traits studied.

CONCLUSION

Among all PCS, PC1 has higher yield potential and having positive association with plant height, number of primary and secondary fingers, TSS, dry matter per cent and yield per fresh plant. Genotypes of first cluster represent high yield potential and late maturity (Table 3) than remain clusters. Proportional contribution of 13 yield and quality attributing traits for first three PCS revealed grouping pattern of ginger genotypes (Fig. 2). The genetic diversity analysis could be helpful to select diverse parents and strengthen breeding programs of India.

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