International Archive of Applied Sciences and Technology
Int. Arch. App. Sci. Technol; Vol 10 [4] December 2019 : 185-190

[ISO9001: 2008 Certified Organization]
www.soeagra.com/iaast.html

IAAST
ONLINE ISSN 2277- 1565
PRINT ISSN 0976 - 4828

CODEN: IAASCA ORIGINAL ARTICLE

DOI: .10.15515/iaast.0976-4828.10.4.185190

Genetic Divergence and Clustering of some elite Ginger Genotypes in Terai region of West Bengal (*Zingiber officinale* Rosc.)

D. Basak[1], S. Chakraborty[2], Sahanob Nath[3]
Department of Genetics and Plant Breeding, Faculty of Agriculture
Uttar Banga KrishiViswavidalaya, Pundibari, Cooch Behar, 736165, Terai Region, West Bengal.
Email: emonbasak4mtripura@gmail.com

ABSTRACT
18 genotypes of ginger were collected from different regions of the states of India to evaluate the genetic potential and divergence of the genotypes and their suitability of growing inTerai region of West Bengal. The multivariate analysis by means of Mahalanobis D^2 statistic for estimating genetic divergence was done where D2 statistical methods were applied for finding out the genetic divergence of the genotypes and all the genotypes were grouped into 8 clusters. Maximum number of genotypes were accommodated in cluster-I followed by cluster-VII. Relative contribution of rhizome yield to the total divergence was highest (58.82) followed by rhizome thickness (25.49) and plant height (5.23). The more diverse the parents, within overall limits of fitness, the greater the chances of obtaining higher amount of heterotic expression in F_1 and broad spectrum of variability in segregating generations.
Keywords: *Genetic divergence, multivariate analysis, clusters, variability, D^2 statistics.*

Received 23.08.2019 Revised 21.09.2019 Accepted 14.11.2019

CITATION OF THIS ARTICLE
D. Basak, S. Chakraborty, Sahanob Nath. Genetic Divergence and Clustering of some elite Ginger Genotypes in Terai region of West Bengal (*Zingiber officinale* Rosc.). Int. Arch. App. Sci. Technol; Vol 10 [4] December 2019 :185-190

INTRODUCTION

Ginger is a monocotyledon belonging to family *Zingiberaceae*. Ginger is an important spice and medicinal crop originated in South-East Asia and introduced in many parts of the world. India has been known from prehistoric times as the land of spices. Until the 1970s, India had a virtual dominance in the international spices trade. India still continues to be the largest producer, consumer, and exporter of spices flavour foods in over 130 countries and their intrinsic values make them distinctly superior in terms of taste, colour and fragrance. The USA, Canada, Germany, Japan, Saudi Arabia, Kuwait, Bahrain and Israel are the main markets for Indian spices. The main ginger growing countries are India, China, Jamaica, Taiwan, Sierra Leone, Nigeria, Fiji, Mauritius, Indonesia, Bangladesh, Philippines, Sri Lanka, Thailand, Trinidad, Uganda, Hawaii, Guatemala, and many Pacific Ocean Islands [6]. The widely reported chromosome number of ginger is 2n=2x=22 and the basic chromosome number of the genus is suggested as x=11 [4, 10].

Three types of ginger products are supplied to market in these areas. The first one is fresh ginger which is usually supplied to market in rainy season for immediate cash demand. It is also supplied in dry season as assemblers collect it for re-sell to large traders after sun-drying. Dry season fresh ginger supply also targets local farmers who demand it as a planting material. The second type of marketable ginger product is dried ginger. Dried ginger is favourite ginger product exchanged in large volumes by all market participants at different stages of marketing from local assembling to export market. Dried ginger for this

purpose is harvested8 to 9 months after planting when there is mature rhizome with a full aroma, flavour and pungency. Further delay not only increases fibre but also decreases oil and oleoresin content [3]. The third type of marketable ginger products are extracted ginger products. These include ginger powder, essential oils, oleoresin and others. The extent to which rhizomes are treated prior to drying directly affects fibre and volatile oil content. Removal of the cork skin reduces fibre content but enhances oil loss through rupture of the surface oil-cells; thus, cleanly peeled ginger generally has a lower oil and fiber content [7].

Table 1. Sub families, tribes and representative genera of the *Zingiberaceae* [3]

Subfamily	Tribe	Representative genera
Zingiberoideae	*Hedychieae*	*Boesenbergia, Curcuma, Hedychium, Kaempferia, Scaphochlamys*
	Zingibereae	*Zingiber*
	Alpinieae	*Aframomum, Alpinia, Amomum, Elettaria, Etlingera, Hornstedtia*
	Globbeae	*Globba*
Costoideae		*Costus, Tapeinochilus*

MATERIAL AND METHODS

The present investigation was conducted during the summer season of 2016-2017 and 2017- 2018 at the University Farm of Uttar BangaKrishiViswavidyalaya, Pundibari, Cooch Behar.

Table-2 List of genotypes under the study

Sl. No.	Name of Genotype	Place of origin	Sl. No.	Name of Genotype	Place of origin
1	GCP-51	Dinhata, Cooch Behar,West Bengal	10	ACC-578	IISR, Kerala
2	GCP-56	Totopara, Alipurduar, West Bengal	11	SE-8631	Telengana
3	GCP-5 Local check	Garubathan, Darjeeling, West Bengal	12	ACC-219	IISR, Kerala
4	GCP-46	Mangalabari, Jaigaon, West Bengal	13	SE-8640	TNAU, Tamil Nadu
5	GCP-30	Majhian, South Dinajpur, West Bengal	14	SG-26-40	Kerala
6	GCP-36	Uttar Madarihat, Alipurduar, West Bengal	15	SE-8681	Telengana
7	GCP-39	Totopara, Alipurduar, West Bengal	16	ACC-247	IISR, Kerala
8	GCP-14	Jambari, Cooch Behar, West Bengal	17	VARADA National check	IISR Variety, Kerala
9	SEHP-9	Telengana	18	KARTHIKA	Kerela Agricultural University

A fertilizer dose of N: P2O5:K2O @ 120:60:60 (Kg/ha) were given for conventional plot. The required amount of fertilizer were calculated on the basis of plot size and applied as Urea (46%N), SSP (16% P2O5) and MOP (60% K2O).

STATISTCAL ANALYSES

The present investigation on genetic divergence was worked out on 18 genotypes based on 8 characters.

Estimation of genetic divergence using D^2 statistics

Mahalanobis's D^2 statistic [9] was used for estimation of genetic divergence among 26 genotypes for 17 traits. Genetic divergence (D^2) between two genotypes is given by the formula: $D^2x = \sum_{i=1}^{p} \sum_{j=1}^{p} (\lambda_{ij})\, d_i d_j$

Where, x is the number of metric trait in a point, λij is the inverse of the common dispersion matrix λij, p is the number of populations / genotypes while d_i and d_j are the difference in the means of two populations for i^{th} and j^{th} characters.

The computation of D^2 using this formula gets complicated and laborious when more number of mutually correlated characters is involved in divergence analysis. So the character means were transformed into sets of uncorrelated variables using pivotal condensation of common dispersion matrix following [9]. After this transformation the formula for genetic divergence is

$$D^2 = \sum_{i=1}^{x} d_i^2$$

Where, $d_i$is the difference between the transformed values of any two-population means for the i^{th} character. The relative contribution of individual character towards genetic divergence was assessed from rank average.

Grouping of genotypes into different clusters

Grouping of genotypes into different clusters was done following Tocher's method. Usually a cluster is defined as a group of populations per clusters such that any two populations belonging to the same cluster should on average, show a smaller D^2 than those belonging to two different clusters. A simple device suggested by Tocher [9] for construction of clusters is to start with two most closely related populations (having the smallest D^2) and then find a third one which has small average D^2 from the first two and so on. At certain stage when it is felt that after adding a particular population there is an abrupt increase in the average D^2, then that population is not added to the cluster. Similarly construction of 2^{nd}, 3^{rd} and other clusters are formed till all the populations are included in one or the other cluster.

Average intra- and inter- cluster distance: Estimation of genetic divergence using D^2 statistics

Mahalanobis's D^2 statistic [9] was used for estimation of genetic divergence among 26 genotypes for 17 traits. Genetic divergence (D^2) between two genotypes is given by the formula:

$$D^2x = \sum_{i=1}^{p} \sum_{j=1}^{p} (\lambda_{ij})\, d_i d_j$$

Where, x is the number of metric trait in a point, λij is the inverse of the common dispersion matrix λij, p is the number of populations / genotypes while d_i and d_j are the difference in the means of two populations for i^{th} and j^{th} characters.

The computation of D^2 using this formula gets complicated and laborious when more number of mutually correlated characters is involved in divergence analysis. So the character means were transformed into sets of uncorrelated variables using pivotal condensation of common dispersion matrix following [9]. After this transformation the formula for genetic divergence is

$$D^2 = \sum_{i=1}^{x} d_i^2$$

Where, $d_i$is the difference between the transformed values of any two-population means for the i^{th} character. The relative contribution of individual character towards genetic divergence was assessed from rank average.

Grouping of genotypes into different clusters

Grouping of genotypes into different clusters was done following Tocher's method. Usually a cluster is defined as a group of populations per clusters such that any two populations belonging to the same cluster should on average, show a smaller D^2 than those belonging to two different clusters. A simple device suggested by Tocher [9] for construction of clusters is to start with two most closely related populations (having the smallest D^2) and then find a third one which has small average D^2 from the first two and so on. At certain stage when it is felt that after adding a particular population there is an abrupt increase in the average D^2, then that population is not added to the cluster. Similarly construction of 2^{nd}, 3^{rd} and other clusters are formed till all the populations are included in one or the other cluster.

Average intra- and inter- cluster distance

For the measure of intra-cluster distances the formula $\sum D_i^2/n$ was used, where $\sum D_i^2$ is the sum of distances between all possible combinations (n) of populations (genotypes) included in a cluster.

For calculating inter-cluster distance the formula $\sum D_i^2/n_i\, n_j$was used; where D_i^2 is the sum of all possible pair wise D^2 values between the individuals of one cluster with that of others, n_i is the number of population in cluster 'i' and n_j is the number of population in cluster 'j'.

The data were analyzed in the computer using SPSS 17.0.For the measure of intra-cluster distances the formula $\sum D_i^2/n$ was used, where $\sum D_i^2$ is the sum of distances between all possible combinations (n) of populations (genotypes) included in a cluster. For calculating inter-cluster distance the formula $\sum D_i^2/n_i\, n_j$was used; where D_i^2 is the sum of all possible pair wise D^2 values between the individuals of one cluster with that of others, n_i is the number of population in cluster 'i' and $n_j$is the number of population in cluster 'j'.

RESULTS AND DISCUSSION

Distribution of different ginger genotypes into various clusters. All the genotypes were grouped into 8 clusters. Maximum number of genotypes were accommodated in cluster-I followed by cluster-VII(Table- 4).

Average intra and inter cluster distance D²

The statistical distance represents the index of genetic diversity among the clusters. The diagonal figures in the table represent the intra cluster distances. The study revealed thatthe average intra cluster distance varied from 3.01 in cluster II to 10.16 in cluster VII (Table- 5).The maximum inter cluster distance (15.86) was found between cluster VI and VII followed by cluster IV and VII (15.49), cluster VII and VIII (14.87), cluster II and VII (14.49), cluster I and VII (14.08) and so on.This indicated considerable amount of divergence within and between the clusters. Cluster VI and VII played critical role in inter cluster distance. It would be logical to effect crossing between genotypes separated by considerable statistical distance.

Table 3 : Intra and inter cluster distance

Cluster	I	II	III	IV	V	VI	VII	VIII
I	5.07	4.57	6.43	4.90	9.14	6.51	14.08	6.55
II		3.01	6.46	6.04	10.19	5.10	14.49	7.51
III			3.40	8.61	6.46	9.83	11.37	9.37
IV				3.86	10.50	6.44	15.49	5.85
V					4.40	12.12	8.51	9.69
VI						5.89	15.86	7.15
VII							10.16	14.87
VIII								0.00

Table 4: Distribution of different ginger genotypes in different clusters

CLUSTER	Number of genotypes	Genotypes
I	4	ACC-219, ACC-578, GCP-36, GCP-46
II	2	GCP-5, GCP-51
III	2	GCP-14, SE-8631
IV	2	GCP-56, KARTHIKA
V	2	SE-8640, SEHP-9
VI	2	GCP-30, GCP-39
VII	3	ACC-247, SE-8681, SG-2640
VIII	1	VARADA

Similar results were also obtained by Singh *et al.* [11], Aragaw *et al.* [2] and Parmar [5].

ClusterI- Cluster- I comprised maximum number of 4 genotypes representing ACC-219, ACC-578, GCP-36 and GCP-46 (Table-3).This cluster was characterized by moderate mean for all of characters viz. plant height, height of shoot, number of leaves, leaf length, number of shoots and leaf width, rhizome thickness and rhizome yield (Table-5).

ClusterII- Cluster- II comprised two genotypes representing GCP- 5 and GCP -51(Table-21). It showed high mean values for all the characters viz. plant height, height of shoot, number of leaves, leaf length, number of shoots and leaf width, rhizome thickness and rhizome yield(Table-5).

ClusterIII- Cluster- III had two genotypes GCP-14 and SE-8631(Table-3). It showed moderate mean values for all the characters viz. plant height, height of shoot, number of leaves, leaf length, number of shoots and leaf width, rhizome thickness and rhizome yield(Table- 5).

Cluster IV- Cluster IV has comprising two genotypes representing GCP-56 and KARTHIKA (Table-3). It showed highest mean values for number of leaves (16.25 cm) and rest of thecharacters viz. plant height, height of shoot, number of leaves, leaf length, leaf width, rhizome thickness and rhizome yield showed high mean values(Table-5).

ClusterV- Cluster- V has two genotypes representing SE-8640 and SEHP-9 (Table-3). This cluster showed lowest mean values for all the morphological traits viz. plant height (52.15 cm), height of shoot (34.19 cm), number of leaves (11.33), leaf length (17.76 cm), leaf width (2.02 cm) and number of shoots (4.08) and rhizome thickness and rhizome yield showed high mean values(Table-5).

ClusterVI- Cluster-VI has two genotypes representing GCP-30 and GCP-39 (Table-3). This cluster had the highest mean values for almost all the morphological traits viz. plant height (67.99 cm), height of shoot (49.92 cm), leaf length (23.35 cm), leaf width (2.50 cm) and number of shoots (8.17). Rhizome thickness and rhizome yield showed high mean values (Table- 5).

Cluster VII- Cluster VII comprising has three genotypes representing ACC-247, SE-8681 and SG-2640 (Table-3). It showed highest mean values for rhizome thickness (2.47 cm) and rhizome yield (8.43 t/ha) (Table- 5).

Table 5- Cluster means of 8 characters in Ginger

Clusters	Plant height (cm)	Height of shoot (cm)	Number of leaves	Leaf length (cm)	Number of shoots	Leaf width (cm)	Rhizome thickness (cm)	Yield (t/ha)
I	60.95	45.08	15.01	21.71	6.58	2.20	2.17	4.22
II	63.77	46.53	15.25	23.16	8.00	2.34	2.23	4.64
III	53.84	36.66	13.67	21.32	5.67	2.17	2.41	4.69
IV	63.13	47.89	16.25	21.13	6.25	2.18	2.03	3.69
V	52.15	34.19	11.33	17.76	4.08	2.02	2.35	6.23
VI	67.99	49.92	15.83	23.35	8.17	2.50	2.04	5.29
VII	57.40	38.79	13.50	20.08	4.56	2.12	2.47	8.43
VIII	54.86	37.31	12.33	20.21	5.50	2.22	1.87	5.37
RELATIVE CONTRIBUTION %	**5.23**	**0.00**	**0.00**	**3.27**	**1.96**	**5.23**	**25.49**	**58.82**

ClusterVIII- Cluster VIII was monogenotypic cluster and represented by VARADA. (Table-21)(Table-3).It showed low mean values for all the characters viz. plant height, height of shoot, number of leaves, leaf length, number of shoots and leaf width, rhizome thickness and rhizome yield(Table- 5). (Table- 5).Earlier workers like Singh *et al.* [11], Argaw *et al.* [2] and Parmar [5] have also indicated the significance of genetic divergence for these traits in ginger.

CONCLUSION

Relative contribution of rhizome yield to the total divergence was highest (58.82) followed by rhizome thickness (25.49) and plant height (5.23). Thus, on the basis of cluster means of these characters, effective collection of genotypes can be made for getting superior high yielding varieties in ginger from rhizome thickness in order to create a broad genetic base of collection in a particular region

REFERENCES

1. Anand, I. J. and Rawat, D. S. (1984). Genetic diversity, combining ability and heterosis in brown mustard. *Indian J. Genet.*, **44**: 226-234.
2. Aragaw, M., Alamerew, S., Girma, M. H. and Tesfaye, A. (2011). Variability of ginger (*Zingiber officinale* Rosc.) accessions for morphological and some quality traits in Ethiopia. *International Horticultural Science Series-5*, New India Publishing Agencies, New Delhi. 67-68.
3. Mabberley, D. J.(1997). The plant-book: a portable dictionary of the vascular plants. 2nd edn. Cambridge University Press: Cambridge.
4. Moringa, T., Fukushina, E., Kanui, T. and Tamasaki, Y. (1929). Chromosome numbers of cultivated plants. *Bot. Mag. (Tokyo),***43**, 589–594.
5. Parmar, R. (2011). Molecular characterization of *Zingiber officinale* Rosc. germplasm in H.P. using RAPD as molecular markers. M.Sc. thesis. Dr.YSP UHF, Nauni, Solan, HP.
6. Peter, K. V. (2007). Spices. Anand, I. J. and Murthy, B. R. 1968. Genetic divergence and hybrid performance in linseed. *Indian J. Genet.*, **28**: 178-185.
7. Pruthi, J. S. (1998). Spices and Condiments. National Book Trust, A-5 Green Park, New Delhi, 147-154.
8. Raghavan, T.S. and Venkatasubban, K.R. (1943). Cytological studies in the family *Zingiberaceae* with special reference to chromosome number and cyto-taxonomy. *Proceedings of Indian Academy of Sciences Series,* **17**: 118–132.
9. Rao, C. R. (1952). Advanced Statistical Methods in Biometrical Research. *John. Wiley and Sons*, New York.
10. Ravishanker, Kumar, S., Baranwal, D.K., Chatterjee, A. and Solankey, S.S. (2013). Genetic Diversity Based on Cluster and Principal Component Analyses for Yield and Quality Attributes in Ginger (*Zingiber officinale* Roscoe). *International Journal of Plant Breeding and Genetics*, **7**: 159-168.
11. Singh, P. P., Singh, V.B., Singh, H. P. and Rajan, S. (2000). Genetic diversity in ginger (*Zingiber officinale* Rosc.) with reference to essential oil content. *Journal of Spices and Aromatic Crops*, **9**(2): 161-164.