DOI: 10.21276/haya.2016.1.3.2

Haya: The Saudi Journal of Life Sciences **ISSN 2415-623X (Print)**
Scholars Middle East Publishers **ISSN 2415-6221 (Online)**
Dubai, United Arab Emirates
Website: http://scholarsmepub.com/

Research Article

Genetic Diversity Analysis of Some Extinct Local Aman Rice Genotypes (*Oryza Sativa* L.) in Bangladesh

Shajedur Hossain [1], Md. Maksudul Haque[2]*, Jamilur Rahman[3]

[1]Assistant Plant Breeder, Research & Development (Rice), Supreme Seed Company Limited, Mymenshing, Bangladesh
[2]Scientific officer (Golden Rice), Plant Breeding Division, Bangladesh Rice Research Institute, Gazipur 1701, Bangladesh
[3]Professor, Department of Genetics & Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka 1207, Bangladesh

***Corresponding Author:**
Md. Maksudul Haque
Email: maksudulhq@gmail.com

Abstract: The experiment was conducted with 34 local rice genotypes with one check varieties at the Sher-e-Bangla Agricultural University experimental field to study characterization and genetic diversity of 35 local rice genotypes and to find out the association among the genetic characteristics. PCA showed the highest inter-cluster distance was observed between the cluster II and V (46.71) followed by III and V (46.40) and IV and V (45.43). Genotypes from these three clusters may be involved in hybridization as wide genetic variations exist among the groups. Cluster IV exhibited the highest intra-cluster distance (38.36), while the lowest distance was observed in cluster V (23.09). Further study of this experiment is needed in different locations of Bangladesh for accuracy of the results obtained from the present experiment. Considering diversity pattern and other agronomic performance lines G-10, G-13, G-15, G-18 and G-24 could be considered suitable parents for efficient hybridization in future.
Keywords: Genetic Diversity, PCA, PCO, CVA, Rice (*Oryza Sativa* L.).

INTRODUCTION

Rice is a self-pollinated cereal crop belonging to the family Gramineae (synomym-Poaceae) under the order Cyperales and class Monocotyledon having chromosome number 2n=24 [20]. The genus *Oryza* includes a total of 25 recognized species out of which 23 are wild species and two, *Oryza sativa* and *Oryza glaberrima* are cultivated [1]. It can survive as a perennial crop and can produce a ratoon crop for up to 30 years but cultivated as annual crop and grown in tropical and temperate countries over a wide range of soil and climatic condition.

Rice and agriculture are still fundamental to the economic development of most of the Asian countries. In much of Asia, rice plays a central role in politics, society and culture, directly or indirectly employs more people than any other sector. A healthy rice industry, especially in Asia's poorer countries, is crucial to the livelihoods of rice producers and consumers alike. Farmers need to achieve good yields without harming the environment so that they can make a good living while providing the rice-eating people with a high-quality, affordable staple. Underpinning this, a strong rice research sector can help to reduce costs, improve production and ensure environmental sustainability. Indeed, rice research has been a key to productivity and livelihood.

Rice is the second largest produce cereal in the world in 158.3 million hectare area with annual production of about 685.24 million metric tons [3] and also the staple food for over one third of the world's population [2] and more than 90% to 95% of rice is produced and consumed is Asia [4]. Rice (*Oryza sativa* L.) is the staple food in Bangladesh, and grown in a wide range of environments ranging from the upland areas like Chittagong Hill Tracts, Sylhet and Garo Hills, with little moisture, to situations where the water is 3-4 meter deep [5]. Bangladesh is ranked as fourth in rice production with annual production of 47.72 million metric ton in the world [3]. Bangladesh has a population density of 977/square km [6] which is the highest in the world. The land scarcity therefore, usually calls for vertical increased in yield or total production. To solve this problem, the production must be increase from less land, with less labor, less water and fewer pesticides.

Knowledge of genetic diversity among existing cultivars of any crop is essential for long term success of breeding program and maximizes the exploitation of the germplasm resources [7]. Hybridization is one of the major tools for the

improvement of a crop that needs the analysis of genetic diversity is important for the source genes of particular traits within the available germplasm [8]. Multivariate analysis with D^2 technique measures the amount of genetic diversity in a given population in respect of several characters and assesses relative contribution of different components to the total divergence both at intra and inter-cluster levels. A good knowledge of genetic resources might also help in identifying desirable genotypes for future hybridization program. Considering all these aspects the research has been conducted for achieving the following objectives: To identify the promising genotypes for desirable characters.

MATERIALS AND METHODS

The study was conducted at the experimental farm of Sher-e-Bangla Agricultural University (SAU), Sher-e-Bangla Nagar, Dhaka-1207. The experimental field was located at 90º 33.5´ E longitude and 23º 77.4´ N latitude at an altitude of 9 meter above the sea level. The soil of the experiment site was a medium high land, clay loam in texture and having pH 5.47-5.63. The land was located in Agro-ecological Zone of 'Madhupur Tract' (AEZ No. 28). The climate of the experimental site is sub-tropical characterized by heavy rainfall during April to July and sporadic during the rest of the year. The experimental plots were laid out in randomized complete block design (RCBD). The field was divided into three blocks; representing three replications. Thirty five genotypes were distributed to each plot within each block randomly. The experimental materials of the study comprised of 35 rice genotypes. The seeds were collected from Bangladesh Institute of Nuclear Agriculture, Mymensingh (BINA). The details of these genotypes are given in Table 1.

Table 1: List of thirty five rice genotypes along with their sources

Sl. No.	Indicating Symbol	Genotypes	Source
1	G-1	KathiGoccha	BINA
2	G-2	Hamai	BINA
3	G-3	KhakShail	BINA
4	G-4	Hari	BINA
5	G-5	Tal Mugur	BINA
6	G-6	DakhShail	BINA
7	G-7	MoinaMoti	BINA
8	G-8	Nona Bokhra	BINA
9	G-9	Bogi	BINA
10	G-10	Patnai	BINA
11	G-11	LedraBinni	BINA
12	G-12	Lalanamia	BINA
13	G-13	Hogla	BINA
14	G-14	JamaiNaru	BINA
15	G-15	Jota Balam	BINA
16	G-16	KhejurChori	BINA
17	G-17	Ghunshai	BINA
18	G-18	Malagoti	BINA
19	G-19	BazraMuri	BINA
20	G-20	Nona Kochi	BINA
21	G-21	MoghaiBalam	BINA
22	G-22	Ghocca	BINA
23	G-23	Mondeshor	BINA
24	G-24	MotaAman	BINA
25	G-25	Golapi	BINA
26	G-26	BhuteShelot	BINA
27	G-27	Mowbinni	BINA
28	G-28	KaloMota	BINA
29	G-29	Ponkhiraj	BINA
30	G-30	Jolkumri	BINA
31	G-31	Lalbiroi-31	BINA
32	G-32	Karengal	BINA
33	G-33	SadaGotal	BINA
34	G-34	HoldeGotal	BINA
35	G-35	BRRI Dhan-33	BRRI

BINA= Bangladesh Institute of Nuclear Agriculture
BRRI= Bangladesh Rice Research Institute

Statistical Analysis of data

Genetic diversity

Genetic diversity was analyzed using GENSTAT 5.13 software program (copyright 1987, Lawes Agricultural Trust, Rothamasted Experimental Station, UK). Genetic diversity analysis involves several steps, i.e., estimation of distance between the varieties clustering and analysis of inter-cluster distance. Therefore, more than one multivariate technique are required to represent the results more clearly and it is obvious from the results of many researchers [9-16].

Principal component analysis (PCA)

Analysis of genetic diversity in rice following multivariate techniques was used and mean data for each character were subjected to use. Principal components were computed from the correlation matrix and genotype scores obtained from first components (which has the property accounting for maximum variance) and succeeding components with latent roots greater than the unity [17] and contribution of the different morphological characters towards divergence are discussed from the latent vectors of the first two principal components. To divide the varieties of a data set into some number of mutually exclusive groups clustering was done using non-hierarchical classification. The algorithm is used to search for optimum values of chosen criterion. Starting from some initial classification of the varieties into required number of groups, the algorithm repeatedly transfers varieties from one group to another so long as such transfer improve the value of the criterion the algorithm switches to a second stage which examines the effect of swapping two varieties of different classes and so on.

Principal coordinates analysis (PCO)

Principal coordinate analysis is equivalent to PCA but it is used to calculate inter unit distances. Through the use of all dimension of P it gives the minimum distance between each pair of the N point using similarly matrix [18].

Canonical vector analysis (CVA)

Canonical vector analysis (CVA) complementary to D^2 statistic is a sort of multivariate analysis where canonical vector and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes, respectively and derived. Canonical vector analysis finds linear combination of original variability than maximize the ratio of between groups to within group's variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus in this analysis a series of orthogonal transformation sequentially maximize the ratio of among groups to within group variation.

Computation of average intra-cluster distances

The average intra cluster distance for each cluster was calculated by taking all possible D2 values within the members of a cluster obtained from PCO. The formula used to measure the average intra-cluster distance was as follows:

$$\text{Intra-cluster distance} = \sum D^2/n$$

Where,

D^2 is the sum of distances between all possible combinations (n) of the genotypes included in a cluster. The square root of the D^2 values represents the distance (D) within cluster.

Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula suggested by Singh and Chaudhury [19]:

$$\text{Inter cluster distances} = \frac{\sum D_{ij}^2}{n_i x\ n_j}$$

Where,

$\sum D_{ij}$ = the sum of distances between all possible combinations of the populations in cluster i and j

n_i = number of population in cluster i

n_j = number of population in cluster j

Cluster diagram

Using the values of intra and inter cluster distances ($D=\sqrt{D^2}$), a cluster diagram was drawn according to Singh and Chaudhury [19] that gave a brief idea of the pattern of diversity among the genotypes included in a cluster.

RESULT AND DISCUSSION

The experiment was conducted with 34 local rice genotypes with one check varieties at the Sher-e-Bangla Agricultural University experimental field to study characterization and genetic diversity of 35 local rice genotypes and to find out the association among the genetic characteristics.

The analysis of variance showed significance differences among 35 genotypes for all 13 characters studied indicating the presence of genetic variability among the genotypes. On the basis of cluster analysis, studied genotypes were grouped into five clusters (Table 2). This distribution pattern indicated that the highest number of genotypes was comprised in cluster IV (10) and the lowest were in cluster V (2).

Intra and inter cluster distances (D^2) for 35 genotypes are shown in Table 3. The highest inter-cluster distance was observed between the cluster II and V (46.71) followed by III and V (46.40) and IV and V (45.43) (Figure 1). Genotypes from these three clusters may be involved in hybridization as wide genetic variations existed among the groups. While the lowest distance was observed in between the cluster I and II (34.25) followed by I and IV (36.02), suggesting a close relationship among these clusters (Figure 1). Cluster IV

exhibited the highest intra-cluster distance (38.36), while the lowest distance was observed in cluster V (23.09).

Table 2: Distribution of 35 rice genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations	Percent	Name of genotypes
I	G-1, G-2, G-5, G-9, G-19, G-21 and G-28	7	20.00	Kathi Goccha, Hamai, Tal Mugur, Bogi, BazraMuri, MoghaiBalam and KaloMota
II	G-3, G-7, G-8, G-13, G-14, G-22, G-24, G-27 and G-30	9	25.71	KhakShail, MoinaMoti, Nona Bokhra, Hogla, JamaiNaru, Ghocca, MotaAman, Mowbinni and Jolkumri
III	G-4, G-10, G-11, G-15, G-16, G-17 and G-26	7	20.00	Hari, Patnai, Ledra Binni, Jota Balam, Khejur Chori, Ghunshai and Bhute Shelot
IV	G-6, G-20, G-23, G-25, G-29, G-31, G-32, G-33, G-34 and G-35	10	28.57	Dakh Shail, Nona Kochi, Mondeshor, Golapi, Ponkhiraj, Lalbiroi-31, Karengal, Sada Gotal, Holde Gotal and BRRI Dhan-33
V	G-12 and G-18	2	5.71	Lalanamia and Malagoti

Table 3: Intra (Bold) and inter cluster distances (D^2) for 35 genotypes

Cluster	I	II	III	IV	V
I	1067.58 **(32.67)**	1172.86 (34.25)	1569.92 (39.62)	1297.77 (36.02)	1683.22 (41.03)
II		1063.08 **(32.60)**	1320.19 (36.33)	1360.99 (36.89)	2182.20 (46.71)
III			1206.87 **(34.74)**	1664.34 (40.80)	2153.41 (46.40)
IV				1471.19 **(38.36)**	2063.57 (45.43)
V					533.10 **(23.09)**

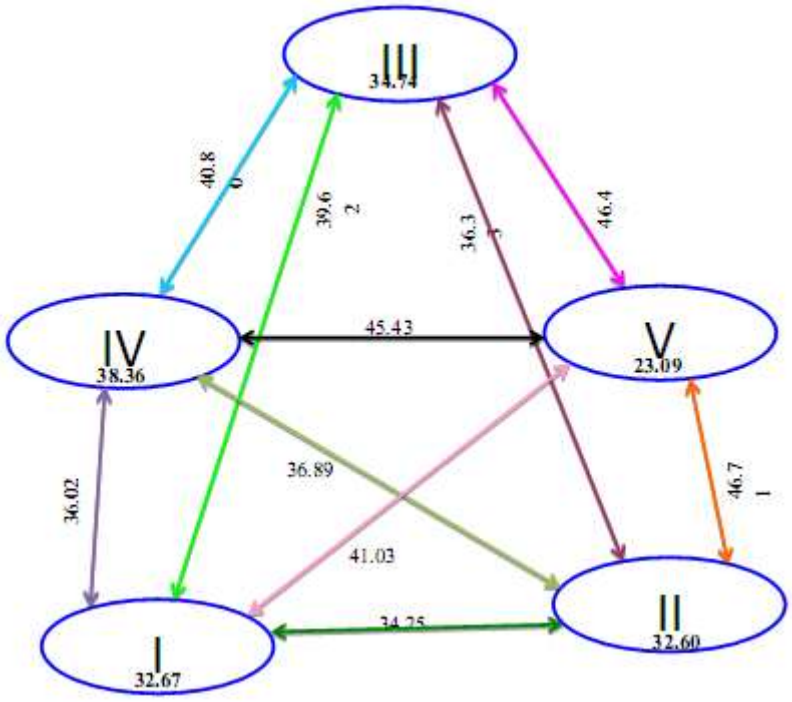

Fig-1: Diagram showing intra and inter-cluster distances of 35 genotypes of rice

Table 4: The nearest and farthest clusters from each cluster between D^2 values

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	I	II (34.25)	V (41.03)
2	II	I (34.25)	V (46.71)
3	III	II (36.33)	V (46.40)
4	IV	I (36.02)	V (45.43)
5	V	I (41.03)	II (46.71)

In the Table 10 Cluster I consisted of nearest cluster with D^2 values cluster II (34.25) and farthest cluster with D^2 values cluster V (41.03). Cluster II consisted of nearest cluster with D^2 values cluster I (34.25) and farthest cluster with D^2 values V (46.71). Cluster III consisted of nearest cluster with D^2 values cluster II (36.33) and farthest cluster with D^2 values V (46.40). Cluster IV consisted of nearest cluster with D^2 values cluster I (36.02) and farthest cluster with D^2 values V (45.43). Cluster V consisted of nearest cluster with D^2 values cluster I (41.03) and farthest cluster with D^2 values II (46.71).

The cluster mean for 13 characters of 35 genotypes of rice are presented in Table 5. The result revealed that cluster the highest intra cluster means for yield were obtained from cluster III and other most important reproductive characters were obtained from cluster I. Therefore, more emphasis should be given on this cluster for selecting genotypes as a variety and as well as parents in crossing with other genotypes.

Table 5: Cluster mean values of 13 different characters of 35 rice genotypes

Characters	I	II	III	IV	V	Max	Min
PH	157.94	164.50	163.05	163.88	143.88	164.50	143.88
NET	7.28	4.22	5.95	3.33	6.16	7.28	3.33
LP	27.46	29.61	29.92	29.37	25.68	29.92	25.68
DF	108.28	110.44	109.85	107.90	101.50	110.44	101.50
NPBP	9.61	10.70	11.57	10.93	10.50	11.57	9.61
NSBP	24.28	24.48	33.57	25.56	36.33	36.33	24.28
NFGP	116.23	110.63	127.00	130.43	105.00	130.43	105.00
NUFGP	25.85	32.44	37.09	29.43	35.67	37.09	25.85
1000GW	22.36	21.69	23.75	23.74	23.08	23.75	21.69
RL	9.38	8.96	11.23	10.49	7.33	11.23	7.33
NRH	1290.76	1044.70	1361.28	973.89	1248.67	1361.28	973.89
RW	65.99	54.33	57.80	54.23	49.33	65.99	49.33
GYH	22.25	26.47	26.90	21.20	15.15	26.90	15.15

PH = Plant height (cm) , NET = Number of effective tiller, LP = Length of panicle, DF = Days to flowering, NPBP = Number of primary branches per panicle, NSBP = Number of secondary branches per panicle, NFGP = Number of filled grain per panicle, NUFGP = Number of unfilled grain per panicle, 1000 GW = 1000 grain weight , RL = Root length , NRH = Number of root hair, RW = Root weight, GYH = Grain yield per hill (g).

Table 6: Latent vectors for 13 characters of 35 rice genotypes

Characters	Vector 1/PCA1	Vector 2/PCA2
Plant height	0.046	0.374
Number of effective tiller	0.134	-0.011
Length of panicle	0.068	0.309
Days to flowering	0.464	-0.190
Number of primary branches per panicle	0.240	-0.374
Number of secondary branches per panicle	0.447	0.060
Number of filled grain per panicle	-0.069	0.417
Number of unfilled grain per panicle	-0.116	0.337
1000 grain weight	0.118	-0.412
Root length	-0.072	0.058
Number of root hair	0.489	0.254
Root weight	-0.060	0.049
Grain yield per hill (g)	0.472	0.240

Contribution of the characters towards divergence is presented in Table 6. The PCA (Principal Component Analysis) revealed that in vector I; most of the characters were positive divergence except for number of filled grain per panicle, number of unfilled grain per panicle, root length and root weight. Similarly, in vector II most of the characters showed positive divergence except for number of effective

tiller, days to flowering, number of primary branches per panicle and 1000 grain weight. Such result indicates that most of the characters contributed maximum towards divergence. It is interesting that greater divergence in the present material due to these characters will offer a good scope for improvement of yield through rational selection of parents. A two-dimensional scattered diagram constructed using principal component I on X-axis and component II on Y-axis, reflecting the relative position of the genotypes (Figure 2).

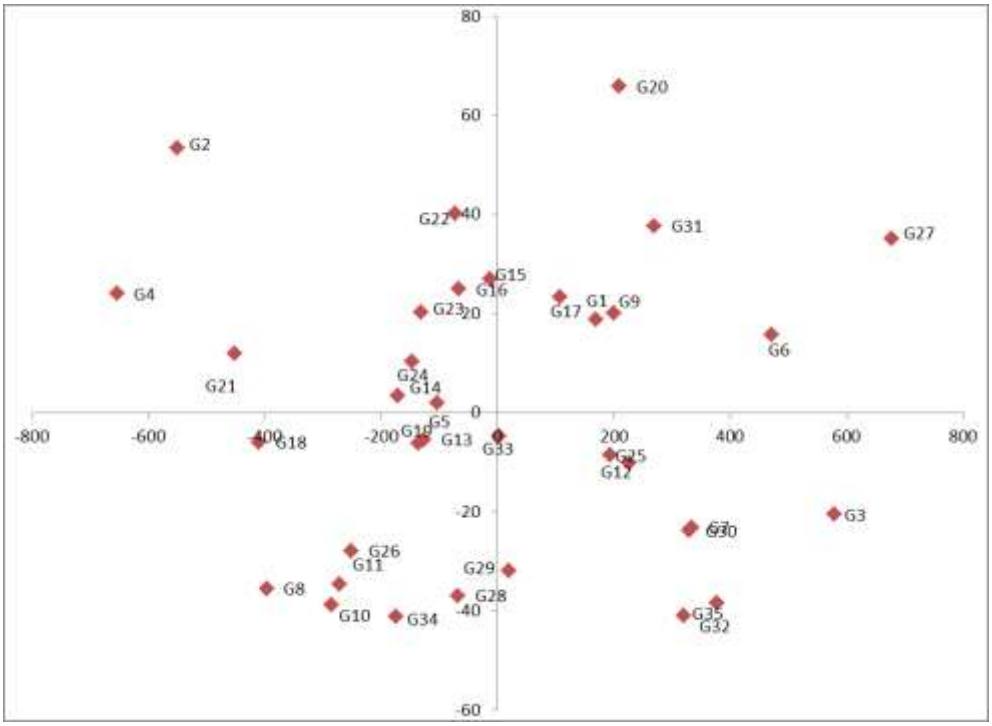

Fig-2: Scattered diagram of 35 rice genotypes based on their principal component scores

CONCLUSION

Thirteen genetic characteristics of 34 local rice genotypes with one check varieties were evaluated to study the genetic divergence through multivariate analysis. Genotypes were grouped into five different clusters considering diversity pattern and other agronomic performance lines G-10, G-13, G-15, G-18 and G-24 could be considered suitable parents for efficient hybridization in future. Further study of this experiment is needed in different locations of Bangladesh for accuracy of the results obtained from the present experiment.

REFERENCES

1. Brar, D. S., & Khush, G. S. (2003). Utilization of wild species of genus Oryzae in rice improvement. In: J. S. Nanda, S. D. Sharma (eds.), *Monograph on Genus Oryzae*, 283-309.
2. Poehlman, J. M., & Sleper, D. A. (1995). Breeding Field Crops. Panima Publishing Corporation, New Delhi, India, 278.
3. Anonymous. (2011). Food and Agricultural Organization of the United Nations. Production: FAOSTAT. Available: http://faostat.fao.org/site/567/defaults.aspx#ancor
4. Virmani, S. S. (1996). Hybrid Rice. *Adv. Agron., 57*, 379.
5. Alim, A. (1982). Bangladesh Rice, 35-39.
6. BBS (Bangladesh Bureau of Statistics). (2009). Monthly Statistical Bulletin August, 2009. Bangladesh Bur. Stat. Div. Min. Planning, Dhaka. *Bangladesh, 54.*
7. Belaj, A., Satovic, Z., Rallo, L., & Trujillo, I. (2002). Genetic diversity and relationship in olive germplasm collection as determined by RAPD., *Theor. Appl. Genet., 105*(4), 638-644.
8. Roy, A., & Panwar, D. V. S. (1993). Genetic divergence in rice. *Oryza, 30*, 197-201.
9. Bashar, M. K. (2002). Genetic and Morpho-physiological basis of heterosis in rice. Ph. D Thesis. Department of Genetics and Plant Breeding. BSMRAU, Gazipur, 20-23.
10. Uddin, M. J. (2001). Morphogenetic diversity and gene action in sesame (*Sesammum indicum* L.) Ph. D Thesis. Department of Genetics and Plant Breeding. BSMRAU, Gazipur, 59.
11. Juned, S. A., Jackson, M. T., & Catty, J. P. (1988). Diversity in the wild potato species (S. chacoenseBtt.) *Euphytica, 37*(2), 149-156.
12. Ariyo, O. J. (1987). Multivariate analysis and choice of parents for hybridization in Okra. *Thero. Appl. Genet., 74*, 361-363.
13. Patil, F. B., Thombre, M. B., & Sindde, W. M. (1987). Genetic divergence in onion. *J. Maharastra Agril. Univ., 12*(2), 252-253.

14. Dani, R. G., & Murthy, B. R. (1985). Genetic variability, correlation and path analysis of yield components of rice. *Madras Agric. J.*, *81*(9), 468-470.
15. Anand, I. J., & Rawat, D. S. (1984). Genetic diversity, combining ability and heterosis in brown mustard. *Indian J. Genet*., *44*(2), 226-234.
16. Balasch, S., Nuez, F., Palomares, G., & Cuartero, J. (1984). Multivariate analysis applied to tomato Hybrid production. *Thero. Appl. Genet.*, *69*, 39-45.
17. Jeger, M. I., Garethojones, D., & Griffith, E. (1983). Component of partial resistance of wheat seedlings to Septorianodorum. *Euphytica*, *32*, 575-584.
18. Digby, P., Galway, N., & Lane, P. (1989). GENSTATS, A second course, Oxford science publications, Oxford, 103-108.
19. Singh, R. K., & Chaudhary, B. D. (1985). Biometrical methods of quantitative genetic analysis. *Haryana J. Hort. Sci.*, *12*(2), 151-156.
20. Hooker, J. D. (1979). The Flora of British India. Vol. 2L.Reeve. Co. Kent, England, 25.