Assessment of genetic diversity studies using D^2 statistics in brinjal of North Bengal

Abstract

Aim: Assessment of genetic diversity studies using D^2 statistics in Brinjal of North Bengal

Study design: Diversity D^2 analysis

Methodology: The present study was undertaken to study the genetic divergence of the 32 brinjal genotypes collected from different locations of North Bengal region. Through diversity D^2 analysis whole genotypes were categorized under seven groups with no evidence for geographical diversity as necessarily cause of genetic diversity.

Results and Conclusion: However, highest genetic diversity was recorded in cluster I and V argued for their utilization to develop transgressive segregate lines. Genotypes under cluster VI and VII found to be effective for the improvement of yield related attributes. The cross combinations between cluster VI and V, cluster VI and II, cluster VI and VI, cluster VI and I, cluster VI and III, cluster VI and cluster VII could be effectively utilized to develop improved heterotic population or recombinant.

Keywords: Brinjal, Genotypes, Genetic divergence

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1. INTRODUCTION:

Brinjal (*Solanum melongena* L.) also known as Eggplant in United States, Aubergine in France and England belongs to Solanaceae family is a kind of principle vegetable which has been cultivated worldwide (Barik *et al.* 2020). It is highly consumed vegetable of South East Asia grown throughout the year (Anbarasi and Haripriya, 2021). It is considered as poor man's crop (Praneetha 2018; Nayak *et al.* 2020) originated and cultivated in India from long back. In India, it is popularly known as baigan, bhanta, badankai, vangi, etc (Ansari and Singh, 2014). It is grown extensively in India, Bangladesh, Pakistan, China, Japan and Philippines. In India major producing states are Orissa, Bihar, Karnataka, West Bengal,

Andhra Pradesh, Maharashtra and Uttar Pradesh (Sahana *et al.* 2020). According to the national horticultural board data brinjal cultivated in 736000 ha and produced 12777 MT in 2019-20. Brinjal has also got high demand for its high nutritional and medicinal values like decholestrolizing property primarily due to presence lenoleic and lenolenic fatty acids which are present abundant in flesh and seeds (Hanchinmani and Imamsaheb, 2015) and minerals like Ca, Mg, P and fatty acids are present in the fruits. It has medicinal use like curing diabetics, asthma, cholera, bronchitis, diarrhea and liver complaints (Santhosha *et al.* 2017). Brinjal is a good source protein, dietary fiber, and minerals like potassium, manganese, magnesium, and copper. It also contains good quantities of vitamin B1 (thiamine), vitamin B3 complex (niacin), vitamin B6 (pyridoxine), folate. Phytonutrients composition of brinjal has good quantities of nasunin and chlorogenic acid and phytonutrients have a power to neutralize the levels of free radicals and other toxins attributed to their antioxidant property. Brinjal is devoid of cholesterol and it has been used in treatments of hypercholesterolemia and nasunin is good antioxidant and scavenger of free radical it protects cell membranes damage. It is helpful in preserving fats and other lipids inside the brain cell membranes from getting oxidized. Antimicrobial, antimutagenic, anti-viral and anti-LDL properties of chlorogenic acid are highly helpful. In brinjal oblong fruited variety have high Total Soluble Solids (TSS), long fruited cultivars have high content of free reducing sugars, anthocyanin, phenols, glycoalkaloids (such as solasodine), dry matter, and amide proteins. Brinjal is used in the improvement of cardiovascular and liver health (Patel *et al.* 2013).

Evaluation of brinjal genotypes helps in recommending particular genotype in terms of yield, quality and resistance to major pest and diseases. And it also helps in developing in variety with high yield, colour, size, shape, weight, quality parameters and resistance to major pest and diseases. A large indigenous biodiversity exists in eggplant with variation in plant type, stem color, leaf size, leaf tip, midrib color, fruit size, fruit shape, fruit color, fruit yield, fruit quality, cooking quality, and tolerance to pests and diseases (Ullah *et al.* 2014). India is being primary centre of origin shows greater extent of variability and there will be high chances of effective selection for desirable types in the population with more variability

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(Vavilov, 1951). The varietal acceptance of brinjal is region specific. For the improvement of heritability the existence of variability in a particular trait is an important one. The qualification of genetic diversity has made it possible to choose genetically diverse parents for a successful hybridization program. Knowledge on genetic diversity, its nature and degree is useful for selecting desirable parents from a germplasm for the successful breeding programme. So, based on this the present experiment was conducted to obtain information on genetic diversity among 32 genotypes of brinjal based on qualitative and quantitative characters respectively in the region of North Bengal, West Bengal, India.

2. MATERIALS AND METHODS:

The experiment was carried out at Experimental Farm of Uttar Banga Krishi Viswavidyalaya, Pundibari, West Bengal, India during *Rabi* seasons of 2016-17 and 2017-18. The farm is situated at 26 ^{0}19'86" N latitude and 89^{0} 23'53" E longitude, at an elevation of 43 meter above mean sea level. The details of the collected experimental material in North Bengal region and their sources have been presented in Table 1. Mahalanobis (1936) D^2 statistics was used for assessing the genetic divergence between brinjal genotypes. The original correlated unstandardised character mean values were transformed into standardised uncorrelated values to simplify the computational procedure. The D^2 values were obtained as the sum of squares of the differences between the pairs of corresponding uncorrelated (Ys) values of any two genotypes. Using all D^2 values, the genotypes were grouped into clusters using Tocher's method as described by Rao (1952). The intra- and inter-cluster distances were calculated by the formula given by Singh and Chaudhary (1985). The character contribution towards genetic divergence was computed using the method given by Singh and Chaudhary (1977).

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Figure 1: Filed preparation, view, data collection and lab analysis during research work

3. RESULTS AND DISCUSSION:

3.1 Genetic divergence

Multivariate analysis serves as a useful tool to quantify the degree of divergence between the biological populations at genotypic level and to assess the relative contribution of different components to the total divergence both at intra and inter and cluster levels. D^2 technique of Mahalanobis based on multivariate analysis serves to be a good index for estimating genetic diversity (Gadekar*et al.,* 1992). Therefore, Genetic divergence among 32 genotypes of brinjal was assessed by adopting Mahalanobis D^2 statistic based on 15 characters.

3.2 Grouping of genotypes into different clusters

Result obtained from D^2 analysis presented in the table.2 showed that all the 32 genotypes under study were broadly categorized into seven different clusters. Among the entire, cluster I showed to be consisting of maximum number of genotypes viz., UBB 1, UBB 2, UBB 3, UBB 4, UBB 5, UBB 6, UBB 7, UBB 8, UBB 9, UBB 10, UBB 11, UBB 12,

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Table.1. Different collected brinjal germplasm and their sources

Sl. No.	Genotypes	code	Location of Collection	Sl. No.	Genotypes	Code	Location of Collection
1	Long and thick brinjal	UBB 1	Pundibari, WB	17	Black Beauty	UBB 17	Nadia, WB
2	KabraGol	UBB 2	Malda, WB	18	Kokila	UBB 18	Alipurduar, WB
3	Phasidewa local 2	UBB 3	Pundibari, WB	19	Pusa Purple Long	UBB 19	IARI, New Delhi
4	AshpuriGhia Brinjal	UBB 4	Malda, WB	20	Ram Begun	UBB20	Malda, WB
5	Long Brinjal	UBB 5	Pundibari,WB	21	Nababganj	UBB 21	North 24 Pargana, WB
6	Chanda Tara Brinjal	UBB 6	Malda, WB	22	Pundibari 2	UBB 22	Pundibari, WB
7	Long Golden Brinjal	UBB 7	Dinhata, WB	23	Jhuri Begun	UBB 23	Pundibari, WB
8	Mukhta Brinjal Green	UBB 8	Malda, WB	24	Thick Brinjal	UBB 24	Pundibari, WB
9	AspuriChanga Brinjal	UBB 9	Malda, WB	25	Tufanganj 1	UBB 25	Tufanganj, WB
10	Panjipara Local	UBB 10	Khoribari, WB	26	Special Mukra	UBB 26	Nadia, WB
11	Phasidewa local 1	UBB 11	Malda, WB	27	Shitali	UBB 27	Jateswar, WB
12	Muktakeshi	UBB 12	Nadia, WB	28	White Brinjal	UBB 28	Pudibari, WB
13	Jhosna Brinjal	UBB 13	Malda, WB	29	Swarna Mani	UBB 29	Vegetable science, UBKV, WB
14	Long Black	UBB 14	Pundibari, WB	30	PusaKranthi	UBB 30	Vegetable science, UBKV, WB

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15	HajipurBhasta Brinjal	UBB 15	Malda, WB	31	Punjab Sadabahar	UBB 31	Vegetable science, UBKV, WB
16	DebjhuriHajari	UBB 16	Malda, WB	32	KasiTaru	UBB 32	Vegetable science, UBKV, WB

UBKV: Uttar Banga Krishi Viswavidyalaya: WB: West Bengal; IARI- Indian Agricultural Research Institute.

Table.2. Clustering pattern of 32 genotypes of Brinjal

Sl. No.	Cluster number	Total number of genotypes	Name of genotypes
1	I	22	UBB 1, UBB 2, UBB 3, UBB 4, UBB 5, UBB 6, UBB 7, UBB 8, UBB 9, UBB 10, UBB 11, UBB 12, UBB 13, UBB 14, UBB 15, UBB 16, UBB 17, UBB 18, UBB 19, UBB 20, UBB 29, UBB 30
2	II	2	UBB 23, UBB 28
3	III	2	UBB 22, UBB 25
4	IV	2	UBB 27, UBB 32
5	V	2	UBB 24, UBB 31
6	VI	1	UBB 21
7	VII	1	UBB 26

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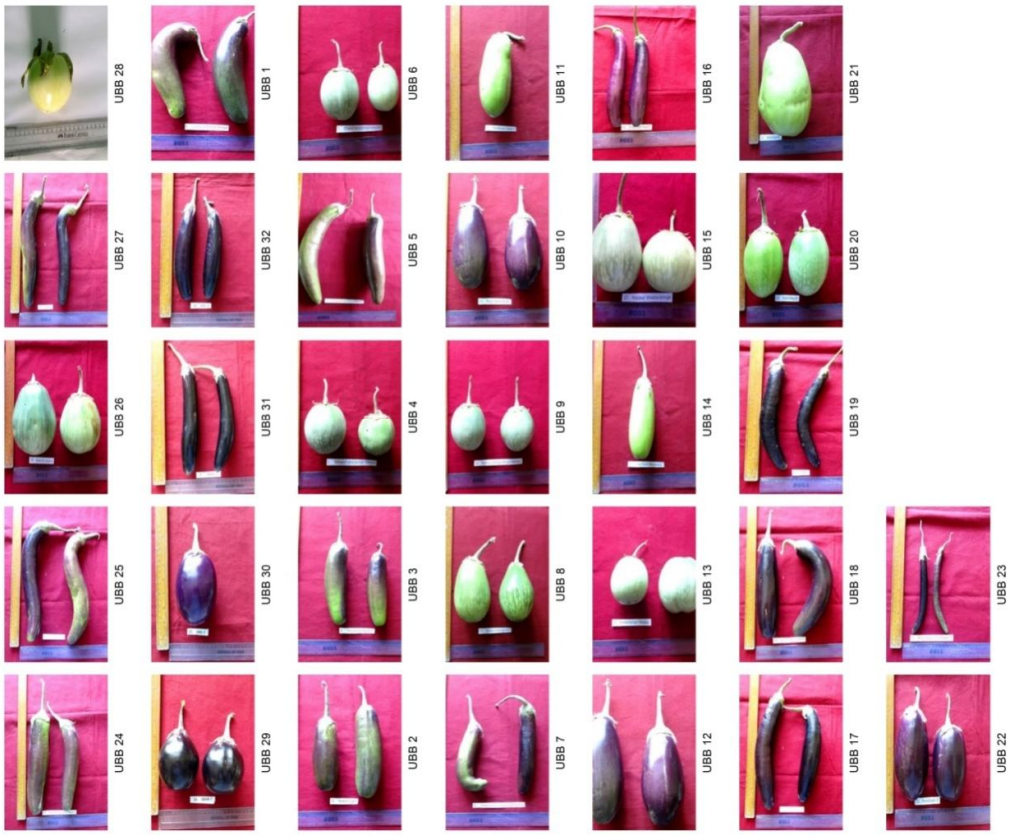

Figure 2: Fruit of different types of brinjal varieties

UBB 13, UBB 14, UBB 15, UBB 16, UBB 17, UBB 18, UBB 19, UBB 20, UBB 29, UBB 30. Other than this, total four number clusters i.e., cluster II, cluster III, cluster IV and cluster V were consisting of two genotypes in each. Rest two clusters, cluster VI and cluster VII were comprised of single genotype in each.

After evaluating the source of collection of genotypes and the pattern of cluster distribution indicated that, the geographical diversity need not necessarily be related to the genetic diversity. Among the genotypes from one geographical area, parallelism was not noticed between geographical diversity and genetic diversity. Similar finding was earlier reported by the Vanaja *et al.* (2003), Arunkumar and Biradar (2004), Sreelathakumary and Rajmony (2004) and Senapathi *et al.* (2005).

3.3 Mean intra and inter cluster distance

Mean intra and inter cluster distances were presented in table 3. It was observed that average inter cluster distance was higher than the average intra cluster distance indicated

wide genetic diversity among the genotypes of different groups than those of same cluster. Similar results were reported by Mahesha*et al*. 2006, Kumar *et al.* (2007), Dutta*et al.* (2009), Sekhar*et al.* (2008) and Islam *et al.* (2011) in brinjal. The intra cluster D^2 values ranged from 0.000-1932.26. Highest intra cluster distance was recorded for cluster I (1932.26) followed by cluster V (1033.35), cluster IV (734.35), cluster III (728.95), cluster IV (734.35) and cluster II (516.00). Whereas, there was no intra cluster distance observed for cluster VI and cluster VII.

In the present study, inter cluster distance found to be maximum for combination between cluster VI and cluster V (9459.58) followed by cluster VI and II (8576.57), cluster VI and cluster VI (8513.05), cluster VI and cluster I (7474.44), cluster VI and cluster III (7027.58) and cluster VI and cluster VII (5953.15). However, minimum inter cluster distance was recorded for combination between cluster IV and cluster II (636.51) followed by cluster VII and cluster III (1172.78), cluster V and cluster II (1205.75) and cluster V and cluster IV (1227.81).

However, the reason of no intra distance in the cluster VI and cluster VII in the present investigation was that both the clusters were comprises of single genotype in each case. Highest cluster distance of cluster I and cluster V indicated existence of genetic divergence among these genotypes in these each cluster and thereby could be used for improvement of yield through recombination breeding and also could be used to develop transgressive segregating lines or heterotic population due existence of high level heterogeneity (Mehta and Asati, 2008). The lowest magnitude of inter cluster distance was recorded for the combination between cluster IV and II followed by cluster VII and III indicated that there were no significant genetic diversity among the genotypes of these clusters and could not be possible to utilize in cross breeding improvement programme among them.

Again, the combinations of cluster VI and V followed by cluster VI and II, cluster VI and VI, cluster VI and I, cluster VI and III, cluster VI and cluster VII these showed greater extent of inter cluster distance which indicated on inter-cross hybridization among the genotypes under each cluster combinations might result in a wide spectrum of segregating population

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as genetic diversity is very distinct among the groups and there by predicted the Possibility of using these genotypes under each cluster to develop improved heterotic population or recombinant

3.1.3 Cluster mean of individual characters and their contribution towards diversity

The mean performance of 32 genotypes from 7 different clusters for 15 characters under study was presented in table.4. Cluster VI registered highest mean for plant height (115.94 cm) followed by cluster VII (107.65 cm) while lowest mean was noticed in cluster II (69.40 cm). Highest mean for number of primary branches was recorded in cluster III (7.21) followed by cluster VII (7.15) and lowest mean was found in cluster V (4.68). Highest mean

Figure 3: Different types of brinjal genotypes collection

Table.3. Inter and Intra cluster (Diagonal) distance of Brinjal

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	**1932.26**	1872.88	1447.69	1822.12	2547.82	7474.44	1953.74
Cluster II		**516.00**	1674.34	636.51	1205.75	8576.57	2670.44
Cluster III			**728.95**	1590.35	2532.40	7027.58	1172.78
Cluster IV				**734.35**	1227.81	8513.05	2596.60
Cluster V					**1033.35**	9459.58	3562.85
Cluster VI						**0.00**	5953.15
Cluster VII							**0.00**

N.B: Bold values indicate inter cluster distance

Table.4. Cluster mean of individual characters and their percent of contribution

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Number of first rank	% contribution
PH	99.90	69.40	99.22	104.75	85.42	115.94	107.65	22	4.44
PB	5.27	5.71	7.21	6.75	4.68	6.29	7.15	1	0.20
CL	3.95	4.14	4.41	5.35	4.49	3.99	4.12	18	3.63
DFF	63.67	72.18	64.61	69.15	63.82	70.86	70.35	0	0.00
DFM	38.58	41.03	41.74	38.80	43.81	48.10	37.36	0	0.00

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FS	98.04	103.08	101.89	102.36	102.19	101.14	95.15	1	0.20
FD	7.95	4.76	7.14	8.88	8.39	13.22	10.73	42	8.47
FL	18.86	13.62	22.25	25.02	22.19	17.93	12.53	1	0.20
FW	311.40	80.73	307.38	177.55	161.32	899.27	428.32	104	20.97
FPP	11.35	34.96	6.53	14.78	15.57	2.30	4.34	143	28.83
VC	9.26	11.69	9.79	9.40	9.35	9.74	8.43	6	1.21
TSS	5.60	5.89	5.39	5.60	5.54	5.74	5.35	6	1.21
PHOL	71.22	54.68	113.70	111.84	120.05	14.05	13.50	3	0.60
ANTH	1.16	1.43	1.15	1.32	1.21	1.43	1.02	0	0.00
YP	42.18	33.76	33.17	46.10	35.07	32.42	42.25	149	30.04

PH: Plant height (cm); PB: Number of primary branches; CL: Calyx length (cm); DFF: Days to first flower; DFM: Days to fruit maturity; FS: Fruiting span: FD: Fruit diameter (cm); FL: Fruit length (cm); FW: Fruit weight (g); FPP: Number of fruit per plant; VC: Ascorbic acid (mg/100g); TSS: TSS (°B); PHOL: Phenol (mg/100g); ANTH: Anthocyanin (mg/100g); YP: Yield per ha (t/ha).

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For calyx length was recorded in cluster IV (5.35cm) followed by cluster V (4.49cm) and lowest mean was found in cluster I (3.95cm). Cluster I recorded lowest mean for days to first flowering (63.67 days) followed by cluster V (63.82 days) whereas highest mean was observed in cluster II (72.18 days). Cluster VII showed minimum mean for days to fruit maturity (37.36 days) followed by cluster I (38.58 days) while maximum mean was noticed in cluster VI (48.10 days) followed by cluster V (43.81 days). Highest mean for fruiting span was noticed in cluster II (103.08 days) followed by cluster IV (102.36 days) and lowest mean was observed in cluster VII (95.15 days) followed by cluster I (98.04 days). Cluster VI recorded maximum mean for fruit diameter (13.22 cm) followed by cluster VII (10.73 cm) and minimum mean was recorded in cluster II (4.76 cm) followed by cluster III (7.14 cm). Mean for fruit length was highest in cluster IV (25.02 cm) followed by cluster III (22.25 cm) and lowest in cluster VII (12.53 cm) followed by cluster II (13.62 cm). Cluster VI recorded maximum mean for fruit weight (899.27 g) followed by cluster VII (428.32 g) and minimum mean was recorded in cluster II (80.73 g) followed by cluster V (161.32 cm). Cluster II has shown highest mean for number of fruits per plant (34.96) followed by cluster V (15.57) while lowest mean was observed in cluster VI (2.30) followed by cluster VII (4.34). Highest mean for ascorbic acid was recorded in genotypes of cluster II (11.69 mg/100g) followed by cluster III (9.79 mg/100g) while lowest mean was shown by cluster VII (8.43 mg/100g) followed by cluster I (9.26 mg/100g). Cluster II showed highest mean for total soluble solid (5.89 °B) followed by cluster VI (5.74 °B) while lowest mean was recorded in cluster VII (5.35 °B). Highest mean for Anthocyanin (IU) was recorded in genotypes of cluster V (120.05 IU) followed by cluster III (113.70 mg/100g) while lowest mean was shown by cluster VII (13.50 mg/100g) followed by cluster VI (14.05 mg/100g). Highest mean for Phenol (mg/100g) was recorded in genotypes of cluster II & VI (1.43 mg/100g) followed by cluster IV (1.32 mg/100g) while lowest mean was shown by cluster VII (1.02 mg/100g) followed by cluster III (1.15 mg/100g). Highest mean for Yield/ha (t/ha) was recorded in genotypes of cluster IV (46.10 t/ha) followed by cluster VII (42.25 t/ha) while lowest mean was shown by cluster VI (32.42 t/ha) followed by cluster III (33.17 t/ha).

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Contributions of the characters towards total diversity of the genotypes were represented in the table.4. It indicate that characters viz., total yield per hectare (30.04 %), number of fruit per plant (28.83) and fruit weight (20.97%) were principal contributing characters towards total divergence. However, comparatively moderate contribution was recorded for fruit diameter (8.47%), plant height (4.44%) and calyx length (3.63%). Other than these, low contributions were recorded for ascorbic acid (1.21%), total soluble solid (1.21%), anthocyanin (0.60%), fruit length (0.20%) and number of primary branch (0.20%). Whereas, for rest of the characters viz., phenol content, days to first flowers and days to fruit maturity did not showed any contribution towards the total diversity. Similar results were reported by Manju and Sreelathakumary (2002) and Senapati*et al.* (2003) in chilli and Sharma and Maurya (2004), Kumar *et al.* (2007), Dutta*et al.* (2009), Das *et al.* (2010) and Islam *et al.* (2011) in brinjal.

However, on the basis of mean of cluster performance cluster VI and VII were important for plant height, fruit diameter, primary branches, fruit weight, total soluble solid and total yield. Whereas, for the for the quality traits viz., anthocyanin, phenol and ascorbic acid as well as calyx length, number of fruit plant cluster II and cluster III could be consider as important. So, selection of the genotype from these cluster as crossing breeding parent could emerged most effective. In the other hand, total yield per hectare, number of fruit per plant and fruit weight showed maximum contribution towards the diversity followed by fruit diameter, plant height and calyx length. Result indicated that diverse genotypes can be utilized for improvement of yield productivity. The greater diversity in the present materials was due to these characters which will offer a good scope for improvement of yield through rational selection of parent's genotypes for brinjal. The genotypes of highly divergent clusters may also be utilized in a breeding programme for development of high yielding varieties with desirable attribute and can also be utilized in heterosis breeding programme for development of F_1 hybrids with superior yield and quality characters.

4. CONCLUSION:

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It emerged conclusively from the present investigation on evaluation of brinjal germplasm for winter season that all the 32 genotypes collected from different locality of north Bengal were highly diversified and manifestation was less effected by the environment. Selection of the characters under study, specifically number of fruit per plant, fruit weight, fruit diameter, calyx length and plant height will likely to be effective in increasing fruit yield per plant due to having effect of more additive gene action and will be effective in developing heterotic population due to having more diversity. Genotypes under cluster VI and VII will be most effective for the improvement of yield related attributes. The cross combinations between cluster VI and V, cluster VI and II, cluster VI and VI, cluster VI and I, cluster VI and III, cluster VI and cluster VII can be effectively utilized to develop improved heterotic population or recombinant.

5. REFERENCES

Anbarasi D, Haripriya K. Genetic divergence in brinjal genotypes for growth and yield parameters. *Electron. J. Plant Breed*, 2021;*12*(4):1408-1412.

Ansari AM, Singh YV. Molecular diversity of brinjal (*Solanum melongena* L. and *S. aethiopicum* L.) genotypes revealed by SSR markers. *Electron. J. Plant Breed*. 2014;*5*(4):722-728.

Arunkumar B, Biradar BD. Genetic divergence studies in Rabi sorghrum. *Karnataka J. Agric. Sci.* 2004;**17**:571-573.

Barik S, Dash L, Das MP, Panigrahi T, Naresh P, Kumari M, Sahu GS, Acharya GC. Screening of brinjal (*Solanum melongena* L.) genotypes for resistance to spotted beetle, *Henosepilachna vigintioctopunctata* (Coccinellidae: Coleoptera). *J. Entomol. Zool. Stud.* 2020;**8**:297-301.

Das S, Mandal AB, Hazra P. Genetic diversity in brinjal genotypes under eastern Indian conditions. *Indian J. Hortic.* 2010;**67**:165-169.

Dutta R, Mandal AK, Maity TK, Hazra P. Multivariate genetic divergence in brinjal (*Solanum melongena* L.). *J. crop weed.*2009;**5**(1):67-70.

UNDER PEER REVIEW

Gadekar DA, Dhonukshe BL, Patil FB. Genetic divergence in tomato. *Veg. Sci.* 1992;**19**(1): 30-35.

Gadekar PT, Mukkolath AV, Tiwari KK. Recovery of nitrophenols from aqueous solutions by a liquid emulsion membrane system. *Sep. Sci. Technol.* 1992;27(4):427-445.

Islam MA, Nasrin AI, Mian MAK, Shahadat MK, Shahjahan M. Genetic diversity in exotic eggplant (*Solanum melongena* L.). *Libyan Agric. Res. Cent. J. Int*. (2011);**2**(1):15-19.

Kumar S, Singh AK, Sharma JP, Sharma N. Genotype clustering in brinjal (*Solanum melongena* L.) using D^2 statistic. *Haryana J. Hort. Sci.* 2007;**68**(3):95-96.

Manju PR and Sreelathakumary I. Genetic variability, heritability and genetic advance in hot chilli (*Capsicum chinense*). *J. Trop. Agric*. 2002;**40**: 4-6.

Nayak N, Pradhan SS, Mishra S. Evaluation of brinjal (*Solanum melangona* L.) landraces of Odisha for fruit yield and its components. *J. Crop Weed*. 2020;**16**(1):151-4.

Praneetha KJDS. Evaluation of brinjal (*Solanum melongena* L.) local types for yield and its quality characters. *Int. J. Conserv. Sci.* 2018;6(3):292-297.

Rao CR. Advanced statistical methods in biometrical research. *John Wiley and Sons Inc.,* New York. 1952;383.

Sahana KP, Kattegoudar J, Lingaiah HB, Sangeetha CG, Prashanth SJ, Padmanabha K, Ugalat J. Performance of advanced breeding lines of green long brinjal for resistance to bacterial wilt disease resistance, yield and quality attributes. *J. pharmacogn. phytochem.* 2020;**9**(2):155-157.

Senapati BK, Sarkar G. Genetic divergence in tall indica rice (*Oryaza sativa* L.) under rainfed saline soil of sundarban. *Oryza.* 2005;**42**(1): 70-72.

Sharma A, Maurya IB. Genetic divergence in brinjal (*Solanum melongena* L.). *Orissa J. Hortic*. 2004;**32**(2):22-25.

Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. 1977.

Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis, Kalyani Publishers, New Delhi. 1985;pp. 229-252.

UNDER PEER REVIEW

Sreelathakumary I, Rajmony L. Genetic divergence in chilli (*Capsicum annuum* L.). *Indian J. Hortic.* 2004;61(2):137-139.

Ullah S, Ijaz U, Shah TI, Najeebullah M, Niaz S. Association and genetic assessment in brinjal. *European J. Biotechnol. Biosci.* 2014;2(5):41-45.

Vanaja T, Babu LC, Radhakrishnan VV, Unninthan VKG. Genetic divergence in high yielding rice genotypes. *Oryza*. 2003;40(1&2): 40-42.

Vavilov NI. Origin, variation, immunity and breeding of cultivated plants. *Chronol. Bot*. 1951;**13**:4-364.

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