



Genetic divergence study on growth, yield and quality traits in pink brinjal (*Solanum melongena* L.) in the subtropical plains of Jammu, India

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Abstract: In 2022, field investigation was conducted to examine the genetic diversity among 30 pink brinjal (eggplant, *Solanum melongena* L.) genotypes originating from India. Mahalanobis D^2 analysis was performed to analyze the data for eighteen growth, yield and quality characters. Among the traits examined, the total fruit yield per plant made the most significant contribution towards diversity. Thirty genotypes were meaningfully grouped into eight clusters. Cluster I, the largest, had eight genotypes, followed by Cluster II and Cluster IV. There was no direct correlation observed between the geographical distribution and genetic divergence. Among all clusters formed, Cluster VII exhibited maximum intra-cluster distance followed by Cluster VI. Observing the inter-cluster distances, the maximum divergence was noted between Cluster III and Cluster IV suggesting that genotypes within these clusters could serve as valuable parents for hybridization programmes aimed at producing highly heterotic hybrids and identifying transgressive segregants in the F_2 generation.

Keywords: Hybridization, Genetic diversity, intracluster distance, eggplant, *Solanum melongena* L, D^2 analysis

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Introduction

Brinjal or eggplant, scientifically known as *Solanum melongena* L., with a chromosome number of $2n=2x=24$, is a significant vegetable plant within the Solanaceae family. In India, the second largest producer worldwide (FAO, 2021), brinjal is mostly cultivated in West Bengal, Odisha, Gujarat, Bihar and Madhya Pradesh. Although it is a perennial by nature, it is predominantly grown and harvested as an annual crop for its young, unripe fruits, commonly utilized in a variety of cooked dishes. It is considered to be a rich source of abundant nutrients and is the complete set of minerals, vitamins, nutritional fibre, protein, and antioxidants, along with some phytochemicals like caffeic acid,

chlorogenic acid (phenolic components) glucoside, delphinidin, and nasunin (flavonoids) that have scavenging activities (Noda *et al*, 2000; Bhaskar *et al*, 2015).

As per Zeven and Zhukovsky (1975), brinjal's primary origin is traced back to India, while China is considered a secondary centre of its origin. A large indigenous biodiversity exists in eggplant in the Indian subcontinent region, due to the place being its centre of origin, and there exists a great variation in plant type, stem colour, leaf size, leaf tip, midrib colour, fruit shape, fruit size, fruit colour, fruit yield, cooking quality, fruit quality, and tolerance to pests and diseases (Ullah *et al*, 2014).

Understanding the genetic diversity within breeding materials is crucial for plant breeders to effectively select parent plants for crossing schemes, which is a prerequisite in breeding programmes. Genetic diversity serves as important criterion for the selection of diverse parents who are expected to produce high hybrid

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vigour (Harrington, 1940). Crossing parents chosen for their genetic divergence, is likely to yield transgressive offspring, and subsequent selection can be applied in segregating generations. The Mahalanobis D^2 technique, as recommended by (Rao, 1952) is a recognized method based on multivariate analysis, offering a reliable measure of genetic diversity. The objective of this study was to investigate the genetic diversity among 30 diverse brinjal genotypes in the subtropic plains of Jammu, India to assist the breeder in identifying prospective parents that exhibit promising traits and possess genetic diversity to achieve the desired improvement.

One of the primary goals in brinjal breeding is achieving early flowering and early harvest, as these traits enable farmers to catch the early market, leading to higher returns. Plant spread, plant height and number of branches per plant are other important traits that directly impact on number of fruits and, consequently, the yield, leading to higher returns to farmers. Fruit length, fruit diameter and fruit weight are directly linked to fruit yield. Marketable fruit yield and unmarketable fruit yield based on fruits affected by biotic (disease-infected and pest-infested) and abiotic stresses (high and low temperature/freezing injury etc.) are also important traits in brinjal breeding. The ultimate goal of any crop improvement programme is to increase economic yield which is measured as fruit yield per plant and fruit yield per hectare. Germination percentage is a parameter used to measure seed viability, and crop stands in the field primarily depend on this percentage, ultimately determining the final yield. Seed vigour index is another important trait in crop improvement as seeds with a higher vigour index produce an early and uniform stand in the field. Ascorbic acid content in brinjal fruit is an important biochemical character associated with increased nutritive value of the fruits which promotes better retention of colour and flavour (Sasikumar, 1999). Total phenol content helps determine resistance against fruit and shoot borer incidence in brinjal. The higher the phenol content, the lower the incidence of fruit and shoot borer (Jat and Pareek, 2003; Shinde et al, 2009). In addition, higher phenolic levels influence antioxidant content and fruit culinary quality (Stommel et al, 2015). Keeping in view the importance of the above traits in brinjal breeding, these were taken into consideration in the present study.

Materials and methods

Thirty genotypes (Table 1) of pink brinjal grown across various regions of Jammu and Kashmir were gathered, tested and assessed at the Experimental Farm of the Division of Vegetable Science, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu. The material encompasses local landraces, advanced breeding lines and hybrids and is conserved at the institute. Seeds were sown in raised nursery beds of 3m × 1m size on 4 August 2022 in lines spaced 5cm apart. Proper care was taken to water the beds and remove weeds for raising healthy seedlings. Seedlings

were ready for transplanting after four and five weeks. Seedlings were transplanted on 2 September 2022 in a randomized complete block experimental design with three replications with a plot size of 3m × 1m and spacing of 90cm × 75cm. All the prescribed cultural practices were followed throughout the growth and development period of the crop to cultivate a healthy crop as given in Package and Practices for Vegetable Crops (Anonymous, 2020).

Five plants were selected from each plot to record observations on days to first flowering, days to first harvest, plant height (cm), number of branches per plant, plant spread (cm²), number of fruits per plant, fruit length (cm), fruit diameter (cm), fruit weight (g), marketable fruit yield per plant (kg) unmarketable fruit yield per plant (kg), total yield per plant (kg), fruit yield per hectare (q/ha), number of seeds per fruit and germination percentage as per descriptors of the International Board for Plant Genetic Resources (IPBGR, 1990). The seed vigour index was calculated by using the formula given by Abdul and Anderson (1973). Ascorbic acid content (mg/100g) was assayed as described by Rangana (1976) and total phenol content (mg/100g) as per procedure given by Thimmaiah (1999). The D^2 statistic, as introduced by Mahalanobis (1936), was employed to evaluate genetic divergence among genotypes for both quantitative and qualitative traits. D^2 analysis is a valuable tool for determining the degree of genotypic divergence between biological populations and determining the relative contributions of different components to the total divergence, both within and between clusters. The grouping of genotypes was carried out utilizing Tocher's method as outlined by Rao (1952). Statistical analyses were done using INDOSTAT software.

Results

Analysis of variance for various characters revealed significant differences for all parameters under study. Mean performance of 30 genotypes for all traits are presented in Supplemental Table 1. After calculating the D^2 values for every potential pair, the 30 genotypes were categorized into eight groups based on their genetic configurations. This clustering highlighted considerable genetic diversity among the genotypes (Table 2) and (Figure 1). Cluster I constituted the largest group with eight genotypes, followed by Cluster II and IV, which each encompassed six genotypes. Cluster VI had four and Cluster VII had three genotypes. Clusters III, V and VIII comprised only one genotype each (mono-genotypic clusters).

Average inter- and intra-cluster distances in pink brinjal genotypes

Inter- and intra-cluster distances were calculated using the formulae described by Singh and Chaudhary (1977), serving as indicators of genetic diversity among clusters, as shown in Table 3. Inter-cluster distances surpassed intra-cluster distances, indicating a substantial level of

Table 1. List of genotypes of pink brinjal (*Solanum melongena* L.) used in this study and their sources.

No.	Genotype	Biological status	Source
1	SJPB-22-01	Advanced breeding line	SKUAST-Jammu, India
2	SJPB-22-02	Advanced breeding line	SKUAST-Jammu, India
3	SJPB-22-03	Advanced breeding line	SKUAST-Jammu, India
4	SJPB-22-04	Advanced breeding line	SKUAST-Jammu, India
5	SJPB-22-05	Advanced breeding line	SKUAST-Jammu, India
6	SJPB-22-06	Advanced breeding line	SKUAST-Jammu, India
7	SJPB-22-07	Advanced breeding line	SKUAST-Jammu, India
8	SJPB-22-08	Advanced breeding line	SKUAST-Jammu, India
9	SJPB-22-09	Advanced breeding line	SKUAST-Jammu, India
10	SJPB-22-10	Advanced breeding line	SKUAST-Jammu, India
11	SJPB-22-11	Advanced breeding line	SKUAST-Jammu, India
12	SJPB-22-12	Advanced breeding line	SKUAST-Jammu, India
13	SJPB-22-13	Advanced breeding line	SKUAST-Jammu, India
14	Jammu Sel-01	Local landrace	Gajansoo, Jammu, India
15	Jammu Sel-02	Local landrace	Marh, Jammu, India
16	Shalimar Hybrid-1	Public sector hybrid	SKUAST-Kashmir, India
17	Baramulla Local Sel-01	Local landrace	Parihaspura, Kashmir, India
18	Baramulla Local Sel-02	Local landrace	Pattan, Baramulla, India
19	Shalimar Local	Local landrace	Dargah, Kashmir, India
20	Ganderbal Local Sel	Local landrace	Ganderbal, Kashmir, India
21	Long Special	Private sector hybrid	Jyoti Agritec, Jammu, India
22	Kashmiri Long	Private sector hybrid	Jyoti Agritec, Jammu, India
23	Long Kashmiri	Private sector hybrid	Gulshan Seeds, Jammu, India
24	Lal Gulab	Private sector hybrid	Rajdhani Seeds, Jammu, India
25	Pink Long	Private sector hybrid	Shatabdi Seeds, Jammu, India
26	PPL-1823	Private sector hybrid	Sultan Seeds, Jammu, India
27	Manjhi	Private sector hybrid	Kalash Seeds, Jammu, India
28	Pink Raja	Private sector hybrid	Truegenic Seeds, Jammu, India
29	Nisha	Private sector hybrid	HM Clause, Jammu, India
30	Brinjal No. 704	Private sector hybrid	MAHYCO, Jammu, India

Table 2. Clustering of 30 genotypes of pink brinjal (*Solanum melongena* L.) based on D² statistics

Cluster	No. of genotypes	Genotypes
I	8	SJPB-22-01, SJPB-22-02, SJPB-22-04, SJPB-22-05, SJPB-22-07, Shalimar Local, Kashmiri Long
II	6	SJPB-22-03, SJPB-22-12, SJPB-22-13, Ganderbal Local Sel, Jammu Sel-01, Jammu Sel-02
III	1	SJPB-22-09
IV	6	Lal Gulab, Manjhi, Long Kashmiri, SJPB-22-08, SJPB-22-11, Brinjal no. 704
V	1	Pink Raja
VI	4	Baramulla Local Sel-01, Pink Long, Shalimar Hybrid-01, Baramulla Local Sel-02
VII	3	SJPB-22-06, SJPB-22-10, Long Special
VIII	1	Nisha

genetic diversity among the studied genotypes. The highest intra-cluster distance was observed in Cluster VII (42.78), with Clusters VI and IV following closely at 40.27 and 39.57, respectively. Clusters III and IV exhibited the greatest inter-cluster distance (103.96), followed by Clusters III and VI (98.96), and Clusters III and VII (93.04). The proximity between Clusters I and III, as evidenced by the minimum inter-cluster distance of 40.17, suggests a stronger relationship among the genotypes within these clusters.

Cluster means for 18 characters in pink brinjal genotypes

Table 4 displays cluster means for each of the 18 characters studied. The single genotype in Cluster III had the maximum cluster mean value for germination percentage (87.33%) and seed vigour index (1115.67). The maximum cluster mean value for fruit length (15.81cm), unmarketable fruit yield per plant (0.32kg), fruit yield per hectare (303.8q/ha and number of seeds

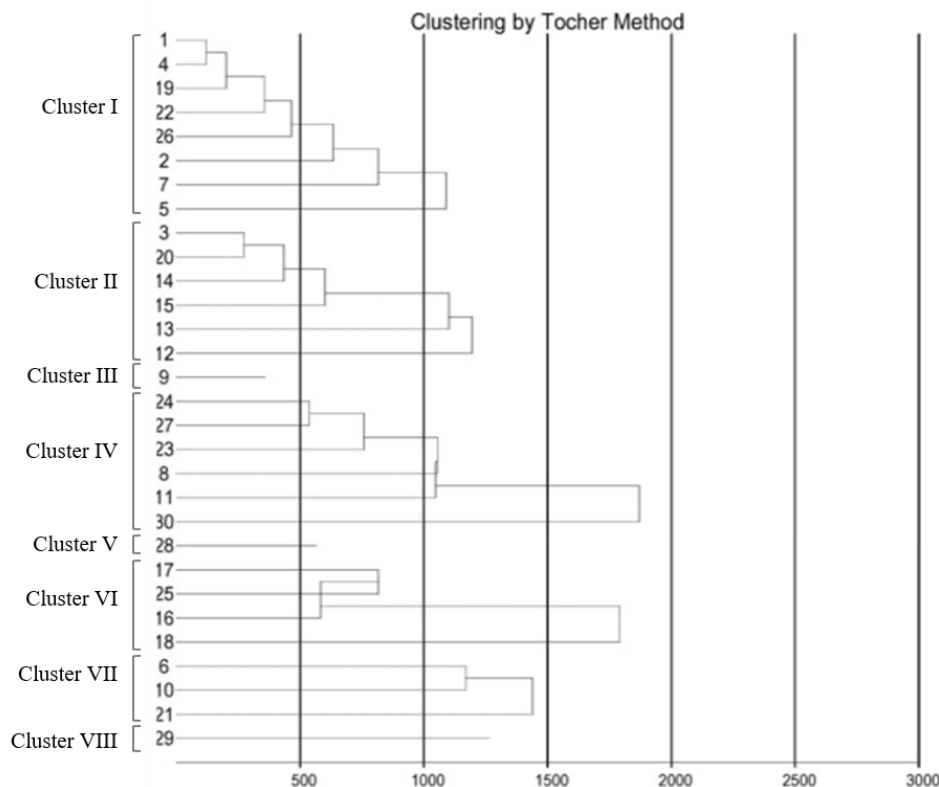


Figure 1. Dendrogram representing clustering pattern of 30 genotypes of pink brinjal (*Solanum melongena* L.). The numbers correspond to genotypes used in this study (see Table 1).

Table 3. Mean intra-cluster distance (highlighted in bold) alongside the inter-cluster distance values (D^2 values) for eight clusters among 30 genotypes of pink brinjal (*Solanum melongena* L.).

Cluster	I	II	III	IV	V	VI	VII	VIII
I	28.47	46.14	40.17	85.92	40.31	72.69	90.16	42.50
II		33.33	71.96	69.31	58.99	56.55	92.26	52.63
III			0.00	103.96	51.53	98.96	93.04	46.59
IV				39.57	80.81	60.29	62.55	64.29
V					0.00	61.75	78.35	45.61
VI						40.27	88.34	70.29
VII							42.78	64.53
VIII								0.00

per fruit (275.11) was observed in Cluster IV. The minimum cluster mean value for days to first flowering (37.00) and days to first harvest (62.33) was observed in Cluster V, whereas desirable cluster mean values for marketable fruit yield per plant (2.05kg) and total fruit yield per plant (2.36kg) were observed in Cluster VI. Cluster VII exhibited the highest mean values among clusters for fruit weight (125.22g), as well as for ascorbic acid content (12.41mg/100g) and total phenol content (2.22mg/100g). Cluster VIII had the maximum cluster mean value for plant height (70.00cm), number of branches per plant (7.33), plant spread (70.00cm²), number of fruits per plant (31.00) and fruit diameter (5.23cm).

Relative contribution of various characters towards divergence

The percentage contribution to genetic divergence by all 18 characteristics is provided in Table 5. Observations revealed that the highest contribution to total divergence was from total fruit yield per plant (33.56%), followed by the number of seeds per fruit (21.38%), seed vigour index (7.94%), marketable fruit yield per plant (7.62%), fruit yield per hectare (3.61%), number of branches per plant (2.52%), days to first flowering (2.25%), plant spread (2.24%), unmarketable fruit yield per plant (2.21%), fruit diameter (2.07%), fruit length (1.89%), fruit weight (1.84%), total phenol content (1.61%), days to first harvest (1.13%),

Table 4. Cluster mean values for different characters in pink brinjal (*Solanum melongena* L.). The lowest values are highlighted in bold, and the highest values are in italic. DFF, days to first flowering; DFH, days to first harvest; PH, plant height (cm); NPB, number of branches per plant; PS, plant spread (cm²); NFP, number of fruits per plant; FL, fruit length (cm); FD, fruit diameter (cm); FW, fruit weight (g); MFYP, marketable fruit yield per plant (kg); UMFYP, unmarketable fruit yield per plant (kg); TFYP, total fruit yield per plant (kg); FYH, Fruit yield per hectare (q/ha); NSF, number of seeds per fruit; G (%), germination (%); SV, seed vigour index; AA, ascorbic acid content (mg/100g); TPC, total phenol content (mg/100g).

Characters	I	II	III	IV	V	VI	VII	VIII
DFF	41.17	40.28	38.00	40.33	37.00	38.92	<i>41.67</i>	41.33
DFH	67.38	67.11	64.67	66.83	62.33	63.75	<i>70.44</i>	63.00
PH	63.83	67.56	61.00	63.78	65.33	57.00	59.56	<i>70.00</i>
NBP	5.71	5.06	6.67	6.28	7.00	6.50	6.11	<i>7.33</i>
PS	63.83	67.56	61.00	63.78	65.33	57.00	59.56	<i>70.00</i>
NFP	23.21	19.89	26.67	26.56	29.33	27.75	25.67	<i>31.00</i>
FL	11.58	13.94	8.83	<i>15.81</i>	9.00	14.50	11.22	10.00
FD	3.86	3.97	3.67	4.31	3.63	4.63	3.63	<i>5.23</i>
FW	63.04	77.50	60.00	117.22	69.00	86.00	<i>125.22</i>	70.00
MFYP	1.30	1.36	1.33	1.71	1.78	2.05	1.26	1.42
UMFYP	0.14	0.17	0.07	<i>0.32</i>	0.24	0.31	0.29	0.17
TFYP	1.44	1.53	1.40	2.05	2.02	2.36	1.56	1.60
FYH	212.91	226.04	207.40	<i>303.85</i>	299.74	249.56	230.61	236.53
NSF	224.79	256.44	207.33	<i>275.11</i>	209.33	260.50	222.56	250.00
G (%)	84.46	83.72	<i>87.33</i>	80.67	82.33	79.17	78.11	85.00
SV	1,030.33	998.39	<i>1,115.67</i>	891.61	919.67	848.25	841.33	1,050.00
AA	10.06	11.05	12.33	11.73	10.22	10.31	<i>12.41</i>	10.94
TPC	1.29	1.70	2.04	1.87	1.15	1.26	2.22	2.01

germination percentage (1.61%) and ascorbic acid content (0.69%).

Discussion

The highest intra-cluster distance was observed in Cluster VII while the greatest inter-cluster distance was observed between Clusters III and IV. The inter-cluster distance was larger than intra-cluster distance suggesting that genotypes within and between clusters were homogenous and diverse, respectively (Pawar *et al*, 2013). The data clearly showed that the clustering of genotypes was not influenced by their geographical distribution. Overall, the distribution pattern of genotypes from different regions into distinct clusters appeared to be random. Several studies (Mangi *et al*, 2020; Silambarasan *et al*, 2020; Kaur *et al*, 2021; Mohanty *et al*, 2021; Verma *et al*, 2021; Anbarasi and Haripriya, 2021; Chaitanya, 2022) have all documented similar findings in their respective research concerning brinjal. One potential explanation may be that it is very challenging to establish the precise place of origin of a genotype. The frequent and open exchange of genetic material among breeders within the country complicates the maintenance of a genotype's true identity. The lack of correlation between genetic diversity and geographical distance suggests that factors beyond geographical origins, like genetic exchange, drift, mutation, variation, and selection, could account for the observed genetic diversity. An alternative explanation could be that the diversity estimates derived from the characters

examined in this study might not fully capture the variability influenced by additional physiological or biochemical characteristics, which could be significant in representing the overall genetic diversity within a population. Consequently, the selection of genotypes for hybridization should prioritize genetic diversity over geographical divergence.

Out of eight clusters, Cluster VIII had the highest mean value for plant height, number of branches per plant, number of fruits per plant and fruit diameter, implying that genotypes in this cluster can be selected directly on the basis of these features and employed in hybridization programmes. Cluster VI also showed the highest mean value for some important traits, namely marketable fruit yield per plant and total fruit yield per plant. The genotypes belonging to this cluster can be used in breeding programmes to develop high fruit-yielding hybrids. Cluster V had the lowest value for days to first flowering and days to first harvest, implying that the genotypes in this cluster are likely to be early maturing types. Hence, these genotypes can be directly employed for developing early crops. Cluster VII exhibited the highest mean value for ascorbic acid and total phenol content along with fruit weight. This implies that this cluster's genotype should be rich in nutritive value, and these genotypes should be employed in quality breeding. The genotypes in Cluster III had the highest cluster mean value for germination percentage and seed vigour index, indicating that genotypes from this cluster exhibit rapid and uniform crop establishment and growth across diverse environmental conditions.

Table 5. Percentage contribution of various traits towards genetic divergence in pink brinjal (*Solanum melongena* L.)

Rank	Characters	Percentage contribution (%)
1	Total fruit yield per plant (kg)	33.56
2	Number of seeds per fruit	21.38
3	Seed vigour index	7.94
4	Marketable fruit yield per plant (kg)	7.62
5	Fruit yield per hectare (q/ha)	3.61
6	Number of fruits per plant	3.34
7	Plant height (cm)	2.99
8	Number of branches per plant	2.52
9	Days to first flowering	2.25
10	Plant spread (cm ²)	2.24
11	Unmarketable fruit yield per plant (kg)	2.21
12	Fruit diameter (cm)	2.07
13	Fruit length (cm)	1.89
14	Fruit weight (g)	1.84
15	Total phenol content (mg/100g)	1.61
16	Days to first harvest	1.13
17	Germination (%)	1.05
18	Ascorbic acid content (mg/100mg)	0.69

A similar comparison of clusters based on the range of mean value of each character was done by earlier works, namely Ravali *et al* (2017); Banerjee *et al* (2018); Sindhuja *et al* (2019); Silambarasan *et al* (2020); Balasubramaniyam *et al* (2021); Kaur *et al* (2021); Verma *et al* (2021); Chaitanya (2022).

Relative contribution of various characters towards divergence

The highest contribution to genetic divergence was observed from total fruit yield per plant. Many researchers including Ravali *et al* (2017); Bhushan *et al* (2018); Sindhuja *et al* (2019); Silambarasan *et al* (2020); Balasubramaniyam *et al* (2021); Mohanty *et al* (2021); Chaitanya (2022) confirmed the substantial contribution of fruit yield per plant to divergence.

The results indicate significant potential for developing new varieties of pink brinjal with increased yield and enhanced economically important attributes by utilizing this elite germplasm. In crop improvement initiatives, effective outcomes could be achieved through interbreeding among genotypes displaying exceptional mean performance for these traits.

Conclusion

Analysis of 18 traits using the Mahalanobis D^2 statistic demonstrated significant diversity among 30 pink brinjal genotypes, resulting in their classification into eight separate clusters. Mahalanobis D^2 proved to be an effective tool in clustering genotypes phenotypically and geographically. The genotypes within Clusters III and IV, which exhibit maximum inter-cluster distance, hold potential for utilization as parents in recombination breeding programmes as these are very diverse from

each other. They could be employed to develop highly heterotic F_1 hybrids or to generate a broad range of transgressive segregants within populations, thereby facilitating the development of high-yielding varieties of pink brinjal. For recovering improved progenies for yield and quality characters, crosses can be attempted between the genotypes belonging to Clusters VI and VII as they show the highest cluster mean value for yield and quality parameters.

Supplemental data

[Supplemental Table 1.](#) Mean values of 18 different characters for 30 genotypes of pink brinjal (*Solanum melongena* L.) described in this study.

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Author contributions

Vishwash Bandhral played a crucial role in drafting the research programme and objectives along with Dr. Anil Bhushan, collecting different genotypes of pink brinjal from different sources, proper sowing and transplanting of field trial, recording field and lab parameters, analyzing data and concluding the results. Dr. Anil Bhushan assisted in drafting the problem of genetic divergence and formulating the objective, Dr. R.K. Samnotra reviewed the trail of divergence, Diksha Rani helped with data collection, and Sonali Sharma assisted with data analysis.

Conflict of interest

Authors have declared that no competing interests exist.

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