Journal of Environmental Biology
p-ISSN: 0254-8704 • e-ISSN: 2394-0379 • CODEN: JEBIDP

JEB®

Original Research Paper
Volume 46 Issue 3 May 2025 pp. 400-409
DOI: http://doi.org/10.22438/jeb/46/3/MRN-5500

J. Environ. Biol., 2025
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Journal website : www.jeb.co.in ★ E-mail : editor@jeb.co.in

Genetic divergence studies of mango germplasms for tree, fruit yield and quality attributes under the Shivalik Foothills of Uttarakhand

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Received: 13 August 2024 **Revised:** 30 October 2024 **Accepted:** 06 January 2025

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Abstract

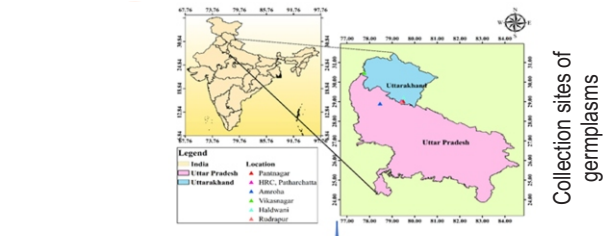
Aim: To evaluate genetic variability and divergence in various traits among mango germplasms in the *Tarai* region of Uttarakhand.

Methodology: The present study was conducted at Horticulture Research Centre, Pantnagar, Uttarakhand for two consecutive years (2021-22 and 2022-23). The genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic gain were estimated by the standard methods. Genetic divergence estimated by Principal Component Analysis (PCA) was subjected to multivariate statistical analysis.

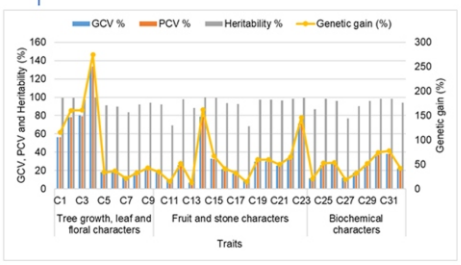
Results: The analysis of variance showed a significant difference for studied attributes, indicating a considerable amount of variability. The phenotypic coefficient of variation (PCV) value was consistently higher compared to genetic coefficient of variation (GCV). Tree growth, flowering, fruit, stone and quality parameters exhibited high genetic coefficient of variation, heritability and significant genetic advance as well as percentage of the mean. The divergence study identified various fruit, yield and plant growth attributes as the most influential trait in determining diversity.

Interpretation: Traits exhibiting high genetic variability are crucial for breeders in selecting suitable germplasm, as highlighted by the Bi-plot analysis, which identified PMSS-7 and PMSS-11 as genetically distinct and particularly valuable for breeding programs.

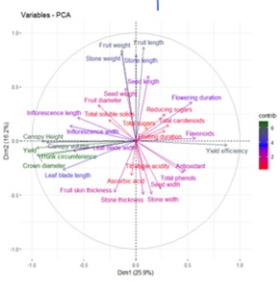
Key words: Bi-plot analysis, Divergence, Germplasms, Genetic diversity, Mango



Collection sites of germplasms



Genetic variability for various characters of mango germplasm



Genetic Divergence for mango germplasm

Promising germplasm *i.e.*, PMSS-7 and PMSS-11

How to cite: Shivran, J.S., A.K. Singh, R. Kumar, I. Kumari, R. Jat and M.L. Jat: Genetic divergence studies of mango germplasms for tree, fruit yield and quality attributes under the Shivalik Foothills of Uttarakhand. *J. Environ. Biol.*, **46,** 400-409 (2025).

Introduction

Mango (*Mangifera indica* L.), belonging to the Anacardiaceae family (order–Sapindales), is known as the national fruit of India and holds immense importance in tropical and subtropical regions globally, particularly in Asia. India, recognized as the primary region of mango origin, produces a diverse range of species/ cultivars with significant genetic variability, leading to its title as the "King of Fruits" in tropical areas (Vincent and Anushma, 2023). It has versatile uses depending on their stage of ripeness, ranging from chutneys and pickles from un-ripened fruits to processed products like squash, nectar, jam, custard powder, and baby food from ripened fruits. Major mango-producing states in India include Uttar Pradesh, Bihar, West Bengal, Maharashtra, Andhra Pradesh and Karnataka, among others. However, mango cultivation in Uttarakhand remains restricted to subtropical regions, covering an area of 21.08 thousand hectares and yielding 112.08 thousand MT annually (Anon., 2023). Analyzing the genetic diversity of fruit crops allows for a better understanding of the available genetic resources, thereby aiding in the improvement of overall quality of the crop. This knowledge is beneficial for breeders when selecting parents for hybridization since greater genetic diversity between parents increases the probability of improving desired traits (Jena *et al.,* 2017).

Over the past few years, several studies have focused on evaluating the genetic diversity and agro-morphological traits of mango (Zhang *et al*., 2020; Carvalho Júnior *et al*., 2021). Kumar *et al.* (2022) assessed the genetic diversity of local mango germplasm using morphological, biochemical markers and DNA barcoding. Recently, Kumar *et al.* (2024) revealed significant differences among the cultivars, with Mallika, Pusa Arunima, and Amrapali emerging as superior varieties in yield, fruit quality, and marketable traits. These studies underscore the growing interest in understanding mango genetic resources to improve fruit quality and adaptability. Despite these efforts, limited attention has been given to mango germplasm under the unique agro-ecological conditions of Uttarakhand, particularly in the *Tarai* region. The *Tarai* belt, characterized by subtropical climatic conditions, presents unique challenges and opportunities for mango cultivation. This study, therefore, differs from previous research by focusing on the genetic diversity, divergence and trait relationships of mango germplasm specifically in the *Tarai* region. The research emphasizes critical traits such as growth, flowering, fruiting and biochemical attributes, employing advanced statistical techniques like Principal Component Analysis (Wold, 1987; Maione and Barbosa, 2019) to classify and characterize mango germplasm. By integrating phenotypic and genotypic variability with environmental influences, this study aims to provide breeders with valuable insights into selecting parents for hybridization and improving desirable traits. Such targeted efforts are vital for developing region-specific cultivars aligned with consumer preferences and environmental conditions.

Materials and Methods

A study was conducted during the two consecutive years 2021 and 2022 at the Horticulture Research Centre, Patharchatta, G.B. Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar (Uttarakhand). The research centre is located at 29.5º N latitude and 79.3º E longitudein the *Tarai* belt, in the foothills of the Shivalik range of the Himalayas, 243.84 m above mean sea level. The experimental site experiences a humid subtropical climate, marked by hot summers and cold winters. During summer, the temperature ranges 32ºC to 45ºC, while in winters, it drops to a minimum range of 5ºC to 10ºC. The annual precipitation measures 1200 mm, with the monsoon typically commencing from the third week of June and lasting until mid-September. A total of 30 germplasms were collected from diverse eco-geographical regions from two states, *i.e.,* Uttar Pradesh and Uttarakhand as detailed in Table 1 and visualized in Fig. 1, to capture a wide range of genetic variability. These germplasms were subsequently conserved at the study center. Horticultural Research Centre, Pattarchatta, Pantnagar. The conserved germplasms represented trees of varying ages, ranging from 5 to 38 years. To ensure experimental precision, the germplasms were planted in a Randomized Block Design (RBD) with three replications. Uniform cultural practices were meticulously applied across all replications throughout the study period to minimize environmental variability and ensure unbiased evaluation of the genetic material.

The measurements of metric features, such as tree growth, flowering and fruiting were recorded according to standard methods (published by International Plant Genetic Resources Institute (IPGRI), Rome, Italy, 2006) in both the year and combined data was taken for analysis. The measurement of total soluble solids was done using a digital refractometer (RX 5000, ATAGO, Japan) in accordance with the normal procedure, and the result was recorded in degrees brix (Ranganna, 1986). Titratable acidity, measured in relation to its malic acid and ascorbic acid levels was determined following the methodology of Ranganna (2007). The estimation of sugars, including both total and reducing sugars, was conducted by the volumetric method developed by Lane and Eynon (1923), as reported by Ranganna (2007). The carotenoid content was quantified by the modified technique outlined by Ranganna (1986).

The flavonoid content was assessed by aluminium chloride technique (Zhishen *et al.,* 1999). The quantification of phenolic compounds in the mango pulp was done by Folin-Ciocalteau method (Singleton *et al*., 1999), with gallic acid serving as reference standard. Brand-Williams *et al.* (1995) described the 2,2-diphenyl-1-picryl-hydrazyl (DPPH) technique for estimating antioxidant activity in fruit pulp, with certain alterations. The parameters of genetic variability *viz.,* GCV, PCV, heritability, genetic advance and genetic gain and PCA were estimated by analysing the pooled data of 2021 and 2022, which consisted of 32 metric attributes of mango germplasms. The heritability was estimated following the standard method suggested by Hanson *et al.* (1956). The expected genetic advance was calculated using the method proposed by Johnson *et al.* (1955). The Genetic gain expressed in per cent ratio of genetic advance and population mean was estimated by the formula suggested by Allard (1960). The principal component

Table 1: List of primary germplasms and commercial varieties (as check) undertaken for characterization in mango

Code No	Accession No.	Method of Crop Improvement	Source	Latitude	Longitude
G1	Dashehari	Seedling Selection	Dashehari (Lucknow), Pantnagar, U.K.	29.0222° N	79.4908° E
G2	Langra	Seedling Selection	Langra (Varanasi), Pantnagar, U.K.	29.0222° N	79.4908° E
G3	PMGC-5	Seedling Selection	SafedaSharbati, Amroha, U.P.	28.9052° N	78.4673° E
G4	PMGC-19	Seedling Selection	Kaloo, Amroha, U.P.	28.9052° N	78.4673° E
G5	PMGC-20	Seedling Selection	Suhag, Amroha, U.P.	28.9052° N	78.4673° E
G6	PMGC-21	Seedling Selection	Beera, Amroha, U.P.	28.9052° N	78.4673° E
G7	PMGC-36	Seedling Selection	ChiknaMulgoa, Amroha, U.P.	28.9052° N	78.4673° E
G8	PMGC-39	Seedling Selection	Gulab Kevera, Amroha, U.P.	28.9052° N	78.4673° E
G9	PMGC-48	Seedling Selection	Surkhuru No. 2, Amroha, U.P.	28.9052° N	78.4673° E
G10	PMGC-50	Seedling Selection	Rahmat Bidiwala, Amroha, U.P.	28.9052° N	78.4673° E
G11	PMGC-51	Seedling Selection	Sharbati, Amroha, U.P.	28.9052° N	78.4673° E
G12	PMGC-72	Seedling Selection	Bhoordas, Amroha, U.P.	28.9052° N	78.4673° E
G13	PMGC-96	Seedling Selection	Surkhuru No. 1, Amroha, U.P.	28.9052° N	78.4673° E
G14	PMGC-97	Seedling Selection	Dadamiyo, Amroha, U.P.	28.9052° N	78.4673° E
G15	PMGC-98	Seedling Selection	Amin Khurd, Amroha, U.P.	28.9052° N	78.4673° E
G16	PMGC-163	Seedling Selection	Pant Sinduri, Pantnagar, U.K.	28.9052° N	78.4673° E
G17	PMGC-164	Seedling Selection	Pant Chandra, Rudrapur, U.K.	28.9875° N	79.4141° E
G18	PMSS-1	Seedling Selection	Nagala, Pantnagar, U.K.	29.0222° N	79.4908° E
G19	PMSS-7	Seedling Selection	1/19, Phoolbag, Pantnagar, U.K.	29.0222° N	79.4908° E
G20	PMSS-8	Seedling Selection	1/104, Phoolbag, Pantnagar, U.K.	29.0222° N	79.4908° E
G21	PMSS-9	Seedling Selection	Lambert Square, Pantnagar, U.K.	29.0222° N	79.4908° E
G22	PMSS-10	Seedling Selection	Sahashpur, Vikasnagar, Dehradun, U.K.	30.4750° N	77.7652° E
G23	PMSS-11	Seedling Selection	Jashowala, Vikasnagar, Dehradun, U.K.	30.4750° N	77.7652° E
G24	PMSS-14	Seedling Selection	1/3, Phoolbag, Pantnagar, U.K.	29.0222° N	79.4908° E
G25	PMSS-15	Seedling Selection	P-23, Patharachatta, U.K.	29.0280° N	79.4131° E
G26	PMSS-17	Seedling Selection	CB-II, Pantnagar, U.K.	29.0222° N	79.4908° E
G27	PMSS-18	Seedling Selection	1/3/5, Phoolbag, Pantnagar, U.K.	29.0222° N	79.4908° E
G28	PMSS-19	Seedling Selection	Shivpuri, Haldwani, Nainital, U.K.	29.2183° N	79.5130° E
G29	PMSS-30	Seedling Selection	HRC, Patharachatta, U.K.	29.0280° N	79.4131° E
G30	PMSS-31	Seedling Selection	Sainik Farm, Patharachatta, U.K.	29.0280° N	79.4131° E

analysisis a multivariate technique estimated by Hotelling (1933). The statistical analysis carried out during study was also performed using the 'R' Statistical Software (v4.1.2; R Core Team 2021).

Results and Discussion

The analysis of variance revealed significant variations in the mean squares attributed to germplasms for all features, suggesting the existence of a wide range of variability and a general mean in mango germplasms (Table 2). The results related to range, variance, coefficient of variation, heritability, genetic advance and genetic gain of various variables are presented in Table 3. It was observed that the phenotypic coefficients of variation were generally higher than their corresponding genotypic coefficients of variation. However, these differences were minimal for most of the attributes, suggesting that the environment had a negligible impact on the estimated traits. A diverse range of genetic diversity was observed in various tree development, leaf and floral features, with values ranging from 11.30% (Flowering duration) to 133.78% (Canopy volume). The tree circumference exhibited a high genotypic coefficient of variation at 78.12%, while the crown diameter showed a similarly high coefficient at 79.19%. The leaf blade width, leaf blade length, and inflorescence length had a medium coefficient of variation at 18.72%, 17.24%, and 16.74% respectively.

While, the coefficient of variation for flowering duration was low at 11.30%. High phenotypic variation was exhibited for canopy volume at 133.99%, followed by crown diameter at 80.23% and tree circumference at 78.33%. Inflorescence width, leaf blade width, and leaf blade length showed moderate coefficients of variation at 22.25%, 19.74%, and 18.04%, respectively. Flowering duration had the lowest coefficient of variation at 12.35%. Regarding heredity, all factors associated with tree development, leaf, and floral characteristics demonstrated a high level of inheritance. The genetic gain for tree growth, leaf and floral qualities was calculated to range from 21.29% to 275.15%, with varying magnitudes. Significant increases in genetic traits were observed for canopy volume (275.15%), crown diameter (161.02%) and tree circumference (160.50%). Moderate improvements were seen for inflorescence width (43.06%), leaf blade width (36.57%) and leaf blade length

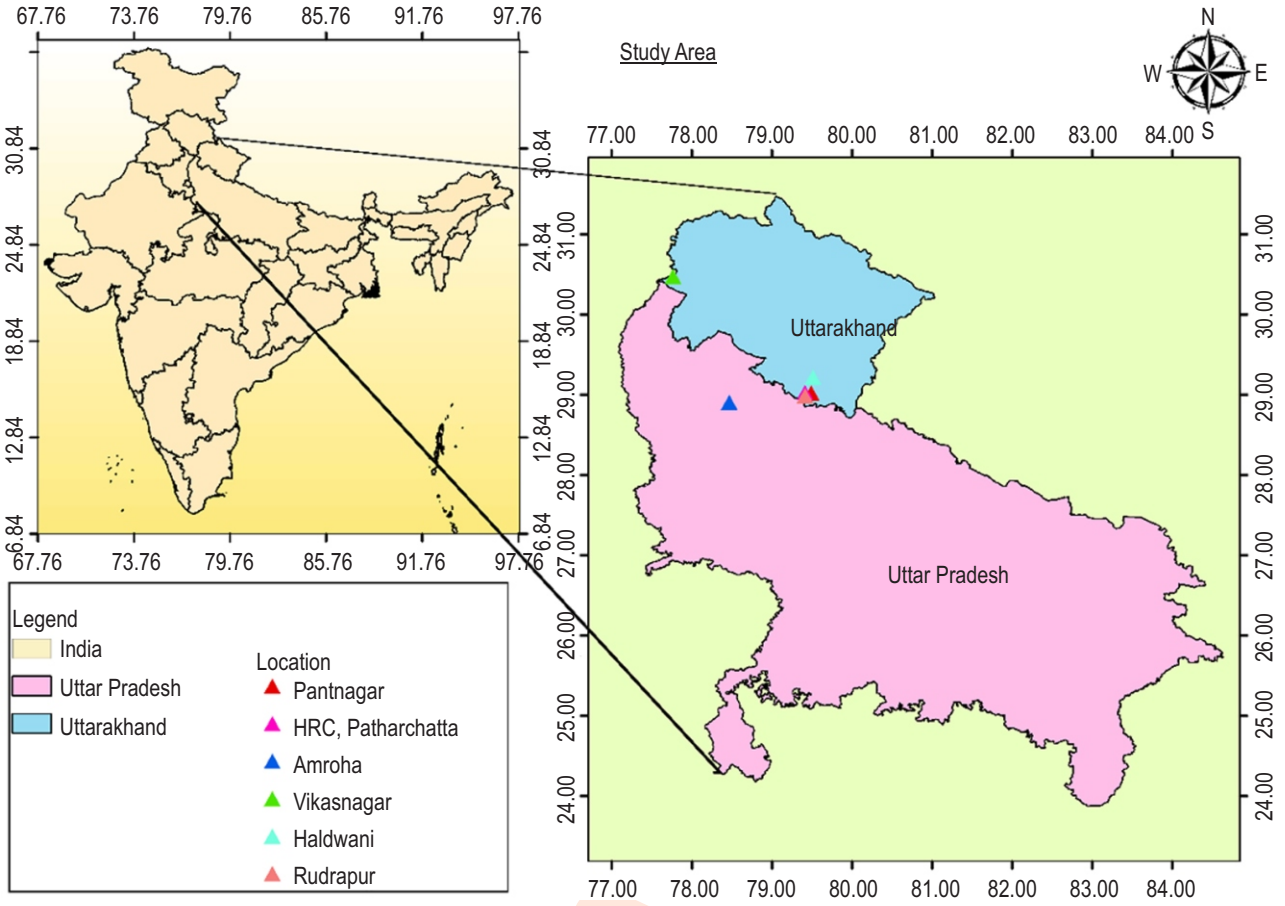


Fig. 1: Collection sites of germplasms from the Uttarakhand and Uttar Pradesh states of India.

(33.94%). The flowering period was observed to be low at 21.29%. A significant variation in genotypic and phenotypic coefficients of variation (GCV and PCV) was observed for fruit and stone characteristics. High GCV was recorded for yield efficiency (78.81%), yield (71.13%), fruit skin thickness (32.74%), and seed weight (31.95%), with PCV estimates similarly high for these traits, including yield efficiency (78.95%) and yield (71.31%). Moderate GCV and PCV were noted for traits like seed length, stone weight, fruit weight, seed width, stone length, and fruit length, while low variability was observed for fruit diameter, stone thickness and fruiting duration in both coefficients.

Heritability estimates were high for most traits, such as yield efficiency (99.65%), yield (99.50%), and fruit skin thickness (99.47%), with medium observed for stone thickness (69.32%) and fruit diameter (68.30%). Genetic gain was highest for yield efficiency (162.06%) and yield (146.17%), moderate for attributes like fruit skin thickness and seed weight, and low for fruit diameter (15.21%), stone thickness (14.05%), and fruiting duration (12.35%). This highlights significant genetic variability, heritability and potential for genetic improvement in these traits.

The genotypic coefficient of variation (GCV) for biochemical traits ranged from 10.44% to 38.14%, with high values observed for total phenol (38.14%) and flavonoid content (36.62%), moderate values for ascorbic acid (26.64%), titratable acidity (25.82%), total carotenoids (25.66%), antioxidant activity (21.15%), and reducing sugars (16.46%), and low values for total soluble solids (10.89%) and total sugars (10.44%). The phenotypic coefficient of variation (PCV) followed a similar trend, ranging from 11.67% to 38.47%, with high values for total phenols (38.47%) and flavonoids (36.97%), moderate levels for ascorbic acid (27.17%), total carotenoids (26.18%), titratable acidity (26.04%), antioxidant activity (21.82%), and reducing sugars (17.31%), and lower levels for total sugars (11.93%) and total soluble solids (11.67%). Heritability was high for most traits, including titratable acidity (98.35%), total phenols (98.33%), and flavonoids (98.15%), while total sugars (76.67%) and total soluble solids (76.67%) showed moderate heritability. Genetic gain was highest for total phenols (77.92%) and flavonoids (74.74%), moderate for ascorbic acid (53.79%), titratable acidity (52.76%), total carotenoids (51.84%), antioxidant activity (42.22%), and reducing sugars (32.25%), and low for total soluble solids (20.92%) and total sugars (18.84%). These results indicate

Table 2: Analysis of variance and mean of morphological and biochemical parameters of mango germplasm

	Mean sum of square			Mean±SE(m)
Source d.f. Characters	Replication 2	Genotypes 29	Error 58	
Canopy height (m)	0.01	18.33*	0.05	4.39±0.13
Trunk circumference (cm)	33.39	14398.79*	25.60	88.60±2.92
Crown diameter (m)	0.20	84.18*	0.74	6.66±0.49
Canopy volume (m3)	790.94	669008.80*	712.95	352.80±15.42
Leaf blade length (cm)	0.13	41.30*	1.27	21.19±0.65
Leaf blade width (cm)	0.03	4.15*	0.15	6.17±0.22
Flowering duration (days)	0.55	16.13*	0.99	19.88±0.57
Inflorescence length (cm)	0.48	65.32*	1.78	27.49±0.77
Inflorescence width (cm)	0.07	18.99*	0.40	11.55±0.36
Fruit length (cm)	0.05	12.84*	0.36	11.53±0.35
Fruit diameter (cm)	0.23	1.56*	0.20	7.58±0.26
Fruit weight (g)	149.50	14425.81*	105.60	272.69±5.93
Fruiting duration (days)	9.71	149.17*	6.39	108.05±1.46
Yield efficiency (kg/m3)	0.0004	0.13*	0.0002	0.26±0.01
Yield (kg/plant)	1.28	847.04*	1.41	0.71±0.01
Fruit skin thickness (mm)	0.0004	0.16*	0.0003	9.50±0.30
Stone length (cm)	0.02	12.00*	0.26	3.98±0.11
Stone width (cm)	0.005	1.31*	0.03	1.87±0.06
Stone thickness (cm)	0.003	0.08*	0.01	40.22±1.16
Stone weight (g)	0.03	425.31*	4.03	5.26±0.15
Seed length (cm)	0.04	7.29*	0.06	2.92±0.08
Seed width (cm)	0.03	1.59*	0.02	30.98±0.29
Seed weight (g)	0.27	362.18*	0.25	23.60±0.69
Total soluble solids (°B)	0.58	11.05*	0.52	17.21±0.42
Titratable acidity (%)	7.36	1.28*	6.54	0.25±0.005
Ascorbic acid (mg/100g)	1.11	322.12*	4.30	38.64±1.20
Total sugars (%)	0.39	6.59*	0.60	13.52±0.45
Reducing sugars (%)	0.01	1.94*	0.07	4.81±0.15
Total carotenoids (mg/100g)	0.04	4.41*	0.06	4.69±0.14
Flavonoids (mg QE/100 g)	0.18	216.27*	1.35	23.11±0.67
Total phenols(mgGAE/100 g)	5.02	1480.21*	8.34	58.08±1.67
Antioxidant activity (mg TE/100 g)	147.62	4863.26*	102.78	188.36±5.85

*Significant at 5% level

significant genetic variability, heritability, and scope for improvement in key biochemical traits.

The genetic coefficient of variation is a valuable tool for enhancing crop quality since it enables the quantification of genetic diversity within germplasm and facilitates the comparison of genetic variability across different traits. According to Vavilov (1951), there is an increased probability of selecting the desired germplasm when there is a higher amount of variation. Significant positive correlations were observed between high values of PCV (phenotypic coefficient of variation) and GCV (genotypic coefficient of variation) for various traits including fruit yield, yield efficiency, canopy volume, canopy diameter, fruit weight, seed weight, fruit skin thickness, total phenol, and flavonoids content. These findings suggest the presence of substantial genetic variability and potential for improvement of these traits through selective breeding. Nayak *et al.* (2013) achieved comparable outcomes in mango. Heritability estimates provide information about the overall amount of variability that can be inherited by future generations. Understanding the heritability of a trait allows a plant breeder to make predictions about the characteristics of future generations and anticipate how they will respond to selective breeding (Sinha *et al*., 2023; Mayavel *et al*., 2024).

Heritability is a valuable metric for forecasting the advancements that can be made through selection. The parameters of maximum canopy volume, yield efficiency, yield, fruit weight, stone width, seed weight, fruit diameter, stone weight, skin thickness, and stone thickness exhibited a significantly high level of heredity. Significant genetic progress, expressed as a percentage of the mean, was seen for fruit yield per tree, yield efficiency, fruit weight, seed weight, and total phenol over both years. Nayak *et al.* (2013) and Das *et al.* (2021) have also documented comparable results in mango. Heritability and genetic progress are two crucial genetic factors. In order to assess the extent of improvement achievable by selection, it is

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Table 3: Estimation of genetic variability for various characters of mango germplasm

Characters	Range	Coefficients of variability (%)		Heritability	Genetic (%)	Genetic gain advance(%)
		Phenotypic	Genotypic			
Tree growth, leaf and floral characters						
C1	1.66-10.50	56.46	56.23	99.19	5.06	115.36
C2	20.17-201.87	78.33	78.12	99.47	142.21	160.50
C3	1.40-16.30	80.23	79.19	97.43	10.73	161.02
C4	6.29-1535.78	133.99	133.78	99.68	970.73	275.15
C5	13.78-26.10	18.04	17.24	91.31	7.19	33.94
C6	4.24-8.87	19.74	18.72	89.93	2.26	36.57
C7	16.50-24.92	12.35	11.30	83.68	4.23	21.29
C8	16.12-37.30	17.43	16.74	92.25	9.11	33.13
C9	7.26-16.76	22.25	21.57	93.97	4.97	43.06
Fruit and stone characters						
C10	7.06-15.1	18.45	17.70	92.08	4.03	35.00
C11	6.28-9.01	10.65	8.87	69.32	1.15	15.21
C12	151.16-422.22	25.62	25.34	97.84	140.78	51.63
C13	86.17-121.50	6.80	6.39	88.16	13.34	12.35
C14	0.02-0.62	78.95	78.81	99.65	0.43	162.06
C15	0.34-1.05	32.83	32.74	99.47	0.48	67.27
C16	5.81-13.11	21.51	20.82	93.73	3.94	41.52
C17	3.07-5.23	17.02	16.36	92.45	1.29	32.40
C18	1.54-2.18	9.99	8.26	68.30	0.26	14.05
C19	16.88-75.24	29.89	29.47	97.21	24.07	59.84
C20	1.60-8.18	29.91	29.52	97.39	3.16	60.00
C21	1.03-4.27	25.27	24.79	96.23	1.46	50.09
C22	11.04-60.47	32.25	31.95	98.17	18.92	65.21
C23	3.55-53.48	71.31	71.13	99.50	34.50	146.17
Biochemical characters						
C24	14.30-22.45	11.67	10.89	87.03	3.60	20.92
C25	0.15-0.43	26.04	25.82	98.35	0.13	52.76
C26	22.31-63.22	27.17	26.64	96.10	20.79	53.79
C27	11.00-15.95	11.93	10.44	76.67	2.55	18.84
C28	3.20-5.94	17.31	16.46	90.45	1.55	32.25
C29	2.93-7.08	26.18	25.66	96.08	2.43	51.82
C30	9.55-42.60	36.97	36.62	98.15	17.27	74.74
C31	22.69-94.39	38.47	38.14	98.33	45.25	77.92
C32	122.67-257.71	21.82	21.15	93.92	79.53	42.22

C1: Canopy height (m); C2: Trunk circumference (cm); C3: Crown diameter (m); C4: Canopy volume (m3); C5: Leaf blade length (cm); C6: Leaf blade breadth (cm); C7: Flowering duration (days); C8: Inflorescence length (cm); C9: Inflorescence width (cm); C10: Fruit length (cm); C11: Fruit diameter (cm); C12: Fruit weight (g); C13: Fruiting duration (days); C14: Yield efficiency (kg m^{-3}); C15: Fruit skin thickness (mm); C16: Stone length (cm); C17: Stone width (cm); C18: Stone thickness (cm); C19: Stone weight (g); C20: Seed length (cm); C21: Seed width (cm); C22: Seed weight (g); C23: Yield (kg/plant); C24: Total soluble solids (°B); C25: Titratable acidity (%); C26: Ascorbic acid (mg 100^{-1} g); C27: Total sugars (%); C28: Reducing sugars (%); C29: Total carotenoids (mg 100^{-1} g); C30: Flavonoids content (mg QE 100^{-1} g); C31: Total phenols (mg GAE 100^{-1} g); C32: Antioxidant activity (mg TE 100^{-1} g).

essential to have knowledge of both the heritability and genetic progress of a particular characteristic (Johnson *et al.,* 1955).

The principal components analysis is a statistical method for identifying patterns in data and highlighting similarities and differences between those patterns (Smith, 2002). The principal component (PC) analysis of 30 mango germplasms based on correlation matrix of morphological and physico-chemical characters reduced the original data set of 32 metric traits to 28 vector or principal components. The eigen values and associated percentage of variation of respective principal component are presented in Fig. 2. The first 12 components in the PCA analysis with eigen values (eigen root) more than one or unity contributed 91.91 % of the total variability among the different germplasm evaluated. The PC1 with eigen value 8.33 accounts for highest variability (26.03 %) in the data of all observed characters, while, PC2 with eigen value 5.17 accounted for 16.17 % of the total variability in all characters observed among the 30-mango

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Table 4: Two most informative principal components for mango germplasm

Characters	Eigenvalue	
	PC1	PC2
Canopy height	0.313	-0.002
Trunk circumference	0.330	-0.056
Crown diameter	0.324	-0.062
Canopy volume	0.297	-0.006
Leaf blade length	0.242	-0.117
Leaf blade width	0.208	-0.040
Flowering duration	-0.188	0.157
Inflorescence length	0.195	0.096
Inflorescence width	0.220	0.063
Fruit length	-0.027	0.382
Fruit diameter	0.126	0.146
Fruit weight	0.046	0.371
Fruiting duration	-0.098	0.040
Yield efficiency	-0.308	-0.015
Fruit skin thickness	0.072	-0.209
Stone length	-0.002	0.350
Stone width	-0.051	-0.215
Stone thickness	-0.022	-0.216
Stone weight	0.049	0.359
Seed length	-0.043	0.264
Seed width	-0.083	-0.194
Seed weight	0.033	0.215
Total soluble solids	0.090	0.085
Titratable acidity	-0.027	-0.121
Ascorbic acid	0.015	-0.140
Total sugars	-0.039	0.052
Reducing sugars	-0.097	0.109
Total carotenoids	-0.109	0.063
Flavonoids content	-0.196	0.011
Total phenols	-0.158	-0.129
Antioxidant activity	-0.165	-0.123
Yield	0.333	-0.026
Eigenvalue	**8.33**	**5.17**
Percentage of Variance	**26.03**	**16.17**
Cumulative Percentage	**26.03**	**42.20**

germplasm. The PC3 showed eigen value 3.64 and accounted for 11.39 % to the recorded variability in all characters. The subsequent PCAs namely PC4, 5, 6, 7, 8, 9, 10, 11 and 12 had Eigen value 2.82, 1.85, 1.60, 1.38, 1.25, 1.07, 0.90, 0.76 and 0.64 summarised 8.80, 5.79, 5.01, 4.30, 3.92, 3.34, 2.80, 2.37 and 2.00 % of the total variability, respectively.

The primary components, that account for 90% of the total variances, have been determined to be adequate and valuable. The initial twelve main components explained 92% of the overall variability in the data. However, the other components had a minimal impact on variance, therefore they cannot be linked to a significant amount of the variation among the germplasm. This study is focused on analysing and interpreting only the first 2 principal components, which have eigenvalues >5. These components explain 42.20% of the variation seen across 30 germplasm. Each primary component is associated with a specific number of characters that contribute to the overall variation. The analysis of Table 4 reveals that the primary factor contributing to the diversity in the first principal component is yield, with a value of 0.333, closely followed by trunk circumference (0.330), crown diameter (0.324), canopy height (0.313), canopy volume (0.297), leaf blade length (0.242), inflorescence width (0.220), leaf blade width (0.208), inflorescence length (0.195), and fruit diameter (0.126), all of which had high positive loadings. On the other hand, yield efficiency (-0.308), flavonoids content (-0.196), flowering duration (-0.188), antioxidant activity (-0.165) and total phenols (-0.158) exhibited the highest negative loadings. The second principal component exhibited the most significant positive correlation with fruit length (0.382), followed by fruit weight (0.371), stone weight (0.359) and stone length (0.350). Conversely, the most substantial negative correlation was observed with stone thickness (-0.216), followed by stone width (-0.215), fruit skin thickness (-0.209) and seed width (-0.194). The factor loadings for the two principal components exhibited both positive and negative values, indicating the presence of both positive and negative correlations. Based on the loadings obtained from the first and second major components, it was found that fruit yield and fruit length were the most optimal options. Using principal component analysis (PCA), able to determine the amount of variation that can be attributed to every axis of differentiation by the largest contributor (Fig 3). PCA of the data showed that the varieties namely PMSS-11 and PMSS-7 were completely distinguishable (Fig. 4) from the other mango germplasm.

The separation is determined by the higher levels of yield and yield efficiency. The data visualisation showed a positive correlation between canopy volume and yield, indicating that a higher canopy volume results in a greater yield. It has been observed that fruit weight, fruit length, stone weight, and stone length were positively connected with each other. The tree growth parameters, including canopy height, trunk circumference, canopy volume and crown diameter, exhibited a positive correlation. The fruit's bio-chemical characteristics, specifically total sugars, reducing sugars and total carotenoids, exhibited a favourable correlation. Ilgbari *et al.* (2019) analyzed the morphological traits of mango cultivars in South-West Nigeria to support classification and conservation. Khadivi *et al.* (2022) identified superior mango genotypes using morphological and pomological traits for breeding and cultivation. Both studies highlight the role of phenotypic diversity in enhancing mango production and conservation.

Esan *et al.* (2024) explored the genetic variability and morpho-agronomic traits of different mango cultivars in Nigeria, providing insights for breeding and conservation. Indian *et al*. (2023) focused on documenting morphological diversity in mango germplasm using Bioversity International descriptors, aiding in systematic classification. These studies contribute valuable data for enhancing mango breeding strategies and germplasm management.

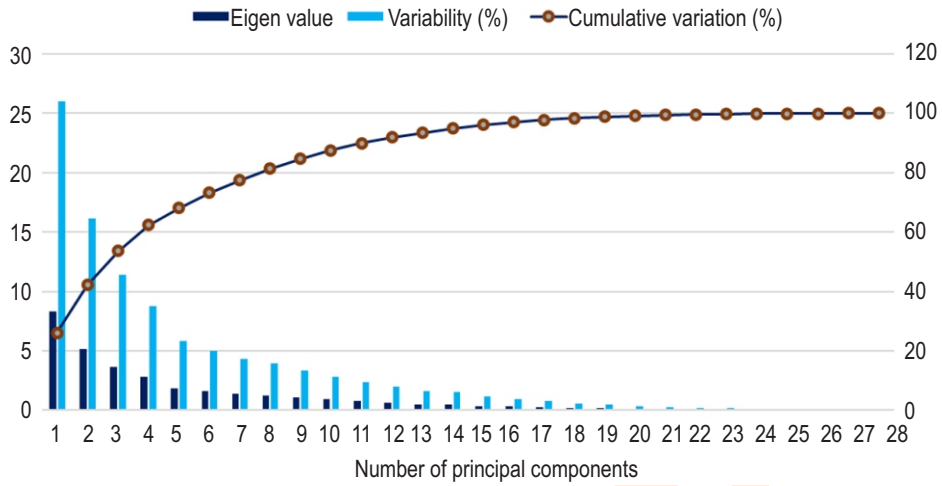

Fig. 2: Eigenvalue, variability and cumulative percentage of variation for different principal components in mango germplasm

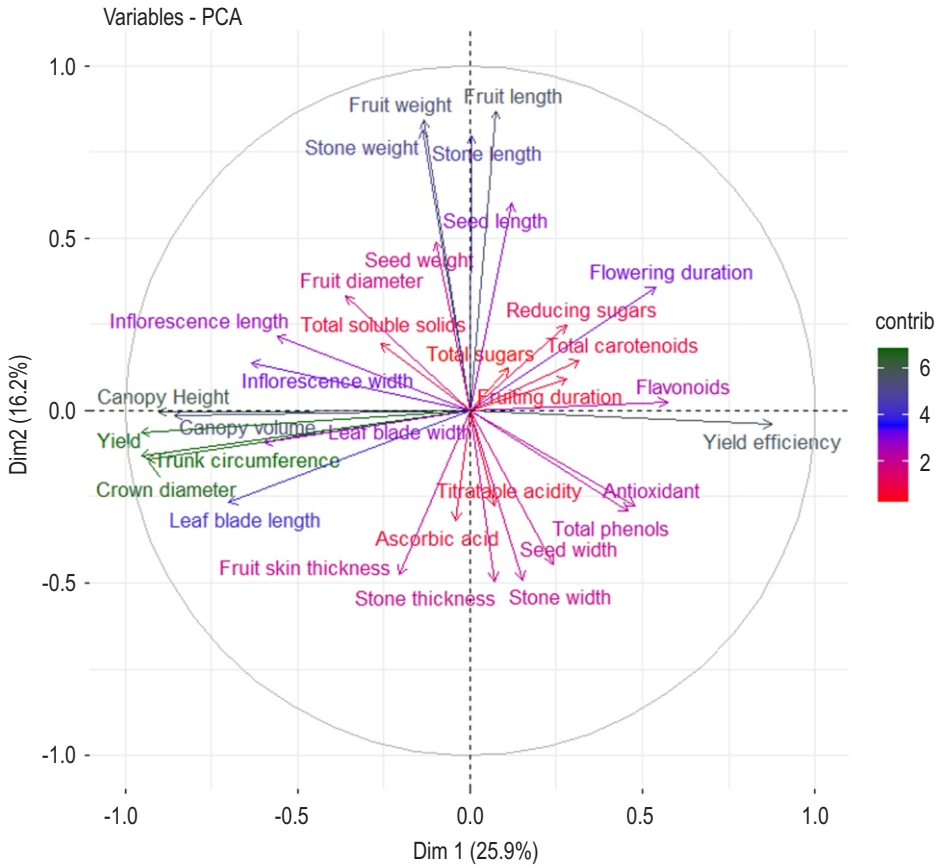

Fig. 3: Character contribution for genetic divergence with respect to PC1 and PC2.

Principal component analysis (PCA) is used to analyse the average data of the germplasms. PCA determines the primary factor that contributes most to the overall variation on each axis of differentiation (Greenacre *et al.,* 2022). The categorisation of mango genetic diversity based PCA is illustrated in Fig. 4. The germplasms were interconnected, providing insight into their individual effects, as indicated by the principal component analysis. It is crucial to prioritise factors that

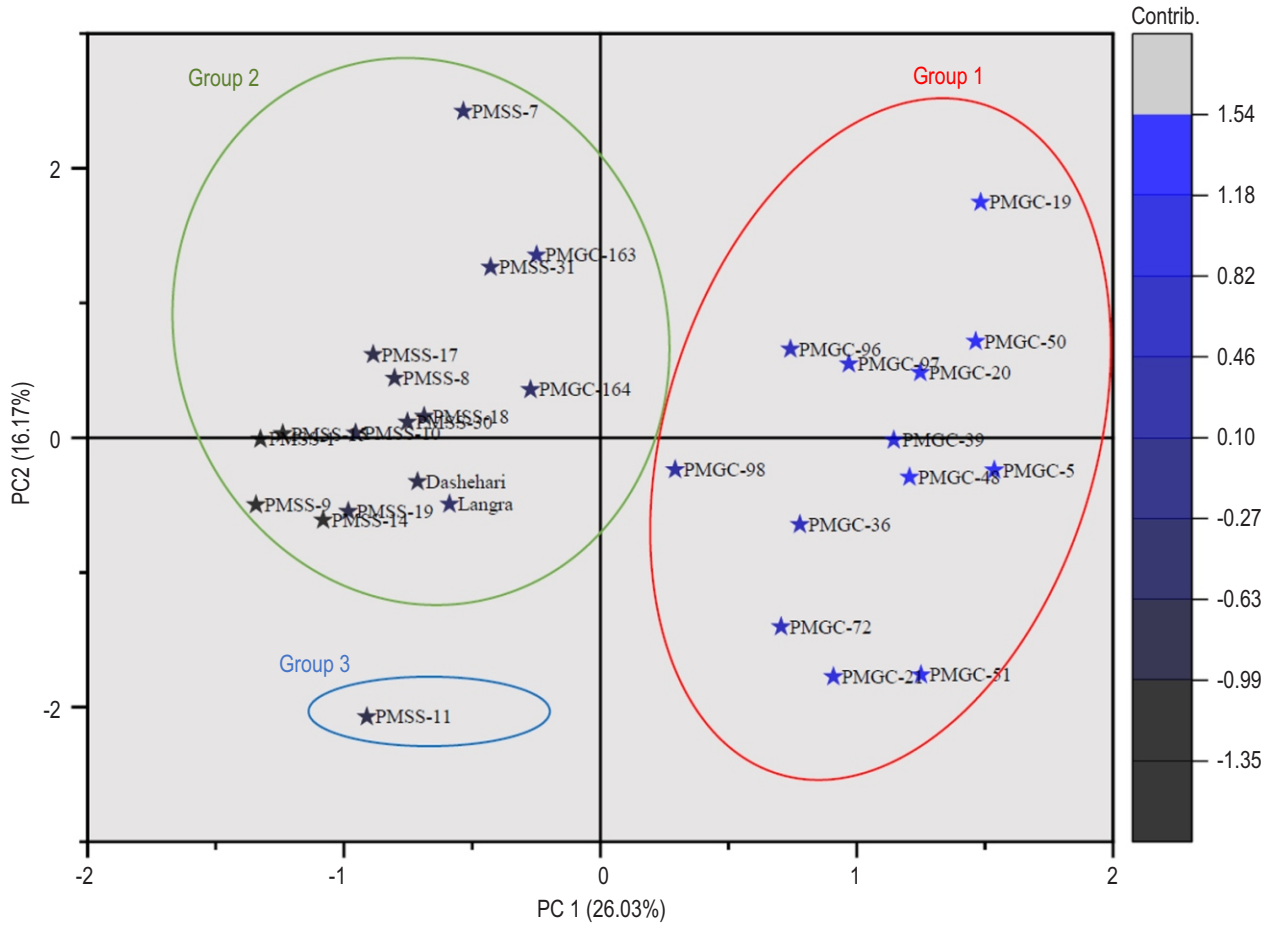

Fig. 4: Distribution of germplasm on the scatter plot along with PC1 and PC2.

have a significant positive or negative relative weight value. Both the first and second principal components exhibited positive loading from half of the germplasm and negative loading from the other half. The range of variation for different germplasm ranged from -1.343 to 1.537 in the first principal component (PC) and from -2.073 to 2.424 in the second PC. The PC1 with the highest positive component loading was PMGC-5 (1.537), followed by PMGC-19 (1.485), PMGC-50 (1.465), PMGC-51 (1.252), PMGC-20 (1.485) and PMGC-48 (1.206). On the other hand, the lowest component loading was recorded from PMSS-9 (-1.343), PMSS-1 (-1.324) and PMSS-15 (-1.238). In the second PC, the range of variability for different germplasm extended from -2.073 to 2.424. The highest positive component loading was observed in PMSS-7 (2.424), followed by PMGC-19 (1.747), PMGC-163 (1.355), and PMSS-31 (1.266). However, the negative component loading was observed in PMSS-11 (-2.073), PMGC-21 (-1.775), PMGC-51 (-1.761), and PMGC-72 (-1.405). These groupings are determined based on the correlation matrix of morphological and physico-chemical characteristics of various germplasm. The PC analysis offered a streamlined categorisation of the mango germplasm and elucidated the primary distinctions among the germplasm, grouping them based on their quantitative values of each parameter. Majumder *et al.* (2013) highlighted significant genetic diversity in mango genotypes through multivariate analysis, aiding breeding programs in Bangladesh. Khadivi *et al.* (2022) identified superior mango genotypes based on morphological and pomological traits, supporting the selection of high-quality cultivars for commercial production. Both studies emphasize the role of genetic and phenotypic evaluation in mango improvement.

Thus, the results of this sudy demonstrated high genetic variation, heritability and genetic gain, making them reliable for breeding programs. Principal component analysis (PCA) highlighted the distinctiveness of PMSS-11 and PMSS-7 among the germplasms, suggesting their potential as superior parental lines for hybridization. This research provides a foundation for genetic improvement and sustainable mango cultivation in the region.

Acknowledgments

The authors would like to thank the Department of Horticulture, GBPUA&T, Pantnagar, Uttarakhand (India) and ICAR-AICRP on Fruits for financial support for the work and also thank to Uttarakhand Council of Biotechnology, Haldi, Uttarakhand for the providing resources and laboratory.

Authors' contribution: J.S. Shivran: Data curation, Formal analysis, Investigation, Methodology, Validation, Writing - original draft; **A.K. Singh and R. Kumar:** Data curation (Supporting), Writing, revision and editing; **I. Kumari, R. Jat, M.L. Jat:** Conceptualization, Software, Data analysis/interpretation, Writing, revision and editing.

Funding: No external financial support, grants, or funding has been received.

Research content: The research content of manuscript is original and has not been published elsewhere.

Ethical approval: Not applicable.

Conflict of interest: The authors declare that is there is no conflict of interest.

Data availability: The original contributions presented in the study are included in the article material, further inquiries can be directed to the corresponding authors.

Consent to publish: All authors agree to publish the paper in *Journal of Environmental Biology.*

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