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Research Article

Variability studies and genetic divergence in chilli (*Capsicum spp.*) genotypes using multivariate analysis

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Abstract
Forty three genotypes of chilli belonging to three different species *viz.,Capsicum annuum, Capsicum chinense, Capsicum frutescens* were evaluated for genetic variability and divergence at College Orchard of Tamil Nadu Agricultural University, Coimbatore. The analysis of variance revealed that the germplasm lines had substantial genetic diversity. Values of close proximity between PCV and GCV indicated that the traits were mostly under genetic control and less affected by the environment. High heritability and genetic advance were observed for almost all the yield contributing traits. PCA showed that five of the 13 main components showed significant results with 77.89% of the total variance, of which the highest variability (26.50%) was exhibited by PC1. Cluster analysis showed maximum intra cluster distance in cluster 3 (515.90). Genotypes in cluster 3 and cluster 4 were genetically distant (2686.11) and can be exploited for the development of hybrid in future breeding programmes.

Keywords: Mahalanobis D², genetic divergence, Clusters, PCA, heritability

INTRODUCTION

Chilli holds an integral place in the diet of every household. Despite its origin in South America, the prevailing climatic conditions in India along with the local ethno-agricultural practices of rural communities have rendered it particularly suitable for the proliferation of chilli species. Numerous native chilli varieties specific to their respective cultivation regions have evolved and attained the designation of geographical indication. Examples of these include Assam's Bhut Jholokia, Goa's Khola chillies, Andhra Pradesh's Guntur Sannam, Karnataka's Byadagi, Sikkim's Dalle Khursani, Manipur's Hathei chilli, Kerala's Edayur chilli, and Tamil Nadu's Ramnad Mundu *etc.,* India ranks first globally in terms of production, consumption, and export (PJTSAU, 2023). The dry tract, high temperature, constant market demand and high price of chilli makes Andhra Pradesh a leader in chilli cultivation with 43% production (Kavitha *et al.,* 2022). The main focus of chilli cultivation is concentrated in the Central and Southern regions of the country, including states like Andhra Pradesh, Karnataka, Maharashtra, and Tamil Nadu. (Usha Nandhini Devi and Pugalendhi 2022). Even though the demand for chilli is on the rise, the nation's current chilli production is notably insufficient and is diminishing due to a range of factors.

One of the primary strategies to enhance the chilli production involves the development of elite cultivars after in-depth exploration of germplasm (Purad *et al.,*2019). The genus *Capsicum* exhibits an immense variation in morphological features and biochemical properties making it the most divergent species. Understanding the diversity between the species provides a broader perspective on genetic variation, evolution and the interconnections between species and their environments. It can also help us to identify novel genes or recombinants that could be introduced into the cultivars through breeding thereby enhancing crop productivity and quality.

The knowledge gained through the assessment of genetic variability paves the way for effective utilisation of the genotypes in breeding programmes and aids in the introduction of a newer variety with advantageous features for commercial exploitation (Pugalendhi *et al.,*2020). GCV and PCV metrics are helpful in determining the genetic coefficient of variability in the germplasm. The influence of environment on character expression and the extent to which improvement is feasible after selection are determined by heritability and genetic advancement. Divergence analysis produces insightful data on the kind and extent of genetic variability among the genotypes. Genetically diverging parents are anticipated to have a strong heterotic effect that will improve the economic characteristics of the offspring that are being taken into account. In segregating generations, the broad spectrum of variation may manifest itself in transgressive and productive recombinants. Additionally, estimating genetic divergence helps to scale down the enormous collection of data on genotypes, which in turn helps in selecting the divergent parents for crossing. A popular dimension reduction technique known as PCA can be used to condense a large number of variables into a smaller set while retaining the majority of the information in the larger set. The PCA analysis creates component scores for the characters by condensing the dimensions of a multivariate dataset to a small number of primary axes, creating an eigenvector for each axis. The eigenvalue of a specific principal component illustrates the extent of variation within traits that are accounted for by that particular principal component. This information holds significant value for subsequent breeding programs.

Hence, the primary aim of this research was to examine the inherent genetic variations present within the chilli genotypes and to categorise these genotypes into distinct clusters using cluster analysis and principal component analysis. Moreover, the study sought to identify the appropriate genotypes for utilisation in chilli hybridisation programs.

MATERIALS AND METHODS

The research was conducted with 43 germplasm accessions of chilli that were sourced from different geographical regions and maintained at the Dept. of Vegetable Science, Tamil Nadu Agricultural University, Coimbatore, to investigate the genetic variations among the accessions (**Table 1)**. The crop was raised in the college orchard. The recommended agronomic practices were strictly followed for proper plant growth and development. Initially, the accessions were raised in protrays and subsequently transplanted in randomised block design with two replications in main field with a spacing of 60 cm x 45 cm, after a period of 45 days.

Observations were recorded on yield and its components namely plant height (cm), primary branches per plant, days to first flowering, duration to 50% flowering, leaf length (cm), leaf width (cm), fruit length (cm), fruit girth (cm), fruit stalk length (cm), individual fresh fruit weight (g), individual dry fruit weight (g), number of fruits per plant, number of seeds per fruit and hundred seed weight (g). The Analysis of variance (ANOVA) (Panse and Sukathme, 1967), genotypic coefficient of variation (GCV) (Burton,1952), phenotypic coefficient of variation (PCV) (Burton,1952), heritability (h^2) (Lush, 1940), genetic advance as a percentage of mean (GAM) (Johnson *et al.,* 1955) was calculated using TNAUSTAT data analysis software (Manivannan, 2014). The assessment of genetic divergence within the population was conducted using Mahalanobis D^2 statistics (Mahalanobis, 1936). To classify genotypes into distinct clusters, Tocher's method was employed and both inter and intra cluster distances were calculated. Using the STAR software of IRRI, principal component analysis, eigenvalues, eigenvectors and biplots were derived.

RESULTS AND DISCUSSION

The Analysis of Variance (ANOVA) (**Table 2)** indicated substantial variations among the 43 genotypes for all the quantitative characters under study, implying genetic variability for the characters under consideration. Estimates for the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2) and GA as a percentage of mean for the traits (GAM) are furnished in **Table 3**. Every attribute under consideration showed coherence between the values of PCV and GCV demonstrating that these traits were less influenced by the environment and that genotype had a highly significant influence on phenotypic expression. High PCV and GCV (>20%) was observed for plant height (29.43, 28.12), leaf length (37.83, 35.98), leaf width (39.08, 37.58), fruit length (47.00, 46.75), fruit girth (37.83, 37.13), single fresh fruit weight (37.78, 37.49), single dry fruit weight (45.49, 43.55), number of seeds per fruit (38.39, 37.80), hundred seed weight (26.83, 24.48) indicating that there are more opportunities for selection-based genetic improvement. The outcome further supported the findings of Kumari *et al.* 2014 and Krishnamurthy *et al*. 2013. High PCV (21.70) but moderate GCV (14.33) was observed for number of fruits per plant. The result is in contrast with the research findings of Jyothi *et al.* 2011 and Sarkar *et al.* 2009 who observed high PCV and GCV for

Table 1. List of genotypes and their sources utilised in this study

S.No	Accessions	Species	Source
01	CA-CBE-116	*Capsicum annuum*	Rahuri,Maharshtra
02	CA-CBE-193	*Capsicum annuum*	Coimbatore, Tamil Nadu
03	CA-CBE-199	*Capsicum annuum*	Mudigree, Karnataka
04	CA-CBE-200	*Capsicum annuum*	Coimbatore, Tamil Nadu
05	CA-CBE-201	*Capsicum annuum*	Kashmir
06	CA-CBE-202	*Capsicum annuum*	Sri Lanka
07	CA-CBE-203	*Capsicum annuum*	Muthukrishnapuram, Cuddalore, Tamil Nadu
08	CA-CBE-204	*Capsicum annuum*	Suloor, Coimbatore,Tamil Nadu
09	CA-CBE-205	*Capsicum annuum*	Coimbatore, Tamil Nadu
10	CA-CBE-206	*Capsicum annuum*	Coimbatore, Tamil Nadu
11	CA-CBE-207	*Capsicum annuum*	Coimbatore, Tamil Nadu
12	CA-CBE-213	*Capsicum annuum*	Bhavani, Erode, Tamil Nadu
13	CA-CBE-215	*Capsicum annuum*	Ramanathapuram, Tamil Nadu
14	CA-CBE-216	*Capsicum annuum*	Cuddalore, Tamil Nadu
15	CA-CBE-217	*Capsicum annuum*	Hampi, Karnataka
16	CA-CBE-218	*Capsicum annuum*	Guntur, Andhra Pradesh
17	CA-CBE-219	*Capsicum annuum*	Virudhunagar, Tamil Nadu
18	CA-CBE-220	*Capsicum annuum*	Virudhunagar, Tamil Nadu
19	CA-CBE-221	*Capsicum annuum*	Virudhunagar, Tamil Nadu
20	CA-CBE-222	*Capsicum annuum*	Aladipatti, Virudhunagar, Tamil Nadu
21	CA-CBE-223	*Capsicum annuum*	Virudhunagar, Tamil Nadu
22	PLR 1	*Capsicum annuum*	Palur,Tamil Nadu
23	CC-CBE-001	*Capsicum chinense*	Coimbatore, Tamil Nadu
24	CC-CBE-002	*Capsicum chinense*	Yercaud, Salem, Tamil Nadu
25	CC-CBE-003	*Capsicum chinense*	Yercaud, Salem, Tamil Nadu
26	CC-CBE-004	*Capsicum chinense*	Tarangapura, Karnataka
27	CC-CBE-005	*Capsicum chinense*	Yercaud, Salem, Tamil Nadu
28	CC-CBE-006	*Capsicum chinense*	Yercaud, Salem, Tamil Nadu
29	CC-CBE-007	*Capsicum chinense*	Yercaud, Salem, Tamil Nadu
30	CC-CBE-008	*Capsicum chinense*	Yercaud, Salem, Tamil Nadu
31	CC-CBE-009	*Capsicum chinense*	Yercaud, Salem, Tamil Nadu
32	CC-CBE-010	*Capsicum chinense*	Yercaud, Salem, Tamil Nadu
33	CC-CBE-011	*Capsicum chinense*	Yercaud, Salem, Tamil Nadu
34	CC-CBE-012	*Capsicum chinense*	Yercaud, Salem, Tamil Nadu
35	CC-CBE-013	*Capsicum chinense*	Yercaud, Salem, Tamil Nadu
36	CC-CBE-016	*Capsicum chinense*	AAU, Jorhat, Assam
37	CC-CBE-017	*Capsicum chinense*	Coimbatore, Tamil Nadu
38	CC-CBE-018	*Capsicum chinense*	Lumpo, Lower Siang District, Arunachal Pradesh
39	CF-CBE-004	*Capsicum frutescens*	Vellanikkara, Tamil Nadu
40	CF-CBE-005	*Capsicum frutescens*	Vellanikkara, Tamil Nadu
41	CF-CBE-006	*Capsicum frutescens*	Coimbatore, Tamil Nadu
42	CF-CBE-007	*Capsicum frutescens*	Sirumalai, Dindigul, Tamil Nadu
43	CF-CBE-008	*Capsicum frutescens*	Pattampakkam, Cuddalore, Tamil Nadu

Table 2. Analysis of variance for 14 characters under study

Character	Mean sum of square		
	Genotype	Replication	Error
Plant height	1559.48*	35.17	71.11
No. of. Primary Branches	0.57*	0.3	0.21
Days for 1st flowering	13.61*	12.66	7.88
Days to 50% flowering	72.12*	320.42*	41.09
Leaf length	14.51*	7.50*	0.73
Leaf width	5.04*	5.23*	0.2
Fruit length	15.92*	0.09	0.08
Fruit girth	5.54*	0.01	0.1
Fruit stalk length	0.39*	0.18*	0.04
Single fresh fruit weight	2.77*	1.92*	0.02
Single dry fruit weight	0.20*	0.08*	0.01
No. of. fruit per plant	126.25*	98.42	42.59
No. of. seeds/fruit	706.82*	198.33*	10.96
Hundred seed weight	0.03*	0	0

* Significance at 5% level

Table 3. Estimation of PCV, GCV, heritability and Genetic advance as a percentage of mean in chilli genotypes

S. No.	Character	Mean	Maximum	Minimum	Coefficient of variation		h2 (%)	GAM (%)
					PCV (%)	GCV (%)		
1	Plant height	97.03	169.00	48.25	29.43	28.12	91.28	55.33
2	No. of. Primary Branches	3.62	4.75	2.70	17.18	11.68	46.22	16.35
3	Days for 1st flowering	31.66	39.50	26.50	10.35	5.35	26.69	5.69
4	Days to 50% flowering	50.67	60.50	35.50	14.85	7.77	27.41	8.38
5	Leaf length	7.30	14.55	4.70	37.83	35.98	90.47	70.50
6	Leaf width	4.14	11.15	2.45	39.08	37.58	92.45	74.43
7	Fruit length	6.02	11.37	2.40	47.00	46.75	98.94	95.80
8	Fruit girth	4.44	7.95	1.71	37.83	37.13	96.34	75.07
9	Fruit stalk length	2.67	3.57	1.10	17.27	15.62	81.84	29.11
10	Single fresh fruit weight	3.13	6.46	0.66	37.78	37.49	98.47	76.64
11	Single dry fruit weight	0.72	1.52	0.10	45.49	43.55	91.66	85.89
12	No. of. fruit per plant	41.28	60.50	31.00	21.70	14.33	43.58	19.48
13	No. of. seeds/fruit	49.34	78.50	21.00	38.39	37.80	96.95	76.68
14	Hundred seed weight	0.45	0.82	0.25	26.83	24.48	83.25	46.02

number of fruits per plant. Moderate PCV and GCV was observed for two traits *viz.,* fruit stalk length (17.27, 15.62) number of primary branches (17.18, 11.68) suggesting that direct selection is less likely to be effective for improvement of these characters. Moderate PCV and low GCV was recorded for days for first flowering (10.35, 5.35) and days for 50% flowering (14.85, 7.77).

Heritability estimates along with genetic advance would be helpful in predicting the gain under selection than heritability estimates alone. The traits like plant height (91.28, 55.33), leaf length (90.47, 70.50), leaf width (92.45, 74.43), fruit length (98.94, 95.80), fruit girth (96.34, 75.07), fruit stalk length (81.84, 29.11), single fresh fruit weight (98.47, 76.64), single dry fruit weight (91.66, 85.89), number of seeds per fruit (96.95, 76.68), hundred seed weight (83.25, 46.02) recorded high heritability (>75%) in combination with high GA (>20%) indicating that these characters were controlled by the additive gene action. Thus, these characters could be considered as reliable indices for selection. Similar results of high heritability coupled with high genetic advance were reported by Jyothi *et al.* 2011. Moderate h^2 and GA were recorded for the traits like number of fruits per plant (43.58, 19.48)

and number of primary branches (46.22, 16.35). While the traits like days to first flowering (26.69, 5.69) and days to 50% flowering (27.41, 8.38) exhibited low h^2 coupled with low GA.

Divergence analysis revealed that the genotypes were grouped into six clusters (**Table 4)**. Cluster 2 comprised of 19 genotypes followed by cluster 1 which comprised of 16 genotypes. Clusters 5 and 6 were solitary with single genotype each. Geographical barriers inhibiting gene flow and intense natural and human selection for unique and adaptable gene complexes must be accountable for this genetic variety, which may explain the emergence of solitary clusters. Thus, the genotypes CA-CBE-215 and CC-CBE-013 are known for their independent identity and possess unique characters which differentiate them from other genotypes. The genes which are responsible for their uniqueness are conserved from genetic erosion. The combination of the distinct species *C. annum, C. chinense,* and *C. frutescens* in cluster 1 may be explained by cross-fertilization occurring at the geographical location. This result support the findings of Thul *et al.*2006 and Thul *et al.*2009. Some of the genotypes which were collected from the same origin were grouped into different clusters and this may be because of broad genetic base present in the genotypes. The result supports the findings of Hasan *et al.* 2015. The clustering pattern in the current study did not match the taxonomic labels or geoclimatic zonal distribution, indicating that variables other than geographic boundaries are also involved in divergence. This is in accordance with the findings of Mamatha and Devaraju, 2017 and Thul *et al.* 2009.

Greater genetic divergence can result from genetic drift and environmental factors than from geographic distance. Before initiating hybridisation work, emphasis must be given for calculating the genetic distance as genetically distinct parents can exhibit high heterosis. While choosing genotypes for crossing program, they must be selected from different clusters for obtaining novel recombinants as the genotypes from same cluster may diverge only a little and may not lead to the desirable segregants. Cluster 3 and cluster 4 showed maximum inter cluster distance (2686.11) followed by cluster 2 and cluster 4 (1436.30) (**Table 5**). Cluster 1 and cluster 6 showed minimum inter-cluster distance (516.59) followed by clusters 2 and 5 (539.44) which indicates that the genotypes found in these clusters were almost similar. Therefore, the genotypes from cluster 3 when crossed with the genotype from cluster 4 are expected to contribute a greater heterotic effect in the first generation and broad spectrum of variability can be noticed in the segregating generations. The intra-cluster distance ranged from 0 to 515.90. This is in accordance with the findings of Hasan *et al.* 2015.

Cluster 3 and cluster 6 secured maximum mean values for most of the characters (**Table 6**). The highest mean values for fruit girth (7.128), fruit stalk length (3.073), single fresh fruit weight (5.968), single dry fruit weight (1.165) and hundred seed weight (0.568) were found in cluster 3. This clearly shows that cluster 3 exhibited maximum variations for the fruit parameters. Number of fruits per plant (48.00), number of seeds per plant (70.00) scored highest cluster mean values in cluster 5. Cluster 4 secured minimum values for most of the characters. The

Table 4. Cluster composition of genotypes based on D^2 values

Cluster number	Number of genotypes	Genotypes
1	16	CC-CBE-009, CC-CBE-010, CC-CBE-007, CC-CBE-012, CC-CBE-011, CC-CBE-003, CC-CBE-008, CC-CBE-017, CC-CBE-016, CC-CBE-002, CC-CBE-018, CA-CBE-216, CC-CBE-001, CF-CBE-005, CC-CBE-006, PLR 1
2	19	CA-CBE-218, CA-CBE-220, CA-CBE-193, CA-CBE-219, CA-CBE-205, CA-CBE-207, CA-CBE-223, CA-CBE-221, CA-CBE-222, CA-CBE-204, CA-CBE-206, CA-CBE-202, CA-CBE-201, CA-CBE-199, CA-CBE-203, CA-CBE-213, CA-CBE-200, CA-CBE-217, CA-CBE-116
3	2	CC-CBE-005, CC-CE-004
4	4	CF-CBE-004, CF-CBE-007, CF-CBE-008, CF-CBE-006
5	1	CA-CBE-215
6	1	CA-CBE-013

Table 5. Average inter and intra cluster distance among 43 genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	319.1229	889.78	995.51	826.09	570.09	516.59
Cluster 2		277.9261	1090.66	1436.30	539.44	1217.06
Cluster 3			515.902	2686.11	1048.53	1413.11
Cluster 4				285.3943	1099.62	937.69
Cluster 5					0	983.25
Cluster 6						0

Table 6. Cluster wise mean values of 14 characters of genotypes in chilli

CLUSTER	Plant height	No. of. Primary branches	Days for 1st flowering	Days to 50% flowering	Leaf length	Leaf width	Fruit length	Fruit girth	Fruit stalk length	Single fresh fruit weight	Single dry fruit weight	No. of. fruits per plant	No. of. seeds / fruit	Hundred seed weight
1	115.350	3.563	31.531	53.063	6.281	4.256	3.682	5.544	2.510	3.320	0.675	41.000	35.000	0.518
2	82.134	3.692	31.395	47.263	7.808	3.703	8.729	3.397	2.877	3.166	0.851	41.895	66.247	0.408
3	98.025	3.475	32.250	51.750	5.825	3.000	6.215	7.128	3.073	5.968	1.165	43.750	44.000	0.568
4	87.213	3.313	31.125	56.500	7.838	4.688	2.818	2.629	2.094	0.805	0.194	37.250	27.875	0.333
5	89.800	4.750	32.000	42.000	7.400	3.650	6.795	7.100	2.770	2.720	0.235	48.000	70.000	0.475
6	131.350	3.550	39.500	60.500	14.550	11.150	3.455	5.850	2.685	3.370	0.585	38.500	33.500	0.550

result showed that the genotypes having high values for a particular trait may be selected and utilised in the selection of parents for the hybridisation programme. Similar divergence studies were carried out by Binoli *et al.* 2023; Indrabi *et al.*2021; Saisupriya *et al.* 2022; Sushmitha *et al.* 2019; Nagaraju *et al.* 2018, Pujar *et al.* 2017; Pradhan *et al.* 2017; Lakshmi devamma *et al.* (2021); Hasan *et al.* (2015). From the **Table 7** and **Fig. 1**, it is clearly shown that Fruit length contributed maximum towards divergence (42.85%) followed by single fresh fruit weight (23.69%), number of seeds per fruit (12.62%), fruit girth (8.63%), single dry fruit weight (5.20%), leaf width (2.32%), leaf length (1.99%), hundred seed weight (1.43%) while the least contribution was by plant height (0.99%). The results were in accordance with the earlier reports by Thul *et al.* (2009) suggesting that fruit characteristics contributed much to the genetic divergence and can be taken into account for consideration. Number of primary branches, Days to first flowering, Days to 50% flowering, number of fruits per plant did not contribute towards divergence. This is in accordance with the results published by Saisupriya *et al.*(2022). The characters that contribute the maximum need to be given a greater emphasis in the selection of parents for hybridisation. The yield characteristics such as fruit length, fruit diameter and fruit weight with high genetic variation and heritability could be considered as reliable selection criteria for yield enhancement in chilli. In this study widespread range of variability for economically important traits was observed among the genotypes which support the findings of Raghuveer *et al.*(2022).

The proportional contribution of the various features to the overall variance of the genotypes of chillies under study has been explained by PCA. Eight components with eigen values more than 0.5 account for 92.69% of the variance, whereas five of the thirteen principal components with substantial eigenvalues (eigenvalue > 1) accounted for 77.89% of the overall variance (**Table 8)**. The PC1 showed the highest level of variability (26.50%), followed by the PC 2 (17.90%), PC 3 (14.41%), PC4 (11.81%) and PC 5 (7.27%). The contributions of each principal component to the overall phenotypic variance are depicted in **Fig. 2**. A scree plot that represents the relationship

Table 7. Percent contribution of different characters towards divergence

S.No.	Character	Times ranked 1st	Contribution %
1	Plant height	9	0.99
2	Number of primary branches	0	0
3	Days for 1st flowering	0	0
4	Days to 50% flowering	0	0
5	Leaf length	18	1.99
6	Leaf width	21	2.32
7	Fruit length	387	42.85
8	Fruit girth	78	8.63
9	Fruit stalk length	2	0.22
10	Single fresh fruit weight	214	23.69
11	Single dry fruit weight	47	5.20
12	Number of fruits per plant	0	0
13	Number of seeds per fruit	114	12.62
14	Hundred seed weight	13	1.43

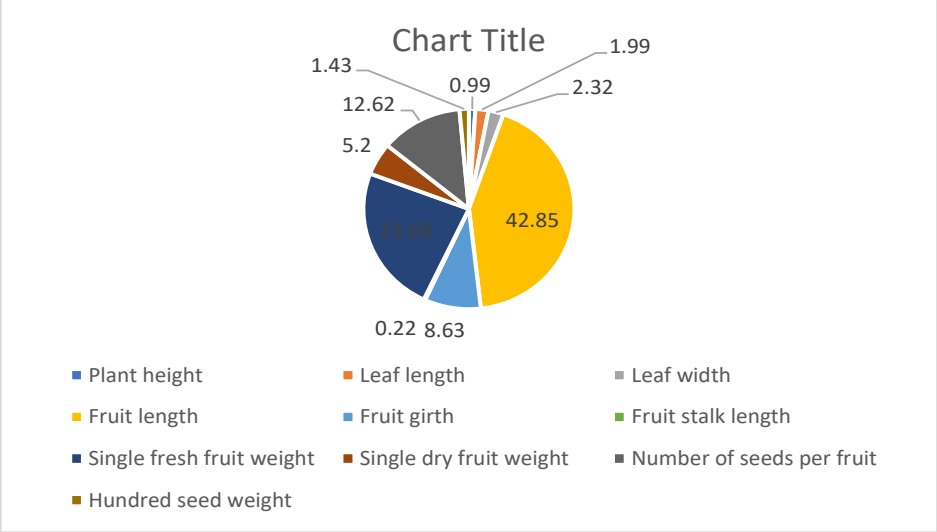

Fig. 1. Pie chart representing percent contribution of each characters towards divergence

Table 8 Table depicting Eigen values, percentage of variability, cumulative variability and attributes that contributed towards variability

Statistical variable	PC1	PC2	PC3	PC4	PC5
Eigen value	3.7095	2.5059	2.0173	1.6532	1.0172
Variance percent	26.50	17.90	14.41	11.81	7.27
Cumulative variance percent	26.50	44.40	58.80	70.61	77.88
Variables	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**
Plant.height	-0.30	0.33	-0.11	0.06	-0.41
No.of.primary.branches	0.14	-0.12	0.63	0.01	-0.02
Days.for.first.flowering	-0.10	0.19	-0.03	-0.33	0.52
Days to50flowering	-0.32	-0.09	0.14	-0.06	0.60
Leaf.length	-0.07	-0.20	0.00	-0.63	-0.32
Leaf.width	-0.27	-0.03	0.02	-0.61	-0.10
Fruit.length	0.47	-0.02	-0.07	-0.17	-0.12
Fruit.girth	-0.18	0.38	0.33	-0.06	-0.08
Fruit.stalk.length	0.30	0.27	-0.09	-0.15	0.07
Single.fresh.fruit.weight	0.17	0.47	0.11	-0.07	0.02
Single.dry.fruit.weight	0.29	0.33	-0.09	-0.13	0.20
Number.of.seeds.per.fruit	0.46	-0.05	-0.05	-0.18	0.07
Number.of.fruit.per.plant	0.14	-0.09	0.64	-0.02	-0.07
Hundred.seed.weight	-0.12	0.48	0.12	0.03	-0.12

between the eigen values and principal component is obtained and that clearly shows that with an eigenvalue of 3.7095, PC 1 showed the largest variance of 26.50%, which steadily decreased in other principal components. The curve virtually becomes a straight line after PC 5 indicating that there is lesser variance in each PCs (**Fig. 3**). The graph makes it evident that PC1 experienced the greatest fluctuation when compared to the other four PCs, hence choosing lines for characters in PC1 may be preferable. Similar experimental results were obtained by Singh *et al.* 2020, Rahevar *et al.*2021.

The traits like fruit length (0.47), number of seeds per fruit (0.46), fruit stalk length (0.30), single dry fruit weight (0.29), single fresh fruit weight (0.17), number of primary branches (0.14) and number of fruits per plant (0.14) contributed positively to PC1 while other characters like leaf length, days to first flowering, hundred seed weight,

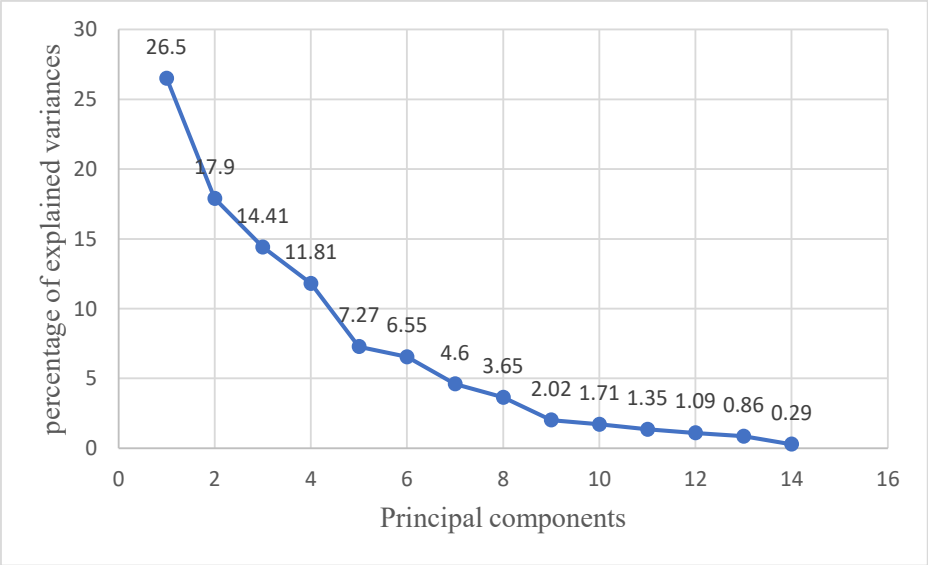

Fig. 2. Graph showing contributions of each principal component to the overall phenotypic variance

fruit girth, leaf width, plant height and days to 50 % flowering contributed negatively (**Table 8**). On the other hand, PC2 was contributed positively by hundred seed weight (0.48), single fresh fruit weight (0.47), fruit girth (0.38), plant height (0.33), single dry fruit weight (0.33), fruit stalk length (0.27) and days to first flowering (0.19). While other traits like fruit length, leaf width, number of seeds per fruit, days to 50% flowering, number of fruits per plant, number of primary branches and leaf length contributed negatively to PC2. A two-dimensional PCA plot was constructed based on the first two principal components which accounted for 44.40% variation (**Fig. 4**). Rahevar *et al.* (2021) and Devi *et al.* (2017) also reported that principal component values can be used for genetic divergence.

Analysis of variance and multivariate statistical analysis indicated that a diverse array of variations were present among the genotypes studied. Traits like plant height, leaf length, leaf width, fruit length, fruit girth, single fresh fruit weight, single dry fruit weight, number of seeds per fruit, and hundred seed weight have scored highly for

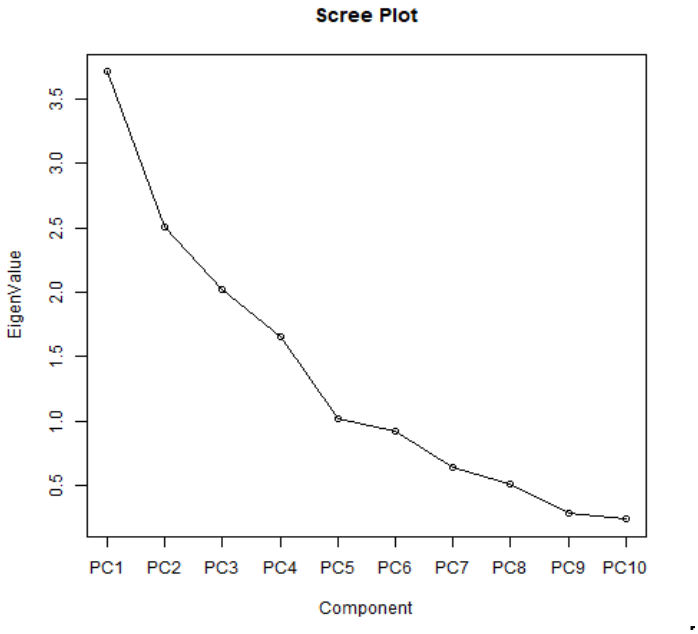

Fig. 3. Scree plot of chilli germplasm showing relationship between eigen values and principal components

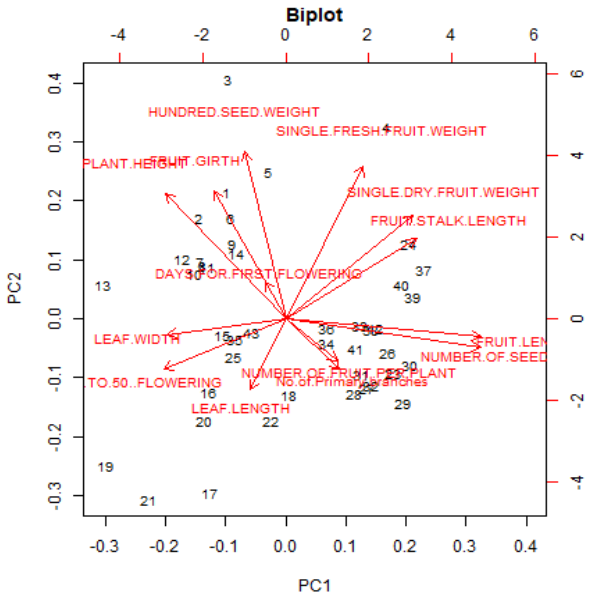

Fig. 4. Biplot scatter diagram of chilli germplasm

PCV, GCV, h2 and GA. Therefore, these characteristics could be regarded as reliable criteria for improving the crop through selection processes. Principal Component Analysis (PCA) demonstrated that out of the 14 main components, five held significance (with eigenvalues exceeding 1), contributing to 77.89% of the variability. The first principal component (PC1) was primarily influenced by factors related to economically important characters. Consequently, opting for genotypes with higher PC1 scores could lead to increased yield. Genotypes displaying strong performance from clusters located further apart (such as clusters 3 and 4, 2 and 4) have the potential to be incorporated into breeding programs to create superior hybrids by capitalizing on heterosis during subsequent generations.

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