Received: 07 Oct 2020 | Revised: 24 May 2021 | Accepted: 28 May 2021

Electronic Journal of Plant Breeding

Research Article

Genetic diversity study in chilli (*Capsicum annuum* L.) using multivariate approaches

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Abstract

An experiment was conducted to analyze the genetic diversity among 58 genotypes with 7 quantitative and 5 qualitative characters in chilli and two multivariate techniques; principal component analysis and cluster analysis. Based on D^2 cluster analysis, the 58 genotypes were grouped into three distinct clusters. The highest inter cluster distance was observed between clusters I and III. The maximum contribution towards genetic divergence was shown by green fruit yield per plant (0.59) and primary branches per plant. Principal component analysis indicates that the first five principal components explain 74.90 per cent of the total variation. PC1 which accounted for the highest variation was mostly related to days to initiation of flowering and days to first picking as most of the important yield attributing and quality traits were present in PC1, PC2 and PC5. This study generally indicated that there was a significant genetic diversity among the test genotypes.

Key words

Chilli, genetic divergence, Mahalanobis clustering, principal component analysis

INTRODUCTION

Chilli (*Capsicum annuum*L.) is an important vegetable and condiment crop having immense commercial and therapeutic value with great export potential. Chilli is also known as bird pepper, cayenne, paprika, hot and sweet pepperbelongstothegenus*Capsicum*ofSolanaceaefamily, subfamily Solanoideae and tribe Capsiceae (Hunziker, 2001; Knapp *et al*., 2004). It is a diploid (2n=2X=24), annual or short-lived perennial herb with several cultivated forms differing from each other in shape, size, colour, position (erect or pendent)and pungency of the fruits. The Bhutjolokia hottest chilli in the world (1,041,427 SHU), also known as a ghost pepper, ghost chilli, U-morok, red-naga, nagajolokia and ghost jolokia, is an interspecific hybrid pepper cultivated in the Northeast Indian states of Arunachal Pradesh, Assam, Nagaland and Manipur. The genus *Capsicum* consists of approximately 22 wild and 5 cultivated species, which includes *C. annuum*, *C. baccatum, C. chinense, C. frutescens*and *C. pubenscens.* Peppers are considered the first spice to have been used by human beings and there is archaeological evidence of pepper and other fossil foods from as early as 6000 years ago (Hill *et al*., 2013). As the maximum diversity for the genus *Capsicum* is observed in Mexico, it is assumed to be the centre of origin of this crop. Molecular analysis (Loaiza Figueroa *et al.,* 1989) also confirmed that the centre of domestication of *C. annuum var. longum,* the cultivated variety, is the upland region of central-eastern Mexico; while Guatemala is considered as a secondary centre of origin (Salvador, 2002). *Capsicum annuum* species includes the vast majority of the cultivated pungent and non-pungent (sweet) chillies in temperate as well as some tropical areas.

The success of selection depends on the presence of wide genetic diversity in the experimental material. Generally, diverse plants are expected to give high hybrid vigour (Harrington, 1940). The knowledge regarding the extent of variability and genetic diversity is of much importance while improving in a complex trait like yield. Hence, it necessitates the study of genetic divergence among the existing varieties and germplasm collection for identification of parents for hybridization programme. The information on genetic divergence of various traits particularly of those that contribute to yield and quality would be of most useful in planning the breeding programme. D^2 statistics developed by Mahalanobis (1936) and described by Rao (1952) provides a measure of magnitude for the divergence between two genotypes under comparison. It considers the variation produced by any character and their consequent effect that it bears on other characters. The technique was first used by Mahalanobis in an anthropometric survey of the united province in India.

Principal Component Analysis (PCA) involves a mathematical procedure that transforms several (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal component. PCA is an important statistical method through which we can easily identify important polygenic characters which are of great importance in a plant breeding programme. PCA provides an idea for how to reduce a complex data set to a lower dimension to reveal the sometimes hidden, simplified structures that often underlies it. The PCA analysis reduces the dimensions of a multivariate data to a few principal axes, generates an eigenvector for each axis and produces component scores for the characters. The eigenvalue of a particular principal component depicts the amount of variation present in traits and explained by that principal component which is very useful for the further breeding programme.

MATERIALS AND METHODS

Plant materials: Diverse fifty-eight chilli accession, collected from different research stations were evaluated at the Main Vegetable Research Station, Anand Agricultural University, Anand during the late *kharif* season in 2017–2018.

The thirty-five days old seedlings were transplanted using 60 x 60 cm plant to plant and row to row distance using a randomized complete block design. Five competitive plants were selected at random from each single row plot in each replication and phenotypic data were recorded for seven morphological characters viz., days to initiation of flowering, plant height (cm), fruits per plant, fruit length (cm), fruit diameter (cm), single green fruit weight (g) and green fruit yield per plant (g) and five biochemical parameters viz.,moisture content (%), chlorophyll content (mg/g), capsaicin content (%), ascorbic acid content (mg/100 g) and total phenol (%) using standard protocols.

D^2 analysis was carried out using a procedure developed by Mahalanobis (1936) and first suggested by Rao (1952) for the assessment of genetic diversity in plant breeding whereas PCA was performed using R and R-studio software using factoextra and ggbiplot packages.

Table 1. Clustering pattern of fifty-eight genotypes of Chilli based on genetic divergence

Clusters	Number of genotypes	Genotypes	sources
I	55	ACGP–2,ACGP–7,ACGP–10,ACGP–15,ACGP–19,ACGP–25,ACGP–26,ACGP–27,ACGP–29,ACGP–37,ACGP–38,ACGP–46,ACGP–48,ACGP–49,ACGP–50,ACGP–57,ACGP–58,ACGP–66,ACGP–67,ACGP–69,ACGP–74,ACGP–76,ACGP–78,ACGP–84,ACGP–88,ACGP–96,ACGP–99,ACGP–112,ACGP–113,ACGP–119,ACGP–125,ACGP–129,ACGP–130,ACGP–134,AVNPC–131,GVC–101,GVC–111,GVC–121,GAVC–112 and local selection	AAU, Anand.
		Anugraha, Byadagidabbi, Ajeet-6, Arkaabhir, DCL-2, PC-56	NAU,Navsari
		Kashi anmol and Kashi gaurav	Varanasi
		Mathania type – 1	Bikaner
		Arkalohit and Arkasuphal	Bengaluru
		Jawerivani	Nipani (KA)
		Gondaldhholar and US Agri 702	Gondal
		Seedco – 202	Anand (Pvt)
		Gujarat chilli – 3	Jagudan
II	2	ACGP –111	AAU, Anand.
		Gujarat chilli – 1	Jagudan
III	1	ACGP –135	AAU, Anand.

ACGP – Anand Chilli Germplasm, AVNPC – Anand vegetable no pungent chilli, GVC – Gujarat vegetable chilli and GAVC – Gujarat anand vegetable chilli

RESULTS AND DISCUSSION

Based on Mahalanobis D^2 (1936) statistics, all the genotypes were grouped into 3 clusters (**Table 1**). A maximum number of genotypes were accommodated in the Cluster-I (55) followed by cluster-II (2), and cluster-III (1). The clustering pattern of genotypes suggested that the geographic diversity may not necessarily be related to genetic diversity.It may be due to genetic drift or selection in different environments.Therefore, the selection of genotypes for hybridization should be based on genetic diversity rather than geographic diversity. Hasan *et al.* (2015) and Razzaq *et al.* (2016) found similar results by grouping 30 genotypes and 25 genotypes in 5 clusters, respectively.

Averages inter and intra cluster divergence (D^2) values have been presented in **Table 2** and **Fig. 1.** The diagonal figures (bold) in the table represent the intra cluster distances. The intra cluster distance was found the maximum in cluster I (3642.7) and minimum in cluster III (0). Whereas, the highest inter cluster distance (22195.58) was recorded between clusters I and III and the lowest (8501.38) was observed between clusters II and III. Based on the high inter-cluster value crossing of genotypes of cluster I and III could be useful to get maximum hybrid vigor and desirable segregants. Inter cluster distance was observed higher than intra cluster. The reason behind that may be due to distinct individual genotypes that were highly distinctive than most of the others and utmost contributing to the formation of new clusters. Similar results for inter and intra cluster distance and clustering were observed by Hasan *et al.* (2014), Srinivas *et al.*(2015) and Dutonde *et al.* (2008).

The cluster means for various traits have been presented in **Table 3**. The highest mean values for chlorophyll content (mg/g), capsaicin content (%) and total phenol (%); whereas the lowest mean values for days to first picking, fruit length (cm), single green fruit weight (g), green fruit yield per plant (g), moisture content (%) and ascorbic acid content ware present in cluster I. The highest mean values for plant height (cm), primary branches per plant and the number of fruit per plant; whereas the lowest mean values for days to initiation of flowering and fruit diameter (cm) were present in cluster II. Cluster III contains the maximum mean values for days to initiation of flowering, days to first picking, fruit length, fruit diameter (cm), moisture content (%), single green fruit weight (g), green fruit yield per plant (g) and ascorbic acid content (mg/100g) along with minimum mean values for plant height (cm), primary branches per plant, the number of fruit per plant, chlorophyll content (mg/g), capsaicin content (%) and total phenol. Cluster III contains single genotype which means all the mean values intended for representing cluster III belongs to that genotype only (ACGP-135). These results are in accordance with the findings of Smitha and Basavaraja (2006), Dushyantha *et al.* (2010), Farhad *et al.* (2010), Kumari *et al.* (2010), Datta and Das (2013), Janaki *et al.* (2016), Aklilu *et al.* (2016), Abhinaya *et al.* (2016) and Pradhan *et al.* (2017).

Table 2. Average intra (diagonal bold) and inter cluster distance (D^2)

Clusters	I	II	III
I	**3642.7**	10927.78	22195.58
II		**202.8**	8501.38
III			**0**

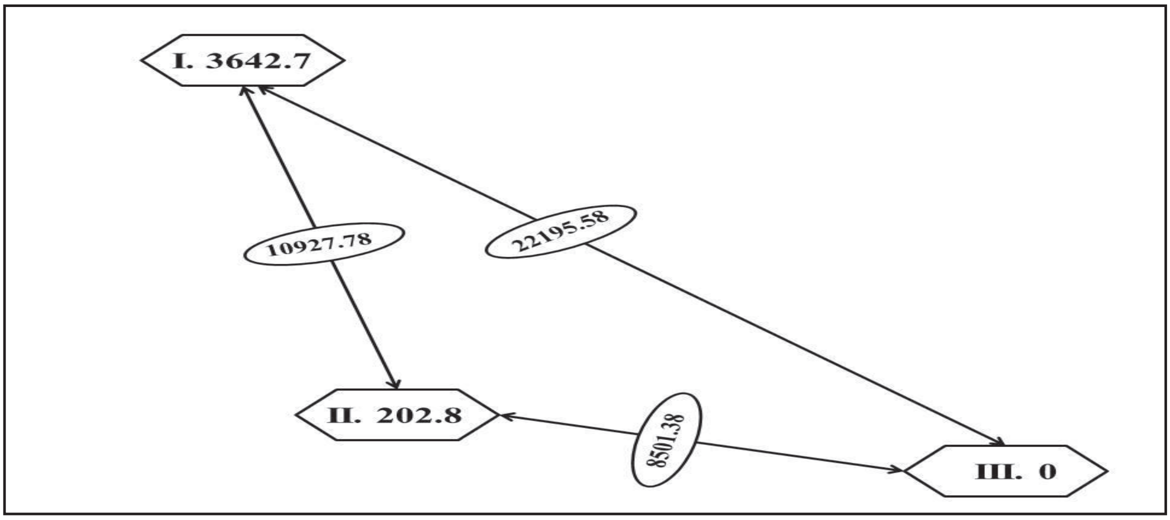


Fig. 1. Clustering pattern of different groups with inter-cluster and intra-cluster distance among the chilli genotypes

Table 3. Cluster means of different characters in chilli

	Days to initiation of flowering	Days to first picking	Plant height (cm)	Primary branches per plant	Number of fruits per plant	Fruit length (cm)	Fruit diameter (cm)	Single green fruit weight (g)	Green fruit yield per plant (g)	Moisture content (%)	Chlorophyll content (mg/g)	Capsaicin content (%)	Ascorbic Acid content (mg/100g)	Total phenol (%)
I	45.76	74.75	51.57	2.03	125.89	7.03	3.74	3.00	371.62	85.47	14.61	0.26	115.56	0.52
II	42.34	77.02	54.51	2.10	159.10	7.69	3.62	3.20	504.33	85.57	13.05	0.22	167.48	0.43
III	56.33	81.33	22.83	2.00	44.83	7.83	13.25	20.17	839.47	89.10	12.80	0.17	231.23	0.42
GM	45.82	74.5	50.83	2.04	125.64	7.1	3.9	3.31	384.26	85.38	14.52	0.25	119.37	0.52
SEm	4.77	3.64	5.25	0.18	18.23	1.06	0.7	1.06	81.83	0.67	1.22	0.03	17.51	0.05
CD	ns	10.18	14.65	0.5	ns	2.96	ns	ns	228.45	ns	ns	ns	48.89	ns
CV%	25.36	11.92	25.14	21.55	35.33	36.41	43.72	78.23	51.85	1.92	20.55	32.3	35.72	25.63
R^2	0.07	0.36	0.29	0.59	0.08	0.27	-	-	0.59	0.13	0.18	-	0.39	0.05
CV_b	7.36	8.92	16.06	25.85	10.67	22.24	-	-	62.33	0.74	9.68	-	29.04	6.33

R^2: Ratio of the inter-cluster variance/total variance, **-**: Not estimated due to –ve variance, **CV_b**: Inter-cluster coefficient of variation

The analysis of variance for each character was carried out using a mean of the 58 genotypes. Estimation of inter-cluster and intra-cluster variances, along with ratio (R^2) of inter-cluster variance to the total variance for the fourteen characters were worked out and presented in T**able 3**. The maximum value of R^2 was observed for green fruit yield per plant (0.59) and primary branches per plant (0.59) followed ascorbic acid content (0.39), days to first picking (0.36), plant height (0.29), fruit length (0.27) and chlorophyll content (0.18). The maximum contribution of fruit yield per plant towards the total divergence was also observed by Hasan *et al.* (2014), Srinivas *et al.*(2015) and Hasan *et al.* (2015). These traits had more contribution to genetic divergence. Hence, the selection of divergent parents based on these characters will be useful for selection in heterosis breeding in chilli. The R^2 value of total phenol was the least (0.05) among all the characters under study depicting the minimum contribution of the trait for the divergence. As regards the fruit diameter, single green fruit weight and capsaicin content, it has no contribution to the divergence because the value of R^2 was not estimated due to negative variance. Similar result for the contribution of fruit diameter and single green fruit weighttowards the total genetic divergence was also observed by Srinivas *et al.* (2015) and Yatung *et al.* (2014).

Inter-cluster coefficient of variance was maximum for green fruit yield per plant (62.33) followed by ascorbic acid content (29.04), primary branches per plants (25.85), fruit length (22.24), plant height (16.06), the number of fruits per plant (10.67) and chlorophyll content (9.68). These traits manifested higher CV_b values demonstrating an important role in the genetic discrimination of the genotypes included under study. The minimum CV_b (0.74) was observed for moisture content.

Earlier workers like Smitha and Basavaraja (2006), Dutonde (2008), Dushyantha *et al.* (2010), Farhad *et al.* (2010), Kumari *et al.* (2010), Datta and Das (2013), Hasan *et al.* (2014), Yatung *et al.* (2014), Hasan *et al.* (2015), Srinivas *et al.* (2015), Janaki *et al.* (2016), Razzaq *et al.* (2016), Aklilu *et al.* (2016), Pradhan *et al.* (2017) and Vanitha and Jansirani (2017) have also indicated the significance of genetic divergence in chilli.

PCA is a well-known method of dimension reduction that can be used to reduce a large set of variables to a small set that still contains most of the information present in the large set (Singh *et al.,* 2020). The result of the PCA explained the genetic diversity of the chilli genotypes. There are no standard tests to prove the significance of proper values and coefficients. Principal component analysis has shown the genetic diversity of the germplasm lines. **Table 4** indicated that out of fourteen principal components, eleven components exhibited >0.5 eigenvalues and showed about 97.27 per cent variability whereas five components exhibited >1 eigenvalue and showed about 74.90 per cent variability among the traits studied. The PC1 had the highest variability (23.01%), followed by PC2 (18.35%), and PC3 (13.05 %). The high value of PC1 is in accordance with the findings of Janaki *et al.* (2015), Singh *et al.* (2020) and Singh *et al.* (2020). A Scree plot (**Fig.2**) explained the percentage of variance associated between eigenvalues and principal components with each principal component (PC) obtained by drawing a graph. PC 1 indicated the highest variation of 23.01 per cent with eigenvalue 1.79 which then declined gradually in other principal components. Semi curve line is obtained which after the eight PC tended to straight with little variance observed in each PC (**Fig.2**). From the graph, it is clear that maximum variation was observed in PC1 in comparison to the other thirteen PCs, therefore

Table 4. Eigenvalues, % variance and cumulative Eigenvalues of germplasm

PC	Eigenvalues	% of variation	Cumulative %
PC1	1.794	23.01	23.01
PC2	1.602	18.35	41.36
PC3	1.351	13.05	54.42
PC4	1.318	12.41	66.83
PC5	1.062	08.07	74.90
PC6	0.900	05.79	80.69
PC7	0.829	04.91	85.60
PC8	0.750	04.02	89.63
PC9	0.646	02.98	92.61
PC10	0.599	02.56	95.18
PC11	0.540	02.08	97.27
PC12	0.488	01.70	98.97
PC13	0.326	00.76	99.74
PC14	0.190	0.25	100.00

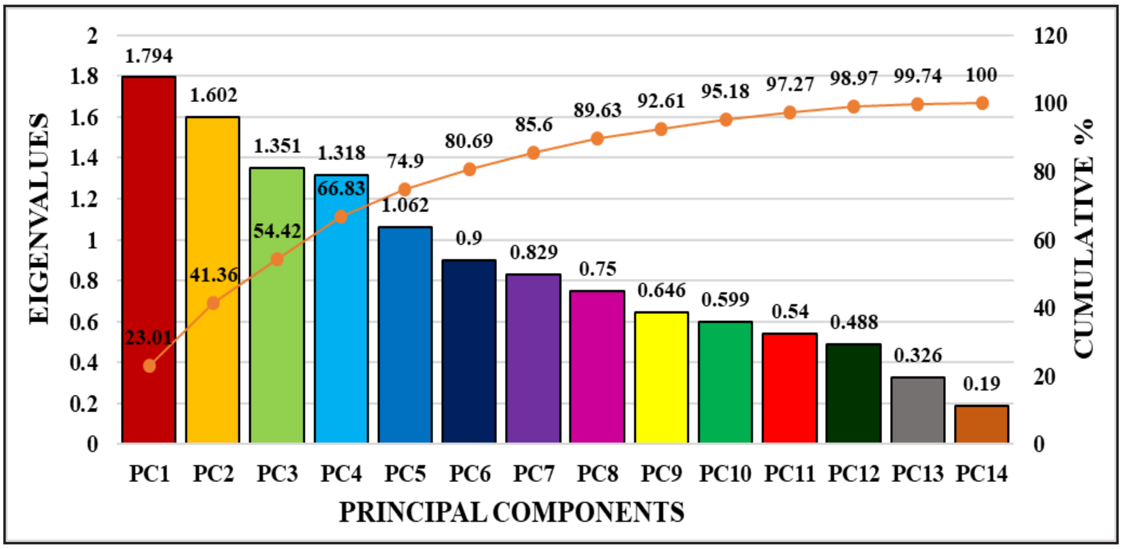


Fig. 2. Scree plot

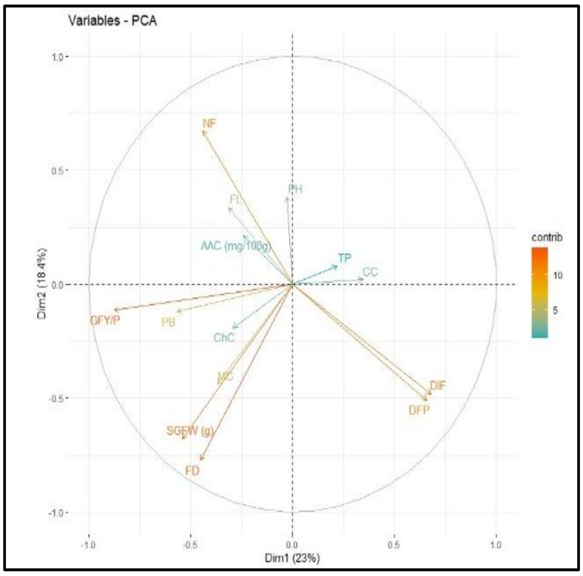
the selection of lines for characters under PC1 may be desirable. A similar curve line was also observed by Singh *et al.* (2020).

Rotated component matrix revealed that eleven PCs are representing the maximum variability (97.27%) hence, the traits falling in these PCs may be given due importance in chilli breeding. It revealed that the first principal component (PC1) which accounted for the highest variation was mostly related to days to initiation of flowering and days to first picking. Thus, PC1 allows for the simultaneous selection of that particular phenological trait whereas other PCs are allowing selection of other respective traits (**Tables 5**). Based on PCA, most of the important yield attributing and quality traits were present in PC1, PC2 and PC5. **Fig.3** represents the contribution of each variable towards the cumulative variability in the genotypes studied.The result of the present findings is similar to the findings of Sreenivas *et al.* (2019), Usman *et al.* (2014), Sarmah *et al.* (2018), Belay *et al.* (2019).

The PC scores of each component had positive and negative values (**Table 6**). These scores can be utilized to propose precise selection indices whose intensity can be decided by variability explained by each principal component. A high PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype Singh *et al.* (2020). Based on the highest PC scores promising genotypes were categorized in **Table 7**. Here, genotype ACGP –129

Table 5 Principal Components for 10 yield contributing traits of Chilli

Traits	Principal Components													
	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**	**PC10**	**PC11**	**PC12**	**PC13**	**PC14**
Days to initiation of flowering	0.378	-0.301	0.099	-0.006	0.292	-0.098	0.042	-0.154	0.314	-0.121	0.139	-0.704	0.076	-0.051
Days to first picking	0.367	-0.319	0.076	-0.015	0.214	0.158	-0.009	-0.321	-0.141	-0.117	-0.661	0.284	-0.152	0.093
Plant height (cm)	-0.015	0.239	0.019	0.193	0.665	0.486	0.088	0.232	-0.315	-0.166	0.171	-0.022	0.070	0.062
Primary branches per plant	-0.317	-0.075	-0.101	0.327	0.066	0.175	0.621	-0.377	0.418	0.099	0.015	0.150	0.084	-0.013
Number of fruits per plant	-0.246	0.420	0.134	0.108	0.220	-0.399	-0.057	0.059	0.138	-0.003	-0.526	-0.189	0.333	0.279
Fruit length (cm)	-0.175	0.208	0.054	-0.381	-0.316	0.648	-0.096	-0.209	0.055	-0.056	-0.222	-0.342	0.179	-0.035
Fruit diameter (cm)	-0.252	-0.482	0.021	-0.184	0.139	-0.010	0.038	0.345	-0.046	0.072	-0.178	0.081	0.502	-0.482
Single green fruit weight (g)	-0.302	-0.423	0.102	-0.326	0.063	0.021	0.000	0.070	0.032	-0.123	0.184	0.066	0.040	0.741
Green fruit yield per plant (g)	-0.487	-0.071	0.184	-0.044	0.204	-0.005	-0.151	0.109	0.202	-0.125	-0.150	-0.127	-0.697	-0.254
Moisture content (%)	-0.205	-0.273	0.025	0.467	-0.277	0.009	0.131	0.014	-0.564	0.163	-0.143	-0.430	-0.084	0.114
Chlorophyll content (mg/g)	-0.163	-0.120	0.327	0.419	0.003	0.074	-0.619	-0.368	0.069	-0.105	0.208	0.162	0.251	-0.064
Capsaicin content (%)	0.193	0.013	0.586	0.034	0.002	0.195	0.036	0.242	0.185	0.684	-0.011	0.052	-0.067	0.099
Ascorbic Acid content (mg/100g)	-0.134	0.133	0.387	-0.386	0.180	-0.274	0.234	-0.491	-0.428	0.106	0.191	0.005	0.012	-0.175
Total phenol (%)	0.122	0.049	0.554	0.114	-0.317	-0.016	0.334	0.242	0.028	-0.615	-0.003	0.086	0.045	-0.056



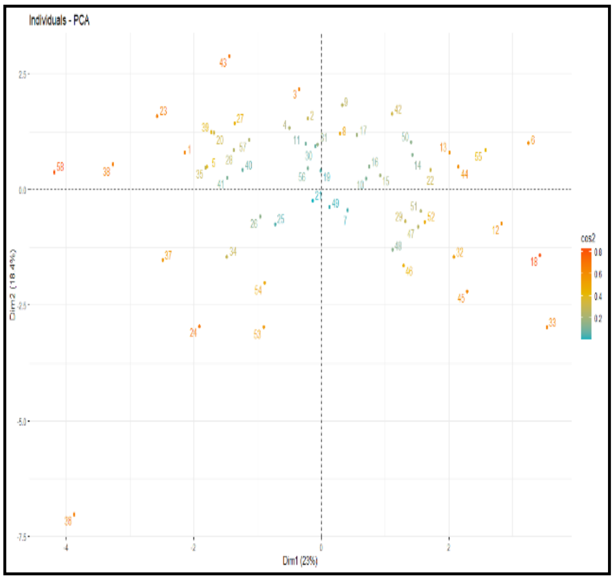


Fig. 3.Contribution of each variable towards the cumulative

Fig. 4. Contribution of each genotypes towards the cumulative variability

https://doi.org/10.37992/2021.1202.047

Table 6. PCA scores of Chilli genotypes

Genotypes	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14
ACGP – 2	-2.160	-0.812	-0.812	1.021	-0.256	-0.347	-0.613	0.584	-0.426	-0.090	0.084	0.153	-0.038	0.267
ACGP –7	-0.217	-1.551	-0.600	1.526	0.287	1.232	-0.297	0.462	-0.154	0.381	-0.153	-0.930	-0.137	0.237
ACGP –10	-0.350	-2.188	0.426	1.075	-0.194	0.131	-0.258	-0.951	-0.285	0.253	-0.135	-0.086	0.099	-0.026
ACGP –15	-0.507	-1.350	-1.563	0.838	1.278	-0.566	-0.463	0.072	1.059	-0.040	0.662	-0.343	0.351	0.163
ACGP –19	-1.813	-0.498	0.123	0.842	1.011	-0.880	-0.490	-1.229	0.450	0.315	0.237	0.052	-0.694	0.046
ACGP –25	3.276	-1.007	1.199	1.252	0.678	1.481	0.481	-0.917	-0.045	0.861	0.215	-0.148	-0.268	0.173
ACGP –26	0.418	0.456	-0.898	-2.388	0.900	0.321	0.889	-0.410	-0.304	0.136	-0.862	0.238	0.665	-0.186
ACGP –27	0.294	-1.219	-0.251	-0.038	-0.910	-0.192	0.329	0.002	-0.294	-0.053	-0.497	-0.025	0.407	-0.102
ACGP –29	0.333	-1.847	1.301	1.249	-0.582	0.494	2.132	-0.734	0.370	-0.967	-0.003	0.107	-0.185	0.006
ACGP –37	0.706	-0.246	0.358	1.382	-0.010	-0.200	-0.295	0.848	0.956	0.118	0.370	0.675	0.132	0.293
ACGP –38	-0.250	-0.994	-1.939	1.192	1.473	-0.481	-0.770	-0.436	1.298	0.185	-0.447	0.169	-0.219	-0.125
ACGP –46	2.848	0.744	-1.042	0.324	-0.640	-0.037	-1.620	-0.458	-0.949	-0.064	0.457	0.390	-0.176	0.119
ACGP –48	2.025	-0.816	-0.035	0.000	-0.191	0.231	0.072	-0.644	1.033	1.038	-0.645	-0.386	0.101	-0.247
ACGP –49	1.440	-0.751	-1.256	2.262	0.051	-2.949	-0.882	0.269	-1.075	-0.170	0.578	-0.416	0.214	-0.003
ACGP –50	0.931	-0.307	-0.414	1.332	-0.487	0.253	0.109	0.983	0.336	-0.092	-0.764	0.300	0.041	0.066
ACGP –57	0.755	-0.498	-0.535	1.723	0.214	0.223	0.358	0.932	0.301	-0.228	-0.294	-0.420	-0.605	-0.054
ACGP –58	0.560	-1.181	2.017	-0.369	1.339	0.341	0.804	0.230	-0.101	0.263	-0.354	-0.466	-0.251	-0.295
ACGP –66	3.457	1.429	-0.471	-0.170	-0.457	0.067	0.126	0.115	0.436	0.692	1.306	0.251	-0.362	0.012
ACGP –67	-0.013	-0.417	-1.374	-0.263	-0.808	-0.162	0.433	0.330	0.449	0.352	-0.105	-0.244	-0.076	-0.152
ACGP –69	-1.700	-1.238	-2.073	-1.133	0.580	-0.738	0.412	-0.539	-0.789	1.013	0.031	-0.152	0.629	-0.003
ACGP –74	-0.140	0.235	-0.536	-2.409	-0.791	0.926	1.043	-0.994	-0.249	-1.467	0.541	-0.903	-0.088	-0.286
ACGP –76	1.728	-0.434	0.960	-0.308	-0.622	1.229	-0.346	-0.808	-0.600	0.540	-0.247	1.548	0.126	-0.191
ACGP –78	-2.598	-1.606	-1.504	-0.688	-0.611	-0.210	-0.243	-0.759	0.139	-0.608	0.285	0.530	0.481	-0.075
ACGP –84	-1.932	2.988	0.459	-1.522	0.558	0.105	-0.282	-0.663	-0.008	1.229	-0.716	0.198	0.023	0.349
ACGP –88	-0.733	0.759	-3.005	-2.660	-0.825	0.680	1.381	1.029	-0.158	0.406	1.279	-0.396	-0.097	-0.156
ACGP –96	-0.970	0.582	-1.791	0.512	0.319	-0.696	-0.827	-1.087	0.006	-1.015	-0.498	-0.555	-0.176	0.044
ACGP –99	-1.373	-1.444	-1.749	0.122	-0.075	-0.123	-0.231	0.513	-0.840	0.268	-0.027	0.689	0.195	-0.105
ACGP –111	-1.383	-0.862	-0.567	0.644	1.020	0.526	0.816	2.059	-0.597	0.042	-0.906	-0.033	-0.116	0.153
ACGP –112	1.325	0.682	-1.002	-0.074	-0.514	-0.504	0.256	1.288	0.086	-0.886	0.004	0.987	-0.281	-0.233
ACGP –113	-0.094	-0.944	-2.434	0.132	1.348	1.071	-0.845	-0.545	0.977	0.214	0.390	-0.138	0.016	-0.059
ACGP –119	-0.060	-0.974	-0.224	-0.065	-1.388	1.113	0.984	-0.020	0.081	0.029	0.048	-0.084	0.589	0.309
ACGP –125	2.095	1.461	-0.532	-0.236	-1.651	-0.980	0.708	-0.025	-0.012	0.791	0.490	0.401	-0.165	-0.165
ACGP –129	3.566	2.995	-0.152	-1.747	2.268	-0.970	1.324	-0.534	-0.596	0.011	-0.053	-0.136	0.137	0.298
ACGP –130	-1.495	1.471	1.055	0.666	-2.393	0.104	0.429	-1.101	-0.094	-0.579	0.998	0.481	0.192	0.444
ACGP –134	-1.832	-0.483	1.984	0.386	-1.048	-0.603	1.082	-1.233	-0.095	-0.035	-0.436	-0.017	-0.212	0.276
ACGP –135	-3.909	7.078	0.860	5.437	0.635	1.061	0.400	-0.042	-0.292	0.425	0.408	-0.216	0.625	-0.470
AVNPC – 131	-2.511	1.535	0.075	-1.687	0.161	0.893	-0.378	0.396	-1.255	0.393	-0.030	0.173	-0.962	-0.169
GVC – 101	-3.296	-0.554	0.149	-1.301	-0.700	0.002	-1.698	0.380	-0.029	-0.080	0.347	0.314	-0.043	-0.055
GVC – 111	-1.738	-1.249	1.806	-0.492	-0.953	0.014	-1.187	-0.302	0.044	0.935	-0.075	-0.317	-0.112	-0.067
GVC – 121	-1.245	-0.422	3.759	-1.629	1.854	-0.423	-0.406	-0.232	-0.092	0.408	0.447	0.007	-0.146	-0.041
GAVC – 112	-1.487	-0.259	2.803	-0.694	-1.444	-1.623	0.469	1.214	1.704	0.045	-0.018	-0.595	0.075	-0.103
Anugraha	1.119	-1.647	0.842	1.357	-1.552	0.597	-0.269	0.021	-1.476	-0.142	0.000	-0.714	-0.183	0.069
Byadagidabbi	-1.455	-2.907	0.437	0.261	-0.284	1.906	0.378	-0.071	-0.044	-0.327	-0.007	-0.324	0.414	-0.155
Ajeet-6	2.167	-0.491	-0.653	-0.023	-0.800	-0.332	-0.830	-0.599	-0.464	0.546	-0.052	-0.693	-0.102	-0.146
Arkaabhir	2.306	2.222	0.923	0.265	-1.254	-1.228	-0.144	-0.163	0.074	-1.158	-0.213	-0.731	-0.078	-0.160
DCL-2	1.298	1.649	-1.071	-0.364	-0.148	0.627	0.770	0.441	1.359	0.842	0.179	-0.049	-0.247	0.074
PC-56	1.528	0.803	0.200	0.540	-1.950	-1.073	0.695	0.686	-0.345	0.576	-1.388	0.293	0.054	0.167
Kashi anmol	1.124	1.315	1.881	-1.726	-1.494	1.028	-2.678	0.616	0.891	-0.601	-0.366	0.166	0.204	-0.188
Mathania type – 1	0.127	0.387	-0.058	-0.771	0.351	-1.950	0.221	-0.406	0.053	-0.158	-0.816	0.553	0.209	-0.238
Arkalohit	1.420	-1.027	3.052	-0.932	1.842	-1.473	-0.323	0.522	-0.523	0.198	1.066	-0.541	0.563	-0.061
Arkasuphal	1.575	0.466	1.306	-0.872	0.489	1.423	-0.885	1.612	-0.376	-0.213	0.629	0.021	0.340	0.233
Jawerivani	1.638	0.714	-1.387	-0.002	0.242	0.393	-0.499	-0.053	0.493	-0.840	-0.206	-0.100	0.084	0.117
Gondaldhholar	-0.914	2.997	-0.381	-1.760	0.619	0.455	-0.987	0.534	-0.297	-0.551	-1.079	-0.966	0.069	0.302
US Agri 702	-0.899	2.042	-0.484	-0.825	1.139	0.394	0.128	-1.029	0.523	-1.048	0.028	0.252	-0.231	0.214
Seedco – 202	2.597	-0.859	1.533	0.771	2.232	0.761	0.004	-0.007	0.411	-1.012	-0.077	0.811	0.355	-0.043
Gujarat chilli – 1	-0.215	-0.469	0.251	0.538	0.435	0.120	-0.265	-0.750	-0.520	-0.350	-0.264	0.437	-0.549	-0.154
Gujarat chilli – 3	-1.139	-1.077	0.394	0.510	1.826	-0.399	0.935	1.177	-0.874	-0.776	0.291	0.530	-0.364	-0.060
Local selection	-4.226	-0.380	0.637	-1.011	-0.114	-1.060	0.846	0.429	0.725	0.045	0.366	0.398	-0.222	0.141
Range	3.56-1.11	7.07-1.31	3.75-1.05	5.43-1.02	2.26-1.01	1.90-1.02	2.13-1.04	2.05-1.02	1.70-1.03	1.22-1.01	1.30-1.06	0	0	0

Table 7 Genotypes selected based on PC score in each component having highest positive values

S. No.	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
1	ACGP –129	ACGP –135	GVC – 121	ACGP –135	ACGP –129	Byadagidabbi	ACGP –29	ACGP –111	GAVC – 112	ACGP –84	ACGP –66	ACGP –76
2	ACGP –66	Gondaldhholar	Arkalohit	ACGP –49	Seedco – 202	ACGP –25	ACGP –88	Arkasuphal	DCL-2	ACGP –48	ACGP –88	
3	ACGP –25	ACGP –129	GAVC – 112	ACGP –57	GVC – 121	Arkasuphal	ACGP –129	ACGP –112	ACGP –38	ACGP –69	Arkalohit	
4	ACGP –46	ACGP –84	ACGP –58	ACGP –7	Arkalohit	ACGP –7	ACGP –134	GAVC – 112	ACGP –15			
5	Seedco – 202	Arkaabhir	ACGP –134	ACGP –37	Gujarat chilli – 3	ACGP –76	ACGP –74	Gujarat chilli – 3	ACGP –48			
6	Arkaabhir	US Agri 702	Kashi anmol	Anugraha	ACGP –38	ACGP –119		ACGP –88				
7	Ajeet-6	DCL-2	GVC – 111	ACGP –50	ACGP –113	ACGP –113						
8	ACGP –125	AVNPC – 131	Seedco – 202	ACGP –25	ACGP –58	ACGP –135						
9	ACGP –48	ACGP –130	Arkasuphal	ACGP –29	ACGP –15	Kashi anmol						
10	ACGP –76	ACGP –125	ACGP –29	ACGP –38	US Agri 702							
11	Jawerivani	ACGP –66	ACGP –25	ACGP –10	ACGP –111							
12	Arkasuphal	Kashi anmol	ACGP –130	ACGP – 2	ACGP –19							
13	PC-56											
14	ACGP –49											
15	Arkalohit											
16	ACGP –112											
17	DCL-2											
18	Kashi anmol											
19	Anugraha											

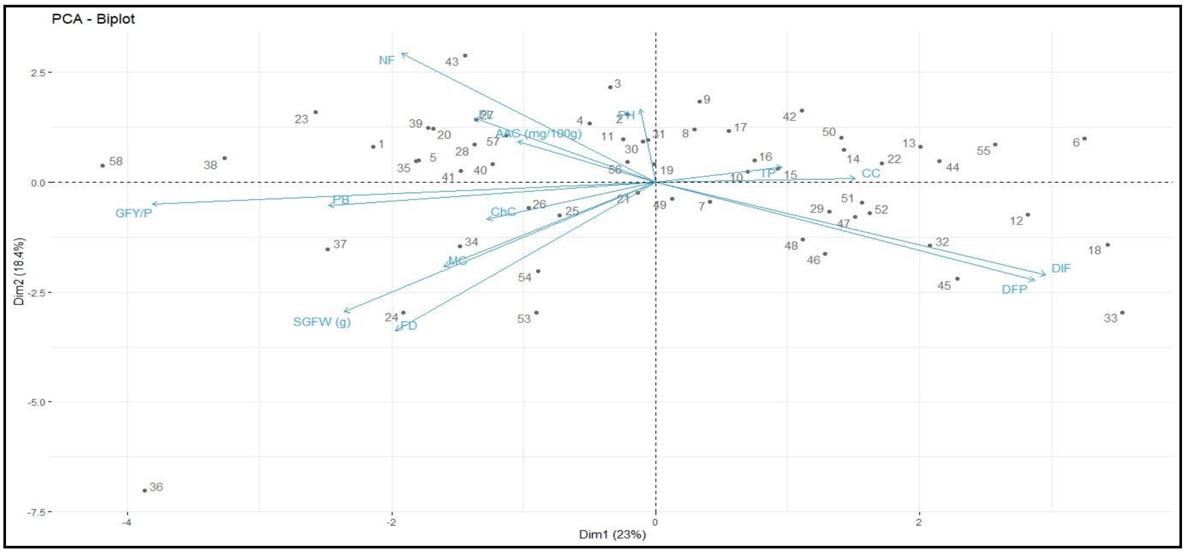


Fig. 5. Bi plot formation on the basis of PC1 and PC2 values

obtained the highest positive PC score in PC1, followed by ACGP –66, ACGP –25 and ACGP –46 indicated that these genotypes possess high values of traits viz. days to initiation of flowering and days to first picking. The range of positive scores in PC1 ranged from 3.56 to 1.32. In PC2 the highest positive PC score was obtained by ACGP –135, followed by Gondaldhholar, ACGP –129 and ACGP –84 which were mainly related tothe number of fruits per plant. The range of positive scores in PC2 ranged from 7.07 to 1.31. Similarly, the best genotypes with high positive scores present in its respective PCs; relative traits and their range are given in **Tables 6 and 7**. The PC scores of each component should have positive values. PC13 and PC14 have no any positively scored genotypes. Genotypes showing maximum positive PC scores and common in PC1 to PC14; which are mostly related to yield traits are ACGP –129, ACGP –25, arkalohit, arkasuphal and kashianmol.

Fig.4 represents the contribution of each genotype towards the cumulative variability of all the genotypes studied whereas **Fig.5** signify Biplot formation on basis of PC1 and PC2 values and it contains the relative contribution of both traits and genotypes. An intensive selection procedure can be designed to bring about rapid improvement of dependent traits i.e., yield traits in chilli by selecting lines. Thus, the selection of these lines can help in the further development of new high yielding and good quality varieties of chilli. Findings of this experiment were supported by Janaki *et al.* (2015), Usman *et al.* (2014), Sarmah *et al.* (2018), Sing *et al.* (2019), Sreenivas *et al.* (2019), Belay *et al.* (2019) and Singh *et al.* (2020).

The results presented here demonstrates abundant variation among the genotypes for most of the characters studied as well as the utility of cluster analysis and PCA in partitioning the genetic variation among chilli genotypes and in identifying different genotypes that would serve as potential sources of unique breeding material for future crop improvement. Considering group distance, inter genotypic crosses between clusters I and III were found to be useful for future hybridization programmes. Considering this, genotype ACGP – 135 of cluster III were identified as promising genotypes for fruit yield per plant therefore, a multiple crossing programme can be proposed involving genotypes from clusters I and III for the development of superior segregants by way of diallel or line x tester analysis. The principle component contributed maximum towards genetic divergence in chilli genotypes by phenological traits weresingle green fruit weight, capsaicin content (%) and plant height. This study generally indicated that there was significant genetic variability or diversity among the test genotypes. Thus, there is an enormous opportunity in the improvement program of chilli. This implies a great potential for breeding through hybridization programmes or direct use as a variety for successful chilli production.

ACKNOWLEDGMENT

We are thankful to Main Vegetable Research Station, AAU, Anand for providing resources and Directorate of research, AAU along with B. A. College of agriculture and a center of excellence in agricultural biotechnology for providing research facility and funding to conduct the trial.

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