



RESEARCH ARTICLE

# Genetic variability appraisal: Identifying potential chilli *Capsicum annuum* genotypes through detailed phenotypic analysis for breeding under drought prone regions in Tamil Nadu

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## Abstract

Genetic diversity provides a broader genetic pool from which a breeder can select varieties that are resistant to climate change-related challenges. Diverse chilli genotypes are more likely to possess genes that confer resistance to emerging diseases and pests, reducing the need for chemical interventions. This study focused on identifying elite chilli genotypes suitable for rainfed conditions in the North-Western zone of Tamil Nadu, an area prone to dry spells during the growing season. Forty-two chilli genotypes were evaluated for growth and yield parameters, revealing significant variability among them. Genotypes, such as Sidlagatta local (SDL local), Japoni Longi and S2 local, exhibited superior performance in terms of fresh fruit yield, number of fruits per plant, individual fruit weight, fruit length and dry fruit yield. Correlation analysis indicated strong relationships between yield and various fruit characteristics, validating their importance for crop improvement. Principal Component Analysis (PCA) highlighted key traits contributing to genetic variance, such as plant height, number of primary branches and fruit dimensions, aiding in genotype selection for future targeted breeding programs. Cluster analysis grouped the genotypes based on genetic similarity, suggesting potential strategies for hybridization to harness genetic diversity effectively. These findings emphasize the significance of genetic exploration and trait-based selection in enhancing chilli productivity under rainfed conditions amidst changing climatic scenarios.

## Keywords

Rainfed Chilli; genetic diversity; correlation; PCA analysis; clustering analysis

## Introduction

Climate change is an inevitable player and likely to affect horticulture crops especially chilli (1). This leads to flower drop in chilli which is a major issue resulting in significant loss at an industrial scale. Flower drop and yield loss is primarily caused by elevated temperature and precipitation resulting in 70 % reduction in yield (2). The North-Western zone of Tamil Nadu is often characterised by erratic rainfall and high frequency of dry spells in the

growing season (3). Chilli is primarily a rainfed crop in these areas. However changing climate, erratic rainfall, elevated temperature leads to huge reduction in production. Irrigation can overcome above mentioned problem, however, considering the economics for irrigation infrastructure and technologies for small scale land holders identifying elite genotypes suited for dry tracts are the top priority solution.

Identifying elite genotypes involves thorough exploration of germplasm as this genus exhibits immense variation (4). Exploiting the genetic diversity paves for identifying novel genes that code for crop improvement and quality (5, 6). Divergence analysis reveals the nature and degree of genetic variability among genotypes. Genetically divergent parents are expected to produce progeny with strong heterotic effects, enhancing desirable economic traits (7). Genetic divergence analysis also aids in simplifying the selection of divergent parents for breeding programs, reducing the complexity of genotype data (8). Principal Component Analysis (PCA), a widely used dimension reduction technique, condenses a large number of variables into a smaller set while retaining most of the information. PCA generates component scores that summarize multivariate data into primary axes, with each axis represented by an eigenvector (9). The eigenvalue of each principal component indicates the variation explained by that component within the traits, offering valuable insights for future breeding efforts. On the other hand, cluster analysis groups genotypes based on similarities and differences, considering a combination of complex traits rather than focusing on individual characteristics. It is generally more effective than PCA in unsupervised learning when the goal is to identify distinct subgroups driven by complex trait patterns. While PCA is primarily a tool for dimensionality reduction and data visualization, it does not directly classify data into groups. However, applying PCA before clustering can help reduce dimensionality, enhancing the clustering process by simplifying the data and improving performance. Considering above the present aim of the study is done to identify elite genotypes among germplasm with high yield and suitable for rainfed conditions suited for North Western Zone of Tamil Nadu.

## Materials and Methods

The experimental trial was conducted with 42 genotypes which were obtained from different sources (Table 1) to assess the best performing variety suitable for rainfed alfisols of North Western Zone of Tamil Nadu. Throughout the cropping season crop production guidelines suggested by TNAU (10) were followed. All the genotypes were screened for growth and yield parameters. Statistical analysis such as principal component analysis (PCA) and Pearson correlation was carried out using R software version 4.4.1 and Ward's minimum clustering was carried out using Darwin software.

## Results and Discussion

The 42 genotypes were statistically analysed and results are furnished in the Table 2. The genotypes significantly varied for all the parameters evaluated. The genotypes SDL local, Japoni Longi, S2 local, Slocal, S3local, PKM1, LCA335, K2, Bydagi kaddi, DCA 93, LCA 424, AR 75, Karamadai, V guntur and DCA96 recorded fresh fruit yield of more than 250 g per plant. Among them SDL local recorded the highest red ripe fruit yield of 420.75 g/plant followed by Japoni longi which recorded 365.67 g/plant. With regard to the number of fruits per plant, the accession Japoni longi recorded the highest number of 110 fruits per plant followed by PKM1 and DCA 96 with 73.83 and 69.00 fruits per plant respectively. The accession Bydagi local recorded the highest fruit length of 16.97 cm followed by S local (15.33 cm). DCA 96 recorded 7.35 cm girth of the fruit while Thaliyur local observed 6.00 cm girth. The height of the plant varied from a minimum of 42.93 cm to a maximum height of 111.70 cm by Pochampalli local. The mean dry fruit yield was found to vary significantly in all the accession ranging from 0.41 to 2.55 t/ha. The highest mean dry fruit yield was noted in the accession SDL local with 2.55 t/ha followed by Japonilongi (2.21 t/ha) and S2 local (2.04 t/ha). Among the germplasm accession twenty lines SDL local, Japoni longi, S2 local, S local, S3local, PKM1, LCA335, K2, Bydagi kaddi, Bydagidabbi, Arka lohit, DCA 93, LCA424, AR75, Karamadai, Vguntur and DCA96 were found superior over the other lines based on growth and dry fruit yield in the rainfed conditions (Table 2). Genotypic variations in quantitative traits have been documented by (11-13) utilising divergent materials across range of environmental conditions.

Correlation analysis (Fig. 1) revealed that dry fruit yield is highly correlated with yield/ha (1.00\*\*\*). The findings confirmed the results (14) and (4) who suggested that ripe fruit yield and number of fruits were highly correlated. Other traits such as number of primary branches (0.78\*\*\*), fresh fruit yield (0.73\*\*\*), number of fruits per plant (0.45\*\*) were also highly correlated with yield/ha. Number of primary branches (0.77\*\*\*) and fresh fruit yield (0.75\*\*\*) is highly correlated with dry fruit yield. Association of plant height and fruit girth with other traits was negligible. The results were in accordance with findings (15). However, the results contradict findings who reported significant and positive correlation of plant height with fruit characters (16). The correlation between the yield and fruit characteristics were similar to results obtained except for the fruit girth which were found non-significant in this study (17-19). Thus, correlation analysis revealed close association between fruit and yield characters. These characteristics could be exploited in the future crop improvement programmes. Further, PCA analysis is done to facilitate the variation (Fig. 2).

Principal Component Analysis (PCA) was conducted on 8 quantitative morphological traits to determine the primary factors influencing overall yield and its components (Table 3). The first 3 PCs with eigen value (>1) contributed 74.18 % of variance (Fig. 2A). The first principal component (PC1) depicted the highest proportion of variance (38.75 %) among the number of informative principal components

**Table 1.** Details of 42 genotypes used in this study.

Sl. No.	Genotypes	Source
1	SDL local	University of Agricultural Sciences, Bangalore
2	Japonilongi	Indian Institute of Vegetable Research, Varanasi
3	S2 local	University of Agricultural Sciences, Bangalore
4	Slocal	University of Agricultural Sciences, Bangalore
5	S3 local	University of Agricultural Sciences, Bangalore
6	PKM1	Horticulture College and Research Institute, Periyakulam, TNAU
7	LCA 335	Indian Institute of Vegetable Research, Varanasi
8	K2	HC&RI, Coimbatore, TNAU
9	Bydagi kaddi	University of Agricultural Sciences, Bangalore
10	Bydagi dabbi	University of Agricultural Sciences, Bangalore
11	Arka lohit	Indian Institute of Horticultural Research, Bangalore
12	Bydagi local	University of Agricultural Sciences, Bangalore
13	Sundampalayam	Local collection from Coimbatore
14	DCA71	University of Agricultural Sciences, Bangalore
15	Samrudhi	University of Agricultural Sciences, Bangalore
16	Poondi	Local collection from Coimbatore
17	Guntur local	University of Agricultural Sciences, Bangalore
18	Pochampalli	Collection from Dharmapuri
19	Palladam	Local collection from Coimbatore
20	Vlocal	University of Agricultural Sciences, Bangalore
21	Chikbellapur	University of Agricultural Sciences, Bangalore
22	Eriyur	Collection from Dharmapuri
23	Chilli local	Collection from Dharmapuri
24	Metupalyam	Local collection from Coimbatore
25	Thaliyur	Local collection from Coimbatore
26	K1	HC and RI, Coimbatore, TNAU
27	Sirumugai	Collection from Coimbatore
28	Dhallylocal	University of Agricultural Sciences, Bangalore
29	Kasi Anmol	Indian Institute of Vegetable Research, Varanasi
30	Dharmapuri	Local collection from Dharmapuri
31	HMT 1	University of Agricultural Sciences, Bangalore
32	Guntur 5	University of Agricultural Sciences, Bangalore
33	DCA93	University of Agricultural Sciences, Bangalore
34	LCA424	Indian Institute of Vegetable Research, Varanasi
35	AR75	University of Agricultural Sciences, Bangalore
36	Karamadai	Local collection from Coimbatore
37	Thondamuthur	Local collection from Coimbatore
38	Vguntur	University of Agricultural Sciences, Bangalore
39	DCA96	University of Agricultural Sciences, Bangalore
40	Madampatti	Local collection from Coimbatore
41	PusaJwala	Indian Institute of Vegetable Research, Varanasi
42	KA2	Indian Institute of Vegetable Research, Varanasi

**Table 2.** Mean performance of 42 genotypes under dry tracts of North Western zone for characters such as plant height, number of primary branches, fruit length, fruit girth, fresh fruit yield, dry fruit yield, number of fruits per plant and yield.

Sl. No.	GENOTYPE	PH	NPB	FL	FG	FFY	DFY	NFPP	YPH
1	SDL local	69.8	7.3	8.63	5.8	420.75	2.55	51.33	8928.57
2	Japoni longi	48.3	8.1	7.42	2.6	365.67	2.21	110.53	7738.1
3	S2 local	68.45	7.55	14.38	4.75	342.8	2.04	68.67	7142.86
4	Slocal	74.65	6	15.33	5	338.01	1.98	49.83	6944.44
5	S3 local	68.5	8.2	12.75	4.9	334.45	1.97	48.9	6904.76
6	PKM1	65.1	6.4	7.13	3.65	322.9	1.93	73.83	6746.03
7	LCA 335	66	5.4	14.75	5	300.8	1.81	39.67	6349.21
8	K2	96.7	6	13.85	3.85	296.8	1.76	57.8	6150.79
9	Bydagi kaddi	71.85	7.5	14.07	4.05	290	1.7	51.5	5952.38
10	Bydagi dabbi	67.45	4.7	13.45	5.7	234.28	1.47	29.5	5158.73
11	Arka lohit	79.55	5.9	9.3	3.25	220.97	1.41	60.17	4920.63
12	Bydagi local	73.45	6.2	16.97	3.7	220.68	1.59	46.17	6349.21
13	Sundampalayam	68.1	7.5	11.15	3.9	212.8	1.44	60.8	5753.97
14	DCA71	67.05	6.4	8.1	3.8	205.96	1.19	43.67	4761.9
15	Samrudhi	72.3	4.6	8.22	3.65	186.25	0.99	37.5	3968.25
16	Poondi	65.4	5	8.23	3.85	156.12	0.94	53.83	3769.84
17	Guntur local	105.1	5.3	5.83	3.55	210.11	0.79	60.9	3174.6
18	Pochampalli	111.7	6.1	8.8	4.6	203	0.79	58.5	3174.6
19	Palladam	81.2	5.6	7.92	4.15	179.96	0.74	40.9	2976.19
20	Vlocal	98.28	4.9	6.86	3.3	165.6	0.64	46	2579.37
21	Chikbellapur	102.75	4.5	2.92	2.5	145.34	0.6	42.33	2400.79
22	Eriyur	103	5	10.23	4.05	177.22	0.55	36.67	2182.54
23	Chilli local	87.65	4.3	8.78	4.75	158.34	0.44	42	1765.87
24	Metupalyam	69.6	4.7	6.45	3.6	152.57	0.41	36.5	1640.87
25	Thaliyur	71	3.8	9.4	6	122.74	0.53	32.3	2104.96
26	K1	68.65	5	9.98	4.4	146.59	0.56	47.8	2242.06
27	Sirumugai	59.95	4	12.6	4.55	196.23	0.47	41.17	1866.47
28	Dhallylocal	74.15	4.5	11.72	3.45	169.4	0.44	44	1767.8
29	Kasi Anmol	48.15	3.5	9	4.15	145.79	0.75	54.33	3017.26
30	Dharmapuri	82.78	4.7	8.5	4.65	242.51	0.43	45.9	1706.15
31	HMT 1	67.4	4.8	12.13	2.8	236.31	0.55	50.1	2182.54
32	Guntur5	80.3	5.7	6.7	3.6	226.59	0.53	52.9	2103.57
33	DCA93	58.55	5.6	14.27	4.25	268.65	0.95	66.33	3780.36
34	LCA424	50.7	2.9	8.85	4.3	325.72	0.51	36.67	2028.57
35	AR75	80.25	3.9	7.88	3.65	294.49	0.88	65.2	3519.25
36	Karamadai	77.55	4.1	7.95	4.55	279.01	0.87	60.11	3472.22
37	Thondamuthur	53.78	4.5	5.51	4.75	111.71	0.89	29.33	3579.17
38	Vguntur	90.85	5.7	8.97	5	264.31	0.87	36.67	3483.73
39	DCA96	67.7	4.9	11.48	7.35	269.1	0.89	69	3572.62
40	Madampatti	54.2	3.9	9.38	3.75	177.66	0.79	38.83	3175.99
41	PusaJwala	42.93	4.2	11.25	3.05	173.72	0.75	49.17	2986.9
42	KA2	47.6	3.9	7.17	3.7	158.85	0.8	42.55	3194.84
	SE(D)	2.57	0.51	0.493	0.263	11.413	0.107	1.844	189.5
	CD (0.05)	5.191	1.03	0.996	0.526	23.054	0.215	3.725	382.92

<b>PH</b>	Plant height (cm)	<b>NPB</b>	Number of primary branches
<b>FL</b>	Fruit length (cm)	<b>FG</b>	Fruit girth (cm)
<b>FFY</b>	Fresh fruit yield (g/plant)	<b>DFY</b>	Dry fruit yield (t/ha)
<b>NFPP</b>	Number of fruits per plant	<b>YPH</b>	Yield (kg/plot)



Chikbellapur, Sirumugai, Thaliyur, Madampatti, Eriyur, Dharampuri, Palladam, Samrudhi) followed by cluster 1 with 11 genotypes (SDL local, S3 local, S2 local, S local, By Kaddii, PKM 1, Sundampalayam, K2, DCA 93, Bydagi local, DCA 96) and cluster 2 with 10 genotypes (Guntur local, Poondi, Guntur5, HMT 1, DCA 71, Karamadai, Arka lohit, Pochampalli, AR75. Cluster 4 contains only 4 genotypes namely, Bydagi dabbi, LCA 335, Vguntur a) and LCA 42. Cluster 5 is a monogenic cluster with single genotype (Japoni longi). Geographical barriers that inhibit gene flow, along with strong natural and human selection for specialized and adaptable gene complexes, likely contribute to the formation of isolated clusters (20). The genotype Japoni longi is unique and distinct from other genotypes. The genes responsible for its uniqueness are likely to be protected from genetic erosion. The inter-cluster distance indicated that the greatest distance was observed between clusters 2 and 5 (8.63), followed by clusters 2 and 3 (8.57) and clusters 1 and 5 (7.37). The lowest distance was recorded between the clusters 4 and 5 (4.85). Cluster mean analysis (Table 4) clearly indicated that genotypes in cluster 2 recorded the highest number of primary branches (8.10), fruit length (110.53) and number of fruits per plant (365.67). However, they recorded the lowest values for plant height (48.3), fruit girth (7.42), fresh fruit yield (2.60), dry fruit yield (3.31) was recorded the lowest. The genotypes in cluster 1 possess the highest yield/ha (6202.36) while those in cluster 4 recorded the highest plant height (81.59). Hybridization between clusters 2 and 5 is recommended to develop genotypes with desirable traits. Further, the genotypes identified in the study not only serve as valuable donors for breeding programs but also provide a genetic foundation for enhancing specific traits, such as yield and environmental adaptability. By incorporating these genotypes into breeding strategies, the potential for developing superior cultivars with improved agronomic performance is significantly increased. Additionally, their diverse genetic makeup offers opportunities for creating resilient varieties that can thrive in varying environmental conditions, thereby contributing to sustainable agricultural practices.

## Conclusion

Thus, evaluation of 42 genotypes of chilli for growth and yield-related traits under rainfed conditions clearly revealed significant variation among the genotypes for all parameters assessed. Several genotypes, including SDL local, Japoni Longi, S2 local and others, demonstrated superior performance in terms of fresh fruit yield, number of

**Table 4.** Cluster mean values of 5 clusters for different yield and yield contributing traits.

Cluster	1	2	3	4	5
PH	71.17	48.3	68.75	81.59	71.65
NPB	6.65	8.10	4.68	5.24	4.45
FL	58.56	110.53	35.63	56.15	41.60
FG	12.73	7.42	11.51	8.32	8.58
FFY	4.65	2.60	5.00	3.74	4.03
DFY	4.93	3.31	7.79	4.27	4.02
NFFPP	301.54	365.67	281.28	225.84	165.32
YPH	6202.36	7738.10	4255.06	3453.24	2538.56

fruits per plant, individual fruit weight, fruit length and dry fruit yield. Notably, SDL local exhibited the highest red ripe fruit yield and dry fruit yield. Correlation analysis indicated strong associations between yield and fruit characteristics, affirming their potential in targeted breeding programmes, genetic engineering for those responsible genes can help in crop improvement programs. Principal Component Analysis (PCA) is a powerful tool which identified key traits contributing to variance, highlighting the importance of traits like plant height, number of primary branches and fruit characteristics in determining overall variation among genotypes. The clustering analysis categorized the genotypes into distinct groups based on genetic similarity, suggesting strategies for future hybridization programs to exploit genetic diversity effectively. Identifying genetic clusters like cluster 2 and cluster 5 can help in preserving genetic diversity by ensuring that different genetic lineages for targeted breeding programs. This study helps in understanding the genetic basis of traits like yield, fruit quality and stress tolerance breeders can develop more productive and resilient chilli varieties.

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## Authors' contributions

The authors mentioned in the research paper contributed to the research in way of visualization and collection of germplasm, lay out, designing by SS, observations at various stages by PT, lab analysis by MD, diversity studies by UND and dendrogram studies by BS interpretations of the results by KD and statistical analysis by EJ and preparation of the manuscript, reviews correction by the authors.

## Compliance with ethical standards

**Conflict of interest:** The authors have declared that no conflict of interest exists.

**Ethical issues:** None

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