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Diversity analysis of chilli (capsicum species) genotypes using dus descriptors

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Abstract
Chilli exhibits a wide range of variability in morpho-physiological traits. A logical way to start any breeding program is to collect precise information on the nature and degree of genetic divergence that would help the plant breeder in choosing the right type of parents for purposeful hybridization. The present investigation entitled was carried out at College Orchard, Department of Vegetable Science, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore with fourteen genotypes in order to study the variability for identifying the best performing chilli genotypes. Principal Component Analysis for the 32 morphological characters elucidated that, ten principle components with eigenvalues more than one accounted for 98.69 per cent of the total variability and the maximum variation was exhibited by the plant growth habit, anthocyanin colouration at nodes, intensity of anthocyanin colouration at nodes, leaf size, fruit colour at maturity unripened stage, fruit colour, fruit colour intensity, fruit sinuation of pericarp, branching habit, stem pubescence, stem pubescence intensity, fruit shape at longitudinal section whereas remaining traits exhibited low variability. Based on PCA and H' the nine genotypes CC-CBE-005, CA-CBE-201, CA-CBE-202, CA-CBE-199, CC-CBE-004, CF-CBE-007, CC-CBE-001, CC-CBE-003 and CC-CBE-002 were identified as the most diverse genotypes.

Keywords: Chilli, DUS, variability, PCA, descriptors

Introduction
Chilli is one of India's most significant commercial vegetable cum spice crops, belonging to the Solanaceae family, which constitutes a diversified plant group (Harini and Sita, 1993; Prakash *et al.*, 1988). The cultivation of chilli expanded quickly from Spain to Europe. Chillies gained popularity throughout Asia, and native Asians and started producing this crop as well. Chilli has been cultivated since ancient times for its pungency, colour, flavour, and taste, and it also has a distinct position in the diet till date. *C. annuum, C. frutescens L., C. baccatum L., C. pubescens Ruiz. & Pav, and C. chinense Jacq* are the five most economically grown chilli species (Bosland and Votava, 2000; Ince *et al.*, 2010). The Capsicum genus has a great degree of diversity in its morphological characteristics. The descriptors provided by "The Protection of Plant Varieties and Farmers' Rights Authority" (PPV&FRA) for Capsicum species aid in variety identification, distinguishing the distinctness of emerging unique varieties, and assessing varietal purity. The DUS descriptor score points helps in the identification of the extremely variable chilli genotypes utilised in the current investigation. Knowing the variability paves the path for effective exploitation of available genotypes in breeding programmes and also aids in the introduction of a newer variety with desirable characters for commercial exploitation (Balaguru *et al.*, 2020) [1]. As a result, this study was conducted to investigate the diversity of 14 chilli genotypes gathered from Sri Lanka and different parts of India, to select the best performing genotpyes using DUS testing, and multivariate analysis.

Materials and Methods
During 2019, 14 genotypes (CA-CBE-199, CA-CBE-200, CA-CBE-201, CA-CBE-202, CF-CBE-004, CF-CBE-005, CF-CBE-006, CF-CBE-007, CC-CBE-001, CC-CBE-002, CC-CBE-003, CC-CBE-004, CC-CBE-005, CC-CBE-016) of capsicum species were raised at College Orchard, Department of Vegetable Science, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, India using Randomized Block Design (RBD) with two replications, and all recommended package of practises were followed for all fourteen genotypes. At the proper stage of chilli plant development, about 32 qualitative characteristics were recorded using the DUS criteria given by PPV and FRA, 2001.

Scores from one to ten were given to all the 14 genotypes for 32 characters. A single observation for a group of plants or plant parts (VG) was done by visual observation for the characters such as seedling anthocyanin colouration of hypocotyl, plant growth habit, branching habit, anthocyanin colouration at nodes, stem pubescence, stem pubescence intensity, stem colour, leaf colour, leaf size, leaf pubescence, leaf shape, corolla colour, anther colour, flower and fruit orientation, fruit bearing habit, fruit colour at mature unriped stage, fruit colour at intermediate stage, fruit colour at maturity, fruit shape at longitudinal section, fruit shape at cross
section, fruit curvature, fruit curvature intensity, fruit neck at basal end, fruit shape at apex, fruit shape at base, fruit sinuation of pericarp, fruit texture surface. Measurement by a single observation of a group of plants or plant parts (MG) was made for plant height (cm), leaf length (cm) and leaf width (cm).

Principal components (PCs) with an eigenvalue of more than one were selected (Jeffers, 1967) [4] and the standardized values of the PAST 3 application and computer software Microsoft Excel were used to conduct the PCA. The components contributing a major share in the total variation were visually assessed by the scree plot. For all the 32 characters correlation matrix were computed using PAST 3.

Results and Discussion

Principal Component Analysis (PCA) is a powerful method for determining the fewest number of components while explaining the most variability out of total variability (Morrison., 1982) [7]. PCA aids in genotype ranking based on PC scores. As a result, for 14 genotypes, Principal Component Analysis was used to analyse the diversity of chilli genotypes collected from Srilanka and different parts of India. The analysis of 32 characters (DUS) yielded 10 principal components with eigenvalues greater than one (Table 1). The PC1 had the highest variability of 30.46% followed by PC2 (20.50%) and PC3 (17.16%). The overall variability of the ten principal components is 98.69%. Only two of the ten PCs had a greater variability of 50.97%. An experiment conducted by Pragya Singh *et al.* (2020) [10] accounted for 100% of the total variance and three PCs with more than one eigenvalue in chilli.

Table 1: Eigen values, variance and cumulative variability of chilli genotypes

Principal component	Eigenvalue	Percent variance	Cumulative variance
1	40.71	30.468	30.468
2	27.3952	20.503	50.971
3	22.9282	17.16	68.131
4	15.0177	11.24	79.371
5	9.33051	6.9831	86.3541
6	5.79716	4.3387	90.6928
7	3.89572	2.9156	93.6084
8	3.68545	2.7583	96.3667
9	1.86492	1.3957	97.7624
10	1.25221	0.93717	98.69957

Figure. 1 shows a Scree plot graph that explains the percentage of variance linked with eigenvalues and principal components, with each principle component (PC) produced by drawing a graph. The X-axis was used to represent the component number, while the Y-axis was used to represent the eigenvalues. PC 1 revealed the largest variance of 30.46 percent with eigenvalue 40.71, which subsequently dropped gradually in other principal components as reported by Gour *et al.* (2017) [5]. After the eight PC, the semi-curve line tended to straighten out with minimal fluctuation noted in each PC. As a result, the most variable lines were chosen for characters under PC1, PC2, and PC3.

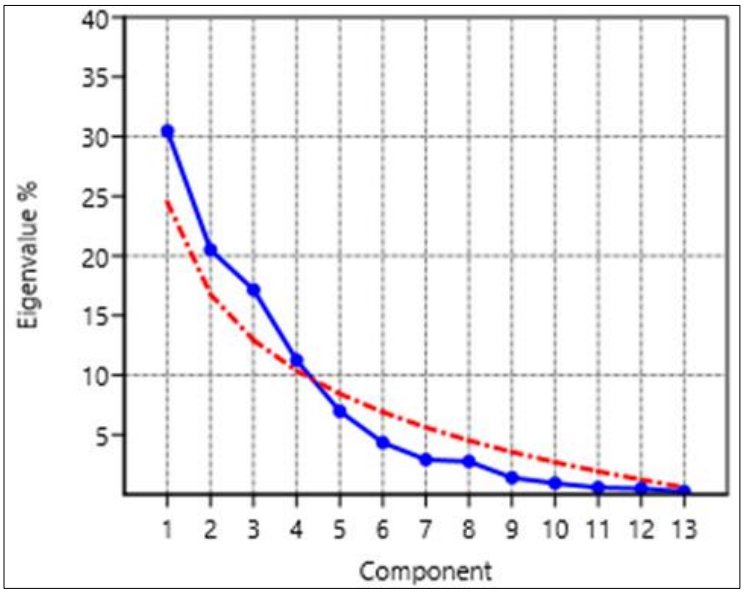

Fig 1: Scree lot graph based on Eigenvalues

Rotated component matrix revealed that two PCs are representing maximum variability (50.97%) 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 (30.46%) was mostly related to plant growth habit, anthocyanin colouration at nodes, intensity of anthocyanin colouration at nodes, leaf size, fruit colour at maturity unripened stage, fruit colour, fruit colour intensity, fruit sinuation of pericarp. Thus, PC1 allows for the simultaneous selection of phenological traits. PC2 accounted for characters for branching habit, stem pubescence, stem pubescence intensity, fruit shape at longitudinal section, (Table. 2 and Fig. 2).

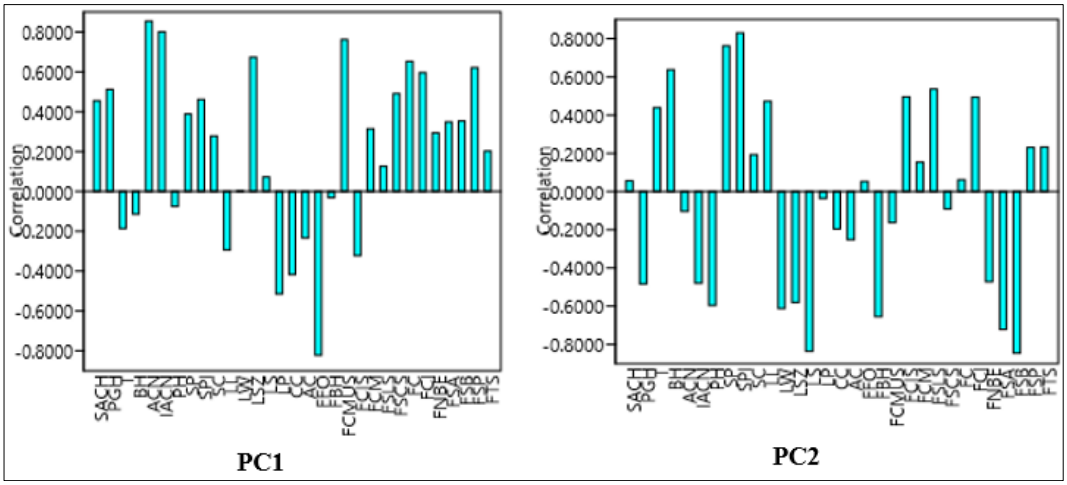

Fig 2: Graphical representation of rotated component matrix for different morphological traits in PC1 and PC2

Table 2: Interpretation of PCA for the morphological traits having value >0.5 in each PCs

	PC 1	PC 2
Morphological traits	Plant growth habit Anthocyanin colouration at nodes Intensity of anthocyanin colouration at nodes Leaf size Fruit colour at maturity unripened stage Fruit colour Fruit colour intensity Fruit sinuation of pericarp	Branching habit Stem pubescence Stem pubescence intensity Fruit shape at longitudinal section

PC scores of genotypes

Positive and negative values were found in the PC scores of each component (PC1 and PC2) (Table 3). These scores may be used to suggest exact selection indices, the strength of which is determined by the variability described by each main component. A high PC score for a specific genotype in a specific component implies high values for the variables in that specific genotype. Based on the highest PC scores promising genotypes were categorized in Table 4.

Table 3: PCA scores of chilli genotypes

Genotypes	PC 1	PC 2
CF-CBE-004	-1.8723	-3.5097
CA-CBE-200	-0.76065	0.42456
CF-CBE-007	-1.3437	-2.8443
CA-CBE-202	-3.2173	2.5371
CC-CBE-003	2.7971	-0.90534
CC-CBE-005	7.4601	0.58845
CC-CBE-004	-1.154	3.05
CA-CBE-199	-0.52066	3.2798
CC-CBE-002	2.7697	-1.081
CC-CBE-001	2.6184	-1.3239
CF-CBE-005	-2.8692	-0.71253
CA-CBE-201	-0.49203	4.3312
CF-CBE-006	-2.2192	-3.3461
CC-CBE-016	-1.1963	-0.48824

Table 4: Selection of genotypes on the basis of PC scores in each component having positive values and more than >1.0 in each PCs

S.no	PC 1	PC 2
1	CC-CBE-005 (7.4601)	CA-CBE-201 (4.3312)
2	CC-CBE-003 (2.7971)	CA-CBE-199 (3.2798)
3	CC-CBE-002 (2.7697)	CC-CBE-004 (3.05)
4	CC-CBE-001 (2.6184)	CA-CBE-202 (2.5371)

Note: = PC scores

Scatter plots including PC1 and PC2 show a strong grouping trend across the 14 chilli genotypes (Fig. 3a). The genotypes that occupied the convex of the hull are CC-CBE-005, CA-CBE-201, CA-CBE-202, CA-CBE-199, CC-CBE-004, CF-CBE-007, CC-CBE-001 and CC-CBE-002. The maximum variation was observed for stem pubescence, stem pubescence intensity, fruit curvature, fruit curvature intensity, fruit colour at intermediate stage, seedling anthocyanin coloration of hypocotyl, and fruit shape at longitudinal section based on the results of principal components, scatterplot for PC1 and PC2 (Fig.3b). The remaining DUS figures exhibited a low level of diversity.

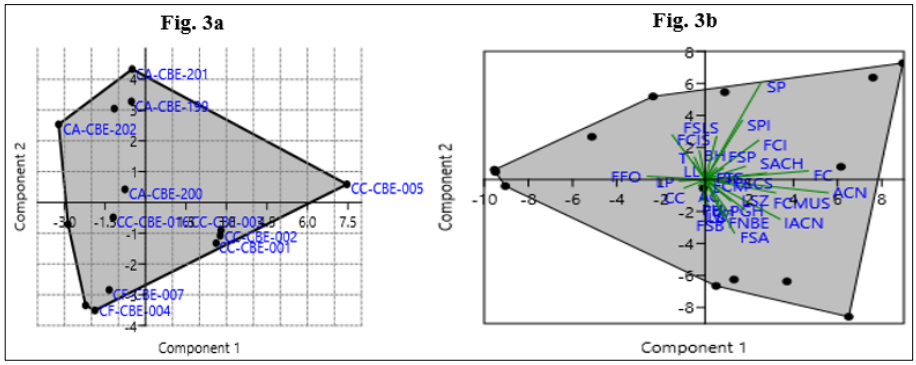

Fig 3: Genotype scatter plot illustrating the relationship between PC1 and PC2

Shannon-Weaver diversity indices (H') revealed that the corolla colour (2.627), leaf size (2.625), leaf length (2.624), plant growth habit (2.615), Fruit colour at intermediate stage (2.612) contributed to the maximum variation in the 14 chilli genotypes (Table 5).

Table 5: Shannon-Weaver diversity indices (H')

S.no	DUS descriptors	(H')
1	Seedling anthocyanin colouration of hypocotyl	2.376
2	Plant growth habit	2.615
3	Tillering	2.585
4	Branching habit	2.602
5	Anthocyanin colouration at nodes	2.44
6	Intensity of anthocyanin colouration of nodes	2.461
7	Plant height	2.626
8	Stem pubescence	2.109
9	Stem pubescence intensity	2.351
10	Stem colour	2.33
11	Leaf length	2.624
12	Leaf width	2.615
13	Leaf colour	2.589
14	Leaf size	2.625
15	Leaf shape	2.456
16	Leaf pubescence	2.593
1	Corolla colour	2.627
18	Anther colour	2.563
19	Flower and fruit orientation	2.609
20	Fruit bearing habit	2.566
21	Fruit colour at mature unriped stage	2.373
22	Fruit colour at intermediate stage	2.612
23	Fruit colour at maturity	2.579
24	Fruit shae at longitudinal section	2.591
25	Fruit shape at cross section	2.213
26	Fruit curvature	2.324
27	Fruit curvature intensity	2.192
28	Neck at basal end	2.273
29	Fruit shape at apex	2.591
30	Fruit shape at base	2.571
31	Fruit sinuation of pericarp	2.585
32	Fruit texture surface	2.376

Conclusion

The variability studies (PCA and H') for morphological characters (DUS descriptors) resulted in the identification of nine genotypes CC-CBE-005, CA-CBE-201, CA-CBE-202, CA-CBE-199, CC-CBE-004, CF-CBE-007, CC-CBE-001, CC-CBE-003 and CC-CBE-002 which are highly variable in characters such as stem pubescence, fruit curvature, fruit colour at intermediate stage, seedling anthocyanin coloration of hypocotyl, fruit shape at longitudinal section, corolla colour, leaf size, leaf length, plant growth habit, fruit colour at intermediate stage plays an important role in explaining the diversity among the genotypes.

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