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Studies on Genetic Divergence in Chilli (*Capsicum annuum* L.) under Southern Telangana Region

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ABSTRACT: Thirty genotypes were evaluated in Randomized Block Design with three replications in *rabi* seasons of the year 2016-17 at the experimental, field of Sri Konda Laxman Telangana State Horticultural University, Rajendranagar. Results indicated that in the year 30 genotypes were grouped into eleven highly divergent clusters. Some of genotypes were so divergent in all the character; hence each single genotype formed a separate cluster. Thus seven clusters *viz*., IV (EC-391088), V (IC-255958), VI (IC-255944), VIII (EC-390033), IX (IC-208591), X (EC-399569), XI (IC-255916) were solitary with one genotype in each cluster. The two genotypes were, hence they have formed two separate clusters *viz*., II (LCA-999, LCA-620), VII (IC25913, LCA-625). The remaining two clusters were having maximum number of genotypes. Cluster II was biggest with 10 genotypes followed by Cluster III was found with 9 genotypes. The intra cluster D^2 values ranged from 0.00 (Cluster VI, V, VI, VIII, IX, X and XI) to 139.55 (Cluster III). The cluster III had the maximum D^2 value (139.55) followed by Cluster VII (81.71) and cluster II (26.76). The inter cluster D^2 values of the eleven clusters revealed that highest inter cluster generalized distance (10154.92) was between cluster I and II followed by cluster I and IV (8723.77). The per cent contribution of each character towards divergence. It was observed that capsanthin content contributed maximum (42.53 %) towards divergence followed by plant height (16.32 %), ascorbic acid content (8.74), oleoresin content (5.52 %), days to first flowering (5.29 %), total number of fruits per plant (3.91 %), days to first fruiting (1.38 %), capsaicin content (1.15 %), fresh fruit yield per plant, fruit length, fruit diameter, fruit pedicel length, fresh fruit weight (0.92 %), seed content (0.23 %). Suggested exploitation of these two clusters by intermating genotypes in a definite breeding design to explore the fullest range of heterosis and to realize good recombinant lines.

Keywords: Chilli, Genotypes, Genetic divergence, Clusters, Improvement.

INTRODUCTION

Chilli (Capsicum spp.) is an important vegetable cum spice crop grown all over the world including India. Though, India used to produce an appreciable quantity of chilli but its productivity is still low. India is the major producer, consumer and exporter of chilli, covering an area of dry chilli 0.75 million hectares with a production of 2.1 million tonnes averaging a productivity of 1.93 metric tonnes per hectare (Indian Horticulture Database, 2018). The genus capsicum consists of a diverse range of plants and fruits, and varies enormously with respect to morphology, yield and nutrition related parameters. Chillies are grown as annual crop, although it can also be grown as perennial shrub in suitable climatic conditions. Among the five cultivated species, *Capsicum annuum* L. is the most widely cultivated species for its pungent (hot pepper) and non pungent (sweet pepper) fruits throughout the world.

The presence of capsaicinoids is specific to the genus capsicum, which varies widely among the varieties, seasons, places of origin, etc (Prasath *et al*., 2007). The chilli fruits are consumed at different ripening stage (green, red or partial red-ripe). Besides, it is used in many processing industries for various products such as pepper sauce, pickled pepper, ground pepper and dried pepper.

Improvement in both quantitative and qualitative traits needs precise information on the nature and degree of genetic divergence, which helps in choosing the right

parents for an efficient breeding programme. It is expected that, genetically divergent parents result in transgressive and productive recombinants. More diverse the parents within a reasonable range, better are the chances of improving economic characters in the F1 population. In the process of formulating the crop improvement programmes, understanding the nature and degree of genetic divergence in the available germplasm plays a pivotal role (Sreelathakumary and Rajamony, 2004).

Understanding about the nature and degree of genetic divergence in the available germplasm plays a pivotal role in selection for crop improvement programme. Genetic divergence among the collected genotypes of green chilli may help the breeders in selecting promising genetically diverse parent for the desired improvement.

The divergence analysis using Mahanalobis D^2 statistics, (Mahanalobis, 1936) which measure the forces of differentiation at intra and inter cluster level, is a variable tool for quantitative estimates of divergence Information on genetic divergence of chilli for the Southern Telangana scanty. Keeping in view the present investigation was under taken to study the nature and degree of genetic divergence among the chilli genotypes grown in southern part of Telangana. This information can be exploited in future for varietal improvement programme of chilli.

MATERIALS AND METHODS

To study the divergence of chilli (Capsicum spp.) genotypes, thirty chilli genotypes were transplanted during *rabi* season of year 2016-17. The accession numbers of the respective genotypes with source are presented in Table 1.

Table 1: List of chilli genotypes used in the experiment and their source.

Acc. No.	Genotype	Source
A_1	**EC-399569**	NBPGR Regional Station, Hyderabad
A_2	**EC-390033**	NBPGR Regional Station, Hyderabad
A_3	**IC-255916**	NBPGR Regional Station, Hyderabad.
A_4	**EC-399535**	NBPGR Regional Station, Hyderabad
A_5	**EC-391083**	NBPGR Regional Station, Hyderabad
A_6	**IC-255944**	NBPGR Regional Station, Hyderabad
A_7	**IC-208591**	NBPGR Regional Station, Hyderabad
A_8	**IC-255958**	NBPGR Regional Station, Hyderabad
A_9	**IC-25913**	NBPGR Regional Station, Hyderabad
A_{10}	**EC-391088**	NBPGR Regional Station, Hyderabad
A_{11}	**IC-214966**	NBPGR Regional Station, Hyderabad
A_{12}	**IC-208534**	NBPGR Regional Station, Hyderabad
A_{13}	**EC-399572**	NBPGR Regional Station, Hyderabad
A_{14}	**AAT-22**	NBPGR Regional Station, Hyderabad
A_{15}	**SR-3429**	NBPGR Regional Station, Hyderabad
A_{16}	**NIC-19967**	NBPGR Regional Station, Hyderabad
A_{17}	**PSR-7074**	NBPGR Regional Station, Hyderabad
A_{18}	**LCA-625**	NBPGR Regional Station, Hyderabad
A_{19}	**LCA-999**	NBPGR Regional Station, Hyderabad
A_{20}	**LCA-620**	NBPGR Regional Station, Hyderabad
A_{21}	**Bydagi**	Variety, Dharwad, Karnataka
A_{22}	**Devanur Deluxe**	Variety, Dharwad, Karnataka
A_{23}	**Warangal Chapata**	Landrace, Warangal, Telangana
A_{24}	**EC-246019**	NBPGR Regional Station, Hyderabad
A_{25}	**AVPP0514**	AVRDC, Regional Station, Hyderabad
A_{26}	**AVPP9813**	AVRDC, Regional Station, Hyderabad
A_{27}	**EC-334182**	NBPGR Regional Station, Hyderabad
A_{28}	**EC-382175**	NBPGR Regional Station, Hyderabad
A_{29}	**IC-214965**	NBPGR Regional Station, Hyderabad
A_{30}	**EC-399533**	NBPGR Regional Station, Hyderabad

The experiment was laid out in RBD with three replications at the experimental field of SKLTSHU, Rajendranagar. The area lies under the southern semi arid and Tropical zone of Telangana, India. The experimental soil was sandy loam. Healthy and uniform seedlings were transplanted in plots of 3.2 m × 1.4 m size with a spacing of 60 cm × 50 cm during middle of October Organic manure @ 25 t ha^{-1} was applied as basal. Inorganic fe1iilizers were applied @ 120: 60: 50 kg N: P_20_5: K_20 ha· respective season. Crop was raised following recommended package of practices. Observations were recorded on different morphological, yield attributing characters and quality parameter from ten randomly selected plants per plot. Ascorbic acid in chilli was estimated as per the procedure given and was expressed in mg/100 g of sample (Ranganna, 1986).

Capsaicin content (%) of red fruits was estimated by colorimetric method (balasubramanian *et.al*, 1982). Total extractable colour *i.e.* capsanthin (in ASTA unit) of red fruits was measured by American Spice Trade Association techniques (1986). Mahanalobis D^2 statistics was used for assessing the genetic divergence between the groups. The grouping of the population was done by using Tocher's method as described by (Rao, 1952).

RESULTS AND DICUSSION

Grouping of genotypes into different clusters (D^2 analysis): The D^2 values between any two genotypes was calculated as the sum of squares of the differences between the mean values of all the twenty characters and used for the final grouping of the genotypes. Procedure suggested by Tocher Rao, (1952) was used to group 30 genotypes into eleven clusters by treating the estimated D^2 values as the square of the generalized distance. Based on D^2 values, the 30 genotypes were grouped into eleven highly divergent clusters (Table 2). Some of genotypes were so divergent in all the character; hence each single genotype formed a separate cluster. Thus seven clusters *viz.*, IV (EC-391088), V (IC-255958), VI (IC-255944), VIII (EC-390033), IX (IC-208591), X (EC-399569), XI (IC-255916) were solitary with one genotype in each cluster. The two genotypes were also divergent in some character, hence they have formed two separate clusters *viz*., II (LCA-999, LCA-620), VII (IC25913, LCA-625). The remaining two clusters were having maximum number of genotypes. Cluster II was biggest with 10 genotypes *viz.*, (Bydagi, EC399533, Devanur Deluxe, Warangal Chapata, PBC-81, AVPP0514, AVPP9813, EC-334182, EC-382175 and IC-214965) followed by cluster III with 9 genotypes *viz.*, (NIC-19967, PSR-7074, SR-3429, AAT-22, IC208534, EC-399535, EC-399572, EC-391083 and IC-214966 are presented in Table 1 and three dimensional diagram in (Fig. 1). Similar results were reported by Smitha and Basavaraja, (2006); Ajjapplavara and Channagoudra, (2009); Dushyantha *et al.*, (2010); Tasso *et al.*, (2014); Janaki *et al*., (2016).

Table 2: Cluster classification of 30 genotypes of chilli.

Cluster	No. of genotypes	Genotypes
I	10	Bydagi, EC-399533, Devanur Deluxe, Warangal Chapata, PBC-81, AVPP0514, AVPP9813, EC-334182, EC-382175, IC-214965
II	2	LCA-999, LCA-620
III	9	NIC-19967, PSR-7074, SR-3429, AAT-22, IC-208534, EC-399535, EC-399572, EC-391083, IC-214966
IV	1	EC-391088
V	1	IC-255958
VI	1	IC-255944
VII	2	IC-25913, LCA-625
VIII	1	EC-390033
IX	1	IC-208591
X	1	EC-399569
XI	1	IC-255916

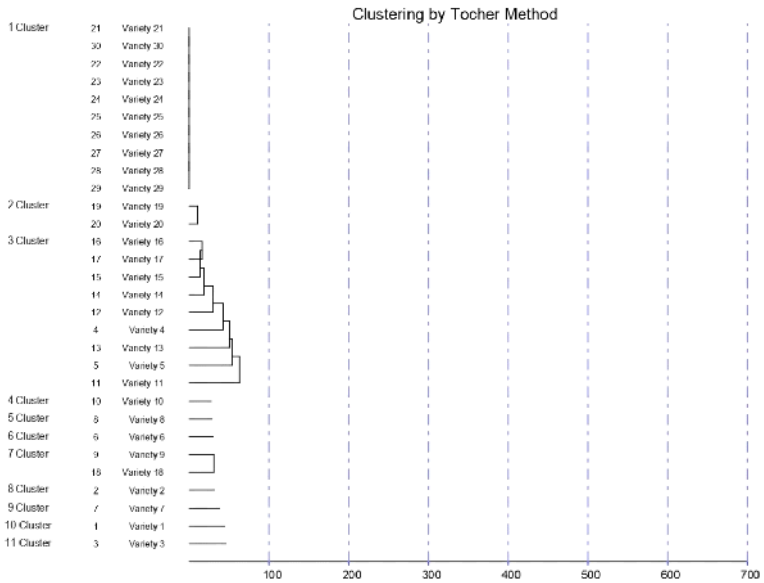

Fig. 1. Dendrogram showing clustering pattern (Tocher's method) in 30 genotypes of chilli.

Average intra and inter cluster distances: The mean intra and inter cluster D^2 values among the eleven clusters are given in the Table 3 & Fig. 2.

The intra cluster D^2 values ranged from 0.00 (Cluster VI, V, VI, VIII, IX, X and XI) to 139.55 (Cluster III). The cluster III had the maximum D^2 value (139.55) followed by Cluster VII (81.71) and cluster II (26.76).

The inter cluster D^2 values of the eleven clusters revealed that highest inter cluster generalized distance (10154.92) was between cluster I and II followed by cluster I and IV (8723.77), while, the lowest (26.76) was between cluster II. Cluster II followed by the VII is the most diverse as all other clusters showed maximum inter cluster distance from it showed in (Fig. 1). Several earlier reports Mishra *et al*., (2004); Ajjapplavara, (2009); Kumar *et al*., (2010); Suryakumari *et al*., (2010); Pandit *et al*., (2010); Yatung *et al*., (2014) also indicate the presence of a high genetic divergence among chilli genotypes in their respective experiments

Table 3: Average intra (bold) and inter-cluster D^2 values for twenty clusters in 30 genotypes of chilli

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	0	10154.92	7489.85	8723.77	6495.44	6624.97	7885.68	6508.44	7035.21	8530.06	7700.16
II		26.76	403.13	237.44	602	749.54	402.4	476	521.93	171.02	438.59
III			139.55	222.88	220.38	288.56	244.49	200.33	242.8	238.44	310.39
IV				0	344.34	314.21	224.8	276.64	193.61	315.05	230.54
V					0	110.39	285.69	84.84	172.08	288.02	324.25
VI						0	271.97	193.46	191.04	471.42	340.01
VII							81.71	261.72	391.89	312.79	245.21
VIII								0	122.45	225.23	204.71
IX									0	388.71	236.65
X										0	319.49
XI											0

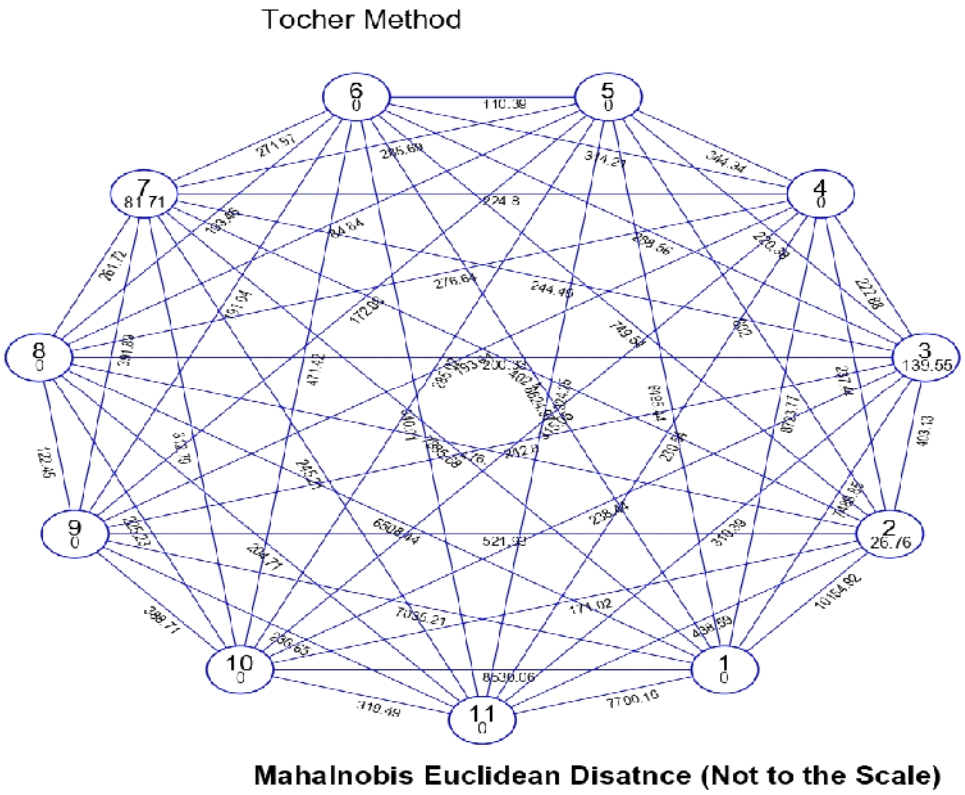

Fig. 2. Statical distance among 30 chilli genotypes (not to scale).

Nearest and distant clusters: The nearest and distant clusters from each of the cluster based on D^2 values are presented in Table 4. Cluster I was nearest to cluster V (6495.44) and distant from cluster II (10154.92). Cluster II exhibited close proximity with cluster II (26.76) and maximum divergence with cluster I (10154.92).

Cluster III was nearest to cluster III (139.55), while it was farthest from cluster I (7489.85). Cluster IV showed close proximity with cluster III (222.88) and maximum divergence with cluster I (8723.77). Cluster V exhibited intimate relation with cluster VIII (84.84) and wide diversity with cluster I (6495.44).

Cluster VI was nearest to cluster V (110.39) and distant from cluster I (6624.97). Cluster VII exhibited close proximity with cluster IV (224.80) and maximum divergence with cluster I (7885.68). Cluster VIII was nearest to cluster V (84.54), while it was farthest from cluster I (6508.44).

Cluster IX was nearest to cluster VIII (122.45), while it was farthest from cluster I (703521). Cluster X showed close proximity with cluster II (171.02) and maximum divergence with cluster I (8530.06). Cluster XI exhibited intimate relation with cluster VIII (204.71) and wide diversity with cluster I (7700.16). Similar results were reported by Misra *et al.*, (2011); Datta and Das; (2013); Suryakumari *et al.*, (2014).

Relative Contribution of different characters towards divergence: The per cent contribution of each character towards divergence is presented in Table 5 & (Fig. 3). It was observed that capsanthin content contributed maximum (42.53 %) towards divergence followed by plant height (16.32 %), ascorbic acid content (8.74), oleoresin content (5.52 %), days to first flowering (5.29 %), total number of fruits per plant (3.91 %), days to first fruiting (1.38 %), capsaicin content (1.15 %), fresh fruit yield per plant, fruit length, fruit diameter, fruit pedicel length, fresh fruit weight (0.92 %), seed content (0.23 %). The remaining characters *viz.*, number of primary branches per plant, number of flowers per axil, days to maturity, duration of the crop, dry fruit weight and anthracnose resistance did not contribute to the total divergence.

Table 4: The nearest and farthest clusters from each cluster based on D^2 values in chilli genotypes.

Cluster No.	Nearest cluster with D^2 values	Farthest cluster with D^2 value
I	V (6495.44)	II (10154.92)
II	II (26.76)	I (10154.92)
III	III (139.55)	I (7489.85)
IV	III (222.88)	I (8723.77)
V	VIII (84.84)	I (6495.44)
VI	V (110.39)	I (6624.97)
VII	IV (224.8)	I (7885.68)
VIII	V (84.54)	I (6508.44)
IX	VIII (122.45)	I (703521)
X	II (171.02)	I (8530.06)
XI	VIII (204.71)	I (7700.16)

Table 5: Per cent contribution of different characters towards diversity in chilli genotypes.

S.No.	Characters	Times ranked 1st	Per cent contribution
1.	Plant height (cm)	71	16.32
2.	Number of primary branches per plant	0	0.00
3.	Days to first flowering	23	5.29
4.	Number of flowers per axil	0	0.00
5.	Days to first fruiting	6	1.38
6.	Days to maturity	0	0.00
7.	Duration of the crop	0	0.00
8.	Total number of fruits per plant	17	3.91
9.	Fresh fruit yield per plant (g)	4	0.92
10.	Fruit length (cm)	4	0.92
11.	Fruit diameter (cm)	4	0.92
12.	Fruit pedicel length (cm)	4	0.92
13.	Fresh fruit weight (g)	0	0.92
14.	Dry fruit weight (g)	4	0.00
15.	Seed content (%)	1	0.23
16.	Ascorbic acid content (mg / 100g of fruit)	38	8.74
17.	Oleoresin content (%)	24	5.52
18.	Capsanthin content (ASTA units)	185	42.53
19.	Capsaicin content (%)	5	1.15
20.	Anthracnose resistance	0	0.00

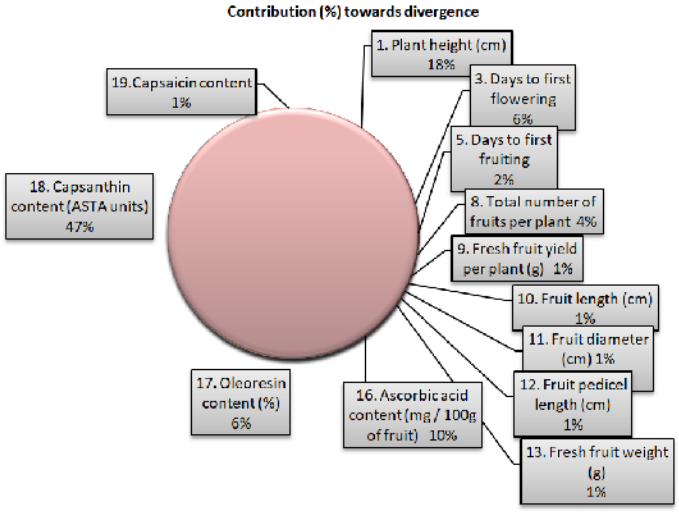

Fig. 3. Per cent contribution of different traits towards divergence of chilli genotypes.

In the present study, thirty germplasm lines of chilli were grouped into eleven clusters. The magnitude of D^2 values confirmed that there was considerable amount of diversity in the experimental material evaluated.

Statistical distance represents the extent of genetic diversity among clusters. The inter cluster distance was minimum between cluster II and VII indicating close relationship and similarity for most of the characters of the genotypes included in these clusters. The maximum inter cluster distance was observed between clusters II and I followed by between clusters II and X, indicating wider genetic diversity among the genotypes included in these groups. Selection of parents from these diverse clusters for hybridization programme would help in achieving novel recombinants. Cluster II displayed least intra cluster distance denoting the similarity of genotypes. While, maximum intra cluster distance was recorded in cluster III and this might be due to limited gene exchange or selection practices among the genotypes for diverse characters. Therefore, hybridization programme between the genotypes belonging to cluster II and of clusters may be undertaken for getting good segregants.

Emphasis should be laid on characters contributing maximum D^2 values for choosing the cluster for the purpose of further selection and choice of parents for hybridization. Highest contribution towards divergence in this regard was put forth by capsanthin content, plant height, ascorbic acid content, oleoresin content, days to first flowering, total number of fruits per plant, days to first fruiting, capsaicin content, fresh fruit yield per plant, fruit length, fruit diameter, fruit pedicel length, fresh fruit weight and seed content. Thus, these were the major traits contributing to divergence. Hence, selection for divergent parents based on these characters will be useful for heterosis breeding in chilli.

Genetic divergence among thirty genotypes revealed that the genotypes *viz.*, Warangal Chapata, LCA-620, LCA-999 and Devanur Deluxe were identified as genetically divergent for plant height and hence, these genotypes can be utilized in crop improvement programme as donor parents for improving fruit length**.** The genotypes IC-255958, IC-208591, LCA-620 and LCA-625 were more divergent for improving number of primary branches per plant**.** The genotypes Warangal Chapata, EC-334182 and Devanur Deluxe were found to be promising line for days to first flowering. The genotypes *viz.*, IC-255916 and EC-399535 are found to be promising line for number of flowers per axil, whereas, the genotypes *viz.*, IC-255958, NIC-19967 and AAT-22 can be used for improving days to first fruiting, the genotypes *viz.*, EC-391083, NIC-19967, IC-255958 can be used for improving days to maturity**.** The genotype Devanur Deluxe, Warangal Chapata, EC-399533 can be used for improving duration of the crop, such as genotypes IC-255916, LCA-625 and Devanur Deluxe can be used for improving total number of fruits per plant. Parameters like fresh fruit yield per plant, the genotypes Warangal Chapata, Devanur Deluxe, EC-399569 and IC-255916 can be used for improving the existing cultivars. Similarly the genotypes IC-255944, IC-208591, AVPP0514 can be used for imparting fruit length character in a hybrid variety. By using the genotypes, Warangal Chapata, EC-399572 and IC-214966 fruit diameter can be improved. Genotypes AVPP0514, AVPP9813 and LCA-620 can be improved and fruit pedicel length. Genotypes EC-399572 and Warangal Chapata can be brought under breeding programme to improve local cultivars for fresh fruit weight. The genotypes EC-399572, IC-214966 and Warangal Chapata with higher dry fruit weight and Warangal Chapata, IC-214965 and EC-399569 with more seed content can be used for improving existing cultivars. The genotypes Warangal Chapata, AVPP9813 and Devanue Deluxe with Ascorbic acid content character can be used for further improvement in breeding programme. The genotypes Warangal Chapata, AVPP0514 and Bydagi with high oleoresin

content. Similarly, AVPP0514, NIC-19967, EC-399569 and IC-255958 were with high capsanthin content and Warangal Chapata, PSR-7074 and PBC-81can be used for high capsaicin content. Bydagi, Devanur Deluxe and Warangal Chapata can be used for hybridization programme.

CONCLUSION

On the basis of present investigation, we could conclude that, the selection of genotypes from Thus seven clusters *viz.*, IV (EC-391088), V (IC-255958), VI (IC-255944), VIII (EC-390033), IX (IC-208591), X (EC-399569), XI (IC-255916). Can be utilized as potential parents and crossing between this genotypes results is high heterotic expression for high yield and its components. So the genotypes from above clusters may be including in hybridization programme for obtaining superior and desirable recombinants. Hence, it will be rewarding to bring improvement in chilli.

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Conflict of Interest. Nil.

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