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Analysis of Genetic Divergence in Chilli (*Capsicum annuum* L.) Genotypes

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ABSTRACT

Chilli (Capsicum annuum L.) is a spice cum vegetable crop belonging to the family Solanaceae. It has different uses at mature green, red ripe and dried stages. Crop improvement in chilli has so far been achieved by exploiting the available sources of the variability. Naturally, the genetic variation or diversity for most of the yield attributes is considerably high in chilli. In the present study we used 63 chilli genotypes which include germplasm accessions, local cultivars, and released varieties. This experiment was undertaken to study genetic diversity and selection of suitable genotypes for future hybridization program. 26 character were studied for the better assessment of genetic diversity present between 63 genotypes. Using Mahalanobis[4] D^2 statistics method, 63 genotypes were grouped into 5 divergent clusters. The 63 chilli genotypes included in the present study had considerable diversity as observed by the magnitude of all possible D^2 values, which ranged from 25.45 to 64.66. These 63 genotypes were grouped into 5 clusters based on similarity of D^2 values. It is desirable to select genotypes from clusters having high inter cluster distance and with high fruit yield as parents in the recombination breeding programmes.

Key words: *Diversity, Cluster, D2 statistics, Hybridization*

INTRODUCTION

Chilli (*Capsicum annuum* L.) is a spice cum vegetable crop belonging to the family Solanaceae. Chillies are nature's wonder. Its fruit appear in different sizes, shapes and colours. Chillies have two important qualities. Chilli is grown for its spice and vegetable green fruits of commerce. It has different uses at mature green, red ripe and dried stages.

Chilli is mainly used for its pungency and pleasant flavor. Consumption of small amount of chilli enriches diet and considered as of minerals, vitamins and other food components[2,17]. The genus *Capsicum* originated in the American tropics. Five species of capsicum were cultivated in different parts of the World[8]. It is probably introduced by Portuguese into Southern parts of India and cultivation spread out throughout India by the end of 19 centuries.

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Due to long history of cultivation, selection and popularity of crops sufficient genetic variability has been generated. Rich variability in morphological traits in hot pepper occurs throughout India particularly in south peninsular region, North Eastern foot hills of Himalayas and Gangetic plains[10]. Collection and maintenance of the genetic diversity in capsicum are important to avoid genetic erosion. Besides the identification of species, the characterization and evaluation of genotypes maintained in gene banks are of fundamental importance[16].

Looking to the market potential of chilli, there is a need to expand area, production and productivity. Hence, there is a prime need for development of varieties or hybrids suited to specific agro-ecological conditions with high quality fruits.

The plant breeders are always interested to know the genetic divergence among the varieties available due to reasons that crosses between genetically diverse parents are likely to produce high heterotic effect[11] and crosses involving distantly related parents within the same species produce wide spectrum of variability. 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 in heterosis breeding[7].

Studies on genetic diversity are important as the individual plant selection is solely dependent on variability. More the diversity, better are chances of improving the economic characters under consideration in the resulting offspring. Crop improvement in chilli has so far been achieved by exploiting the available sources of the variability. Naturally, the genetic variation or diversity for most of the yield attributes is considerably high in chilli. There is a need to seek improvement in complex quantitative trait such as yield. As a result of free exchange of chilli germplasm and lot of introgression of characters has taken place in many local chilli cultivars resulting in enhancement of variability and new genetic combinations. This experiment was undertaken to study genetic diversity and selection of suitable genotypes for future hybridization program.

MATERIAL AND METHODS

Experimental location: The experiment was conducted in field of department of Crop improvement and biotechnology of Kittur Rani Channamma College of Horticulture, Arabhavi, which is located at Zone-3 of Karnataka

Plant materials: Germplasm were collected from HRS (Horticulture Research Station), Devihosur along with two established popular local cultivars Byadagi Kaddi and Byadagi Dabbi and some other were from local farmers. The accession numbers of the genotypes with codes are given in Table 1.

Nursery raising and cultivation practices: The germplasm accessions raised were sown in raised seed beds and 25 days later transplanted in the main field in randomized block design with two replications consisting of one row of 15 plants for each entry. A spacing of 60 cm × 60 cm was followed and the crop was raised as per the recommended package of practices.

Observations recorded: Five random competitive plants per treatment/genotypes were selected, tagged and observations were recorded on these plants for different characters like, plant height (cm), number of primary and secondary branches, plant spread in east west and north south (cm), stem girth (cm), days to first and fifty percent flowering, fruit set percentage, green fruit length and girth (cm), number of fruits per plant and fruit yield per plant (Kg). The data recorded on five

plants per treatment was averaged and for other characters such as ascorbic acid content (mg/100g) and capsaicin content (%) was calculated and estimated by random picking of green fruits which are taken for recording fruit characters. In these characters also estimated quantities are averaged and the average data of both plant and fruit quality characters were taken for statistical analysis.

Statistical Analysis: Average of values of each parameter or characters were used for analysis. Statistical analysis of the data was carried out by using Statistical Package for Agricultural Research (SPAR) and Indostat. For diversity analysis Mahalanobis[4] D^2 statistical methods was used.

RESULT AND DISCUSSION

Genetic Diversity

The importance of genetic diversity has been widely appreciated. Multivariate analysis utilizing the concept of statistical distance has been found to be a very powerful statistical tool in estimating diversity in biological populations. It has been successfully employed even in situations where overlapping of characters rendered the conventional methods of classification ineffective[6,14]. Ecological diversity has been regarded as a reasonable index of genetic diversity[5,18]. Assuming this, the cultivars from widely separated localities have been included in the hybridisation programme by most of the plant breeders for recovering promising sergeants. But, Sachan and Sharma[13], Kumar *et al*[3]., and Rameshbabu and Patil[12] could not find any direct relationship between geographical distribution and genetic diversity in crops belonging to different breeding systems. The 63 chilli genotypes included in the present study had considerable diversity as observed by the magnitude of all possible D^2 values, which ranged from 25.45 to 64.66 (Table 2). These 63 genotypes were grouped into 5 clusters based on similarity of D^2 values.

Intra-cluster distances (Table 3) revealed, cluster II with 3 genotypes shared maximum intra-cluster distance (D^2= 21.72) followed by cluster I (D^2=18.33) shared with 57 genotypes showing that the genotypes belonging to cluster I are very closely related. The clusters III, IV and V (D^2=0.00) had only one genotype each. However, present study has showed that there was comparatively high intra-cluster distance among the genotypes in cluster I and II indicating the presence of sufficient amount of diversity with genotypes of respective clusters. Thus, there is scope for selection among the genotypes within the clusters. Similar results were also obtained by Farhad *et al*[2]., Datta *et al*[1]., and Tasso *et al*[17].

Based on distance between clusters *i.e.* inter-cluster distance, the maximum divergence was observed between cluster-III and cluster-V (64.66) followed by cluster-II and cluster-V (57.65), cluster-III and IV (52.01), cluster-II and III (44.72), cluster-I and V (43.51), cluster-II and IV (37.87), cluster-I and II (32.73), cluster-I and III (31.89), and cluster-I and IV (29.79). The inter cluster distance was least between cluster-IV and V (25.45).

Analysis of cluster means

All genotypes spread over 5 clusters and means were scored across the clusters for all the 26 characters. (Table 4)

The lowest cluster mean was given the first rank and next cluster possessing next best means were given 2nd, 3rd, and so on up to 5th rank for all the traits accordingly cluster III with overall score of 54 across 26 characters secured first rank followed by clusters I, II, V and IV indicating presence of most promising genotypes in them and can be extensively used for further breeding programme to generate new material. Similar reports are also given by Prabhudeva[9] and Smitha and Basavaraja[15].

Table 1: List of 63 genotypes used for the study

Sl. No.	Lines	Sl. No.	Lines	Sl. No.	Lines
1	Samriddhi	22	V-20	43	G22
2	Gadag Local	23	V-22	44	G23
3	V-1	24	V-23	45	G24
4	V-2	25	VN2	46	G176
5	V-3	26	G1	47	G178
6	V-4	27	G2	48	G179
7	V-5	28	G4	49	G180
8	V-6	29	G5	50	G181
9	V-7	30	G6	51	G189
10	V-8	31	G9	52	G190
11	V-9	32	G11	53	G191
12	V-10	33	G12	54	G192
13	V-11	34	G13	55	G194
14	V-12	35	G14	56	G197
15	V-13	36	G15	57	G198
16	V-14	37	G16	58	G199
17	V-15	38	G17	59	G201
18	V-16	39	G18	60	Byadagi Kaddi
19	V-17	40	G19	61	Byadagi Dabbi
20	V-18	41	G20	62	Arka Lohit
21	V-19	42	G21	**63**	**Pusa Jwala (Check variety)**

Table 2: Clustering pattern of 63 genotypes of chilli, based on D^2 values

Cluster	Number of genotypes	Genotypes included
I	57	Gadag local, Samriddhi, G-1, G-2, G-4, G-5, G-6, G-9, G-11, G-10, G-11, G-12, G-13, G-14, G-15, G-16, G-17, G-18, G-19, G-20, G-21, G-22, G-23, G-24, G-176, G-177, G-178, G-179, G-180, G-181, G-182, G-183, G-184, G-185, G-186, G-187, G-188, G-189, G-190, G-191, G 192, G194, G-197, G-198, G-199, G-200, G-201.
II	3	Arka Lohit, Pusa Jwala and V 11
III	1	VN2
IV	1	G 13
V	1	V 18

Table 3: Average intra and inter cluster D^2 values of chilli germplasm

Cluster Distances	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Group. 1	18.33	32.73	31.89	29.79	43.51
Group. 2		21.72	44.72	37.87	57.65
Group. 3			0	52.01	64.66
Group. 4				0	25.45
Group. 5					0

Table 4: Per cent contribution of each character

Sl. No.	Character	Times Ranked 1st	Contribution %
1	Plant height (cm)	16	0.82%
2	Number of primary branches	0	0.00%
3	Number of secondary branches	9	0.46%
4	East West (cm)	0	0.00%
5	North South (cm)	24	1.23%
6	Stem Girth (cm)	1	0.05%
7	Days to First Flowering	0	0.00%
8	Days to 50% Flowering	0	0.00%
9	Fruit set percentage	1	0.05%
10	Green fruit girth (cm)	14	0.72%
11	Green fruit length (cm)	57	2.92%
12	Green fruit weight in (g)	331	16.95%
13	Number of green fruits/plant	528	27.04%
14	Green fruit yield /plant (kg)	1	0.05%
15	Green fruit yield /plot (kg)	81	4.15%
16	Green fruit yield /ha (t)	0	0.00%
17	Dry fruit girth (cm)	0	0.00%
18	Dry fruit length (cm)	5	0.26%
19	Dry fruit weight in (g)	0	0.00%
20	Dry fruit yield /plant (kg)	1	0.05%
21	Dry fruit yield /plot (kg)	0	0.00%
22	Dry fruit yield /ha (t)	0	0.00%
23	Number of seeds per fruit	64	3.28%
24	1000-seed weight (g)	6	0.31%
25	Ascorbic acid content (mg/100 g)	801	41.01%
26	Capsaicin content (%)	13	0.67%

CONCLUSION

Genetic diversity is largely contributed by pericarp weight, dry fruit yield per plant, number of fruits per plant and number of branches per plant. Thus, these characters may be given high emphasis while selecting the lines for hybridization programme to generate large variability and it will provide immense scope for improvement of yield through selection.

REFERENCES

1. Datta S. and Das, L., Characterization and genetic variability analysis in *Capsicum annuum* L. germaplasm. *SAARC J. Agri.*, **11(1):** 91-103 (2013).
2. Farhad, M., Hasanuzzaman, M., Biswas, B.K., Ariifuzzaman, M. and Islam, M.M., Genetic divergence in chilli (*Capsicum annuum* L.*). Bangladesh Research Publications Journals*, **3(3):** 1045-1051 (2010).
3. Kumar, S.R., Verma, S.P. and Ganguli, D.K., D^2 analysis for fruit yield and component characters in brinjal (*Solanum melongena* L.). *South Indian Horti*., **46(5-6):** 251-255 (2000).
4. Mahalanobis, P.C., On the generalized distance in Statistics. Proc. Natl. Inst. Sci., India. **2:** 49-55 (1936).
5. Moll, R.H., Salhwana, W.S. and Robinson, H.F., Heterosis and genetic diversity in variety crosses in maize. *crop sci*., **2:** 197-198 (1962).
6. Murthy, B. and Anand, I.J., Combining ability and genetic diversity in some varieties of *Linum usitatissimum*. Indian J. Genet., **26:** 21-36 (1966).
7. Patel, M.Z., Reddi, M.V., Rana, B.S. and Reddy, B.J., Genetic divergence in

safflower (*Carthamus tinctorius* L.). *Indian J. Genet*., **49(1):** 113-118 (1989).

8. Pickersgill, B., Genetic resources and breeding of *Capsicum spp. Euphytica*, **96:** 129- 133 (1997).
9. Prabhudeva, S.A., Variability, genetic diversity and heterosis study in chilli (*Capsicum annuum* L.). *M. Sc. Thesis*, Univ. Agric. Sci., Dharwad, Karnataka, India (2003).
10. Pradheep, K. and Veeraragavathatham, D., Characterization of *Capsicum spp.* germplasm *Indian Journal of Plant Genetic Resources*, **19(2):** 180-183 (2006).
11. Ramanujam, S., Tiwary, A.S. and Mehra, R.B., Genetic divergence and hybrid performance in mungbean. *Theor. Appi. Genet*., **44(5):** 211-214 (1974).
12. Rameshbabu, and Patil R.V., Studies in brinjal genotypes. Part-II. Genetic divergence. *Indian J. Pl. Gen. Res*., **15(1):** 71-70 (2002).
13. Sachan, K.S. and Sharma J.R., Multivariate analysis of genetic divergence in tomato. *Indian J. Gen. Pl. Bred*., **31(1):** 86-93 (1971).
14. Sakal, R.R., Statistical Methods in Systematics. *Biological Review*, **40:** 337-391 (1965).
15. Smitha, R.P. and Basavaraja. N., Genetic divergence studies in chilli (*Capsicum annuum* L.). *Karnataka J. Agric. Sci*., **19(4):** 978-979 (2006).
16. Sudre, C.P., Gonçalves, L.S.A., Rodrigues, R., Amaral Júnior do A.T., Riva Souza, E. M. and Bento, C. dos S., Genetic variability in domesticated *Capsicum* spp as assessed by morphological and agronomic data in mixed statistical analysis. *Genetics and Molecular Research*, **9(1):** 283-294 (2010).
17. Tasso, Y., Rakesh Kr. Dubey, Vikas Singh, and Garima, U., Genetic diversity of chilli (*Capsicum annuum* L.) genotypes of India based on morpho-chemical traits. *AJCS* **8(1):** 97-102 (2014).
18. Vavilov, N.I., Studies on the origin of cultivated plants. *Bul Appli Botany*., **16:** 2 (1926).