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Genetic variability and inter-relationship studies among growth, yield and quality parameters in Chilli (*Capsicum annuum* L.)

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Abstract

Chilli (*Capsicum annuum* L.) is probably one of the commercial and important vegetable crop after tomato at the global level. In India, Chilli is cultivated on an area of 3.76 lakh hectares with a production of 3.78 lakh tonnes and productivity of 10.02 tonnes per hectare (NHB, 2019). Since the productivity of the crop is low there is a demand for development of new varieties and hybrids with high productivity. Genetic divergence and extent of genetic variability are important for the genetic improvement of any crop in the germplasm stock. Magnitude of genetic variability present in the germplasm is always proportional to the improvement in any crop. Greater the chances of desirable genotypes and cultivars, greater is the variability in the population. Screening of available germplasm helps to estimate the variation and diversity and also to classify and select superior parents for hybridization purposes. The degree of genetic divergence can be calculated by using the Multivariate Analysis from Mahalanobis D^2 , which is as an important method for determining the relative contribution of different characters to total divergence in crops that are often cross-pollinated.

Keywords: Variability, heritability, genetic advance, divergence, Chilli

Introduction

Chilli (*Capsicum annuum* L.) with chromosome number, $2n= 24$ belonging to Solanaceae family is one of the most important commercial vegetable as well as spice crop grown in India both for domestic consumption as well as for export. The origin of chilli is Central America. It has wide range of diverse uses such as spice, sauce, vegetable and medicinal purposes. It is considered as an important source of nutrients, vitamin A and C as well as phenolic compounds, which are important antioxidants in human diet (Litoriya *et al.* 2014) [2]. The presence of crystalline volatile alkaloid capsaicin makes chilli pungent while red colour of chilli is due to presence of capsanthin. Health benefits of chilli are anti-bacterial properties, prevention of diabetes, anti-inflammatory, improves vision and clear digestion (Hosmani, 1993). In Punjab, chilli is cultivated in an area of 7.69 thousand hectares with production of 14.50 thousand hectares and productivity of 5.3 t/ha (NHB, 2019).

In chilli improvement programme, characterization and evaluation of germplasm are one of the important prerequisite. In any breeding work, assessment of genetic variability present in the indigenous genotypes for yield and its components is necessary. Parameter of genotypic and phenotypic coefficients of variation is useful in detecting the amount of variability present in the germplasm. Heritability and genetic advance help in determining the influence of environment in expression of the characters and the extent to which improvement is possible after selection. Hence, new genotypes must be characterized to assess the variability and identify promising genotypes which can be used in further breeding programmes. The complex character like yield is controlled by a large number of yield contributing characters and their interactions. Correlation studies between different quantitative characters provide an idea about association which is further exploited to formulate selection strategies for improvement of yield and its components. The path coefficient technique helps in estimating direct and indirect contribution of various components in building up total correlation towards yield. In the hybridization programme, genetically diverse parents are with high heterotic effect and genetically distant parents in the segregating generations could generate a wide range of variability. D^2 statistics by Mahalanobis (1936) is an important tool which provides a measures of magnitude for divergence between two genotypes under comparison. The first step to effective selection and using genotypes in the breeding programme is the study of genetic diversity along with heritability.

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Table 1: Genetic variability, Heritability (h^2) and Genetic advance (GA)

Aspect	Recommendation	Reference
Genetic variability, h^2 GA		
94 genotypes	High GCV and PCV with high heritability and high genetic advance for number of matured fruits and dry fruit yield/plant, 100 seed weight, capsaicin, capsanthin and ascorbic acid content.	SuryaKumari <i>et al.</i> (2010) ^[3]
34 genotypes	High PCV than GCV with number of fruits per plant (86.05%, 85.02%), fresh fruit weight (119.95%, 111.26%), 100 seed weight and weight of red ripe fruit (111.63%, 110.97%) and high heritability and genetic advance for no. of fruits/plant, ascorbic acid content(mg/100g) and green fruit yield/plant.	Chattopadhyay <i>et al.</i> (2011) ^[4]
53 genotypes	High heritability with high genetic advance in no. of fruits/plant, capsaicin content and in primary branches/ plant.	Datta and Das (2013) ^[5]
23 genotypes	High phenotypic variation coefficient and genotypic variation coefficient for fruit number, fruit weight and dry (red) yield per plant. High heritability estimates were demonstrated by all the characters. However, the number of fruits/plant, the yield of green fruits per plant, the dry (red) yield per plant, the number of seeds per plant and the height of the plant showed high genetic improvement as a percentage of the mean additive gene effect.	Amit <i>et al.</i> (2014) ^[6]
63 genotypes	High magnitude of PCV and GCV for per cent fruit set, number of matured fruits per plant, fruit diameter, average dry fruit weight, considering the wide range of genetic variability in germplasm.	^[7] Janaki <i>et al.</i> (2015)
25 genotypes	High PCV for fruit width (21.00%), fruit weight of dry chilli (23.38%) seed yield/plant (28.94%), number of primary branches per plant (21.88%) and number of fruits/plant (42.00%) where as high GCV was seen in number of fruits per plant (41.77%), dry fruit yield (29.61%), seed yield per plant (27.67%) and fruit weight of dry chilli (21.67%).	Kadwey <i>et al.</i> (2016) ^[8]
24 genotypes	Hyb-(2)-2 showed maximum-- fruit yield per plant, fruit length, fruit girth, and pericarp thickness among the most promising one. Genetic variability of number of fruits per plant, fruit yield/plant, fruit girth and number of seeds/fruit have emerged as the most accurate selection characters due to their probable conditioning by the additive gene action. In three characters, moderate GCV was reported in combination with high broad sense heritability and moderate genetic advance, namely fruit yield per plant, number of fruits per plant, fruit girth and seeds per fruit.	Murmu <i>et al.</i> (2017) ^[9]
11 genotypes	Genotypic and phenotypic variances were recorded highest for fruit yield per plant, followed by fruit weight and fruit number per plant. Phenotypic coefficient of variation and genotypic coefficient of variation were maximum for the number of plants affected by leaf curl per plot supplemented by fruit weight and number of wilted plants per plot. Heritability was highest for fruit weight followed by the number of fruit per plant and the amount of fruit affected per plant. Maximum genetic advance was observed in the number of plants affected by leaf curl per plot followed by fruit.	Nahak <i>et al.</i> (2018) ^[10]
34 genotypes	The GCV and PCV were higher in fruit yield per plant, average dry fruit weight and average fresh fruit weight. Strong heritability was achieved with TSS, average dry fruit weight and average fresh fruit weight. Genetic advance as a percentage of average was higher in the case of dry fruit yield per plant and average dry fruit weight.	Kumar <i>et al.</i> (2019) ^[11]
60 genotypes	The high heritability estimates for number of fruits/plant (99%), fruit diameter (68%), fruit length (96%), fruit weight (95%), and fruit yield per plant (99%) were found.	Farwah <i>et al.</i> (2020) ^[12]
19 genotypes	For chlorophyll, ascorbic acid (mg/100 g), capsaicin (SHU), fruit yield / plant (g), fruit yield/ ha and number of fruits/ plant, higher GCV and PCV values suggested the existence of greater genetic variability and less environmental impact. Stalk to fruit ratio, number of fruits/plant, fruit yield/plant(g), average dry fruit weight (g),fruit yield/ha, ascorbic acid (mg/100 g), chlorophyll and capsaicin (SHU) showed high heritability coupled with high genetic advance as a percentage mean, indicating the existence of additive gene action for inheritance of these yield characteristics.	Kumar <i>et al.</i> (2020) ^[13]

Report: From the above table maximum workers in different locations stated that high PCV and GCV, heritability and genetic advance were found maximum in the characters like plant height, no. of fruits/plant, fruit weight, fruit length, seed weight, no. of seeds/fruit. This shows that selection is most preferable for quality and yield traits.

Correlation and Path coefficient analysis

Kumar *et al.* (2012) reported that the chilli traits such as No. of branches at 150 DAT, days to flowering anthesis, number of fruits/plant, average fruit weight, ascorbic acid, capsaicin content and length of fruit showed a positive correlation with fruit yield per plant (g), while incidence of leaf curl showed negative genotypic correlation ^[14]. Jogi *et al.* (2013) tested correlation and path coefficient analysis in 50 genetically diverse cultivated and wild genotypes of chili and recorded a significantly positive phenotypic and genotypic association of all characteristics of fruit yield except days to first flowering and weight of 10 fruits and established a positive correlation of early fruit yield and late fruit yield with total fruit yield. The genotypic path coefficient analysis showed that ascorbic acid and chlorophyll content had high direct positive effect on

total fruit yield ^[15]. Green fruit yield per plant exhibited significant positive and substantial correlation with average green fruit weight, fruit length and fruit breadth, while dry fruit yield showed a similar correlation with fruit length and yield per plant (Vikram *et al.* 2014) ^[16]. Correlation studies found a negative association of capsanthin with oleoresin content and capsaicin content. Oleoresin content had a positive correlation with fruit length, pericarp weight, fruit number per plant and dry fruit yield per plant (Vijaya *et al.* 2015) ^[17]. The findings of correlation studies showed that for all the features, genotypic correlation coefficients were greater in magnitude than their corresponding coefficients of phenotypic correlation. At both genotypic and phenotypic levels, green fruit yield/plant had a high, important and positive association with the number of fruit/plant, average fruit weight, moisture content and chlorophyll content, suggesting that these characteristics were the main yield attributing characteristics. Path analysis showed that characteristics such as the number of secondary branches per plant, the number of fruits per plant, and the mean weight of the fruit had a high and positive direct impact on the yield of green fruit Patel *et al.* (2015) ^[18].

Hasan *et al.* (2016) conducted a study with 30 chilli genotypes of fruit length, fruit weight, 100 seed weight, and fruits per plant showed a significant and positive correlation with yield per plant at both genotypic and phenotypic levels. Path coefficient analysis revealed that fruits per plant had maximum positive direct effect on yield ^[19]. Pujar *et al.* (2017) conducted field experiments to study the correlation and path analysis of 63 chili genotypes and demonstrated that fruit yield was correlated positively and extremely significantly with the percentage number of fruits per plant ^[20]. Path analysis and correlation tests of 20 chilli genotypes were performed with 14 different qualitative and quantitative characteristics. At the genotypic and phenotypic level, correlation coefficients indicated that the fruit length, fruit diameter showed a highly significant and positive genotypic and phenotypic correlation coefficient with fruit yield per plant. Path coefficient analysis found that the fruit diameter, days to first flowering, had a negative direct impact on fruit

yield per plant. The fruit diameter had a very high direct positive effect on fruit yield per plant. Days to first harvest had a small direct positive effect on fruit yield per plant. The height of the plant and the days before the first harvest had a negligible impact on the fruit yield per plant (Vidya *et al.*, 2018) ^[21]. Negi and Sharma, (2019) performed a study during the summer-rainy season of 2017 and experimental material consisting of 33 chilli genotypes including 'Surajmukhi' was evaluated as a standard check in randomised complete block design with three replications. The majority of characteristics displayed a high degree of heritability along with moderate PCV, GCV and genetic improvement projections. Correlation analysis found that marketable red ripe fruit yield / plant exhibited a positive correlation with fruit length, fruit diameter, fruit width, plant height, average red ripe fruit weight, marketable red ripe fruit / plant, total red ripe fruit / plant, marketable red ripe fruit / plant proportion, average dry fruit weight, and both dry fruit yield / plant levels ^[22].

Table 2: Positive and negative correlation

Characters	Positive correlation with yield	Negative correlation with yield	Positive direct effect with yield	Negative direct effect with yield
Plant height	8	-	1	-
No of fruits/plant	1,4,5,6	-	1,3,4,5	-
Fruit length	1,3,5,7,8	-	3,5,8	-
Fruit weight	2,3,4,5	-	3,4,5,6	-
Days to first flowering	2	-	3	7
Fruit diameter	7	-	7	-
Fruit set %	6	-	6	-
Ascorbic acid	1	-	1,2	-
Capsaicin content	1	-	8	-

References

- 1- Kumar *et al.* (2012), 2-Jogi *et al.* (2013)
- 3-Vikram *et al.* (2014), 4-Patel *et al.* (2015)
- 5-Hasan *et al.* (2016), 6-Pujar *et al.* (2017)
- 7-Vidya *et al.* (2018), 8-Negi *et al.* (2019)

Report: From the above table it is clearly observed that maximum characters are positively correlated with yield and showed a positive direct effect on yield. So direct selection for the characters can be used for the improvement in chilli.

Genetic Divergence

The study on genetic diversity was conducted by Hasanuzzaman and Golam (2011), with twenty chilli accessions grouped into six clusters. Cluster I consisted of a single genotype, three accessions of Cluster II and Cluster III, two genotypes of Cluster IV and a maximum of seven genotypes of Cluster V, while Cluster VI consisted of four genotypes, respectively. The highest intra-cluster divergence was invariably smaller for cluster VI than the lowest divergence between cluster III and cluster VI, thus authenticating the pattern of clustering identified in this analysis. The intra-cluster divergence ranged from 0.00 to 0.07288 to 1.7153 while the inter-cluster divergence ranged from 3.247 to 12.677 between clusters III and VI and clusters I and V ^[23]. (Datta and Das, 2013), with 53 genotypes grouped into 17 clusters, and results indicated that Cluster I and Cluster VII included 29 and 9 genotypes. The remainder of the clusters each consisted of one genotype. Variability tests showed that all of the characters analyzed had a wide range of variation. In capsaicin content in fruit, number of fruits, yield and primary branches per plant, high heritability along with higher genetic advance (as a percentage of mean)

has been found. These characters can be regarded as accurate indices of selection as they may be controlled by the influence of additive genes ^[24]. (Yatung *et al.*, 2014) performed a D² statistics analysis to estimate genetic divergence with thirty genotypes of chilli and divided into six clusters below. Cluster III had a large number of genotypes and had the highest intra-cluster gap while the lowest was found in Cluster II, since the greatest contribution to divergence was provided by characters such as capsaicin and ascorbic acid material. The highest inter-cluster difference between Cluster II and Cluster IV was observed, and the lowest was identified among both Cluster I and Cluster IV. So, this can be taken into account in selecting better parents for an effective hybridization system in chill ^[25]. Hasan *et al.* (2015) used D² statistics to study the genetic variation of 13 chilli genotypes based on six characters. The findings suggested a maximum contribution of fruits per plant to total divergence followed by length of fruit and yield per plant. Cluster IV provided the highest mean for fruit weight, plant fruits and plant yield. Cluster V produced the highest mean for length of fruit, pedicel length and diameter of fruit. Cluster I and III recorded the lowest overall mean for nearly all characters. Hence genotypes of Cluster IV and Cluster V can be used as possible parents in the future hybridization system for the production of the desired superior chilli variety ^[26]. Abhinaya *et al.* (2016) conducted an experiment in 32 genotypes and studied the genetic divergence, variability and correlation studies for yield and its components. The study indicated the presence of genetic variability, less environmental influence of plant height, secondary branches per plant, weight of the fruit, length of stalk, fruits per plant, seeds per fruit, yield of fruit, vitamin C and capsaicin content ^[27]. Sharma *et al.*, (2017) conducted an experiment using 64 genotypes and concluded

that genetic diversity assessment can be useful in selecting the most successful genotypes for breeding strategy design to generate genetic variability in the current chilli germplasm pool [28]. Gawande *et al.* (2018) assessed 29 chilli genotypes on the basis of seven yield and yield contributing characteristics for genetic diversity studies as per Mahalanobis D² statistics. The 29 chilli genotypes were grouped into 9 clusters. Maximum genotypes were grouped into cluster 1 followed by cluster 2 and 4 followed by cluster 2 and 6 clusters found to have one genotype in each cluster. The maximum intra-cluster distance was in cluster 4 followed by cluster 2 where cluster 4 and 6 showed as the highest inter-cluster distance [29]. Bandela *et al.* (2019) studied twenty-five

genotypes of chilli and grouped into 7 clusters, based on Mahalanobis D² statistics. The maximum number of genotypes for the cluster I is seven whereas cluster IV contained one genotype only. The maximum number of genotypes accommodated among the clusters was cluster-I (7), followed by cluster-II (5), cluster-VI (5), cluster-III (3), cluster-V (2), cluster-VII (2) and cluster-IV (1). Between clusters I and VII, the highest inter-cluster distance was observed (6.978) and the lowest inter-cluster distance between clusters V and VI (2.828). The highest intra-cluster gap was observed in cluster VII (2.768) and the lowest was observed in cluster IV (0.001) [30].

Table 3: Show the genotypes and method used analysis

Year of study	No. of genotypes taken	Method used for analysis	No of clusters	High intra cluster distance	High inter cluster distance	Reference
2011	20	Mahalanobis D ²	6	Cluster 6	Cluster 3,6	Hasanuzzaman and Golam (2011)
2013	53	D ²	17	Cluster 7	Cluster 17,16	Datta and Das (2013)
2014	30	D ²	6	Cluster 3	Cluster 2,4	Yatung <i>et al.</i> (2014)
2015	13	Mahalanobis D ²	5	Cluster 4	Cluster 1,4	Hasan <i>et al.</i> (2015)
2016	32	D ²	3	Cluster 3	Cluster 2,3	Abhinaya <i>et al.</i> (2016)
2017	64	D ²	8	Cluster 6	Cluster 4,7	Sharma <i>et al.</i> (2017)
2018	29	Mahalanobis D ²	9	Cluster 4	Cluster 4,6	Gawande <i>et al.</i> (2018)
2019	29	Mahalanobis D ²	7	Cluster 7	Cluster 1,7	Bandela <i>et al.</i> (2019)

Report: From the above table studies were conducted at different locations on the divergent characters by dividing them into clusters based on the Mahalanobis D² and it can be concluded that with specific clusters of intra and inter cluster distance which has different diversity of gene action indicates a better scope for the selection of traits in the improvement of chilli.

Conclusion

In this paper, the reviewed literature highlighted the genetic divergence and variability available in genotypes of chilli. Awareness of the relationship between yield and its components is very useful for the efficient selection of the desired type of plant. Genetically divergent genotypes may also be used for the potential improvement of chilli crops.

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