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EXPLORING GENETIC VARIABILITY OF CHILLI GENOTYPES IN RELATION TO YIELD AND ASSOCIATED TRAITS

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Abstract

Chilli peppers, integral to Capsicum spp., are globally vital crops valued for culinary, economic, and nutritional contributions. Assessing genotypes is essential for improving varieties with traits like higher yield, disease resilience, and enhanced nutritional value. This study was conducted at the Spices Research Centre in Shibganj, Bogura, during the period of 2019-20 to evaluate 20 genotypes of chilli. Employing an alpha lattice design with two replications, the evaluation considered genetic diversity, variation, heritability, clustering, and trait associations as key components. All the traits exhibited remarkable significance (P< 0.01) for the studied genotypes, underscoring the genetic variability inherent to the traits in focus. Heritability varied from 79% to 99% for the traits investigated. Foremost in yield was found in the AVPP 1111 genotype (21.62 t/ha), trailed by the Indch 39 (21.19 t/ha), and A1511050 (20.57 t/ha). The cluster analysis dendrogram visually demonstrated the proximity among different genotypes concerning their similarities, ultimately forming six distinct clusters. While the studied traits displayed higher genotypic co-efficient of variation (GCV), and phenotypic co-efficient of variation (PCV) values, however, GCV values were closely aligned with PCV values across the traits. Notably, a robust positive correlation existed between yield and both single fruit weight and the weight of fruit per plant. The outcomes of this study, i.e., the promising genotypes AVPP 1111, Indch 39, A1511050 etc.; grouping; and significant positive correlations of different traits with grain yield, hold valuable insights for future chili improvement initiatives.

Keywords: Chilli, GCV, Genetic diversity, Heritability, PCV, Variability

Introduction

Chilli (*Capsicum annuum* L.) is an important valuable commercial spice-cum-vegetable crop belonging to the family Solanaceae, and originated in Latin American regions of New Mexico, Guatemala and Bulgaria (Prajapati *et al.,* 2020). Chilli is diversely used as a spice, condiment, culinary supplement, medicine, vegetable and

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ornamental plant. It is also one of the most widely used spice crop in Bangladesh. It is widely cultivated throughout the year. It is a self-pollinated crop but chances of cross-pollination are also high. It has wide variability especially on shape, size, skin color, hotness etc. Germplasm collection followed by evaluation is a continuous process in crop breeding program and is also important for the maintenance of biological diversity and food security. Improvement of any crop depends on the extent of genetic variation present, and the degree of improvement depends on magnitude of the available beneficial genetic variability. Therefore, it is necessary to explore the mutual relationship between yield and yield components for efficient utilization of the genetic stock in crop improvement program of chilli.

Heritability is used to denote the relative degree to which a character is transmitted from parent to offspring. The magnitude of such estimates suggests the extent to which improvement is possible through selection (Nechifor *et al.*, 2011). It also indicates how much of the genetic variability has a genetic origin and gives necessary information for the genetic selection process (Falconer, 1981). The correlation between the yield and its component characters are not often real because of inter-relationship existing between the component characters themselves. Therefore, analysis of inter component correlation is very essential to expose the direct and indirect contributions of each component (Wright, 1921; Srinivas *et al*., 2020). In Bangladesh, the cultivated area of chilli is 1.03 lakh hectare, and the total production is 1.41 lakh metric tons (dry chilli) with an average yield of 1.37 t/ha (BBS, 2018). Though there are quite a few popular chilli varieties introduced by public research institutes and private seed companies, has higher yield potential, but still we are well short in production than the expected demand. So, we are trying to develop new varieties with higher yields and better quality that will compete with the existing popular chilli varieties. By keeping the view in consideration, the present experiment was conducted to evaluate chilli genotypes collected from different agro-ecological zones and to identify the potential genotype(s) in terms of yield and its attributing traits suitable for mass production while conserve the land races for future research purposes.

Materials and Methods

Germplasm

A total of 20 chilli lines collected from all over the Bangladesh were included in the study. Commercially available chilli variety developed by public research institute were used as standard check. Details of the germplasm were given in supplementary table S1.

Location

The chilli lines were evaluated at Spices Research Center, BARI, Bogura during winter (Rabi) season of 2019-20. The weather details prevailed during cropping seasons of different years at the location were given in supplementary table S2.

Experimental plan

The field trial was laid out in Alpha lattice design accommodating the genotypes under study with 2 replications. The seeds of the different genotypes were sown in seed bed on 26 September, 2019 and four weeks old seedlings were transplanted on well-prepared raised bed in the field on 31 October, 2019. The unit plot size was 3 m x 1 m keeping 0.5 m space between beds. A 50 cm x 50 cm spacing was maintained for row to row and hill to hill during planting. The crop was fertilized with recommended dose of cow dung 5t/ha, $N_{100}P_{52}K_{100}S_{22}Zn_3B_2$ kg/ha. Other intercultural practices were done as and when required in which timely irrigation was provided to ensure moisture availability and plant protection measures were taken to repel pest infestation.

Observations recorded

Various morpho-physiological traits observations were recorded using standard protocol for chilli phenotyping (IPGRI, AVRDC and CATIE. 1995). Plant height, number of fruits per plant, single fruit weight, weight of fruits per plant, was recorded on randomly taken five plants, and then averaged. Fresh yield (Green chilli) was recorded from field weight on whole plot basis at harvestand converted to tons per hectares.

Statistical analysis

The analysis of variance for individual traits was carried out using R software (R Core Team 2021). The theoretical formula for calculation of ANOVA implemented in R was in accordance as for Alpha lattice design (Patterson and Williams 1976). Analysis was required to test whether the genotypes differed significantly among themselves or not. Clustering of genotypes were done using 'Dendextend' package (Tal Galili, 2015) in R software (R Core Team 2021).

Linear model of observations in alpha lattice design as follows

$$Yijk=\mu + ti + rj + bjk + eijk \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots..(1)$$

Where,

Yijk- observed trait for i-th treatment received in the k-th block within j-th replicate

ti - fixed effect of the i-th treatment

rj- effect of the j-th replicate

bjk- effect of k-th incomplete block within the j-th replicate

eijk- experimental error

Phenotypic and genotypic variance were calculated according to the formula given by (Lush , 1949). Heritability in broad sense for all the characters was computed as suggested by (Lush, 1949). Heritability was classified in to low (0-30 %), moderate (30-60 %) and high (>60 %) as suggested by (Robinson et al, 1949). Correlation analysis was performed in 'R' software (R Core Team 2021) using 'Agricolae' package (de Mendiburu, 2015).

Results and Discussion

Variability estimates

Twenty chilli genotypes were studied for estimating genetic diversity and variability based on some morphological traits. All the morphological characters studied in this study showed highly significant variability (GV) ($P < 0.01$) (Table 1). These significant differences indicate that the genotypes were genetically variable for the studied traits. Variations in growth, and yield components have been reported in many studies (Sharma *et al.*, 2010; Thul *et al.*, 2009; Alam et al., 2022; Alam et al., 2023; Khan et al., 2022).

In the present study, it was found that the GCV and PCV value was higher for all the traits (Table 1); however, GCV values were near to PCV values for all the studied traits. Higher values of PCV and GCV indicated that there was high variability exiting among the genotypes. High genotypic coefficients of variation (GCV) were observed for the traits single fruit weight (54.6%), weight of fruit per plant (35.5%), fresh yield (26.57%), and number of fruits per plant (22%). On the contrary, the lowest genotypic coefficient of variation was exploited by the trait plant height (11.3%). High phenotypic coefficients of variation (PCV) were observed for traits single fruit weight (55.3%), weight of fruit per plant (35.6%), fresh yield (27.7%) and number of fruits per plant (23.9%). On the contrary, the lowest phenotypic coefficient of variation was exploited by the trait plant height (14.0%).

The results from all the genotypes depicted that, phenotypic variances (PV), and phenotypic coefficient of variation (PCV) were higher than genetic variances (GV) and genotypic coefficient of variation (GCV) for all the studied characters suggesting some environmental influence on those characters. Similar result was found by Yanti (2016) with sixteen genotypes of chilli indicating high contribution of genotypic effect for phenotypic expression of such characters. Kannan *et al*., (2016) conducted a study on evaluating eight diverse genotypes of chill, and they found that high genotypic and phenotypic coefficient of variation, heritability and genetic advance. Similarly, high heritability found in the studied genotypes for fruits per plant, fruit weight, flowers per branch, fruits per branch and clusters per plant, revealed these traits are under the control of additive gene action. This indicated high response to selection for genetic improvement of chilli genotypes.

Table 1. Co-efficient of variance and heritability of the different traits in chilli

Trait	h^2_b	GV	PV	GCV	PCV	GA	GG
PH	0.79	140.82**	215.78	11.34	14.04	19.75	18.87
NF	0.92	779.75**	920.03	21.97	23.87	52.96	41.67
SFW	0.99	5.28**	5.41	54.61	55.29	4.68	111.11
WFP	0.99	29834.38**	30037.85	35.49	35.61	354.61	72.86
FY	0.96	16.52**	17.96	26.57	27.70	8.03	52.51

Note: PH=Plant height; NF=Number of fruits per plant; SFW=Single fruit weight; WFP=Weight of fruit per plant; FY=Fresh yield; h^2b=Heritability; GV=Genetic variance; PV=Phenotypic variance; GCV= genotypic coefficients of variation; PCV= phenotypic coefficients of variation; GA=Genetic advance; GG=Genetic gain.

Heritability and genetic advance

Heritability estimates often as a measure of precision of trials (Schmidt et al., 2019), is of tremendous significance to the breeder, as its magnitude indicates the accuracy with which a genotype can be recognized by its phenotypic expression. Heritability of the studied traits in the present study was ranged from 79-99%. The higher values of the estimates indicated that majority of the variation in a trait is due to variation in genetic factors (Wray and Visscher 2008; Visscher et al., 2008), which means traits are less influenced by the surrounding environment, ultimately reflects the precision/ accuracy of the trial (Schmidt et al., 2019). Most of the traits such as single fruit weight (h^2b=99%), weight of fruit per plant (h^2b= 99%), fresh yield (h^2b= 96%), number of fruits per plant (h^2b= 92%) and plant height (h^2b= 79%) exhibited high heritability (>60%) accompanied with high to moderate genotypic and phenotypic coefficient of variance (Table 1). High heritability of those traits indicated that influence of environment on these characters was negligible or low. Therefore, selection can be effective on the basis of phenotypic expression of those traits in the individual plant by implementing simple selection methods. High heritability does not always indicate a high genetic gain; heritability should be used together with genetic advance in predicting the ultimate effect for selecting superior varieties. (Muchie and Fentie, 2016).

The estimates of high heritability (>60%) coupled with high genetic advance (>20%) were recorded in weight of fruit per plant (h^2b=99 %, GA=354.61%), in Table 1 which exhibited good scope for improving these traits through phenotypic selection due to additive gene action. High genetic advance associated with high heritability of fruit weight, fruit weight per plant, single fruit weight, fresh yield, number of fruits per plant and plant height suggested appreciable level of improvement could be possible for these characters subjected to selection. High estimates of heritability for these characters suggested that the selection based on phenotypic performance would be effective as propounded by Johnson *et al*., (1955). High heritability coupled with high genetic advance has been reported for yield and fruit weight per plant in chilli (Munshi and Behra, 2000; Sreelathakumary and Rajamony, 2004; Singh and Yadav, 2008).

Means and range

Plant height ranged from 82.86 cm to 127.12 cm, with a mean of 104.65 cm, (Table 2). The tallest genotype was Indch 36 (127.12 cm) followed by TOZP 11 (117.08 cm) and the dwarf one was BARI Morich-3 (82.86 cm). Average number of fruits per plant varied from 80.08 to 187.86 with a mean of 127.09. Most profuse bearing genotype was found in EW 1009 while least one was found in Indch 41. Single fruit weight ranged from 1.51 g to 10.45 g with a mean of 4.21 g. Most light weight fruit was found from genotype VTNMCH 2, whereas healthy one was from genotype Indch 41. Average weight of total fruits per plant varied from 211.31 g to 781.37 g with a mean of 486.72 g. The maximum fruit weight per plant was observed in genotype Indch 41 and the minimum was found in genotype VTNMCH 2. Fresh yield ranged from 9.12 t/ha to 21.62 t/ha with a mean of 15.30 t/ha. The highest yielding genotype was AVPP 1111 (21.62 t/ha) followed by genotypes Indch 39 (21.19 t/ha), and A1511050 (20.57 t/ha). In contrast, the genotype AVPP 1236 was recorded for the lowest yield (9.12 t/ha) (Fig. 1).

Table 2. Performances of twenty chilli genotypes evaluated during 2019-2020

Genotype	PH	NF	SFW	WFP	FY
AVPP 1111	90.4	103.6	7.6	777.4	21.6
Indch 39	100.9	99.3	6.3	602.1	21.2
A1511050	103.7	148.5	4.2	625.7	20.6
EW 2050	109.7	111.7	6.5	720.3	19.2
LTMCH	114.3	120.9	3.8	465.1	19.2
Indch 23	94.2	172.21	3.2	563.0	18.6
TOZP 11	117.1	141.3	3.3	468.8	17.6
Indch 41	98.5	80.1	10.5	781.4	17.8
Indch 33	104.6	109.2	6.4	698.0	16.6
F1HC	102.9	130.4	3.2	410.6	14.5
LTMHCH	112.0	141.7	3.3	464.9	14.4
Indch 36	127.1	122.7	4.4	523.6	13.9
KSMRCH 1	115.0	132.9	2.9	387.6	12.8
Mohona 2	91.2	83.9	5.7	450.8	12.7
AVPP 1245	95.9	136.6	2.2	296.6	12.2
BARI Morich-3	82.7	122.1	2.6	315.9	11.5
VTNMCH 1	110.1	144.4	1.9	264.7	11.5
VTNMCH 2	104.8	139.7	1.5	211.3	10.6
EW 1009	109.5	187.9	2.2	422.8	10.2
AVPP 1236	108.0	113.17	2.6	283.8	9.1
Grand Mean	104.7	127.1	4.21	486.7	15.3
Min.	82.9	80.1	1.51	211.3	9.1
Max.	127.1	187.9	10.45	781.4	21.6
LSD (1%)	11.87	18.82	0.55	27.02	1.9
CV%	8.27	9.32	8.66	2.93	7.83

Note: PH=Plant height; NF=Number of fruits per plant; SFW=Single fruit weight; WFP=Weight of fruit per plant; FY=Fresh yield. LSD=Least significant difference; CV%=Coefficient of variation

Clustering pattern

Cluster dendrogram from cluster analysis showing the closeness of different genotypes in terms of their similarity (Fig. 1). The phenotypic relatedness was found in cluster analysis, with two major clusters. Furthermore, the grouping of evaluated genotypes, clusterted into six sub-groups. This may probably have genotypes with less diversity, so the base gene pool was narrow (Madu and Uguru, 2006). The top yielding genotypes AVPP 1111, Indch 39 and A1511050 were in a same cluster, and entirely different from other genotypes. The check entry BARI Morich-3 were in a cluster with four other genotypes. The dendrogram provides insights into the genetic diversity of the chilli genotypes and can be useful in selecting suitable parents for breeding programs to improve the yield and quality of chilli crops. The phenotypic relatedness also evidenced by the narrow range o similarity coefficient (0.637-0.866) (Votava *et al*., 2005).

Correlation analysis

The interrelationship among traits is utmost importance for effective selection in cultivar development. Correlation coefficients give reliable and useful information on the relationship between the traits in terms of the nature, extent and direction of selection (Zeeshan *et al*., 2013). The type of genotypic (r_g) and phenotypic (r_p) correlations in plant breeding can have important implications for the selection of breeding lines and the development of new cultivars. Table 3 showed the correlation coefficients (r_g and r_p) between different traits. For number of fruits per plant, both r_g and r_p were positive for plant height and yield indicating a moderate correlation with the other traits. For example, there was a positive correlation between number of fruits per plant and yield, both in terms of r_g and r_p (r_g=0.26, r_p=0.33). This suggests that the plants with a higher number of fruits per plant tend to have a higher yield.

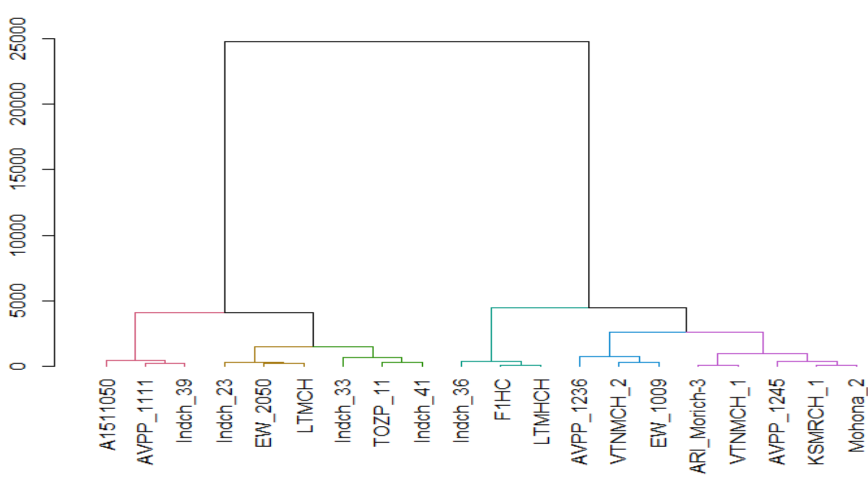

Fig. 1. Dendrogram showing the cluster pattern of genotypes of chilli

Table 3. Correlation among different yield and yield contributing traits of chilli genotypes

Traits	Type	PH	NF	SFW	WFP
NF	r_g	0.31			
	r_p	0.25			
SFW	r_g	-0.23	-0.73**		
	r_p	-0.21	-0.73**		
WFP	r_g	-0.09	-0.42	0.89**	
	r_p	-0.09	-0.44	0.90**	
FY	r_g	0.15	0.26	0.64**	0.84**
	r_p	0.08	0.33	0.67**	0.81**

Note: PH=Plant height; NF=Number of fruits per plant; SFW=Single fruit weight; WFP=Weight of fruit per plant; FY=Fresh yield; $r_{g=}$Genotypic correlation; $r_{p=}$Phenotypic correlation

From the study, it was also found that the weight of fruit per plant and single fruit weight were strongly positively associated with yield, while weight of fruit per plant and single fruit weight are negatively associated with plant height and number of fruits per plant. Similar results have been reported in chili by Hosamani (2008) where they observed significant correlation of various yield attributing traits with fruit yield. In case of weight of fruit per plant, both r_g and r_p were negative, indicating a weak negative correlation with the other traits. For example, there was a negative correlation between weight of fruit per plant and number of fruits per plant (r_g=-0.42, r_p=-0.44) and weight of fruit per plant and plant height (r_g=-0.09, r_p=-0.09). But there was a strong positive correlation between single fruit weight and yield (rg=0.84, r_p=0.81). For single fruit weight, both r_g and r_p were negative with number of fruits per plant, plant height and positive with yield, indicating a moderate to strong correlation with the other traits. For example, there was a strong positive correlation between single fruit weight and yield (r_g=0.64, r_p=0.67). There was a negative correlation between single fruit weight and plant height, meaning that as the plant height increases, the single fruit weight tends to decrease. There was also a negative correlation between single fruit weight and number of fruits per plant, suggesting that as the number of fruits per plant increases, the single fruit weight tends to decrease. In case of yield, both r_g and r_p were positive with all the other traits, indicating moderate to strong correlations. For example, there was a strong positive correlation between yield and weight of fruit per plant (r_g=0.84, r_p=0.81).

Overall, the correlation coefficients suggest that weight of fruit per plant and single fruit weight were strongly positively associated with yield, while weight of fruit per plant and single fruit weight were negatively associated with plant height and number of fruits per plant. These relationships can be useful in plant breeding programs for selecting traits that are likely to result in higher yields.

Conclusion

Evaluation of 20 chili genotypes has unveiled significant genetic diversity and variability in morphological traits, which will enhance chili breeding programs. Heritability estimates ranging from 79% to 99% suggest a predominant genetic influence on the studied traits, with minimal environmental impact. Traits such as fresh fruit yield, weight per plant, number of fruits per plant, and single fruit weight exhibit high genetic and phenotypic variability, coupled with moderate to high heritability. These insights provide valuable guidance for breeders aiming to optimize quantitative characteristics in C. annuum crosses. Hierarchical clustering techniques identified six clusters among the accessions, offering a roadmap for selecting ideal parents in breeding programs to enhance productivity and quality. Notably, genotypes such as AVPP 1111, Indch 39, and A1511050, clustered closely with lower genetic distances, displayed the highest yields, emphasizing the significance of genetic relatedness in yield performance. Overall, this study's comprehensive findings hold substantial value for both researchers and producers, contributing to the advancement of chilli cultivation and ultimately enhancing livelihoods of farmers.

Conflicts of Interest

The authors declare no conflicts of interest regarding publication of this manuscript.

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