



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(11): 2075-2080
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www.thepharmajournal.com
Received: 26-09-2022
Accepted: 31-10-2022

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Studies on heritability, genetic advance and correlation in chilli (*Capsicum annum* L.)

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Abstract

The present investigation was carried out at experimental field, Division of Vegetable Science during Kharif 2020. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The experimental material involved forty-nine genotypes of chilli collected from different states of India representing different agro-ecological regions and were evaluated for several quantitative and qualitative traits. The genotypes observed significant differences for all the characters. Analysis of variances revealed significant differences for all the characters observed. The highest phenotypic and genotypic coefficients of variation were observed for Capsaicin followed by number of fruits per plant, fruit yield per plant and fruit diameter. In general, PCV was marginally higher than the corresponding GCV indicating the less influence of environment in the expression of traits under study. High heritability, coupled with high genetic advance as percentage of mean was observed for almost all traits indicating that most of the traits studied were mainly controlled by additive gene effect and thus selection may be effective. Correlation coefficients revealed that the fruit yield per hectare exhibited significant positive association with fruit length, number of fruits per plant, average fruit weight and fruit yield per plant.

Keywords: Chilli, heritability, genetic advance, genotypic variance, phenotypic variance

Introduction

Chilli (*Capsicum annum* L.) is an important vegetable cum spice crop grown in almost all parts of tropical and subtropical regions of the world. It belongs to the family Solanaceae. The genus *Capsicum* includes 30 species, five of which are cultivated: *Capsicum annum* L., *C. frutescens* L., *C. chinense* Jacq, *C. pubescens* R. & P. and *C. baccatum* L. (Perry *et al.*, 2007) [26]. The primary centre of origin of chilli is reported to be Latin American regions of New Mexico, Guatemala and Bulgaria (Salvador, 2002) [31]. Columbus introduced it in Europe in 15th century and thus spread to the rest of the world along the spice trading routes to Africa, India, China and Japan. In India, its introduction is believed to be through the Portuguese from Brazil towards the end of 15th century and its cultivation became popular in the middle of 17th century. In India, there is a lot of variation in the morphological characteristics of hot peppers, especially in the south peninsular region, the north Eastern foot hills of Himalayas and Gangetic plains (Pradheep and Veeraragavatham, 2006) [27]. The crop's high level of variability hasn't, however, been completely exploited in crop improvement programmes up to this point. For the purpose of planning a successful breeding programme to increase the genotype's yield potential, understanding of nature and extent of genetic variability in the population is of utmost importance. Heritability is a genetic relationship between parent and progeny that has been frequently utilised to determine the degree to which a character can be passed down from one generation to the next. The genetic advance through selection can be estimated with knowledge about the character's heritability. To determine whether the observed variation for a specific character is caused by genotype or by environment, heritability studies are therefore crucial. The correlation coefficient analysis measures how different characters are related to one another and identifies the component traits that selection might be based upon to improve results.

The ultimate criterion that a plant breeder must bear in mind while developing superior cultivars of any crop is yield. Yield, on the other hand, is a polygenic trait that is heavily impacted by the environment. Knowledge of the relationship between quantitative characters, especially for yield and its attributes, is quite useful throughout the selection process. Variability studies reveal the amount to which distinct characters may be improved, but they do not reveal the degree and nature of the relationships that exist between various contributing characters and economically significant characters.

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As a result, understanding of the relationship of various characters among themselves and with economic character is required for making indirect selections to enhance economical characters. Correlation studies help to understand the relationship that exists between highly heritable characteristics and the majority of economic characters, as well as the role that each trait plays in the genetic makeup of the crop. The magnitude of the observed association between two characters is indicated by the phenotypic correlations. Because it includes both heredity and environmental effects, this does not provide a complete genetic picture of the relationship. Genotypic correlations measure the inherent relationship between the genes that regulate any two characters. As a result, it is more important and might be useful in developing an effective selection strategy

The goal of the current study was to determine the heritability and correlation in order to identify promising genotypes for use in improving the genetics of chillies in temperate environments. To determine the relative significance of unexpected factors in such a situation, it is crucial to divide the correlation coefficient into components of direct and indirect effects. The goal of the current investigation was to ascertain the degree of association, genetic advance, heritability, and variability among the characters.

Materials and Methods

Planting of genotypes was done in Randomized Complete Block Design (RCBD) with three blocks, during Kharif 2020. The sowing was carried out on 22nd April 2020. Seedlings were transplanted in the field on 8th June 2020 at a spacing of 45 cm between rows and 45 cm between plants in a row. Ten plants of each genotype were transplanted and five randomly chosen plants from each genotype were used for recording data on plant growth habit, branching habit, leaf shape, fruit position, fruits per axil, fruit shape, fruit shape at pedicel attachment, fruit shape at blossom end, plant height, plant spread, number of primary branches per plant, days to 50% flowering, days taken to first fruit set, fruit diameter (cm), fruit length (cm), pedicel length (cm), average fruit weight (g), number of fruits per plant, green fruit yield per plant(kg), fruit yield per hectare (q/ha), average dry fruit weight (g) and number of seeds per fruit. The mean data of five plants was used for statistical analysis.

The data was examined to determine various components of

coefficient of variation, heritability in the broad sense, expected genetic advance as a percentage of Mean and phenotypic and genotypic correlation coefficients.

Genotypic variance and Phenotypic variance was calculated using the method suggested by Johnson *et al.* (1955) [11]. The amount of phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) in a trait was calculated using Burton's formula (1952) [2]. The formula given by Lush (1949) [17] and Johnson *et al.* (1955) [11] was used to calculate genetic advance at 5% selection intensity. Genetic advance as per cent of mean was estimated as per the method suggested by Johnson *et al.* (1955) [11]. Genotypic and phenotypic covariances and correlation coefficients were estimated using formula proposed by Panse and Sukhatme (1985) [23].

Results and Discussion

Components of variation: Phenotypic variation may only be a rough measure of the variation or extent of divergence between genotypes. More trustworthy estimates of genetic variability are those based on phenotypic and genotypic coefficients of variation. Because phenotypic variability estimates cannot distinguish between genetic and environmental effects, phenotypic or observable variation must be divided into heritable (genotype-related) and environmental components. The phenotypic and genotypic coefficients were computed for this purpose and the results are reported in Table-1. The coefficients of genotypic and phenotypic variation can be compared to determine the relative amount of variation for distinct traits.

The degree of relation of plant traits has traditionally been useful for selection in plant breeding. The existence of a relationship between two characters is usually determined by looking at the correlation between them. It's crucial to understand the genetic connection between distinct traits for this reason, as this can reveal information about the linked response to selection. At both the genotypic and phenotypic levels, correlation coefficients were calculated using variances and co variances to evaluate the association between various features and their relationship with an economically desirable trait, namely fruit yield per plant. Table-2 shows the phenotypic and genotypic correlations between various characters.

Table 1: Estimates of phenotypic variance, genotypic variance, phenotypic and genotypic coefficients of variation for various growth and yield attributing characters in chilli (*Capsicum* spp.)

S. No	Parameters	Phenotypic variance (PV)	Genotypic variance (GV)	Phenotypic coefficient of variation (PCV)	Genotypic Coefficient of variation (GCV)	Heritability (bs)	Genetic advance as % of mean
1	Plant height (cm)	125.34	124.79	18.66	18.62	0.99	38.26
2	Plant spread (cm)	112.94	112.59	27.57	27.53	0.99	56.63
3	Number of primary branches	0.76	0.70	16.92	16.24	0.92	32.11
4	Days to 50% flowering	103.83	102.95	16.33	16.30	0.99	33.64
5	Days taken to first fruit set	78.00	77.28	13.64	13.62	0.99	28.10
6	Fruit diameter (cm)	0.21	0.20	35.26	35.05	0.98	71.76
7	Fruit length (cm)	5.99	5.86	26.95	26.66	0.97	54.32
8	Pedicel length (cm)	0.38	0.28	17.95	15.35	0.73	27.03
9	Number of fruits per plant	350.73	350.49	40.10	40.09	0.99	82.55
10	Average fruit weight (g)	4.49	4.46	32.39	32.31	0.99	66.38
11	Fruit yield per plant (g)	13262.77	13211.51	39.68	39.60	0.99	81.42
12	Number of seeds per fruit	625.42	556.37	27.87	26.28	0.89	51.07
13	Average dry fruit weight (g)	0.19	0.17	34.42	32.81	0.91	64.40
15	Fruit yield per hectare (q)	3255.19	3243.07	39.88	39.81	0.99	81.85

Table 2: Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among different characters in chilli (*Capsicum* spp.)

S. No	Parameter	Plant height	Plant spread	Number of primary branches	Days to 50% flowering	Days taken to first fruit set	Fruit diameter	Fruit length	Pedicle length	Number of fruits plant ⁻¹	Average fruit weight	Fruit yield per plant	Average dry fruit weight	Number of seeds per fruit	Fruit yield per hectare
1	Plant height (cm)	1.00	0.659**	0.166	0.176*	0.154	-0.068	0.242**	0.179	0.129	-0.100	0.035	-0.099	-0.105	0.040
2	Plant spread (cm)	0.656**	1.00	0.065	0.348*	0.333*	-0.010	0.006	0.055	0.084	-0.124	0.006	-0.124	-0.109	0.016
3	Number of primary branches	0.160	0.060	1.00	0.142	0.094	0.029	-0.207*	-0.019	0.196*	-0.057	0.109	0.204*	0.291*	0.107
4	Days to 50% flowering	0.176*	0.347**	0.136	1.00	0.926**	0.050	-0.157	0.059	-0.026	-0.228**	0.252**	0.101	0.031	0.242**
5	Days taken to first fruit set	0.153	0.333**	0.090	0.926**	1.00	-0.030	-0.038	0.125	0.015	-0.148	-0.128	0.074	0.046	-0.118
6	Fruit diameter (cm)	-0.068	-0.010	0.023	0.050	-0.030	1.00	-0.298*	0.299**	-0.176*	0.260**	-0.081	0.234**	-0.229**	-0.077
7	Fruit length (cm)	0.238**	0.004	-0.190*	-0.155	-0.038	-0.296**	1.00	0.525**	0.099	0.093	0.255**	0.060	0.137	0.255**
8	Pedicle length (cm)	0.147	0.044	-0.020	0.051	0.107	-0.246**	0.451**	1.00	-0.180	0.001	-0.087	0.034	0.176	-0.088
9	Number of fruits per plant	0.128	0.083	0.189*	-0.026	0.015	-0.175*	0.098	-0.153	1.00	-0.390**	0.607**	-0.165	0.019	0.604**
10	Average fruit weight (g)	-0.099	-0.124	-0.055	-0.228**	-0.148	0.260**	0.090	0.007	-0.399**	1.00	0.410**	0.330*	0.084	0.413**
11	Fruit yield per plant (g)	0.035	0.006	0.104	-0.251**	-0.128	-0.078	0.251**	-0.068	0.605**	0.412**	1.00	0.057	0.071	0.999**
12	Average dry fruit weight (g)	-0.092	-0.119	0.198*	0.096	0.070	0.220**	0.040	0.025	-0.157	0.318**	0.051	1.00	0.173	0.053
13	Number of seeds per fruit	-0.099	-0.100	0.238**	0.029	0.043	-0.212**	0.118	0.152	0.017	0.075	0.064	0.159	1.00	0.066
14	Fruit yield per hectare (q)	0.039	0.015	0.102	-0.241**	-0.118	-0.075	0.252**	-0.069	0.603**	0.415**	0.999**	0.047	0.059	1.00

*, ** = Significant at 5% and 1% respectively

The estimates of phenotypic and genotypic coefficients of variation of all the characters evaluated are presented in (Table 1). In general, the phenotypic and genotypic coefficients of variation were almost identical, with somewhat higher phenotypic coefficients of variation, indicating that environment has a role in the expression of the traits under study. This was in conformity with the study of Shirshat *et al.* (2007) [33]; Gupta *et al.* (2009) [7]; Sharma *et al.* (2010) [32]; Chattopadhyay *et al.* (2011) [4]; Janaki *et al.* (2016) [9]; Sahu *et al.* (2016) [30]; Jogi *et al.* (2017) [12]; Singh *et al.* (2017) [35] and Nahak *et al.* (2017) [20].

The data revealed that the parameters like that plant spread (27.57, 27.53), fruit diameter (35.26, 35.05), fruit length (26.95, 26.66), number of fruits per plant (40.10, 40.09), fruit weight (32.39, 32.31), fruit yield per plant (39.68, 39.60), average dry fruit weight (34.42, 32.81), fruit yield per hectare (39.88, 39.81), number of seeds per plant (27.87, 26.28) showed high phenotypic and genotypic coefficients of variation respectively, implying that genotypes had a broad genetic base for these traits. The results were in agreement

with Sarkar *et al.* (2009) [29]; Patel *et al.* (2009) [25]; Singh *et al.* (2009) [36]; Padhar and Zaveri (2010) [21]; Datta and Das (2013) [5]; Janaki *et al.* (2016) [9]; Singh *et al.* (2017) [35]. Other traits with moderate phenotypic and genotypic coefficients of variation were plant height (18.66, 18.62), number of primary branches (16.92, 16.24), days to 50% blooming (16.33, 16.30), days to first fruit set (13.64, 13.62) and pedicle length (17.95, 15.35). This was in agreement with findings Diwakar *et al.* (2012) [6]; Datta and Das (2013) [5] and Singh *et al.* (2009) [36]. Characters with moderate to high coefficients of variation indicated that there is a greater chance of improvement through selection. A high GCV and PCV ratio, as well as a wide range of variability and high estimates of phenotypic and genotypic coefficients of variation, imply that these traits might respond to selection. Even phenotypic and genotypic coefficients of variation do not provide a complete picture of the character's inheritance. As a result, a character's heritability may be trusted since it allows the breeder to determine the amount of selection pressure to apply in a specific environment, thereby

separating environmental impact from overall variability. As suggested by Panse and Sukhatme (1957)^[22] and Johnson *et al.* (1955)^[11], the estimation of heritability has a greater role to play in determining the effectiveness of character selection if it is considered in conjunction with the predicted genetic advance. Heritability is influenced by bio-metrical method, hybrid generation, sample size of experimental material and environment. Furthermore, the degree of genetic gain is precisely proportional to the success in selection. As a result, the influence of selection manifests itself more swiftly in traits with high heritability and genetic gain. With the use of heritability estimates and genetic advance, the relative amount of heritable component of variance was determined.

When high heritability is coupled with high genetic gain, it implies the prevalence of additive gene effects and selection may be successful. High heritability with low GAM suggests a prevalence of non-additive gene action, in which high heritability is attributed to a favourable environment rather than genotype and selection for such traits may not be rewarding. Low heritability with high GAM is regulated by additive gene effects, in which low heritability is manifested as a result of favourable environmental effects and selection may be successful in such conditions. Low heritability combined with low GAM suggests that character is heavily impacted by external factors (environmental effects), making selection inefficient.

The heritability (b.s.) of all the characters was high, ranging from 73 to 99 percent, indicating the less impact of environmental effects over the characters and hence an effective transmission of characters to the progeny, as well as implying that genetic constitution plays a major role in the expression of a character and thus selection based on phenotypic expression could be relied upon. Verma *et al.* discovered similar results (2004). Number of fruits per plant, fruit length, fruit diameter, fruit weight, number of fruits per plant and fruit yield per plant all showed high heritability. This is in line with the findings of Smitha and Basavaraja (2006)^[37] and Johari and Kumar (2007)^[10]; Sarkar *et al.* (2009)^[29], Ibrahim *et al.* (2001)^[8]; Rathod *et al.* (2002)^[28], Krishna *et al.* (2007)^[14], Janaki *et al.* (2016)^[9], Chakrabarty *et al.* (2017)^[3], Mahantesh *et al.* (2017)^[18] and Jogi *et al.* (2017)^[12]. These qualities had high heritability values, indicating that variation was mostly under genetic control and was minimally impacted by the environment.

For determining the effect of selection, a high estimate of heritability combined with genetic gain (per cent of mean) is more trustworthy than heredity alone (Johnson *et al.*, 1955)^[11]. The characters like fruit diameter, fruit length, number of fruits per plant, average fruit weight, fruit yield per plant, number of seeds per fruit, average dry fruit weight and fruit yield per hectare all had high estimates of heritability, indicating the predominance of additive gene action in control of these traits. This shows that genuine progress in yield enhancement might be accomplished through selection. These results are in agreement with several workers *viz.* Smitha and Basavaraja (2006)^[37] for days to 50% flowering, Sarkar *et al.* (2009)^[29]; Mahantesh *et al.* (2017)^[18]. Vaishnavi *et al.* (2018)^[42] for number of fruits per plant, fruit weight, fruit length, fruit diameter and fruit yield per plant, Varalakshmi and Haribabu (1991)^[43]; Sreelathakumary and Rajamony (2002)^[38]; Khurana *et al.* (2003)^[13]; Verma *et al.* (2004)^[44] and Sarkar *et al.* (2009)^[29] found similar results for plant height and spread.

Fruit yield is a crucial character that determines the hybrid/commercial variety's viability. As a result, the trait should be given top attention in any breeding programme. The high heritability of this feature, as well as the high genetic advance as a percentage of the mean, showed that high yielding cultivars may be selected from the current collection. This was also backed up by Patel *et al.* (2009)^[25], Sharma *et al.* (2010)^[32] and Surya *et al.* (2014)^[39].

Table-2 revealed that the estimates of genotypic correlation were somewhat greater than phenotypic correlation in the current study, suggesting that masking effects of the environment were minimal, demonstrating the presence of inherent relationship between various characters. In all cases, however, the genotypic associations may be relied upon more heavily. The kind of genotypic correlation was identical to the phenotypic correlation that was being studied. Mathew *et al.* (2004)^[19], Patel *et al.* (2015)^[24] and Jogi *et al.* (2017)^[12] all found similar findings.

Fruit length, number of fruits per plant, average fruit weight, average dry fruit weight and fruit yield per plant, all had positive and significant associations with the economically crucial trait of fruit yield per hectare. A non-significant positive correlation was observed with plant height, plant spread, number of primary branches and number of seeds per fruit. However, it also depicted negative and significant relation with days to 50% flowering at both the phenotypic and genotypic levels implying that reasonable yield enhancement may be achieved by selecting for these component characters simultaneously. This clearly demonstrated the independent nature of these traits, implying that fruit yield selection based on them is unreliable. These results are in agreement with findings of Temphurne *et al.* (2008)^[40], Ganeshreddy *et al.* (2008), Gupta *et al.* (2009)^[7], Ullah *et al.* (2011)^[41]; Chattopadhyay *et al.* (2011)^[4], Kumar *et al.* (2012)^[15], Yatung *et al.* (2014)^[45,46], Bijalwan and Mishra (2016)^[1], Singh *et al.* (2009)^[36], Padhar and Zaveri (2010)^[21], Lahbib *et al.* (2013)^[16] and Shweta *et al.* (2018)^[34].

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