HYBRID PERFORMANCE AND ANALYSIS OF GENETIC VARIABILITY IN GREEN CHILLIES (CAPSICUM ANNUUM L.)

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Abstract

In this study, the indigenously developed chilli hybrids were assessed for finding the genetic differences, heritability, genetic advance and meaningful establishment of correlation of the yield with other traits of economic importance. One of the indigenously developed hybrids i.e.; Hyb.5 (1.44 kg/plant) gave significantly high green fruit yield than the commercial hybrid (222-Hyb) with 1.34 kg/plant. However, the parental line (NARC-16/9) and Hyb.4 were found at par not only to each other but also with the commercial hybrid. The small difference (0.2 to 1.5%) between the phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) values indicated the less involvement of the environmental factors in the character expression. Selection for improvement can be made for these traits by adopting proper selection procedures. High heritability (> 60%) with high genetic advance (> 30%) was recorded for the traits like number of primary branches, number of secondary branches and green fruit yield per plant except for plant height which indicated the prediction of valid results by the involvement of the additive gene action. The indigenous hybrid development can be followed up as most of the economically important traits are governed additively. The correlation of green fruit yield per plant was positively associated to all characters (r = 0.64 to 0.90) except for plant height (r = 0.11). High heritability in conjunction with high genetic advance values for green fruit yield per plant (99% and 45.45%), number of secondary branches of days to first blossoming (98% and 32.59%) indicated least influence of environment could be made through selection

Key words: Green chillies, GCV, PCV, GA and h².

Introduction

Chilli (*Capsicum annuu*m L.) is widely known as hot pepper and belongs to the family *Solanaceae* (Poulos, 1993). Globally, chilli is being consumed as both vegetable (green chilli) as well as condiment (dry chilli), and is an important ingredient of sauces and pickles. The green chilli fruit is enriched in vitamin A, C, E and P (Hosmani, 1993). It is supposed that chillies are primarily originated from Mexico however; Guatemala and Bulgaria are considered as its secondary centers of origins (Salvador, 2002). Chilli is self-pollinated and chasmogamous crop having the chromosomes number of 2n = 24. However, 2 to 96% outcrossing has been noticed under open pollination (Hasanuzzaman *et al.*, 2002).

Green chilli is cultivated on an area of almost 1.5 million hectares with the annual production of almost 7.0 million tonnes world widely (http://www.efreshglobal.com/e Fresh/Content/Products.aspx?u=chilli pcer). The area under chillies has been increased about 6-7% approximately from 2002-2011(Vanitha et al., 2013). However, there has been an increase in its production by 15% approximately from 2005-2014 (www.factfish.com > Topics > Geography and Agriculture > Crop) over the years which might have been due to the adaptation of recommended better agronomic practices and reliance upon high yielding and disease tolerant genotypes (Verma et al., 2004). Pakistan is ranked as the third largest producer of the chillies in the world after India and China. Chilli is cultivated over 80% of the area of Sindh while only 10% of the area comes under Punjab province (Iqbal et al., 2012). The total area under chillies cultivation in Pakistan is about 62.74 thousand hectares with an annual

production of 145.8 thousand tonnes approximately. The average production of chilli in Pakistan is 2.32 tonnes hectare⁻¹ (Anon., 2013-2014).

As far as the advancement in research is concerned; vegetables have been neglected in the past as compared to the other crops in Pakistan. One of the basic tools to achieve a quantum jump in yield per hectares is exploitation of heterosis breeding among genetically diverse genotypes. Therefore, to meet this objective in shorter time; an affective programme on heterosis breeding has been initiated to develop and identify the suitable best performing hybrids (Ganeshreddy *et al.*, 2008).

In Pakistan, the total yield hectares⁻¹ of chilli is not sufficient as compared to the advanced agricultural countries. The reason for this low yield is due to the unavailability of highly productive varieties and hybrids. The pace of breeding for developing high yielding genotypes is quite slow in case of chillies because of the insufficient availability and maintenance of the genetic resources. Genetic variability in any breeding programme provides the basis for an affective selection of diversified parents. In fact, the betterment of any crop or cultivar is completely dependent upon the availability of genetic variability.

For this purpose, the philosophy of hybrid development in chillies was employed so as to assess the extent of variability among the indigenously developed hybrids, international hybrids and their parental lines. The second step was the assessment of correlation among the yield and other agronomic traits for getting the information of the linkage of several characters with the ultimate objective of yield.

Materials and Methods

This study was focused on the evaluation of the five elite indigenously developed chilli hybrids at National Agricultural Research Centre, Islamabad, Pakistan. The indigenously developed chilli hybrids (Hybrid-1, Hybrid-2, Hybrid-3, Hybrid-4, and Hybrid-5) along with their six elite parental lines (NARC-15/6, NARC-16/9, NARC-16/4, NARC-16/8, NARC-16/5 and NARC-14/9), two commercial chilli cultivars (Lounghi and Tatapuri) and an international chilli hybrid (HYB-222). The parental lines were maintained through selfing by planting in isolated net tunnel. The hybrids were reconstituted on the basis of their performances in a series of crosses. The best combiners were chosen to constitute crosses from April through May, 2012. The distinctive traits of the parental/inbred lines are represented in Table 1.

The experimental material was sown in the first week of November, 2012 on raised beds of 1 meter under a tunnel structure. The temperature in the tunnel was maintained at $30 \pm 2^{\circ}$ C during the day and $23 \pm 2^{\circ}$ C at night. The nursery was transplanted by the mid of March, 2013. Each entry was represented by three replications in a randomized complete block design (RCBD). Plot size of 3.0 m \times 1.0 m was engaged to accommodating 12 plants in total on both sides of the bed. Distance among the plants and rows were maintained 50 cm and 75 cm respectively. Farm yard manure @ 30 t ha⁻¹ and N-P-K @ 120, 75 and 50 kg ha⁻¹ were also incorporated in field. Whole amount of P, K and half of N were incorporated during soil preparation. The remaining half of N was split in two equal doses for later on application. The characters like number of days to first blossoming, number of days to 50% blossoming, number of primary branches, number of secondary branches, plant height (cm) and green fruits yield plant⁻(kg) were taken into consideration.

The data were analyzed using MSTAT-C (Steel *et al.*, 1997) to determine significant differences. Genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance were estimated as advised by Burton (1952), Allard (1960) and Johnson *et al.* (1956), respectively. Correlation coefficients were computed by the formula outlined by Dewey & Lu (1959) using Minitab programme.

Table 1. Distinctive features of the chillies parental/inbred lines.								
S. No.	Inbred lines	Distinct features						
1.	NARC-14/9	Long and thin fruit with light green in colour						
2.	NARC-15/6	Long fruit size with medium green fruit colour, moderately resistant to chilli mosaic virus and Phytophthora						
3.	NARC-16/4	Long fruit in size with light green in colour						
4.	NARC-16/5	Long, thick fruit in size with medium green in colour, moderately resistant to chilli mosaic virus						
5.	NARC-16/8	Long fruit with light green in colour						
6.	NARC-16/9	Long fruit and light green in colour						

Ta	able 2. Mean	squares from	analysis of	variance	along for	different a	agronomic	traits o	f chillies.
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SOV	df	ND1 st B	NDFB	NPB	NSB	PH	GFYPP		
Replication	ns 2	1.786	0.446	0.008	0.464	15.540	0.001		
Genotypes	13	112.83**	75.63**	0.852**	12.30**	179.73**	0.275**		
Error	26	1.05	1.02	0.05	0.34	18.83	0.001		

 $ND1^{st}B = Number of days to first blossoming, PH = Plant height, NDFB = Number of days to 50\% blossoming, NPB = Number of primary branches, NSB = Number of secondary branches, GFYPP = Green fruit yield per plant$

** = Highly significant at p<0.05 and p<0.01 levels, * = Significant at p<0.05 level

Table 3. Evaluation of chilli h	vbrids/inbred lines along with exotic and l	ocal genotypes.
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S. No.	Genotypes	ND1 st B	NDFB	NPB	NSB	PH	GFYPP
1	HYB-5	28.00	38.50	3.45	11.90	91.30	1.44
2	222-HYB	36.00	40.00	3.45	9.05	69.10	1.34
3	NARC 16/9	36.50	43.00	2.45	9.65	80.80	1.30
4	HYB-4	25.50	40.50	3.65	10.60	90.00	1.30
5	HYB-3	27.50	39.50	3.05	9.95	94.30	1.20
6	NARC 16/5	26.00	35.00	3.25	9.05	67.60	1.20
7	HYB-2	27.00	39.00	2.70	9.05	83.60	1.13
8	NARC 16/8	28.50	41.50	2.65	8.85	79.15	1.10
9	NARC 14/9	28.00	43.00	3.25	8.84	79.20	1.08
10	HYB-1	26.00	33.50	2.90	8.50	82.10	0.97
11	NARC 16/4	32.00	40.00	3.55	7.75	80.80	0.94
12	NARC 15/6	36.50	45.50	3.15	10.25	72.50	0.92
13	Tatapuri	39.00	45.50	2.00	5.65	78.80	0.82
14	Lounghi	45.50	55.00	2.05	3.80	82.50	0.21
	LSD (0.05)	1.72	1.70	0.40	0.98	7.28	0.06

 $ND1^{st}B = Number of days to first blossoming, PH = Plant height, NDFB = Number of days to 50\% blossoming, NPB = Number of primary branches, NSB = Number of secondary branches, GFYPP = Green fruit yield per plant$

genetie advance (GA), for unrerent traits of cupsicum unnuum E.											
Troita	Maan	Damas	Variances			Coefficient of variation			H^2	C A	GA %
Traits	Mean	Kange	Vg	Vp	Ve	GCV%	PCV%	ECV%	H ² (%) GA 98 10.3 97 8.4 87 0.8 94 3.3 79 0.5	GA	(over mean)
ND1 st B	31.6	45.5-25.5	55.4	56.4	1.0	23.6	23.8	3.3	98	10.3	32.59
NDFB	41.5	55.0-37.0	36.8	37.8	1.0	14.6	14.8	2.4	97	8.4	20.24
NPB	03.0	03.6-02.0	00.4	00.4	0.1	20.5	22.0	8.0	87	0.8	26.66
NSB	08.8	11.9-03.8	05.8	06.2	0.3	27.5	28.3	6.7	94	3.3	37.50
PH(cm)	80.8	94.3-67.6	71.0	89.9	19	10.4	11.7	5.4	79	0.5	0.62
GFYPP(kg)	1.1	01.4-00.2	00.1	0.001	34.7	34.9	34.9	3.3	99	0.5	45.45

Table 4. Estimates of mean, range, genotypic (V_g) , phenotypic (V_p) , environmental (V_e) , variation, genotypic (GCV), phenotypic (PCV), environmental (ECV) coefficient of variation, heritability in broad sense (h^2) and genetic advance (GA), for different traits of *Cansicum annuum* I.

 $ND1^{st}B = Number of days to first blossoming, NDFB = Number of days to 50\% blossoming, NPB = Number of primary branches, NSB = Number of secondary branches, PH = Plant height, GFPP = Green fruit yield per plant (kg)$

Results and Discussion

Analysis of variance: The mean sum of squares due to hybrids and parents revealed highly significant differences (Nawab *et al.*, 2011 b) among the different chilli genotypes for the traits under consideration (Tembhurne *et al.*, 2008) which showed the existence of adequate genetic variability (Table 2) and considerable scope for improvement. From this it is deduced that variability can be exploited. The parental lines may be utilized in different cross combinations for the creation of genetic variability among the chilli germplasm.

The mean values of genotypes (Table 3) revealed that HYB-4 took least number of days to first blossoming (25.5 days) following NARC 16/5 (26 days), HYB-1 (26 days) and HYB-2 (27 days) respectively. As the difference between these three genotypes was nonsignificant it meant that these three genotypes were the earliest to flower and were at par with one another for number of days to first blossoming. Whereas, the significant differences were observed between the indigenously developed hybrids, international hybrid 222-HYB (36 days) and local varieties Tatapuri & Lounghi (39 days and 45.50 days respectively) for number of days to first blossoming. It is thus concluded that the parent (NARC 16/5) might be one of the common parents of the early blossoming hybrids (HYB-1, HYB-4 and HYB-2). The lowest number of days to 50% blossoming was observed in HYB-1 (33.5 days) following NARC 16/5 (35 days). Statistically, both of these genotypes were considered at par to each other as the differences between the values of these two are non-significant. HYB-1 and NARC-16/5 were the earliest genotypes marked among all the other genotypes tested with respect to the number of days to first blossoming and days to 50% blossoming which indicated that NARC-16/5 might be one of the parents of HYB-1. The maximum days to 50% blossoming (55 days) was recorded for Lounghi which was significantly higher than NARC 15/6 and Tatapuri with 45.5 days whereas, the international hybrid (222-HYB) took 40 days to 50% blossoming. Significantly, maximum number of primary branches was recorded in HYB-4(3.65) followed by NARC-16/4 (3.55), HYB-5 (3.45) and 222-HYB (3.45) respectively than all the other genotypes. The minimum number of primary branches was recorded for the genotypes Tatapuri (2.0) and Lounghi (2.05). HYB-5 recorded significantly maximum number of secondary branches (11.9). HYB-3 gave the maximum plant height (94.3cm) among the fourteen

genotypes followed by HYB-5 (91.3 cm) and HYB-4 (90.0 cm). The HYB-5 gave significantly highest green fruit yield per plant (1.4 kg) followed by the international hybrid (222-HYB) with 1.34 kg and the local checks (Tatapuri and Lounghi) with 0.82 kg and 0.21 respectively as evident from the Table 3. The parental line (NARC-16/9) and HYB-4 gave 1.30 kg of green fruit yield per plant which was at par to the green fruit yield of the international hybrid (222-HYB) but significantly vary from the highest yielding HYB-5 (1.44 kg).

Variability based on genetic components: The values for phenotypic coefficient of variability (PCV) were observed as higher than the genotypic coefficient variability (GCV), but the existence of difference were very minute which clearly indicated that the environmental factors had a little influence on these variations as shown in (Table 4). Therefore, selection can easily be taken for further improvement by adopting proper selection procedure. Higher PCV and GCV were observed for number of days to first blossoming, number of primary branches, number of secondary branches and green fruit yield per plant. The moderate GCV and PCV were noticed in number of days to 50% blossoming and plant height (Table 4). High PCV and GCV indicated the existence of large variability, which have a very good scope for their better improvement through selection. These results are in accordance with the findings of other researchers for number of days to first blossoming, number of primary branches (Yadeta et al., 2011), number of secondary branches (Tembhurne et al., 2008), green fruit yield per plant (Sreelathakumary & Rajamany, 2002).

Broad sense heritability in for the all characters under consideration was observed as very high (Table 4) which depicted that further improvement can be made through selection. The highest magnitude of heritability was noticed in green fruit yield per plant (99%) followed by number of days to first blossoming (98%) and number of days to 50% blossoming (97%) respectively. Results revealed the presence of substantial extent of phenotypic fluctuation that credited towards genotypic change determination could be made for these attributes on the premise of phenotypic expression. High heritability estimates for fruit yield per plant (Das & Choudhary, 1999; Sreelathakumary & Rajamony, 2002), days to 50% blossoming (Bhardwaj et al., 2007) and plant height (Ibrahim et al., 2001; Bhardwaj et al., 2007) noticed by earlier workers were strongly related with the present research work. Higher values of genetic advance were

observed for number of days to 50% blossoming, number of primary branches, number of secondary branches and green fruit yield per plant indicating the presence of additive genes. Significant improvement can be made using standard selection procedures. However, the genetic advance value (0.62%) was very low for plant height (Sharma et al., 2010). Heritability estimation alone is not sufficient to show the response to selection therefore, it is more significant when it is accompanied and considered with genetic advance (Shashikanth et al., 2010). The present findings depicted high heritability in conjunction with high genetic advance values for fruit yield per plant (99% and 45.45%), number of secondary branches (94% and 37.50%), number of days to first blossoming (98% and 32.59%), number of primary branches (87% and 26.66%) and number of days to 50% blossoming (97% and 20.24%) indicating the least influence of environment on these traits so the improvement could be made through selection as shown in Fig. 1. This implies the presence of additive gene action (Panse, 1957) and these characters can respond well to selection. High heritability and high genetic advance have also been reported by other researchers for green fruit yield per plant (Bhardwaj et al., 2007). However, high heritability with low genetic advance (79% and 0.62%) was observed for plant height (Tembhurne & Rao, 2012) which indicated the engrossment of non-additive type of gene action. The high estimation of genetic variability for plant height was executed through the favourable environmental factor rather than effect of genotype for character expression. Selection for this trait may not be rewarding, however, heterosis breeding and hybridization may bring to forth some significant results.

Table 5. Genotypic (upper	value) and phenotypic (lower
value) correlations among	various Capsicum genotypes.

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Traits	NDFB	NPB	NSB	PH	GFYPP
ND1 st B	0.86*	-0.64*	-0.70*	-0.29	-0.67*
	0.84**	-0.60**	-0.67**	-0.27	-0.66**
NDFB	1.00	-0.60*	-0.66*	-0.03	-0.74*
	1.00	-0.57**	-0.64**	-0.06	-0.73**
NPB		1.00	0.72*	-0.07	0.64*
		1.00	0.70**	0.02	0.62**
NSB			1.00	0.17*	0.90*
			1.00	0.22	0.88**
PH				1.00	0.11
				1.00	0.12

 $ND1^{st}B = Number of days to first blossoming, PH = Plant height, NDFB = Number of days to 50% blossoming, NPB = Number of primary branches, NSB = Number of secondary branches, GFYPP = Green fruit yield per plant$

** = Highly significant, * = Significant

Genotypic and phenotypic correlation: Correlation coefficient is utilized to discover the degree and direction of the relationship between at least two factors. Correlation in plant breeding is a useful tool of indirect selection of the secondary trait with the improvement in the primary trait. A positive value gives the indication of the same direction of the two variables in question and vice-versa (Nawab *et al.*, 2011 a). Simple correlation study was carried for all morphological characters with

green fruit yield per plant (Table 5). The correlation of number of days to first blossoming with green fruit yield per plant was negative but significant at the genotypic level (-0.67) and negatively highly significant at the phenotypic level (-0.66). These observations are in consonance with the results of Ukkund et al. (2007). The green fruit yield per plant was also negative with days to 50% blossoming at both the levels but significant at genotypic level (-0.74) and highly significant at phenotypic (-0.73) level. Our observation is in agreement with the results of Nsabiyera et al. (2009). In both of these cases, it was inferred that late blossoming/late fruit bearing had drastic effect on fruit yield. Hence, the promotion of earliness can bring about a positive difference in yield. Number of primary branches has a positive correlation with the green fruit yield per plant. The correlation is significant at genotypic (0.64) and highly significant at phenotypic (0.62) levels. Positive correlation between yield and number of primary branches was observed by several investigators viz., Ibrahim et al. (2001), Kumar et al. (2012) and Jabeen et al. (2009). The correlation for number of secondary branches was observed as significant at genotypic level (0.90) and highly significant at phenotypic (0.88) level, showing it as one of the yield contributing traits. The more the number of secondary branches, the more will be the green fruit yield per plant. Therefore, an increase in number of secondary branches per plant would likely contribute to increase yield (Jabeen et al., 2009 and Sharma et al., 2010). As a whole, it can be said that branching habit can affect yield. The correlation between plant height and green fruit yield per plant was positive but non-significant both at genotypic (0.11) and phenotypic (0.12) levels (Table 5). The similar positive correlation was also noticed by Jabeen et al. (2009) and Nsabiyera et al. (2009). Therefore, from these reported results it is clear that plant height has no impact on fruit yield. However, negative correlation was recorded for the same character by Marame et al., 2008. The selection on the basis of this trait will not be rewarding.



Fig. 1. Graphical presentation of heritability and genetic advance for different traits in chillies.

Conclusion

It was concluded that one of the indigenously developed hybrids i.e., Hyb.5 (1.44 kg/plant) gave significantly high yield than the commercial hybrid (222-Hyb) with 1.34 kg/plant. However, the parental line (NARC-16/9) and Hyb.4 were found at par not only to each other but also with the commercial hybrid. High estimates of heritability and genetic advance is the clear evidence that most of the economically important traits are governed additively and the best performing parental lines can be utilized in different combinations to exploit hybrid vigour.

Acknowledgements

The research on hybrid development in chillies was conducted under the project "Indigenization of Hybrid Seed Production Technology (IHSPT)" being undertaken at the Vegetable Crops Research Programme, Horticultural Research Institute, NARC, Islamabad. The project activities were funded by the Public Sector Development Programme (PSDP), Government of Pakistan. This project has trained the scientists and students of various universities of the country. For this, the authors duly acknowledge the support and time to time help of the Project Director, IHSPT (Dr Muhammad Shafique Zahid) in the commencement of the research work.

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(Received for publication 23 September 2016)