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Genetic variation, path and correlation analysis in crosses among Indian and Taiwan parents in chilli

SL Krishnamurthy, K Madhavi Reddy and A Mohan Rao

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The most commonly grown spice crop in India is chilli pepper (*Capsicum annuum* L.), which has culinary and medicinal applications. India is the major producer, consumer, and exporter of chilli, contributing almost one fourth of the world production. Indian chilli export is facing competition in the international market from other chilli-growing countries and high domestic consumption. In India, hot pepper is the most widely used spice and vegetable crop with additional importance of offering outstanding job and income generating opportunities for enormous small farmers in the country. The fruits are consumed fresh, processed or when dried as spice or condiment. Hot pepper is a genetically self-pollinated and chasmogamous crop whose flowers open only after pollination takes place however, 11–64% outcrossing was observed under open pollination.

The usefulness of selection depends on the amount of genetic variation present. In chilli, a wide range of variability is available due to its ability to cross pollinate, which provides possibilities to improve fruit yield through a breeding program. When variability is partitioned into heritable and non-heritable components, efficiency of selection is better understood. It is necessary to assess the nature and extent of association between attributes of yield.

For starting any improvement work, information about the genetic variability in the population is a prerequisite. Presence of high variability in this crop offers much scope for its improvement. Hence, an attempt was made to estimate heterosis, genetic variability, heritability and genetic advance in the Indian and Taiwan genotypes of hot pepper *(Capsicum annuum)*.

Twenty four Indian chilli inbreed lines of different regions and six inbreed lines of Taiwan were used as pollen parents and five CMS lines from Taiwan were used as female parents for crossing. In 2006 and 2007, crossings were made between 24 Indian and six Taiwan testers with the five Taiwan CMS A – lines (Table 1) in Line × Tester mating design. Single floret was selected and used for crossing in insect proof net house and pollinated floret was covered with thin layer of cotton to control out crossing. The F_1 seeds were harvested from all the crosses at the end of respective cropping season, 2006 and 2007. The 150 F_1 progenies were obtained from 30 testers and five female parents along with 30 selfed parents and five maintained CMS B Lines.

Seeds of the 35 parental genotypes (30 testers and 5 CMS B Lines) and their 150 F_1s were sown at two locations viz., University of Agricultural Sciences (UAS), Bangalore and Indian Institute of Horticultural Sciences (IIHR) Bangalore during 2008. All the 150 progenies along with their parents were transplanted in randomized complete block design (RCBD) at both locations. All the recommended package of practices was followed to raise a healthy crop. Ten plants in each genotype were tagged from each replication and recorded nine characters viz., Days to 50 per cent flowering, Days to first fruit maturity, Plant height (cm), Fruits plant^{-1}, Fruit length (cm), Fruit width (cm), Hundred seed weight (g), Green fruit yield plant^{-1} (g) and Red fruit yield plant^{-1} (g) in each environment.

Homogeneity of error variance across the two locations was tested by the F test (Gomez and Gomez, 1983) and combined analyses of variances for treatments (150 Crosses, 5 Lines and 30 Testers) across the two locations were performed to determine treatments × environment

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SL Krishnamurthy
Division of crop improvement, Central Soil Salinity Research Institute, Karnal-132001, Haryana, India
E-mail: krishnagene@gmail.com
K Madhavi Reddy
Division of Vegetable crops, Indian Institute of Horticultural Research, Hessarghata, Bengaluru-560089, Karnataka, India
A Mohan Rao
Department of Genetics and Plant Breeding
University of Agricultural sciences, GKVK,
Bengaluru- 560065, Karnataka, India

interaction for each trait using the GLM procedure of SAS. Significant levels were determined as suggested by McIntosh (1983) for combined analysis. The data of the UAS Bangalore and IIHR Bangalore were combined for analysis of variances, variability and path co-efficient. The correlation was estimated as per the method suggested by Al-Jibouri *et al.,* (1958) and path coefficients analyses as per Dewey and Lu (1959) method. Statistical analyses of variances, variability and path co-efficient were performed using 'Indostat' (statistical software developed by Indostat Services, Hyderabad 500 016, India.

Homogeneity of error variance across the two locations, UAS Bangalore and IIHR Bangalore, was tested and none of the error mean squares were significant for any of the traits. Combined analyses of variances for treatments across the two locations were performed to determine treatments × locations interaction for nine traits and noticed non-significant difference among treatments × locations interaction, data of the UAS Bangalore and IIHR Bangalore were combined for estimation of variances, variability and path co-efficient.

The extent of variability present in 35 parents and 150 hybrids of chilli was measured in term of phenotypic variance, genotypic variance, phenotypic co-efficient of variation, genotypic co-efficient of variation, heritability and genetic advance (Table 1). All the treatments (parents and hybrids) differed significantly with respect to different characters studied. Variability was partitioned into genotypic and environmental components. Genotypic variances were of higher magnitude than the corresponding environmental variances for days to first fruit maturity, 50 per cent flowering, plant height and fruit length and it indicating that environment had little influence on genetic variability. Whereas, environmental variances were higher magnitude than the corresponding genotypic variance for polygenic traits namely, fruit width, 100 seed weight, red fruit yield plant^{-1}, green fruit yield plant^{-1} and fruits plant^{-1} indicating influence of environment on variability. Estimates of phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) were high for red fruit yield plant^{-1}, green fruit yield plant^{-1}, fruits plant^{-1} and fruit length (Table 1) in the chilli. The higher PCV and GCV magnitudes indicated the presence of substantial variability, indicating the possibility for improvement through selection for these traits. The PCV and GCV were moderate for fruit width, indicating that these traits have less potential for direct selection. Estimates of PCV and GCV were low for days 50 per cent flowering and days to first fruit maturity. High PCV and moderate GCV for 100 seed weight and plant height indicate that there was comparatively low genetic variation for this trait. These results substantiate findings of Mini and Khader (2004), Sreelathakumary and Rajamony (2004) and Singh *et al.,* (2009) who used different genetic material and were in different locations, indicating the possibility for improvement through selection for these traits.

The heritability estimates ranged from 30.84 per cent for green fruit yield plant^{-1} to 61.04 per cent for plant height (Table 1). The high heritability was noticed in all studied traits viz., days to 50 per cent flowering (54.86%), days to first fruit maturity (59.41%), plant

Table 1. Estmates of variability parameters for nine traits of 185 (5 Lines, 30 Testers and 150 Crosses) chilli genotypes grown at UAS Bangalore during Kharif 2008 and IIHR Bangalore during Rabi 2008

Characters	Variance			Co-efficient of variation (%)			Heritability Broad Sense (h^2) (%)	Genetic Advancement	Genetic Advancement (% of Mean)	GCA:SCA Variance
	Environmental	Genotypic	Phenotypic	Environmental	Genotypic	Phenotypic				
50 per cent flowering	3.52	4.27	7.79	2.24	2.47	3.33	54.86	3.15	3.76	1 : 233
Days to first fruit maturity	10.50	15.38	25.88	2.67	3.23	4.19	59.41	6.23	5.13	1 : 58
Plant height (cm)	139.89	219.15	359.04	14.83	18.56	23.75	61.04	23.83	29.87	1 : 51
Fruit length (cm)	2.11	3.01	5.13	17.60	21.01	27.41	58.75	2.74	33.17	1 : 24
Fruit width (cm)	0.03	0.02	0.05	15.37	12.62	19.89	40.26	0.18	16.50	1 : 45
Fruits plant?^{l}	1037.98	730.80	1768.79	43.41	36.42	56.66	41.32	35.80	48.23	1 : 125
100 seed weight (g)	0.02	0.01	0.03	22.39	16.38	27.75	34.86	0.13	19.93	1 : 2010
Red fruit yield plant?^{l} (g)	5644.49	4134.74	9779.22	38.24	32.73	50.33	42.28	86.13	43.84	1 : 267
Green fruit yield plant?^{l} (g)	9712.62	4330.10	14042.72	37.73	25.19	45.37	30.84	75.27	28.82	1 : 190

height (61.04%), fruit length (58.75%) fruit width (40.26%), fruits plant^{-1} (41.32%), 100 seed weight (34.86%), red fruit yield plant^{-1} (42.28%) and green fruit yield plant^{-1} (30.84%). The heritability is an indication of presence of proportion of fixable additive variance in the population. Heritability value is of much use to breeder, as it indicates the accuracy with which a genotype can be evaluated by its phenotypic expression.

The estimates of heritability when accompanied by estimates of genetic advance are more meaningful from the point of expected gain and type of selection method to be followed. The traits namely, green fruit yield plant^{-1} and red fruit yield plant^{-1} had expressed high heritability (30.84 and 42.28%) with high genetic advance (75.27 and 86.13); fruit width, 100 seed weight, days to 50 per cent flowering, days to first fruit maturity, plant height and fruit length had expressed high heritability associated with less genetic advance and fruits plant^{-1} expressed high heritability associated with moderate genetic advance (Table 1). All the studied traits had expressed the high heritability and low to moderate genetic advance and indicating the role of non additive genes for these traits suggesting thereby that their improvement could be achieved through heterosis breeding. Improvement of these traits through simple selection might not give desirable results and needs to be improved through hybridization (Panse, 1957). Similar results have been reported by Nandadevi and Hosamani (2003), Das and Maurya (2004) and Mini and Khader (2004) using different genetic material and under different environmental conditions, indicating the possibility of improvement through heterosis breeding followed by selection.

A high positive significant correlation of days to 50% flowering and days to first fruit mature suggested that early flowering genotypes would be an appropriate selection criterion to get early marketable (green) fruit yield (Table 2). The number of fruits^{-1} had positive correlation with green fruit and red fruit yield plant^{-1} at genotypic and phenotypic level. Similar findings were noticed by Mishra *et al.,* (1998). Selection on the basis of these traits might lead to higher yield. Significant positive correlations of yield with fruits per plant, fruit length and significant negative association with days to 50 % flowering agree with the findings of Khurana *et al.,* (2003) and Kumar *et al.,* (2003).

Path analysis helps in partitioning correlation coefficients into direct and indirect effects of component characters in yield. Direct and indirect effects of all the traits on yield were computed at the genotypic level. For path analysis at the genotypic level, green fruit (marketable fresh fruit) yield per plant was taken as dependent variables and all other traits used for correlation were considered as causal variables. At genotypic level, fruits plant^{-1} (0.819) had the highest positive direct effect on yield per plant followed by fruit length (0.311), fruit width (0.243) and red fruit yield (0.215). Direct and positive effects on yield were observed for number of fruits per plant, fruit weight, fruit length and fruit width (Kumar *et al.,* 2003; Leaya and Khader, 2002; Verma *et al.,* 2004), emphasizing importance of these characters in chilli improvement. For fresh and dry fruit yields, selection on the basis of average fresh and dry fruit weight and number of total and fruits per plant would be worthwhile. In view at the direct and indirect

Table 2. Estimates of phenotypic (P) and genotypic (G) correlation coefficients for different traits in chilli

Characters		Days to 50% flowering	Days to 1st fruit mature	Plant height (cm)	Fruit length (cm)	Fruit width (cm)	Fruit plant^{-1}	100 seeds weight (g)	Red fruit yield plant^{-1}	Green fruit yield plant^{-1}
Days to 50% flowering	G	1.00	0.60**	0.24**	0.22**	0.07	-0.16**	-0.02	-0.11*	-0.11*
	P	1.00	0.52**	0.23**	0.19**	0.07	-0.13**	-0.02	-0.09	-0.10*
Days to 1st fruit mature	G		1.00	0.30**	0.17**	0.19**	-0.17**	0.01	0.01*	-0.02
	P		1.00	0.29**	0.17**	0.18**	-0.16**	0.01	0.01*	-0.02
Plant height (cm)	G			1.00	0.02	0.09	-0.05	0.05	-0.12*	-0.03
	P			1.00	0.02	0.09	-0.05	0.05	-0.12*	-0.03
Fruit length (cm)	G				1.00	0.26**	-0.25**	0.02	0.04	0.17**
	P				1.00	0.25**	-0.25**	0.02	0.04	0.17**
Fruit width (cm)	G					1.00	-0.36**	0.05	-0.03	0.03
	P					1.00	-0.35**	0.04	-0.03	0.03
Fruit plant^{-1}	G						1.00	-0.12*	0.27**	0.72**
	P						1.00	-0.11*	0.27**	0.71**
100 seeds weight (g)	G							1.00	0.10*	-0.05
	P							1.00	0.10*	-0.05
Red fruit yield plant^{-1}	G								1.00	0.45**
	P								1.00	0.45**
Green fruit yield plant^{-1}	G									1.00
	P									1.00

*: significant at $P < 0.05$ or **: significant at $P < 0.01$.

Table 3. Estimates of direct (diagonal) and indirect effects (off-diagonal) of different traits on green fruit yield in chilli at genotypic (G) levels

Characters	Days to 50% flowering	Days to 1st fruit mature	Plant height (cm)	Fruit length (cm)	Fruit width (cm)	Fruit plant^{-1}	100 seeds weight (g)	Red fruit yield plant^{-1} (g)	Genotypic correlation with grain yield
Days to 50% flowering	**-0.078**	-0.047	-0.019	-0.017	-0.005	0.012	0.001	0.008	-0.11*
Days to 1st fruit mature	0.035	**0.059**	0.018	0.010	0.011	-0.010	0.001	0.001	-0.021
Plant height	-0.004	-0.005	**-0.018**	0.000	-0.002	0.001	-0.001	0.002	-0.031
Fruit length	0.067	0.054	0.007	**0.311**	0.080	-0.079	0.006	0.013	0.17*
Fruit width	0.017	0.046	0.023	0.062	**0.243**	-0.088	0.011	-0.007	0.028
Fruit plant^{-1}	-0.128	-0.140	-0.044	-0.207	-0.296	**0.819**	-0.094	0.221	0.72**
100 seeds weight	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	**-0.003**	0.0001	-0.053
Red fruit yield plant^{-1}	-0.023	0.002	-0.026	0.009	-0.007	0.058	0.023	**0.215**	0.45**

Residual effect = 0.19

contributions of component traits towards fruit yield, selection on the basis of horticultural traits viz., average fruit weight and number of fruits per plant would be a paying preposition in the genotypes included in the study.

Most of the traits under study were showed significant variations, from low to high magnitude of heritability and genetic advance. These can facilitate selecting and utilizing the mot preferred traits of interest and also hint the potential of chilli to further improvement. Some traits with high phenotypic and genotypic coefficient of variation those are detrimental which make possible chilli improvement. The heritability estimates together with genotypic coefficient of variation is important to exploit heterosis.

References

Al-Jibouri HA, Millar PA and Robinson HF (1958) Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. Agronomy Journal 50: 633–636.

Das S and Maurya KR (2004) Heritability study in chilli. Journal of Applied Biotechnology 14(1):22–23.

Dewey DR and Lu KH (1959) A correlation and path analysis of components of crested wheat-grass seed production. Agronomy Journal 51: 515–518.

Gomez KA and Gomez AA (1983) Statistical procedures for agricultural research Wiley, New York. Journal of American Society of Horticultural Sciences 125(4): 448–453.

Khurana DS, Singh P and Hundal JS (2003) Studies on genetic diversity for growth, yield and quality traits in chilli (*Capsicum annuum* L.). Indian Journal of horticulture 60(3): 277–282.

Kumar BK, Munshi AD, Joshi S and Kaur C (2003) Correlation and path coefficient analysis for yield and biochemical characters in chilli (*Capsicum annuum* L.). Capsicum Eggplant Newsletter 22: 67–70.

Leaya J and Khader KMA (2002) Correlation and path coefficient analysis in chilli (*Capsicum annuum* L.). Capsicum Eggplant Newsletter 21: 56–59.

McIntosh MS 1983. Analysis of combined experiments. Agronomy Journal 75:153–155.

Mini S and Khader KMA (2004) Variability, heritability and genetic advance in wax type chilli (*Capsicum annuum* L.). Capsicum Eggplant Newsletter 23: 49–52.

Mishra YK, Ghildiyal PC, Solanki S and Joshi RP (1998) Correlation and path analysis in sweet pepper (*Capsicum annuum* L.). Recent Horticulture 4:123-126.

Nandadevi and Hosamani RM (2003) Variability, correlation and path analysis in *Kharif* grown chilli (*Capsicum annuum* L.) genotypes for different characters. Capsicum Eggplant Newsletter 22: 43–46.

Panse VG (1957) Genetics of quantitative characters in relation to plant breeding. Indian Journal of Genetics 17: 318–328.

Singh Y, Sharma M and Sharma A (2009) Genetic Variation, Association of Characters, and Their Direct and Indirect Contributions for Improvement in Chilli Peppers. International Journal of Vegetable Sciences 15: 340–368.

Sreelathakumary I and Rajamony L (2004) Variability, heritability and genetic advance in chili (*Capsicum annuum* L.). Journal Tropical Agriculture 42(1/2): 35–37.

Verma SK, Singh RK and Arya RR (2004) Genetic variability and correlation studies in chillies.