PATH COEFFICIENT ANALYSIS AND TRAIT ASSOCIATION STUDIES FOR YIELD ENHANCEMENT IN CHILLI (*CAPSICUM ANNUM* L.)

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Abstract

Successful execution of plant breeding programs requires diversity among key yield contributing traits and their positive association with final yield. Association of major traits with chilli fruit yield and their direct and mediated effects through path analysis were explored in this research. During 2018 and 2019, trials were conducted on 6 chilli genotypes using RCB design with three replications. Highly significant ($p \leq 0.01$) diversity, from pooled ANOVA results, was observed among six chilli genotypes for days to flowering, plant height, canopy width, number of main branches, days to fruiting, single fruit weight, fruit length, fruit diameter, number of fruits per plant and fruit yield/plant. Days to flowering and fruiting showed an intermediate positive association (r <0.7) with chilli fruit yield and also their path coefficient analysis revealed no substantial direct or mediated contribution to yield. Number of main branches, plant height, number of fruits/plant and single fruit weight exhibited positive correlation (r >0.7) with fruit yield. Path analysis of number of fruits/plant and single fruit weight showed maximum (>0.5) positive direct effect on yield. Although, number of main branches and plant height exhibited small direct effect on fruit yield, their positive mediated effect on yield, through single fruit weight and number of fruits/plant was high (>0.4). In addition, these traits also showed optimum (>20) genetic advance over mean and high heritability (>80%). Therefore, for superior chilli cultivars development selection should be practiced for number of fruits/plant, single fruit weight, plant height and number of main branches.

Key words: Chilli breeding**,** Path analysis**,** Genetic advance, Capsicum.

Introduction

In the Solanaceae family, after tomato and potato, chilli (*Capsicum annuum* L.) holds third rank (Naz *et al*., 2006) and is considered the most popular spice with over 20% of the world population using it in several forms (Huq *et al*., 2010). Out of the total spice trade in the world, chilli accounts for 18% after black pepper (Geetha & Selvarani, 2017). Regardless of its economic and medicinal importance (Khan *et al*., 2014), chilli remains a neglected crop in many countries and is hardly considered a national agricultural development priority (Anon., 2010).

Pakistan cultivates chilli on about 60 thousand ha and produces about 143 thousand tons of chilli. In the global chilli market, Pakistan's share is about 5-7% and contributes 1.5% to the country's GDP. However, productivity of chilli in Pakistan is much lower as compared to global level (Khan *et al*., 2020). On the other hand, aflatoxin plays one of the major hindrances in chilli export (Iqbal *et al*., 2011). Thus, Pakistan is losing its international position in chilli production due to per hectare lower yield and fruit quality – a two-dimensional problem to be addressed through intensive breeding.

Every breeding program requires phenotypic characterization and exploration of genetic diversity to be employed for superior cultivars development. The *Capsicum* genus has wide genetic diversity and about 292 genes can be used for numerous traits improvement (Padilha & Rosa, 2016). In addition to genetic diversity, high heritability, traits association, and genetic advance should be explored for major yield contributing traits (Magar *et al*., 2021). This provides an insight on how yield can be enhanced, when selection is practiced based on these approaches. Furthermore, the correlation coefficients

need to be dissected through path analysis in order to categorize direct and mediated/indirect yield contributing traits (Jilo & Leta, 2019). The present work aim to establish selection criteria for chilli yield enhancement by investigating major yield contributing traits through correlation and path coefficient analysis.

Material and Methods

This study was conducted at research farm of Nuclear Institute of Agriculture (NIA), Tandojam for two consecutive years during 2018 and 2019. Chilli genotypes were collected in 2016 from several farmers across Sindh province. The following year their seeds were multiplied and based on morphological traits similar plants from each plot were harvested and bulked together which resulted in six chilli genotypes i.e., Laungi-1, Laungi-2, Laungi-3, Laungi-4, Laungi-5 and Laungi-6. The following two years these land races were evaluated in randomized complete block design (RCBD) with three replications. Both years, a 45 days old nursery was transplanted to the field. Each plot contained 4 rows, each 5 m long, with 45×45 cm spacing of row to row and plant to plant. Fertilizers were applied as per doses recommended by Wahocho *et al*., (2016). Data on important morphological and yield traits were recorded according to the method of (Gogoi & Gautam, 2002, Quresh *et al*., 2021). In each replication data were recorded from randomly selected five plants and values were then averaged for each trait.

Data analysis

The data was pooled over years before subjecting it to different statistical tests. Analysis of variance was carried out

through statistical software *R*, using *Agricolae* package 1.3-5 by applying the *"lm"* (linear Modal) function (Mendiburu, 2021). The same fitted model was used for LSD (0.05) test also. Genetic advance over mean and broad sense heritability (h^2) were estimated using *"variability"* package, developed by Popat *et al*., (2020). The package is based on the methods adopted by Singh & Chaudhary (1979).

Simple Pearson's correlation coefficients were estimated from mean values of the parameters and the same correlation coefficients were used to estimate path coefficients using Dewey & Lu (1959) approach through *Agricolae* R package.

Results and Discussion

Genetic diversity and mean performance of the genotypes: Results from pooled ANOVA revealed highly significant ($p \leq 0.01$) diversity among the genotypes for all the traits (Table 1). These results illustrated the existence of sufficient diversity among the genotypes – an essential prerequisite in every plant breeding program. Employing diverse parents in breeding programs results in optimum post hybridization genetic diversity and consequently facilitates breeders in selection of ideotypes from the resulting segregating populations.

Chowdhury *et al*., (2015) studied several chilli traits like number of fruits/plant, single fruit weight and plant height, and found sufficient diversity in four chilli genotypes. Significant genetic diversity in several chilli trials was also confirmed by Hasan *et al*., (2014). Mean

performance, presented in (Table 2) depicted a wide range for all the studied traits, except MBR and FL.

Adequate phenotypic variation was evident from the mean performance of these genotypes for key yield parameters like SFW (0.25-0.43 g), FPP (174-290), and FYPP (50.07-123.92 g). We observed a relatively small variation for FL (1.47-1.55 cm). Elahi *et al*., (2019) studied several chilli genotypes and found no significant difference for fruit length. Maximum Ph (52.39) was achieved by Laungi-2 however, it was statistically at par with Laungi-1 (50.63). Shortest Ph (37.72 cm) was recorded for Laungi-6. This genotype was also a poor performer in other yield contributing traits like MBR (5), SFW (0.29 g), FPP (174) and FYPP (50 g). Likewise, low performance was shown by Laungi-3 and Laungi-4 genotypes. In the studied genotypes, Laungi-2 exhibited highest performance for important yield traits like MBR (9), FL (1.55 cm), and SFW (0.43g), followed by Laungi-1 and Laungi-5. Due to the right combination of key traits, Laungi-2 achieved maximum fruit yield per plant (123.92g) followed by laungi-1 (96.93g) and Laungi-5 (69.95g). High heritability ($h^2 > 0.7$) was observed for most of the traits, except CW (0.67) and FL (0.38). Low GAM (<20) was observed for DFFR (13.9), FL (2.30), and FD (7.8). High GAM (>20) was estimated for Ph (26.9), CW (25.7), MBR (48.3), SFW (41.6) and FFP (31.6). Traits having high heritability coupled with high GAM enable effective traits selection and play key role in cultivar development (Johnson *et al*., 1955, Shukla *et al*., 2016). To compare means, mean performance of the genotypes was subjected to LSD test (Table 2).

Table 1. Mean squares showing significant diversity for morphological traits in the study.

SoV	Df	Ph	CW	DFFL	MBR	DFFR
Genotypes	5	217.29**	162.79**	280.58**	14.58**	221.83**
Reps	2	5.609	19.623	2.333	0.083	15.361
Error	27	2.681	11.558	3.227	0.554	6.164
SoV	Df	FL	Fd	SFW	FPP	FYPP
Genotypes	5	0.005**	0.019**	0.03**	10333.71**	5370.61**
Reps	2	0.001	0.001	0.001	1111.4	271.6
Error	27	0.001	0.001	0.01	598.3	100.7

** Significant at $p \leq 0.01$; SoV = source of variation; Df = degree of freedom
(Ph = Plant height (cm); CW = Canopy width (cm); DFFL = Days to flowering; MBR = Main braches per plant; DFFR = Days to first fruiting; FL= Fruit length (cm); FD: Fruit diameter (cm); SFW= Single fruit weight (g); FPP = Number of fruits/plant and FYPP = Fruit yield/plant (g)

Table 2. Mean performance of morphological and yield contributing traits of six chilli genotypes.

Genotype	Ph (cm)	CW (cm)	DFFL	MBR	DFFR	FL (cm)	FD (cm)	SFW (g)	FPP	FYPP (g)
Laungi-1	50.63[a]	34.12[bc]	57[b]	7[b]	80[b]	1.47[b]	1.41[a]	0.38[b]	253[b]	96.93[b]
Laungi-2	52.39[a]	40.88[a]	60[a]	9[a]	83[b]	1.55[a]	1.38[ab]	0.43[a]	290[a]	123.92[a]
Laungi-3	41.22[bc]	31.82[bc]	45[c]	5[c]	74[c]	1.47[b]	1.27[d]	0.25[e]	205[c]	50.74[d]
Laungi-4	42.27[b]	25.17[d]	57[b]	6[c]	82[b]	1.51[b]	1.33[c]	0.28[d]	203[c]	55.84[d]
Laungi-5	39.92[c]	35.12[b]	60[a]	5[c]	91[a]	1.49[b]	1.36[bc]	0.32[c]	222[c]	69.95[c]
Laungi-6	37.72[d]	30.75[c]	47[c]	5[c]	75[c]	1.48[b]	1.26[d]	0.29[d]	174[d]	50.07[d]
Grand Mean	44.03	32.98	54	6	81	1.49	1.33	0.32	224.5	74.57
LSD (0.05)	1.93	4.02	2.12	0.88	2.94	0.04	0.03	0.02	28.97	11.89
h^2	0.92	0.67	0.93	0.86	0.84	0.38	0.80	0.92	0.73	0.89
GAM	26.9	25.7	24.8	48.3	13.9	2.3	7.8	41.6	31.6	77.5
CV (%)	3.71	10.55	3.19	10.18	3.18	2.51	2.05	6.55	10.57	13.52

cm = Centimeter; g = Gram; h^2= Heritability (broad-sense); GAM= Genetic advance over mean; CV= Coefficient of variation; Means having same alphabets are not significantly different
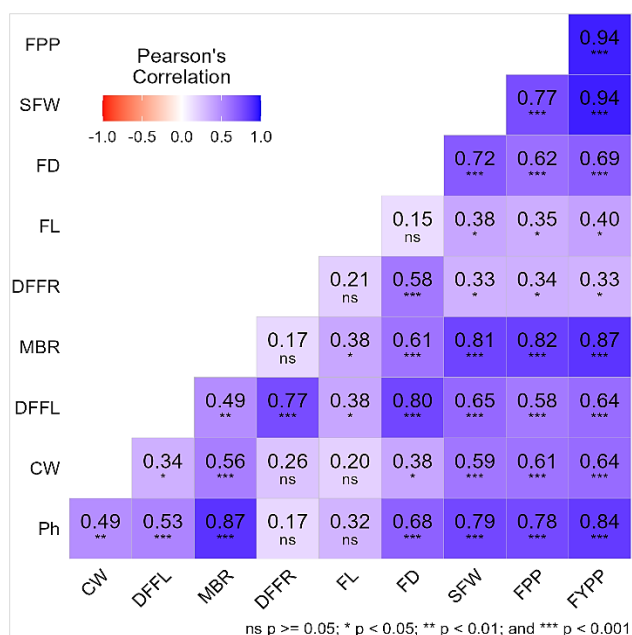
Fig. 1. Heat map of the correlation coefficients among the studied traits.

The LSD test revealed significant distinctness for the studied traits except for FL where only Laungi-2 with 1.55 cm length, was significantly higher than other genotypes. Maximum Ph (52.39 cm) was achieved by Laungi-2, which was however, statistically at par with Laungi-1 (50.63 cm). Laungi-2 also had significantly higher values for key yield contributing parameters like CW (40.88 cm), MBR (9), and FPP (290). Consequently, based on LSD, Laungi-2 had highest significant FYPP (123.92 g). Mean values of FYPP showed that four genotypes had significant distinct performance, enabling effective selection based on fruit yield. MBR and FL exhibited small range and only 1 or 2 genotypes had significant higher mean values. Among the studied genotypes, Launig-1 and Laungi-2 had adequate values for key yield contributing traits, and these two genotypes can be used as parents/inbred lines for development of new and improved chilli cultivars.

Correlation coefficients: Phenotypic correlation (Fig. 1) revealed FYPP had strong positive association with indirect yield contributing traits Ph (r = 0.84) and MBR

(r=0.87). With direct yield contributing traits i.e., SFW and FPP, FYPP showed maximum positive (r = 0.94) correlation. Positive and strong correlation was found for Ph with key yield contributing traits like SFW (r = 0.79), FPP (r = 0.78) and MBR (r = 0.87). A moderate (r = 0.49) correlation was observed between Ph and CW. This association explains that an increased Ph allows space for more MBR and CW, as reported by Belay & Yemane (2020). Consequently, both MBR and CW could accommodate more fruits per plant. This is achieved by adequate light interception in plants having optimum canopy width and positive association with other important traits (Evans *et al.*, 1975).

Among the phenological parameters, DFFR had week relationship with most of the yield traits like SFW (r = 0.33), FPP (r = 0.34) and FYPP (r = 0.33). The study of Vidya *et al.*, (2018) also reported weak correlation for days to first harvesting with fruit yield (r = 0.045) and negattive association with number of fruits per plant (r = -0.144). This suggested that delayed fruiting does not effectively contribute to yield improvement and genotypes having late fruiting should not be selected. In our study we found that SFW, a key yield contributing trait, was strongly correlated with FD (r = 0.72) as compared to FL (r = 0.38). Butcher *et al.*, (2013) also observed positive correlation among FL, SFW and FD. FL also had weak correlation with CW (r=0.21) and MBR (r = 0.38). Silva *et al.*, (2016) observed positive associations between canopy width and chlorophyll content and suggested that the use of correlation approach may improve the effectiveness of genotype selection. They have also reported significant positive association between number of branches and fruit yield in chilli. It could be concluded from these results that Ph positively contributes to more MBR and subsequently CW. Thus, an increased plant size can accommodate more FPP, which in combination with SFW may contribute significantly to yield enhancement.

Path analysis: Through path analysis, phenotypic correlation coefficients were partitioned to explore the direct and mediated contribution of all the traits to chilli FYPP. This approach is useful in dissecting the contribution of traits more effectively, as even significant correlation between traits may not always confirm the presence of linkage among them (Jilo & Leta, 2019).

Table 4. Estimates of direct (bold and diagonal) and mediated effects of different traits on fruit yield/plant in six chilli genotypes.

	Ph	CW	DFFL	MBR	DFFR	FL	FD	SFW	FPP	Total Effects
Ph	**0.032**	0.005	-0.001	-0.015	-0.004	0.005	-0.015	0.427	0.410	0.84**
CW	0.016	**0.009**	-0.001	-0.010	-0.006	0.003	-0.009	0.321	0.317	0.64**
DFFL	0.017	0.003	**-0.002**	-0.008	-0.017	0.006	-0.018	0.352	0.304	0.64**
MBR	0.028	0.005	-0.001	**-0.017**	-0.004	0.006	-0.014	0.434	0.430	0.87**
DFFR	0.005	0.002	-0.002	-0.003	**-0.022**	0.003	-0.013	0.180	0.178	0.33*
FL	0.010	0.002	-0.001	-0.006	-0.005	**0.016**	-0.003	0.200	0.181	0.39**
FD	0.022	0.004	-0.002	-0.010	-0.013	0.002	**-0.022**	0.386	0.325	0.69**
SFW	0.026	0.006	-0.002	-0.014	-0.008	0.006	-0.016	**0.539**	0.402	0.94**
FPP	0.025	0.006	-0.001	-0.014	-0.008	0.006	-0.014	0.415	**0.522**	0.94**

*, ** Significance at 0.05 and 0.01 probability levels, respectively; Residual effect = 0.004

Results from path analysis are presented in Table 4. Out 9 studied parameter, 5 parameters viz., Ph, CW, FL, SFW and FFP had positive direct effect on fruit yield. DFFL, DFFR and FD showed negative direct effect on fruit yield. SFW had maximum positive effect (0.539) on FYPP, followed by FPP with (0.522) direct effect on FYPP. The total effects in (Table 4) are the correlation coefficients of the corresponding trait with FYPP. In case of Ph, its total effect or correlation coefficient with FYPP was (r = 0.84), however, as estimated by path analysis, its direct contribution to fruit yield was very small (0.032). Nevertheless, its positive mediated effect through SFW (0.427) and FPP (0.410) was high. Therefore, Ph may not be directly selected for yield improvement, but its mediated effect on key yield contributing traits can significantly enhance fruit yield in chilli. Similarly, MBR had a very small negative effect (-0.017) on FYPP, but its mediated effect (0.430) through SFW and FPP was high. It can be inferred that selection for MBR may not improve yield directly, however, as it will improve SFW and FPP, consequently chilli yield could be enhanced. Ullah *et al*., (2011) also suggested more fruits per plant as an important parameter for yield enhancement. The study of Yatung *et al*., (2014) also revealed that SFW and number of fruits per plant were the most critical traits for improving FYPP in chilli.

Conclusion

İt is important to explore crops genetic diversity and choices of selection approaches to incorporate that diversity into plant ideotypes. Traits association and path coefficient analysis in combination with heritability and genetic advance over mean can be an effective approach for traits selection and crop improvement. Results from our study illustrated optimum genetic variability for diverse parent selection and subsequent chilli yield enhancement. Single fruit weight (SFW), number of fruits/plant (FPP), Plant height (Ph) and number of branches (MBR) were strongly correlated with fruit yield/plant (FYPP) and also had high heritability and high genetic advance over mean (GAM). SFW and FPP exhibited maximum positive direct effect on fruit yield, thus these two traits can be selected directly for chilli yield improvement. MBR and Ph had no substantial direct effect on fruit yield (FYPP), however, both traits exhibited high mediated effect on yield through single fruit weight (SFW) and fruit yield/plant (FYPP). Therefore, selection for plant height and number of main branches (MBR) can indirectly improve fruit yield in chilli.

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