Variability, Correlations and Path Co-Efficient Analysis IN Pumpkin (*Cucurbita moschata* Duch. ex Poir.)

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Authors' contributions

This work was a part of PhD dissertation of the first author. The author MATM act as a research supervisor and author BA got all the research material from him and he provide all kind of technical assistance. The other authors guided the research work and helped to develop the manuscript.

Original Research Article

ABSTRACT

Nineteen pumpkin inbreds were evaluated to measure the variability, estimate genetic attributes, the association among the characters and their contribution to yield. There was a significant variation observed for all the characters among the inbred. High heritability coupled with the high genetic advance in percent means and high genotypic coefficient of variation was observed for fruit length, cavity length and average fruit weight, indicating additive gene effects of these traits. The positive and strong association of node number of first female flower ($r_g = 0.91$, $r_p = 0.82$), flesh thickness ($r_g = 0.55$, $r_p = 0.47$), fruit diameter ($r_g = 0.46$, $r_p = 0.44$) with yield per plant. On the other hand, days to first male flower ($r_g = -0.27$, $r_p = -0.14$) and days to first female flower ($r_g = -0.1$, $r_p= -0.13$) co-related negatively and insignificantly with fruit yield per plant. Average fruit weight (0.89 kg)

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and fruits per plant (0.52) had direct effect on pumpkin yield, indicating their importance as selection parameters. Moreover, the results indicated that node number to first female flower, average fruit weight, flesh thickness, fruit length, fruit diameter and fruits per plant can be used as useful selection criteria to increase fruit yield per plant in pumpkin.

1. INTRODUCTION

Pumpkin (*Cucurbita moschata* Duch. ex Poir.) is one of the cucurbitaceous vegetables consumed and relished by most of the people of Bangladesh. It is very popular among the peoples owing to its good taste, high nutritive value, good storability and longtime of availability and

Even better transport potentialities [1,2]. It ranks 3rd in respect of both area and production next to brinjal and radish. In Bangladesh, it occupies an area 27,500 ha with an annual production of 2,18,000 tons accounting to an average yield of 7.93 t ha^{-1} [3]. However, cultivation of this multipurpose and nutrition rich vegetable is most desirable for overcoming the malnutrition problem in this country, Pumpkin is a monoecious crop and has high cross-pollination mechanism, and due to its out crossing characteristics, diverse type of genotypes are always generating in this crop, the desirable variations, particularly for fruit types and quality, have been preserved by the farmers. Along with fruit morphotypes, variations for other plant characters are also available. Therefore, there is a need to improve the productivity and fruit yield of this vegetable. Fruit yield is a complex character that is determined by complex associations among several agronomic traits [4], also, to plan an efficient pumpkin breeding program or crop selection program, the knowledge of interrelationships among yield and yield contributing characters are necessary, and correlation studies among yield and other traits of the crop could be the interest of breeders in planning hybridization programs and evaluating the individual plants in the segregating populations.

Path coefficient analysis is a statistical tool which helps the plant breeder to better understand what type of relationship exists between two variables, the relationship between two variables can be such that one variable directly causes and then affects the other variable. Path analysis would help in partitioning the correlation coefficient into direct and indirect effects of various traits on the fruit yield, the concept of path analysis was originally developed by Wright [5], but the technique was first used for plant selection by Dewey and Lu [6]. Path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effects.

Nevertheless, the correlation along with path analysis would give a better appreciation of cause and effect relationship between pairs of character, knowledge of correlations, if accompanied by the understanding of the magnitude of contribution (direct and indirect) of each component characters to the final make-up of the fruit yield, the criteria formulated would be effective in selecting the genotypes and using themselves in the crop improvement program. Therefore, the present study was undertaken to determine the genetic variation, the correlation coefficient and path coefficient for screen out the suitable parental groups for future breeding program.

2. MATERIALS AND METHODS

Nineteen pumpkin inbreds (PK01, PK02, PK03, PK04, PK05, PK06, PK07, PK08, PK09, PK10, PK11, PK12, PK13, PK14, PK15, PK16, PK17, PK18 and PK19) were used in this study. The inbreds were collected from Floriculture Division, Horticulture Research Centre (HRC) and the experiment was setup at the Experimental farm of Bangladesh Agricultural Research Institute (BARI), Gazipur during October, 2011 to May, 2012. The experiment was conducted in RCBD with three replications. So Twenty five days old seedlings were transplanted in well prepared experimental plot. Fertilizers were applied @ 5000-35-75-18-4.3-2 kg ha^{-1} of cowdung-N-P-K-S-Zn-B. The sources of N, P, K, S, Zn and B were urea, TSP, MoP, gypsum, zinc sulphate and boric acid (medicated) respectively. Moreover, the entire amount of cowdung, P, S, Zn, B and 1/3rd of K were applied during pit preparation as basal to each plot. The rest of K was applied in two equal installments at 20 and 35 days after transplanting (DAT). N was applied in four equal installments at 7, 20, 35 and 50 DAT.

Furthermore, necessary intercultural operations were done during the crop period for proper growth and development of the plants and to protect the fruits from routing. The fruits were harvested when the peduncle dried on maturity. Data were collected from at least three mature fruits from all the plants of inbreds. Data were recorded for days to 1st male flower, days to 1st female flower, node number to 1st male flower, node number to 1st female flower, fruit length, fruit diameter, cavity length, cavity diameter, flesh thickness, average fruit weight, fruits per plant, yield per plant and TSS (%). However, the data were analyzed to estimate genotypic and phenotypic co-efficient of variation using the formula of Burton [7], heritability in broad sense using the formula of Hanson et al. 1956 [8], genetic advance was estimated by the using formula suggested by Johanson et al. [9]. Co-relation coefficient and path co-efficient analysis was worked out as suggested by Singh and Chaudhary, [10] and Dewey and Lu [6] respectively.

3. RESULTS AND DISCUSSION

Genotypic, phenotypic and error variance, heritability (%), genotypic and phenotypic coefficient of variation, genetic advance (GA), genetic advance in percent mean have been presented in (Table 1) to show the extant of variation among the nineteen inbreds. In the other side, the magnitude of genotypic variance for days to 1st male flower, days to 1st female flower, fruit length, fruit diameter, cavity length, cavity diameter, flesh thickness, average fruit weight, fruits plant[-1], fruit yield plant[-1] and TSS were higher than the environmental variance and the genotypic and phenotypic variance were observed more or less similar. However, this indicates that the genotypic component of variation was the major contributor to the total variation, the environmental variances of the above traits were observed to be very low, indicating that the environment had very little effect on observed phenotypic variation of the traits. These would also suggest that the above traits have broad variation and improvement can be achieved through the imposition of selection on the traits. Same result was reported by Aruah et al. [11] and Akter et al. [12]. On the other hand, environmental variance was higher than genotypic variance for node number to 1st male flower, node number to 1st female flower and flesh thickness, indicating that these characters were influenced by environment and selection

based on these traits would not be effective reported by Islam et al. [13].

The phenotypic co-efficient of variation (PCV) was the highest in cavity length (53.93%), fruit length (34.92%), fruit yield per plant (33.99%) and average fruit weight (32.88%), and Khan et al. [14] reported that high PCV is an indication of the existence of wide scope of selection for the improvement of the traits from a considerable amount of variability present. Comparatively low PCV observed for days to 1st female flower (6.06%), days to 1st male flower (8.85%), node number to 1st female flower (9.02%), TSS (11.87%), fruit diameter (16.09%), cavity diameter (17.63%) and flesh thickness (18.21%) indicating less scope for selection. The highest genotypic co-efficient variation (GCV) was found for cavity length (50.32%), fruit yield per plant (25.64%) and average fruit weight (21.54%). While, Yadav [15] reported that high GCV is the indication of exploitable genetic variability for these traits which may facilitate selection.

Moreover, a narrow range of difference between PCV and GCV was observed for days to 1st male flower (8.58 and 7.57) followed by days to 1st female flower (6.06 and 4.64), fruit length (33.24 and 34.92), fruit diameter (16.09 and 14.99) and TSS (11.87 and 9.17), therefore, this indicates that the traits are mostly governed by genetic factors with minimal environmental influence on the phenotypic values may be effective as reported by Aruah et al. [11]. However, wide range of variation between PCV and GCV was reported for node number to 1st male flower (21.29 and 2.39), node number to 1st female flower (9.02 and 2.52), average fruit weight (32.88 and 21.54), fruits per plant (25.83 and 16.13) and fruit yield per plant (33.99 and 25.64) indicating venerability of these traits to environmental influence and thereby reducing the response to selection on phenotypic basis reported by Islam et al. [13].

A character can be improved only if it is highly heritable, among the various characters, high heritability coupled with high genetic advance over percent mean was noticed for fruit length (90.50% and 65.13%), cavity length (86.90% and 96.62%), average fruit weight (80.43% and 54.41%). High heritability estimates with fairly high estimates of Genetic Advance in Percent Mean (GAPM) demonstrate the presence of additive gene effect and selection for genetic improvement for these traits would be effective. Such high GA may be due to the action of additive genes reported by Idahosa et al. [16].

Table 1. Estimation of genetic parameters for different traits in 19 pumpkin inbreds

Characters	Genetic parameters							
	Genotypic variance (δ^2g)	Phenotypic variance (δ^2p)	Error variance (δ^2e)	Genotypic Co-efficient variance (GCV)	Phenotypic Co-efficient variance (PCV)	Heritability (Broad sense) h2(%)	Genetic advance (GA)	Genetic advance in percent mean (%)
Days to 1st male flower	13.53	17.30	3.77	7.57	8.58	78.21	6.70	13.82
Days to 1st female flower	7.32	12.45	5.13	4.64	6.06	58.75	4.27	7.33
Node number to 1st male flower	0.03	2.00	2.03	2.39	21.29	1.25	0.04	0.55
Node number to 1st female flower	0.06	3.06	3.0	2.52	9.02	1.89	0.07	0.35
Fruit length (cm)	37.26	41.17	3.91	33.24	34.92	90.50	11.95	65.13
Fruit diameter (cm)	9.05	10.37	1.32	14.99	16.09	87.27	5.79	28.19
Cavity length (cm)	28.87	33.22	4.35	50.32	53.98	86.90	10.31	96.62
Cavity diameter (cm)	2.92	4.80	1.88	13.68	17.63	61.00	2.75	22.14
Flesh thickness (cm)	0.33	0.41	0.09	16.31	18.21	80.28	1.09	31.05
Average fruit weight (kg)	0.98	1.22	0.24	21.54	32.88	80.43	1.8	54.41
Number of fruits per plant	0.70	1.29	0.59	16.13	25.83	54.42	1.27	28.92
Fruit yield per plant (kg)	13.87	24.39	10.52	25.64	33.99	56.86	5.77	39.78
TSS (%)	0.65	1.09	0.44	9.17	11.87	59.90	1.29	14.64

Table 2. Genotypic (r_g) and phenotypic (r_p) correlation coefficient among different characters in 19 pumpkin inbreds

Character		DFF[2]	NFM[3]	NFF[4]	FL[5] (cm)	FD[6] (cm)	CL[7] (cm)	CD[8] (cm)	Fl. T[9] (cm)	Av. FWt.[10]	Fruits /Plant	TSS (%)[11]	Fruit yield/Plant (kg)
DFM[1]	r_g	0.78**	0.06	0.03	0.04	-0.31	0.01	-0.19	-0.06	-0.19	-0.08	-0.13	-0.27
	r_p	0.71**	0.08	0.15	0.09	-0.24	0.07	-0.17	0.01	-0.09	-0.09	-0.16	-0.14
DFF[2]	r_g		-0.21	0.09	0.04	-0.29	-0.22	-0.38	0.01	-0.15	0.03	-0.33	-0.10
	r_p		-0.06	0.19	0.01	-0.22	-0.01	-0.16	-0.01	-0.11	-0.06	-0.26	-0.13
NFM[3]	r_g			0.10	0.10	-0.01	0.11	-0.04	-0.06	-0.01	0.28	0.01	0.12
	r_p			-0.02	0.01	0.08	-0.03	0.19	-0.06	0.07	0.03	-0.10	0.07
NFF[4]	r_g				-0.29	-0.01	-0.29	0.15	-0.04	0.01	0.38	-0.06	0.91**
	r_p				-0.23	0.22	-0.27	0.18	0.04	0.06	0.09	-0.14	0.82**
FL[5] (cm)	r_g					-0.28	0.99**	-0.46*	0.18	0.42	0.10	-0.34	0.22
	r_p					-0.25	0.96**	-0.42	0.18	0.42	0.12	-0.20	0.22
FD[6] (cm)	r_g						-0.38	0.99**	0.69**	0.74**	-0.48*	0.15	0.46*
	r_p						-0.38	0.85**	0.68**	0.73**	-0.34	0.16	0.42
CL[7] (cm)	r_g							-0.54*	0.02	0.29	0.17	-0.32	0.51*
	r_p							-0.53*	0.04	0.27	0.17	-0.24	0.44
CD[8] (cm)	r_g								0.51*	0.52*	-0.55*	0.44	0.18
	r_p								0.36	0.46*	-0.32	0.29	0.18
Fl. T[9] (cm)	r_g									0.88**	-0.59*	-0.00	0.55*
	r_p									0.97**	-0.36	0.01	0.47*
Av. FWt.[10]	r_g										-0.30	-0.11	0.88**
	r_p										-0.20	-0.04	0.79**
Fruits/Plant	r_g											-0.37	0.13
	r_p											-0.33	0.39
TSS (%)[11]	r_g												-0.39
	r_p												-0.25

**Significant at 1% level, *Significant at 5% level, [1]Days to 1st male flower , [2]Days to 1st female flower, [3]Node number to 1st male flower, [4]Node number to 1st female flower, [5]Fruit length, [6]Fruit diameter, [7]Cavity length, [8]Cavity diameter, [9]Flesh thickness, [10]Average fruit weight, [11]Total soluble solid (%)

Table 3. Partitioning of genotypic correlation with fruit yield into direct (bold) and indirect components

Character	DFM[1]	DFF[2]	NFM[3]	NFF[4]	FL[5] (cm)	FD[6] (cm)	CL[7] (cm)	CD[8] (cm)	Fl. T[9] (cm)	Av. FWt.[10]	Fruits/Plant	TSS (%)[11]	Total corr. (r_g) with yield
DFM[1]	**-0.05**	0.04	0.000	-0.01	-0.01	-0.01	0.01	-0.08	-0.00	-0.10	-0.07	0.00	-0.27
DFF[2]	-0.03	**0.06**	-0.00	-0.01	-0.00	-0.01	-0.00	-0.00	0.00	-0.08	-0.03	0.00	-0.10
NFM[3]	-0.01	-0.00	**0.002**	-0.01	0.00	0.00	-0.01	0.00	0.04	0.08	0.02	0.00	0.12
NFF[4]	-0.01	0.08	0.00	**0.04**	0.11	0.07	-0.05	0.08	-0.07	0.08	0.65	0.00	0.91**
FL[5](cm)	-0.00	0.00	0.00	0.01	**-0.09**	-0.11	0.11	-0.10	-0.02	0.37	0.07	0.01	0.22
FD[6] (cm)	0.02	-0.01	0.00	-0.01	0.03	**0.05**	-0.07	0.01	-0.05	0.66	-0.18	-0.00	0.46*
CL[7] (cm)	-0.00	-0.00	-0.00	0.04	-0.06	-0.02	**0.18**	-0.01	-0.00	0.23	0.14	0.01	0.51*
CD[8] (cm)	0.02	-0.02	0.00	-0.02	0.05	0.04	-0.10	**0.01**	-0.04	0.41	-0.16	-0.02	0.18
Fl. T[9] (cm)	-0.00	-0.00	000	-0.00	-0.01	0.03	0.03	0.04	**-0.07**	0.71	-0.19	-0.0	0.55*
Av. FWt.[10]	0.00	-0.01	0.00	-0.00	-0.02	0.06	0.05	0.06	-0.05	**0.89**	-0.10	0.00	0.88**
Fruits/Plant	0.01	-0.00	0.00	-0.05	-0.11	-0.07	0.03	-0.05	0.02	-0.17	**0.52**	0.00	0.13
TSS%[11]	0.01	-0.02	-0.00	0.01	0.00	0.01	-0.04	0.01	-0.06	-0.13	-0.18	**-0.01**	-0.39

*Residual effect = 0.027, **Significant at 1% level, *Significant at 5% level,*
[1]Days to 1st male flower , [2]Days to 1st female flower, [3]Node number to 1st male flower, [4]Node number to 1st female flower, [5]Fruit length, [6]Fruit diameter, [7]Cavity length, [8]Cavity diameter, [9]Flesh thickness, [10]Average fruit weight, [11]Total soluble solid (%

On the other hand, It was estimated that the most of the cases genotypic correlation co-efficient values were higher than the phenotypic values (Table 2). The positive and strong association of node number to first female flower (r_g = 0.91**, r_p = 0.82**), average fruit weight (r_g = 0.88**, r_p = 0.79**), flesh thickness (r_g = 0.55*, r_p = 0.47*), fruit diameter (r_g = 0.46*, r_p = 0.42), and cavity length (r_g = 0.51*, r_p = 0.44) with fruit yield per plant. On the other hand, day to first male flower (r_g = -0.27, r_p = -0.14) and days to first female flower (r_g = -0.10, r_p = -0.13) correlated negatively and insignificantly with fruit yield per plant. Similar positive and strong association in average fruit weight, flesh thickness, fruit diameter with fruit yield per plant were also reported by Sultana et al. [17]; Akter et al. [12] and Aruah et al. [11]. The positive and strong associations of the above characters with yield revealed that the importance of the characters in determining fruit yield and showed that selection for these traits would result in superior fruit yield.

The path coefficient analysis (Table 3) revealed that the highest positive direct effect was recorded in average fruit weight (0.89) to fruit yield and high direct effect was found in fruits per plant (0.52) followed by cavity length (0.18). Considering the high direct contribution of average fruit weight and number of fruits per plant to the fruit yield, it would appear that, these two characters are the most reliable selection criteria for fruit yield improvement. Similar high direct effects of average fruit weight and number of fruits per plant on yield were also reported by Sultana et al. [17]; Akter et al. [12] and Aruah et al. [11]. The highest negative direct effect on yield was exhibited by fruit length (-0.09) and flesh thickness (-0.07). The highest positive indirect effect of average fruit weight on flesh thickness (0.71) followed by fruit diameter on average fruit weight (0.66) and node number to first female flower on fruits per plant (0.65). The residual effects determine how the best causal factors account for variability of the dependent factors i.e. fruit yield per plant.

4. CONCLUSION

All the results indicates that node number to first female flower, average fruit weight, flesh thickness, fruit length, fruit diameter and fruits per plant can be used as useful selection criteria to increase fruit yielding in pumpkin.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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