



P-ISSN: 2349-8528

E-ISSN: 2321-4902

IJCS 2018; 6(2): 2695-2699

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Received: 05-01-2018

Accepted: 08-02-2018

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International Journal of Chemical Studies

Studies on genetic component analysis and gene action for growth, yield and yield attributing traits of pumpkin

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Abstract

Fifteen hybrids of pumpkin developed through diallel mating (excluding reciprocals) using six parents were evaluated for three seasons with the objective to know the nature of inheritance of growth and yield attributes. The present study revealed that the both additive and dominance variance were found important in the inheritance of most of the traits, whereas dominance variance were more prominent than the additive variance in all three seasons. Average degree of dominance revealed the presence of over dominance for all traits in all three seasons (E_1, E_2, E_3). Highly significant values of additive (\hat{D}) and dominance (\hat{H}_1 and \hat{H}_2) effects of components were observed for most of the traits studied in all three seasons (E_1, E_2, E_3) except the values of \hat{D} for node number to first male flower appearance, number of primary branches per plant, polar circumference of fruit and intermodal length in all three seasons and for days to first male flower anthesis in E_2 , for equatorial fruit circumference in E_1 and E_2 which were found non-significant. In general the proportions of dominant and recessive genes in parents $[4\hat{D} - \hat{H}_1]^{1/2} + \hat{F}$ / $(4\hat{D} - \hat{H}_1)^{1/2} - \hat{F}$ were more than unity with positive \hat{F} value for all the traits in all three seasons except fruit length in Y_2 indicating major contribution of dominant genes.

Keywords: Pumpkin, gene action, yield, non-additive

Introduction

Based on commercial significance the cultivated *Cucurbita* sp. ranks among the 10 leading vegetable crops worldwide. China and India lead the world production and other major producers are U. S. Egypt, Mexico, Ukraine, Cuba, Italy, Iran and Turkey (Ferriol and Pico, 2008). The total area of pumpkin in India is 19,760 hectares whereas, the total production is 0.42 million tonne with productivity 21.25 MT/ha (Anonymous, 2017). Robinson and Decker-Walters (1999) [17] concluded that in genus *Cucurbita*, there are 5 cultivated and 10 wild species. Seshadri and More (2009) [18] also stated that the recent recognition of synonyms and taxonomic changes have reduced the number of *Cucurbita* species to 15 or even less. The five cultivated species are *C. argyrosperma* (earlier *C. mixta*), *C. pepo*, *C. maxima*, *C. moschata* and *C. ficifolia*. In India, pumpkin and squashes were introduced from South America by foreign navigators and emissaries. *Cucurbita moschata* is more widely cultivated than other four cultivated species in our country. Since *Cucurbita moschata* is amenable to hotter climates more than other cultivated species, it is also the most widely grown vegetable throughout the tropics of both hemispheres. Pumpkins, like other squash, are thought to have originated in North America. The oldest evidence, pumpkin-related seeds dating between 7000 and 5500 BC, were found in Mexico.

The three economically important species, *C. pepo*, *C. moschata*, and *C. maxima* are highly polymorphic in fruit characteristics, inspiring much research into their inheritance although most of such studies have been done in *C. pepo* and *C. maxima*. The gene list of *Cucurbita* sp. includes 79 loci for phenotypic/morphological traits and 48 polymorphic allozyme loci along with linkage and gene mapping (Paris and Brown, 2005) [15]. However, information on simply inherited characters documented in the gene list is almost lacking for *C. moschata*, and among the few that have been reported so far are Trifluralin (a herbicide) tolerance controlled by a dominant gene "T" (Adeoye and Coyne, 1981) [1], naked kernel (absence of tough seed coat) trait

controlled by a pair of recessive genes (Zhou, 1987) and mottled light and dark green fruit colour, monogenic dominant (“*Mldg*”) over dark green fruit (Cardoso *et al.* 1995) [5]. A wide range of expression of the trait “silver leaf mottling” was observed in *C. moschata* although all the reports indicated that this trait showed dominance over non-mottled leaf. Ribeiro and da Costa (1989) [16] reported that a partially dominant gene was responsible for silver mottling in leaf but modifier genes affected its expression while it was reported to be conditioned by two genes (Latha and Gopalkrishnan, 1993) [13] and a single gene “*M*” (Wessel-Beaver and Katzir, 2000) [23]. Information on polygenic inheritance of quantitative characters in pumpkin is also meager. Non-additive gene action for vine length, number of laterals, nodes of first staminate and pistillate flowers and days to first staminate and pistillate flowers (Doijode and Sulladmath, 1988) [6]; for number of seeds/fruit, 100-seed weight and seed size index (Doijode *et al.* 1987); over-dominance (Galka, 1987) [7] and dominance (Sirohi *et al.* 1986) [21] for fruit weight; over-dominance for vine length, fruit number/plant, flesh thickness, fruit shape index and fruit yield per plant (Sirohi *et al.* 1986) [21] and over-dominance gene action for all the nutritional traits, namely, total soluble solids, carotenoids, ascorbic acid, calcium, and iron content (Sirohi and Yayasanani, 2001) [22] clearly suggested the importance of exploiting heterosis commercially.

The existence of significant amount of non-additive gene action is a prerequisite for exploitation of heterosis. The specific combining variance largely is the measure of dominance variance. If heterosis is high for specific cross and observations made are true for economic trait like yield, it is possible to utilize the cross (Arunachalam, 1989).

Materials and Methods

The experimental materials for the present study comprised of six promising and diverse inbreds and varieties of pumpkin selected on the basis of genetic variability from the germplasm stock maintained in the Department of Vegetable Science, N.D. University of Agriculture & Technology, Kumarganj, Faizabad (U.P.) India. The selected parental lines *i.e.* Narendra Upkar (P₁), NDPK-120 (P₂), Narendra Agrim (P₃), NDPK-39-2 (P₄), Kashi Harit (P₅) and NDPK-11-3 (P₆) were raised and crossed in the all possible combinations, excluding reciprocals, during *Zaid*, 2015 to get 15 F₁ hybrid seeds for the study of variability, character association, heterosis, combining ability, gene action and stability for twenty one quantitative and qualitative traits. Observations were recorded on fourteen economic traits including biochemical analysis *viz.* days to first female flower anthesis, days to first male flower anthesis, node number to first male flower appearance, node number to first female flower appearance, days to first fruit harvest, vine length (m), internodal length (cm), number of primary branches per plant, fruit weight (kg), number of fruits per plant, equatorial circumference of fruit (cm), polar circumference of fruit (cm), flesh thickness (cm), fruit yield per plant (kg).

The genetic components of variation were calculated for the analysis of numerical approach followed the method given by Jinks and Hayman (1953) [11], Hayman (1954a) [8] and Askel and Johnson (1963) [4].

Results and Discussion

The estimates of components of variation provide detailed information of additive and dominant components and allied statistics. The genetic progress in a population largely

depends upon the relative values of these components. The diallel cross analysis through analytical method is based on a number of assumptions regarding applicability of this method as advocated by Hayman (1954a) [8] *viz.*, homozygous parents, diploid segregation, no reciprocal differences, no multiple allelism, no epistasis and absence of linkage, absence of epistatic and random mating. The validity of specific assumptions of diploid segregation, lack of reciprocal differences and multiple allelism were presumed. Pumpkin being cross pollinated crop it is tedious to get complete homozygous parents for all the characters. However, if some traits exhibit the partial non fulfillment of assumption, the estimates of population parameters are still possible (Hayman, 1954a) [8]. However, the results in such cases are less reliable than would have been if all the assumptions are completed. The estimates of the components of variation and their related statistics for different traits of pumpkin have been presented in Table-1.

Highly significant values for additive (\hat{D}) and dominance (\hat{H}_1 and \hat{H}_2) effects of components were observed for most of the twenty traits in all three seasons (E₁, E₂, E₃) except the values of \hat{D} for node number to first male flower appearance, number of primary branches per plant polar circumference of fruit, internodal length in all three seasons and days to first male flower anthesis in E₂, equatorial fruit circumference in E₁ and E₂ in which these parameters were found non-significant. The significant values of \hat{D} , \hat{H}_1 and \hat{H}_2 indicated the importance of both additive and dominance gene action in the expression of these traits, which is in consonance with the findings of Pandey *et al.* (2004) [14], Kathiria *et al.* (2005) [12] and Jha *et al.* (2009) [10]. However, additive (\hat{D}) genetic variance components were lower in magnitude than dominant component of genetic variance for all the fourteen traits over all three seasons which showed preponderance of dominance components of variance in expression of fruit yield and its attributing traits in all three seasons. Similar findings were also recorded by Sharma *et al.* (2010) [19] in pumpkin

The positive values of \hat{F} were found for all traits in all three seasons, which indicated that there were an excess of dominance gene in the inheritance of these traits among the parents.

The average degree of dominance ($(\hat{H}_1/\hat{D})^{1/2}$) revealed the presence of over dominance for all characters in all three seasons (E₁, E₂, E₃). This suggested that heterosis breeding might be advantageous for improvement of yield and its attributing traits in pumpkin. The results are in agreement with the finding of Jha *et al.* (2009) [10] and Sharma *et al.* (2010) [19].

Ratio of $(\hat{H}_2/4\hat{H}_1)$ which estimates frequency of alleles with positive and negative effects in the parents were less than 0.25 in all three seasons for all characters which showed asymmetrical distribution of loci showing dominance for all traits (Table-1). The ratio of $(4\hat{D}\hat{H}_1)^{1/2} + \hat{F} / (4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$ indicated that the dominant alleles were more frequent than recessive alleles for all the traits studied in all the seasons (Table-1). These findings are similar to that of Sharma *et al.* (2010) [19].

The proportion of \hat{h}^2/\hat{H}_2 , which provides information about groups of gene exhibiting little or no dominance. The less than one \hat{h}^2/\hat{H}_2 ratio suggested that at least one gene group mainly governed the characters under study for most of traits. The positive correlation (r) between parental order of dominance ($Wr + Vr$) and parental measurement (Yr) were showed for most of the characters in all three seasons, except total sugars in all three seasons and number of fruits per plant in E_2 and E_3 , dry matter content and reducing sugars in E_1 and node number to first female flower appearance and non-reducing sugars in E_3 . The positive correlation suggesting the preponderance of recessive genes while, positive values suggested preponderance of dominant genes. The results of present investigation suggested preponderance of dominant genes in the expression of most of traits studied. Therefore,

heterosis breeding approach could be advantageous to produce superior hybrids for high fruit yield in pumpkin. The above findings are in agreement with that of Singh *et al.* (2005) [20].

Thus the non-significant values of ' t^2 ' or $(1-b/SEb)$ indicates the validity of assumptions pertaining to diallel analysis, while significant values of ' t^2 ' or $(1-b/SEb)$ showed failure of hypothesis or null hypothesis for diallel cross analysis (Table-1).

The result of present study suggested preponderance of dominance genes in the expression of most of the component traits studied. Therefore, heterosis breeding approach might be advantageous rather than selection to develop superior hybrids for high fruit yield in pumpkin.

Table 1: Estimates of components of variation and their related statistics in 6 x 6 diallel crosses of pumpkin over three seasons (E_1, E_2, E_3)

Components of variation and related statistics	seasons	Days to 1 st male flower anthesis	Days to 1 st female flower anthesis	Node no. to 1 st male flower	Node no. to 1 st female flower	Days to first fruit harvest	Number of primary branches per plant	Equatorial circumference of fruit
\hat{D} (Additive effect)	E_1	17.00**±3.00	20.78**±5.27	0.18±0.15	4.14*±1.43	18.17*±7.03	0.78±0.68	8.08±7.95
	E_2	7.98±7.95	7.41±6.82	0.12±0.33	1.99**±0.21	10.75±10.18	0.45±0.68	1.51±4.04
	E_3	17.01**±2.65	20.83**±2.68	0.18**±0.19	4.15*±2.13	26.04**±7.29	0.78±0.72	8.08*±3.56
\hat{H}_1 (Dominance effect)	E_1	49.91**±7.62	53.31**±13.39	1.88**±0.38	17.94**±3.64	80.91**±17.85	7.79**±1.74	98.43±20.18
	E_2	106.14**±20.20	88.43**±17.33	3.61**±0.84	7.44**±0.52	121.25**±25.84	6.88**±1.73	85.26**±10.25
	E_3	43.72**±6.73	39.65**±6.81	1.85**±0.49	16.05**±5.42	108.81**±18.51	8.61**±1.83	89.94**±9.06
\hat{H}_2 (Dominance indicating asymmetry of +/-effect of genes)	E_1	42.99**±6.81	40.47**±11.97	1.38**±0.34	10.37**±3.25	68.60**±15.95	6.98**±1.55	84.88**±18.02
	E_2	101.83**±18.04	84.04**±15.48	3.17**±0.75	6.80**±0.48	110.83**±23.09	5.69**±1.55	65.26**±9.16
	E_3	37.37**±6.02	35.73**±6.09	1.53**±0.43	10.31*±4.84	92.80**±16.54	7.55**±1.64	84.28**±8.09
\hat{F} (Mean Fr over arrays)	E_1	20.16**±7.34	28.05*±12.89	0.56*±0.36	10.30*±3.50	15.88±17.18	0.56±1.67	17.91±19.42
	E_2	4.58±19.44	6.19±16.68	0.25±0.81	1.24*±0.52	14.76±24.87	-0.17±1.67	7.90±9.87
	E_3	16.77±6.48	16.74±6.56	0.44±0.47	8.47±5.22	32.14±17.82	1.09±1.76	9.74±8.7
\hat{h}^2	E_1	14.80**±3.47	21.20**±6.80	18.50**±5.45	20.80**±7.24	29.60**±2.55	22.50**±3.70	7.70±9.63
	E_2	13.10*±5.26	11.70*±6.20	15.50*±6.04	27.20**±0.26	10.30±9.10	38.80**±2.06	29.00**±0.94
	E_3	25.90**±1.57	30.60**±1.27	8.10±16.95	21.00±16.21	17.50**±3.48	16.30**±5.58	8.40**±1.84
\hat{E} (Environmental component)	E_1	0.08±1.13	0.21±1.99	0.02±0.05	0.10±0.54	0.23±2.65	0.02±0.25	0.95±3.50
	E_2	0.07±3.08	0.19±2.58	0.03±0.12	0.16±0.08	0.30±3.84	0.01±0.25	0.31±1.52
	E_3	0.08±1.00	0.16±1.01	0.01±0.07	0.09±0.80	0.19±2.75	0.02±0.273	0.96±1.34
$(\hat{H}_1/\hat{D})^{1/2}$ (Mean degree of dominance)	E_1	1.71	1.60	3.17	2.08	2.11	3.15	3.48
	E_2	3.64	3.45	5.47	1.93	3.35	3.88	7.51
	E_3	1.60	1.38	3.14	1.96	2.04	3.31	3.33
\hat{H}_2/\hat{H}_1 (Proportion of genes with +/- effects in parents)	E_1	0.21	0.19	0.17	0.14	0.21	0.22	0.21
	E_2	0.24	0.23	0.22	0.22	0.22	0.20	0.19
	E_3	0.21	0.22	0.20	0.16	0.21	0.21	0.23
$(4\hat{D}\hat{H}_1)^{1/2} + \hat{F}/(4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$ (Proportion of dominant and recessive genes in parents)	E_1	2.05	2.47	2.81	3.96	1.52	1.25	1.93
	E_2	1.17	1.27	1.46	1.38	1.51	0.90	2.07
	E_3	1.88	1.82	2.20	3.16	1.86	1.53	1.44
\hat{h}^2/\hat{H}_2 (Number of gene groups)	E_1	1.64	0.66	0.84	0.27	0.48	2.82	1.94
	E_2	1.71	1.84	2.35	0.86	1.41	0.93	1.40
	E_3	1.89	0.75	0.74	0.26	0.80	2.61	1.95
r (Correlation coefficient)	E_1	0.84	0.47	0.30	0.33	0.55	0.61	0.54
	E_2	0.65	0.68	0.21	0.97	0.41	0.74	0.28
	E_3	0.87	0.77	0.31	-0.12	0.88	0.66	0.60
t^2	E_1	0.19	1.43	0.05	0.85	1.25	3.25	15.26
	E_2	2.39	1.26	17.99	2.92	2.64	17.18	4.67
	E_3	2.20	2.05	0.319	0.01	15.54	3.29	2.74
$(1-b/SEb)$	E_1	1.05	0.28	1.25	0.69	0.19	3.36	7.17
	E_2	2.87	2.21	8.51	2.06	3.44	7.04	4.57
	E_3	2.27	2.46	2.09	2.36	5.98	3.27	3.15

Significant at 5 per cent and 1 per cent probability levels, respectively.

Table 1: Contd.

Components of variation and related statistics	Seasons	Vine length (m)	Average fruit weight	No. of fruits per plant	Fruit yield per plant	Polar circumference of fruit	Flesh thickness	Internodal length (cm)
\hat{D} (Additive effect)	E ₁	0.96**±0.19	0.05**±0.01	0.45**±0.11	1.28**±0.43	5.98±6.11	0.05*±0.02	0.47±0.70
	E ₂	0.09**±0.03	0.05**±0.01	0.42**±0.16	0.62**±0.48	3.46±5.76	0.06*±0.02	0.15±0.45
	E ₃	0.96**±0.16	0.05**±0.00	0.45**±0.16	1.52**±0.90	5.93±5.70	0.05*±0.01	0.48±0.50
\hat{H}_1 (Dominance effect)	E ₁	0.23±0.50	0.12**±0.03	1.44**±0.30	7.57**±1.12	73.61±15.52	0.16±0.05	6.62±1.79
	E ₂	0.46**±0.08	0.09**±0.02	1.48**±0.42	5.18**±1.23	140.11**±14.62	0.30**±0.06	4.20**±1.16
	E ₃	2.18**±0.42	0.10**±0.02	1.55**±0.42	9.58**±2.28	65.96**±14.47	0.15**±0.04	5.96**±1.27
\hat{H}_2 (Dominance indicating asymmetry of +/- effect of genes)	E ₁	1.77**±0.44	0.07**±0.02	1.25**±0.26	5.94**±0.99	61.01**±13.86	0.13**±0.04	6.09**±1.60
	E ₂	0.36**±0.07	0.06**±0.02	1.22**±0.37	4.07**±1.10	128.10**±13.06	0.25**±0.05	3.39**±1.04
	E ₃	1.68**±0.38	0.06**±0.02	1.27**±0.38	7.36**±2.04	61.30**±12.92	0.140**±0.04	5.37**±1.14
\hat{F} (Mean Fr over arrays)	E ₁	0.62±0.48	0.06**±0.02	0.47*±0.28	2.24*±1.07	13.23±14.93	0.06±0.04	0.86±1.72
	E ₂	0.16**±0.07	0.03±0.02	0.49±0.40	1.35±1.18	12.16±14.07	0.06±0.06	0.41±1.12
	E ₃	0.62**±0.40	0.05**±0.02	0.57±0.41	3.12±2.20	5.44±13.92	0.05±0.04	0.55±1.22
\hat{h}^2	E ₁	45.30±1.04	47.40±4.06	21.50±3.60	17.90±2.53	14.10*±5.32	14.10±11.24	4.70±30.24
	E ₂	11.90±4.84	54.80±2.13	22.50±6.66	18.50±6.78	4.80±4.52	23.90**±4.24	24.50**±5.98
	E ₃	47.60±0.74	50.50±3.69	19.70±7.54	13.80±8.85	13.60**±4.73	10.80±11.65	15.70**±5.30
\hat{E} (Environmental component)	E ₁	0.04±0.07	0.00±0.00	0.01±0.04	0.06±0.16	1.00±2.31	0.01±0.01	1.52**±0.40
	E ₂	0.02±0.01	0.00±0.00	0.01±0.06	0.03±0.18	0.45±2.17	0.003±0.01	0.01±0.17
	E ₃	0.04±0.06	0.00±0.00	0.01±0.06	0.09±0.34	1.07±2.15	0.01±0.007	0.027±0.19
$(\hat{H}_1/\hat{D})^{1/2}$ (Mean degree of dominance)	E ₁	1.52	1.42	1.77	2.42	3.50	1.79	3.71
	E ₂	2.26	1.34	1.87	2.87	6.36	2.24	5.18
	E ₃	1.50	1.31	1.84	2.50	3.33	1.76	3.53
$\hat{H}_2/4\hat{H}_1$ (Proportion of genes with +/- effects in parents)	E ₁	0.19	0.15	0.21	0.19	0.20	0.20	0.23
	E ₂	0.19	0.17	0.20	0.19	0.22	0.21	0.21
	E ₃	0.19	0.17	0.20	0.19	0.23	0.22	0.22
$(4\hat{D}\hat{H}_1)^{1/2} + \hat{F}/(4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$ (Proportion of dominant and recessive genes in parents)	E ₁	1.53	2.27	1.82	2.12	1.92	2.16	1.63
	E ₂	2.27	1.71	1.91	2.16	1.76	1.64	1.68
	E ₃	1.54	1.96	2.03	2.37	1.31	1.97	1.39
\hat{h}^2/\hat{H}_2 (Number of gene groups)	E ₁	1.13	-0.02	0.83	0.70	0.95	0.45	0.05
	E ₂	-0.033	0.027	0.70	0.60	2.63	0.70	0.38
	E ₃	1.19	-0.02	0.81	0.67	0.94	0.43	0.06
r (Correlation coefficient)	E ₁	0.77	0.66	0.07	0.65	0.49	0.45	-0.07
	E ₂	0.51	0.74	-0.23	0.12	0.55	0.64	-0.07
	E ₃	0.77	0.75	-0.05	0.22	0.29	0.57	0.39
t ²	E ₁	1.42	0.11	1.30	0.38	0.12	0.01	0.83
	E ₂	0.38	0.01	0.16	0.20	0.34	0.02	19.37
	E ₃	3.50	0.01	0.51	0.00	0.00	1.28	1.07
(1-b/Seb)	E ₁	2.16	0.58	3.29	1.63	1.54	1.35	3.27
	E ₂	1.83	0.84	2.19	2.27	1.72	1.07	9.37
	E ₃	3.08	0.65	1.51	1.56	1.47	2.42	2.59

Significant at 5 per cent and 1 per cent probability levels, respectively.

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