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Gene action for growth, yield and yields attributing traits of pumpkin (*Cucurbita moschata Duch ex Poir*)

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Abstract
The present experiment was conducted to assess the nature of gene action for important fruit yield its attributing characters in pumpkin were determined by analyzing one 8 x 8 half diallel population. 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, However, additive (a) genetic variance components were lower in magnitude than dominant component of genetic variance for all the nineteen traits in both generations which showed preponderance of dominance components of variance in expression of fruit yield and its attributing traits in both generations. The positive values of $\hat{F}$ were found for all the traits except days to first female flower appearance, node number to first male flower appearance and number of seeds per fruit in F_1 and F_2 indicated that there was an excess of dominance gene in the inheritance of these traits among the parents. The average degree of dominance revealed the presence of over dominance for all characters in both generations (F_1, F_2). Ratio of genes with positive or negative effects in the parents were less than 0.25 in both generations for all characters which showed asymmetrical distribution of loci. The ratio of dominant and recessive genes in parents indicated that the dominant alleles were more frequent than recessive alleles for most of the traits studied in both generations. Number of gene groups was found less than one suggested that at least one gene group mainly governed the characters under study for most of traits.

Keywords: Pumpkin, half diallel, gene action and yield

Introduction
Pumpkin (*Cucurbita moschata* Duch ex Poir) is an economically important vegetable crop. It is hardy in nature and rich in carotene content and also have very good keeping quality. It is a herbaceous annual sexually propagated vegetable having an identical genomic structure *i.e.* AABB which indicates that it is an amphidiploid. It comprises about 27 species of both wild and cultivated having same chromosome number of 2n = 40. Among these species only five species *Cucurbita moschata, Cucurbita maxima, Cucurbita ficifolia, Cucurbita pepo* and *Cucurbita mixta* are commonly cultivated. These species are considered to be originated in Central America. Because of its wider adaptability and versatility, pumpkin is grown throughout the world either in outdoors or indoors. 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) [6]. In India, the total area covered by pumpkin is 0.104 million hectares whereas, the total production is 2.183 million tonne with productivity 20.99 tonne/ha (Anonymous 2020) [1].

Pumpkin is relatively high in energy and carbohydrates and a good source of vitamins, especially high carotenoid pigments and minerals. The colour of pumpkin is derived from the orange pigments *i.e.* carotene content abundant in fruits. It may certainly contribute to improve nutritional status of the people, particularly the vulnerable groups in respect of vitamin A requirement. Night-blindness is a serious problem of South Asian countries. Fruit are rich in lutein and both α and β carotene content, the latter of which generates vitamin A in the body. Pumpkins are very versatile in their uses for cooking. Most of the parts of pumpkin are edible, including the fleshy shell, seeds, leaves, and even the flowers. Encouraging the mass people to take more pumpkin can easily be solved the problem. The information regarding nature of gene action controlling important quantitative traits is required for devising a suitable breeding strategy and for improvement of pumpkin. The existence of significant amount of non-additive gene action is a prerequisite for exploitation of heterosis.

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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 a as a commercial seed production of hybrids or there exists a male sterility, fertility restoration system (Arunachalam, 1989) [3].

Materials and Methods
The investigations were carried out to evaluate the 64 genotypes (28 F_1, 28 F_2 and 8 parental lines) of pumkin *viz*: Azad Pumpkin - 1 (P_1), P-35-16 (P_2), P-40-16 (P_3), Narendra Agrim (P_4), NDPK-7-24 (P_5), Kashi Harit (P_6), DVRP-2-5 (P_7), and Punjab Samrat (P_8). The 8 parental lines and their 28 F_1 and F_2 were grown in a Randomized Complete Block Design (RBD) with three replications during *Zaid* 2021 at the Department of Vegetable Science, Kalyanpur, CSA University of Agriculture and Technology, Kanpur (U.P.) India. Each 28 F_1, F_2 and parents were grown in rows spaced 3 meters apart with a plant to plant spacing of 0.50 meter. All the recommended agronomic package of practices and plant protection measures were followed to raise good crop.
Observations were recorded on nineteen quantitative traits *viz.*, Days to first male flower appearance, days to first female flower appearance, node numbers to first male flower appearance, node numbers to first female flower appearance, vine length (cm), internodal length (cm), number of primary branches plant^{-1}, days to first harvest, average fruit weight (kg), number of fruits per plant, equatorial circumference of fruit (cm), polar circumference of fruit (cm), flesh thickness (cm), total soluble solids (^{0}Brix), dry matter content(%), moisture content (%), number of seed per fruit, Specific gravity (g/cm^3) and fruit yield per plant (kg). The data recorded from 28 F_1, 28 F_2 and 8 parental lines on nineteen characters were subjected to the analysis of numerical approach followed the method given by Jinks and Hayman (1953) [8], Hayman (1954a) [7] and Askel and Johnson (1963) [4].

Result and Discussion
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 nineteen characters in both generations (F_1 and F_2) except the values of $\hat{D}$ for node number to first male flower appearance, vine length, number of primary branches per plant, days to first harvest, number of fruits per plant, flesh thickness, dry matter moisture content and fruit yield per plant in F_1 and node number of first male flower, number of primary branches per plant, flesh thickness, dry matter content, moisture content, specific gravity in F_2 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 most of the yield and its attributing traits, However, additive ($\hat{D}$) genetic variance components were lower in magnitude than dominant component of genetic variance for all the nineteen traits in both generations which

showed preponderance of dominance components of variance in expression of fruit yield and its attributing traits in both generations which were also verified the results reported by earlier workers (Kumar *et al.*, 2018) [10].

The positive values of $\hat{F}$ were found for all traits except days to first female flower appearance, node number to first male flower appearance and number of seeds per fruit in F_1 and F_2 indicated that there was an excess of dominance gene in the inheritance of these traits among the parents. Similar findings were also reported by Sharma *et al.* (2010) [13] and Singh *et al.* (2019) [14]. The average degree of dominance ($\hat{H}_1/\hat{D}$)$^{1/2}$ revealed the presence of over dominance for all characters in both generations (F_1, F_2) 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 Singh *et al.* (2005) [15], Singh *et al.* (2019) [14], Kumar *et al.* (2018) [10] and Sharma *et al.* (2010) [13]. 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 both generations for all characters which showed asymmetrical distribution of loci showing dominance for all traits. 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 most of the traits studied in both generations. 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 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. 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 which show similarity with the findings of Kumar *et al.* (2018) [10] and Singh *et al.* (2019) [4].

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 most of the yield and its attributing traits, however, additive ($\hat{D}$) genetic variance components were lower in magnitude than dominant component of genetic variance for all the nineteen traits in both generations which showed preponderance of dominance components of variance in expression of fruit yield and its attributing traits in both generations.
Based on the above findings it can be concluded that preponderance of dominance genes in the expression of most of the component traits studied. Therefore, preponderance of dominant gene action along with over dominance in parents for most of the traits suggested that heterosis breeding approach might be more rewarding than selection to develop superior hybrids for high fruit yield in pumpkin.

Table 1: Estimates of genetics components and related statistics for 19 characters in 8 x 8 diallel cross of pumpkin

Characters		Days to first male flower appear	Days to first female flower appear	Node numbers to first male flower appearance	Node numbers to first female flower appearance	Vine length (cm)	Internodal length (cm)
$\hat{D}$ (Additive effect)	F_1	18.49	11.62	-0.003	2.16	0.22	0.66
	SE±	2.42	4.24	0.05	0.33	0.14	0.14
	F_2	10.25	11.30	0.02	2.06	0.21	0.51
	SE±	2.78	2.42	0.06	0.25	0.08	0.23
$\hat{H}_1$ (Dominance effect)	F_1	25.42	44.48	0.42	4.03	1.29	1.54
	SE±	5.56	9.74	0.11	0.75	0.31	0.34
	F_2	39.55	26.74	0.59	2.99	1.55	1.79
	SE±	6.39	5.54	0.14	0.58	0.18	0.53
$\hat{H}_2$ (Dominance indicating asymmetry of +/-effect of genes)	F_1	20.03	35.79	0.37	3.14	1.13	1.23
	SE±	4.84	8.48	0.10	0.65	0.27	0.35
	F_2	31.77	21.43	0.53	2.01	1.45	1.55
	SE±	5.56	4.82	0.12	0.51	0.15	0.46
$\hat{F}$ (Mean Fr over arrays)	F_1	1.12	-12.77	-0.07	1.62	0.20	0.81
	SE±	5.72	10.01	0.12	0.77	0.32	0.35
	F_2	2.71	-2.08	-0.02	0.27	0.22	0.53
	SE±	6.57	5.70	0.14	0.08	0.18	0.54
$\hat{h}^2$	F_1	5.54	8.39	1.24	4.06	0.57	0.48
	SE±	3.25	5.68	0.07	0.44	0.18	0.20
	F_2	21.14	18.13	0.02	3.67	5.87	1.58
	SE±	3.73	3.23	0.08	0.34	0.11	0.31
$\hat{E}$ (Environmental component)	F_1	0.38	0.75	0.05	0.19	0.04	0.41
	SE±	0.81	1.41	0.02	0.11	0.05	0.49
	F_2	0.62	1.06	0.02	0.27	0.04	0.19
	SE±	0.93	0.80	0.02	0.08	0.03	0.07
$(\hat{H}_1/\hat{D})^{.5}$ (Mean degree of dominance)	F_1	1.17	1.96	10.60	1.37	2.44	1.53
	F_2	1.47	1.54	5.13	1.20	2.71	1.87
$(\hat{H}_2/4\hat{H}_1)$(Prop. of genes with +/- effects in parents)	F_1	0.20	0.20	0.22	0.20	0.22	0.20
	F_2	0.20	0.02	0.23	0.17	0.23	0.23
$(4\hat{D}\hat{H}_1)^{.5}+\hat{F}/ (4\hat{D}\hat{H}_1)^{.5}-\hat{F}$ (Prop. of dominant and recessive genes in parents)	F_1	1.05	0.56	0.08	1.76	1.45	2.37
	F_2	1.10	0.88	0.81	2.39	1.48	1.76
$\hat{h}^2/\hat{H}_2$ (Number of gene groups)	F_1	0.28	0.24	3.31	1.29	0.51	0.49
	F_2	0.66	0.84	0.04	1.82	4.03	1.02
R (Correlation coefficient)	F_1	0.69	0.79	-0.01	0.89	0.06	0.54
	F_2	0.83	0.83	0.04	0.85	0.76	-0.27
*, ** Significant at 5% and 1%, respectively.							

Table 1: Contd…

Characters		Number of primary branches/plant	Days to first harvest	Average fruit weight (kg)	Number of fruits/plant	Equatorial circumference of fruit (cm)	Polar circumference of fruit (cm)	Flesh thickness (cm)
$\hat{D}$ (Additive effect)	F_1	0.11	10.58	0.06	0.19	39.11	20.11	-0.01
	SE±	0.13	6.81	0.04	0.11	8.36	4.55	0.001
	F_2	0.08	10.61	0.05	0.19	39.22	19.99	0.001
	SE±	0.15	2.32	0.01	0.08	6.03	2.79	0.001
$\hat{H}_1$ (Dominance effect)	F_1	2.56	75.61	0.42	0.89	80.98	55.31	0.08
	SE±	0.31	15.64	0.09	0.24	19.22	10.46	0.02
	F_2	1.86	24.02	0.34	1.11	35.94	17.90	0.04
	SE±	0.36	5.33	0.03	0.20	5.87	6.42	0.01
$\hat{H}_2$ (Dominance indicating asymmetry of +/-effect of genes)	F_1	2.14	64.04	0.36	0.77	71.47	48.95	0.08
	SE±	0.27	13.61	0.08	0.21	16.72	9.09	0.01
	F_2	1.55	18.08	0.29	0.91	25.67	14.19	0.04
	SE±	0.31	4.63	0.02	0.17	5.11	5.58	0.01
$\hat{F}$ (Mean Fr over arrays)	F_1	0.36	-0.74	0.05	0.21	11.64	6.79	-.001
	SE±	0.32	16.08	0.09	0.25	19.75	10.75	0.01
	F_2	0.12	9.56	0.08	0.31	32.28	9.26	0.001
	SE±	0.37	5.48	0.07	0.21	6.03	6.59	0.01
$\hat{h}^2$	F_1	4.08	32.52	0.75	1.08	71.54	87.59	0.18
	SE±	0.18	9.13	0.05	0.14	11.21	6.11	0.01
	F_2	1.32	4.06	1.62	1.57	43.58	-0.40	0.15
	SE±	0.21	3.12	0.01	0.12	3.42	3.74	0.01

$\hat{E}$ (Environmental component)	F_1	0.71	0.62	0.01	0.01	0.44	0.82	0.004
	SE±	0.4	2.27	0.01	0.04	2.78	1.52	0.002
	F_2	0.09	0.58	0.01	0.01	0.34	0.93	0.001
	SE±	0.05	0.77	0.003	0.03	0.85	0.93	0.001
$(\hat{H}_1/\hat{D})^{.5}$ (Mean degree of dominance)	F_1	4.87	2.67	2.74	2.12	1.43	1.66	6.33
	F_2	4.81	1.51	2.52	2.37	0.96	0.95	8.26
$(\hat{H}_2/4\hat{H}_1)$(Prop. of genes with +/- effects in parents)	F_1	0.21	0.21	0.22	0.22	0.22	0.22	0.25
	F_2	0.21	0.19	0.22	0.21	0.18	0.19	0.22
$(4\hat{D}\hat{H}_1)^{.5}+\hat{F}/ (4\hat{D}\hat{H}_1)^{.5}-\hat{F}$ (Prop. of dominant and recessive genes in parents)	F_1	2.06	0.97	1.43	1.64	1.23	0.82	0.65
	F_2	1.53	1.85	1.90	1.99	2.51	1.65	2.42
$\hat{h}^2/\hat{H}_2$ (Number of gene groups)	F_1	1.90	0.51	2.05	1.39	1.00	1.79	2.27
	F_2	0.85	0.22	3.95	1.72	1.69	-0.03	4.12
R (Correlation coefficient)	F_1	0.48	0.45	0.28	0.68	0.71	0.72	0.21
	F_2	-0.38	0.52	0.92	0.11	0.83	0.47	0.58
*, ** Significant at 5% and 1%, respectively.								

Table 1: Contd…

Characters		Total soluble solids (0Brix)	Dry matter content (%)	Moisture content (%)	Number of seeds per fruit	Specific gravity (g/cm³)	Fruit yield per plant (kg)
$\hat{D}$ (Additive effect)	F_1	0.09	0.03	0.03	435.83	0.004	1.06
	SE±	0.04	0.14	0.14	200.12	0.002	0.80
	F_2	0.10	0.09	0.09	421.17	0.001	1.12
	SE±	0.01	0.08	0.08	53.91	0.001	0.43
$\hat{H}_1$ (Dominance effect)	F_1	0.69	2.09	2.09	1832.78	0.01	12.68
	SE±	0.09	0.31	0.31	460.05	0.01	1.84
	F_2	0.26	0.71	0.71	665.61	0.006	6.36
	SE±	0.02	0.21	0.21	123.93	0.003	1.00
$\hat{H}_2$ (Dominance indicating asymmetry of +/-effect of genes)	F_1	0.62	1.36	1.36	1641.38	0.01	11.73
	SE±	0.08	0.27	0.27	400.25	0.01	1.60
	F_2	0.20	0.48	0.48	574.28	0.005	5.74
	SE±	0.02	0.18	0.18	107.82	0.003	0.87
$\hat{F}$ (Mean Fr over arrays)	F_1	0.12	0.07	0.07	-314.29	0.01	0.63
	SE±	0.09	0.32	0.32	472.88	0.01	1.89
	F_2	0.14	0.18	0.18	-15.70	0.001	1.27
	SE±	0.03	0.21	0.21	127.38	0.003	1.03
$\hat{h}^2$	F_1	2.38	0.87	0.87	1665.02	-0.004	28.98
	SE±	0.05	0.18	0.18	268.42	0.003	1.07
	F_2	0.98	1.47	1.46	45.77	-0.001	26.38
	SE±	0.02	0.12	0.12	72.31	0.002	0.58
$\hat{E}$ (Environmental component)	F_1	0.01	0.09	0.09	44.32	0.001	0.14
	SE±	0.01	004	0.05	66.71	0.001	0.27
	F_2	0.006	0.03	0.03	26.47	0.001	0.07
	SE±	0.003	0.03	0.03	17.96	0.001	0.14
$(\hat{H}_1/\hat{D})^{.5}$ (Mean degree of dominance)	F_1	2.67	8.76	8.77	2.05	1.58	3.46
	F_2	1.61	2.68	2.68	1.26	1.95	2.38
$(\hat{H}_2/4\hat{H}_1)$(Prop. of genes with +/- effects in parents)	F_1	0.22	0.16	0.16	0.22	0.18	0.23
	F_2	0.19	0.17	0.17	0.22	0.18	0.22
$(4\hat{D}\hat{H}_1)^{.5}+\hat{F}/ (4\hat{D}\hat{H}_1)^{.5}-\hat{F}$ (Prop. of dominant and recessive genes in parents)	F_1	1.62	1.34	1.34	0.70	2.29	1.19
	F_2	2.56	2.07	2.07	0.97	1.44	1.62
$\hat{h}^2/\hat{H}_2$ (Number of gene groups)	F_1	3.88	0.64	0.64	1.01	-0.05	2.47
	F_2	4.75	3.04	3.04	0.08	-0.11	4.59
R (Correlation coefficient)	F_1	0.79	-0.21	-0.20	0.78	-0.03	0.55
	F_2	0.99	0.44	0.04	0.97	0.05	0.77
*, ** Significant at 5% and 1%, respectively.							

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