



Short Communication

Inheritance of yield and its components in pumpkin (*Cucurbita moschata* Duch. ex Poir.)

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Ascorbic acid and β -carotene contents are major antioxidants trait found in pumpkin (*Cucurbita moschata* Duch. ex Poir.) [1]. Pumpkin had lot of variability for yield and its components. Many genetic models based on certain assumptions were proposed for the estimation of gene effects. Most of these were developed to estimate the relative importance of additive and dominance gene effects [2]. The present experiment was conducted to analyse the nature and magnitude of different types of gene effects and discuss the implications in the development of appropriate breeding methodology towards evolution of high yielding varieties.

The experimental material consisted of 4 crosses (BP-18 \times NDPK-130, IVPK-226-8 \times IVPK-227-7, Pumpkin-01 \times MKB/SP-01, MKB/SP-02 \times KPS-1), involving 8 parents of diverse pedigree origin. Six generation viz., P₁, P₂, F₁, F₂, BC₁ and BC₂ of four crosses were grown in randomized block design with three replication during summer and *kharif* 2003 (two season). Ten randomly selected plants from each of P₁, P₂, F₁s, 20 plants each of BC₁s, BC₂s and 30 plants from F₂s in each replication used for observation on fruits per plant, fruit weight (kg), polar circumference of fruit (cm), equatorial circumference of fruit (cm), number of ridges per fruit, hundred seed weight (g) and yield per plant (kg). The recorded data were subjected to scaling test for testing the adequacy of additive, dominance model [3]. In the event of inadequacy of additive-dominance model weighted analysis of [4] was used for estimating the various components of generation means.

The investigation has revealed that simple additive dominance model is inadequate in the inheritance of various yield components in most of the crosses. For certain traits in some crosses additive and dominant effects along with all the three types of non allelic interaction (additive \times additive; additive \times dominance, dominance \times dominance) were important while in other crosses one or two types of non allelic interactions were important. Simple additive dominance model was adequate in cross C₄ and C₁ with predominance of additive component in inheritance for number of fruits in crosses C₁, while in C₂ only additive \times dominance

interaction control the inheritance of fruits number. Analysis of cross C₃ indicated the presence of dominance, additive \times additive and dominance \times dominance type of interaction. Importance of dominance, dominance \times dominance type of gene action influencing the inheritance of fruit numbers [5].

Additive dominance model was adequate with predominance of additive component in inheritance of fruit weight in case of crosses, C₁ and C₂, whereas in cross C₃, in addition of additive and dominance gene effect, and additive \times additive and dominance \times dominance type of interaction was observed. Additive dominance model was also adequate with predominance of additive component in inheritance of polar circumference of fruits in cross C₁. So, improvement can be achieved through pedigree selection, while in cross C₂ the digenic model revealed the significance of dominance, additive \times additive and dominance \times dominance type of gene effect. Analysis of cross C₃ and C₄ indicated the presence of additive, additive \times additive and dominance \times dominance type of inheritance.

Simple additive dominance model was inadequate in all the four crosses for equatorial circumference of fruit. In cross C₁ additive and dominance \times dominance gene effects were important, while in cross C₂ additive, dominance and non-allelic interaction dominance \times dominance was significant. In cross C₃ additive, dominance, additive \times additive and dominance \times dominance gene effect, while in cross C₄ dominance, additive \times additive and dominance \times dominance gene effects were found significant.

In cross C₁ both additive and dominance gene effect were significant along with non-allelic interactions, additive \times additive and dominance \times dominance for number of ridges. In cross C₂ and C₄ dominance gene effects were significant along with non allelic interaction, Additive \times additive and dominance \times dominance, while in cross C₃ additive and additive \times dominance gene effect was significant. Additive, dominance, additive \times additive and dominance \times dominance gene effects was important for ridges toughness [6]. All the six parameters of diagenic model were found to be significant in C₁

Table 1. Estimation of different type of gene action in four crosses of pumpkin

Characters	Cross	m	d	h	i	j	l	Epistasis
Fruits per plant	C ₁	1.77**±0.40	0.21**±0.05	-0.41±0.94	-	-	-	
	C ₂	1.67**±.58	0.03±0.12	-0.5±1.58	-	-1.07*±.51	-	Duplicate
	C ₃	0.28±0.38	0.016±0.08	4.33**±1.12	1.03**±0.37	-	-3.15**±0.75	Duplicate
	C ₄	1.53**±0.093	-0.078±0.092	0.245±0.22	-	-	-	
Fruit weight (g)	C ₁	2.24**±0.083	-0.11**±0.083	-0.12±0.16	-	-	-	
	C ₂	2.33**±0.077	-0.52**±0.07	-0.72**±0.15	-	-	-	
	C ₃	6.05**±0.28	0.19**±0.05	-4.52**±0.71	-2.37**±0.28	-	2.04**±0.4	Duplicate
	C ₄	2.20**±0.45	0.40*±0.06	0.59±1.29	-	1.29**±0.42	-	Duplicate
Polar circumference of fruit (cm)	C ₁	53.5**±4.48	0.83**±0.02	-1.16±10.9	-	-	-	Duplicate
	C ₂	9.66**±4.35	1.0±0.55	45.33**±10.43	12**±4.35	-	-0.36**±6.31	Duplicate
	C ₃	42.5**±5.72	-2.16±0.84	23.83±13.73	27.99**±5.65	-	22.33**±8.36	
	C ₄	114.5**±8.01	14.5**±0.47	-135.83**±18.15	-51.33**±8	-28.33**±3.88	83**±10.45	Duplicate
Equatorial circumference of fruit (cm)	C ₁	51.99**±4.93	2**±0.57	18.99±10.61	-	-	-13.99**±5.88	Duplicate
	C ₂	56.0**±3.5	1.33**±0.55	0.19*±9.18	-	-	-22**±5.87	Duplicate
	C ₃	76.33**±4.62	-2.33**±0.72	-49.33**±11.45	-12.66**±4.57	-	54.66**±7.17	Duplicate
	C ₄	89.84**±16.57	0.16±1.05	-70.85**±34.04	-34.67**±16.54	-	49.99**±17.65	Duplicate
No. of ridges per fruits	C ₁	20.16**±1.64	0.05*±0.23	-24.83**±3.96	-7.33**±1.63	-	18.33**±0.98	Duplicate
	C ₂	27.16**±1.69	0.16±0.44	-36.83**±4.15	-11.99**±1.63	-	22.33**±2.80	Duplicate
	C ₃	15.66**±2.5	0.66**±0.23	-2.66±5.47	-	-3.33**±1.05	-	Duplicate
	C ₄	8.16**±1.92	0.5±0.37	17.83**±4.94	4.66**±1.88	-	-13.66**±3.14	Duplicate
100 Seed weight (g)	C ₁	3**±0.72	-2.03**±0.1	24.63**±1.66	8.87**±0.71	11.03**±0.41	-20.15**±0.98	
	C ₂	-16.41**±1.05	2.1**±0.04	71.48**±1.4	26.43**±0.64	-8.64**±0.25	-44.34**±0.77	Duplicate
	C ₃	11.84**±1.05	-1.56**±0.06	-4.12±2.23	-5.04*±1.05	-3.36**±0.3	-	
	C ₄	32.81**±0.36	2.93**±0.02	-33.53**±0.82	-	1.95**±1.11	-	Duplicate
Yield per plant (g)	C ₁	4.24**±0.18	0.27±0.18	-0.48±0.05	-	-	-	
	C ₂	4.84**±1.17	-0.5**±0.13	-4.36±2.56	-	-1.42**±0.49	-	Duplicate
	C ₃	4.95**±1.19	0.32±0.33	8.49*±3.56	-	-	8.2**±2.46	Duplicate
	C ₄	3.99±2.27	0.49*±0.25	0.06±5.09	-	-2.46**±1.1	-	Duplicate

*,**Significant at 0.05 and 0.01 level of probability, respectively; C₁ - BP 18 × NDPK-130, C₂ - IVPK 226-8 × IVPK-227-7, C₃-Pumpkin-01 × MKB/SP-01, C₄- MKB/SP-02 × KPS-1; m = Mean, d = Additive effect, h = Dominance effect, i = Additive × Additive gene effect, j = Additive × dominance gene effect, l = Additive × dominance gene effect

and C₂ suggesting the importance of additive, dominance as well as non-allelic interaction in the inheritance of 100 seed weight. For cross, C₃ additive, additive × additive and additive × dominance gene effects were found significantly, whereas in cross C₄ additive, dominance and additive × dominance gene effects play important role.

The simple additive model was adequate with predominance of dominant component in inheritance of yield in C₁. Therefore improvement in this cross can be achieved in through simple pedigree selection. An additive, dominance gene effect with non-allelic interaction such as additive × dominance in C₂ and dominance gene effect with non-allelic interaction, dominance × dominance in C₃ and additive × dominance in C₄ were influencing the inheritance of yield [7]. The present study suggests that the nature and magnitude of gene effect vary with different crosses for different characters. So, specific breeding strategy has to be adopted for a particular cross to get improvement. In some crosses, inbred can be developed through hybridization following the pedigree method of selection. In other crosses although high magnitude of dominance gene effects and dominance × dominance interactions were present, thus it is difficult to exploit them due to

presence of duplicate epistasis, in such cases some form of recurrent selection like diallel selective or bi-parental mating may be an effective approach.

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