Genetic studies of yield and its component traits using generation mean analysis in summer squash (*Cucurbita pepo* subsp. *pepo*)

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Abstract

The present investigation involved the generation mean analysis of six generations ($P_1, P_2, F_1, F_2, BC_1P_1(F_1 \times PCK-1)$) and BC_1P_2 (F1× Lady Godiva) derived from cross of PCK-1(hulled seed) × Lady Godiva (hull-less seed) in summer squash. The pooled analysis of variances revealed highly significant differences among the generation means of different populations for vine length (cm), leaf length (cm), days to 50% flowering, inter-nodal length (cm), peduncle length (cm), polar diameter (cm), equatorial diameter (cm), flesh thickness (cm), fruit yield per plant (kg), number of seeds per fruit and seed yield per fruit (g). The epistasis was absent for node number of 1st female flower, node number of 1st male flower, number of primary branches, leaf width (cm), days to 1st harvest, number of fruits per plant, average fruit weight (kg), fruit shape index and petiole length (cm), where leaf width, number of fruits per plant, and petiole length with highly significant additive genetic variances and partial dominance can be improved through inbreeding and selection. However, over-dominance in the inheritance of node number to first female flower, node number to first male flower, number of primary branches per vine, days to 1st harvest, average fruit weight and fruit shape index suggested use of heterosis breeding for improvement. Six parameter model unveiled the preponderance of dominance and dominant \times dominant [l] gene interactions for most of the other traits with the inheritance of many dominant genes carrying small and cumulative effects. However, the opposite effects of dominance [h] and the estimates of dominant \times dominant [1] interactions highlighted duplicate type of gene interactions. Therefore, summer squash cross involving PCK-1(hulled seed) × Lady Godiva (hull-less seed) can be used as a source of dominant genes and inter-allelic gene combinations for the expression of yield and related traits that can be exploited in the form of hybrid vigour through heterosis breeding.

Key words: Summer squash, gene action, six-generation mean, dominant gene effect, additive gene effect

Introduction

Pumpkins and squashes are member of *cucurbitaceous* family and cultivated during summer season in India. It has round fruits with more than 200 seeds interspersed in a net like mucilaginous fibres in the central inner cavity. Its seeds have a malleable, chewy texture and a subtly sweet, nutty flavour. When roasted, pumpkin seeds are delicious and nutritious that can be enjoyed throughout the year. The seeds contain 40 to 50% oil (Jacks et al. 1972) and also source of proteins, fatty acids, antioxidants, carotenoids, tocopherol, and minerals (Lazos 1986, Fu et al. 2006 and Stevenson et al. 2007). Its oil is used for cooking, roasting, preservation and natural therapies due to anti-diabetic, antihypertensive, antitumor, antibacterial, anti-hypercholesterolemia, strong hypo-triglyceridemic and anti-inflammatory properties (Abd EI-Aziz and EI-Kalek 2011, Dhiman et al. 2009, El-Adawy and Taha 2001, Makni et al. 2011, Rajakaruna et al. 2002, Tsaknis et al. 1997 and Wenzl et al. 2002). Hull-less Styrian (mutant) seed summer squash (Cucurbita pepo subsp. pepo var. styriaca), discovered in late 19th Century in South-East of the Astro-Hungarian Monarchy lacks complete lignifications of the testa (Zraidi et al. 2003, Latifi et al. 2012). The middle three layers of total five are collapsed into the hyaline without any trace of lignin in the testa (Stuart and Loy 1983). Although, the first reference on hull-less seeds of C. pepo was published in 1934 by an Austrian scientist Techermak-Seysenegg (1934), but breeding efforts were started in early 60's (Winkler 2000). Hull-less seed have evaded expensive decortication process and favored by the oil and nut industries for commercial production (Idouraine et al. 1996). 'Lady Godiva', a vine type selection from European land races was first time released in 1972 by the USDA. This variety was introduced from USA and crossed with bush type variety Punjab Chappan Kaddu-

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1 for studying genetics of economically importance traits in summer squash.

Materials and Methods

The present investigation was carried out during springsummer seasons using six generations $viz P_1, P_2, F_1$ F_{2} , $BC_{1}P_{1}(F_{1} \times PCK-1)$ and $BC_{1}P_{2}(F_{1} \times Lady Godiva)$ derived from cross of PCK-1 × Lady Godiva (hull-less) during spring-summer season of 2014 and 2015. The female parent was bush type and light green with globular-round, smooth skinned fruits having creamishwhite and hulled seeds. The male parent 'Lady Godiva' was characterized with long and dark green vines, ovalround, attractive fruits and yellowish-green, hull-less seeds. Nursery of all the generations was raised in protrays during February and transplanted in the field during first week of March during the spring-summer season of 2014 and 2015. Experiment was planned in randomized block design (RBD) with three replications, wherein, each replication was comprised of 10 plants for each P_1 , P_2 and F_1 ; 60 plants each of BC₁ P_1 ($F_1 \times$ PCK-1) and $BC_1P_2(F_1 \times Lady Godiva)$ and 120 plants of F₂ population. For hull-less seed trait, the plants were randomly selected from all replications in each generation at the end of the season and presence or absence of seed coat was noticed for each. A healthy crop was raised following recommended cultural practices. The data was recorded on various vegetative characters like vine length (cm), inter-nodal length (cm), number of primary branches, leaf length (cm), leaf width (cm), petiole length (cm), node number for 1st female flower, node number for 1st male flower and days to 50% flowering.

For statistical analysis, the presence or absence of seed coat was observed in each plant of each population and the observed frequencies of each were compared with expected frequencies through \div^2 test. For generation mean analysis, the replicated data from individual plants for different traits under investigation was recorded and generation means were worked out by taking the average of all plants in each replication. Pooled data of two years (2014 and 2015) was used for analysis of variances of all the generations. The deviations of means of all possible inbred lines from the cross of parents were estimated and the scaling test suggested by Mather (1949) was applied to test the adequacy of additivedominance model as well as for detecting the presence of non-allelic interactions. In additive dominance model, the generation means were analyzed to get the information about the additive or dominant genetic variances, which were estimated as m, [d] and [h]parameters. The observed generation means were compared with the expected values through genetic expectations. The genetic expectations of the different generations in the absence of epistasis (three parameter model) and presence of epistatic interactions (six parameter model) were defined as F- metric as given by Mather and Jinks (1982). Epistatic interactions included non-allelic interactions ([*i*], [*j*] and [*l*] parameters) as well as new estimates of *m*, [*d*] and [*h*]. The goodness of fit of additive-dominance model or six-parameter model was tested by \div^2 test as follows:

$$a^{2} = \sum (O_i - E_i)^2 \times W_i \text{ for n-p d.f.}$$

i=1

Where, O_i and E_i are observed and expected mean value of ith generation. Degree of freedom was calculated by subtracting the number of generations and number of parameters. Standard errors of the parameters m, [d], [h], ([i], [j] and [l] were computed from the diagonal elements of the inverted information matrix. The significance of individual parameters was tested by »t¹/₄ test.

The goodness of fit model was tested by chi-square test as described earlier, and the model that showed minimum value of chi-square with maximum number of significant parameters was considered the best fit model. The inferences for additive and dominance gene effects were drawn from the best-fit model, when the non-allelic interactions were significant, but from additive-dominance model, when the interactions were absent.

Results and Discussion

Inheritance of hull-less seed trait: The segregating generations derived from a cross of PCK-1 × Lady Godiva (hull-less) were screened for the presence of hull-less trait. The first generation hybrid of cross had hulled seeds that highlighted the monogenic recessive nature of the trait under investigation. Out of 146, 73 and 66 plants in F2, BC_1P_1 and BC_1P_2 for which the data of seed trait was recorded the seeds of 33, 0 and 27 plants were found hull-less, respectively (Table 1). The generations, F2 and BC₁P₂ followed the Mendelian ratio of 3(hulled):1(hull-less) and 1(hulled):1(hull-less) for the inheritance of hull-less seed trait. It suggested that hull-less seed trait in summer squash was controlled by a single recessive gene. For the improvement of this trait, homozygous recessive plants can be phenotypically identified in the segregating generations. The genetic behaviour of hull-less trait has also been reported by Winkler (2000). Gong et al (2008) also reported that four SSR markers closely linked to hull-less locus (h)at 1.5–3.6 cM on *LGp9h* that further be used for early screening of the seedlings for hull-less seed trait.

Domulation	Obser	Observed ratio		Expected ratio		
Population	Hulled	Hull-less Hulled		Hull-less	$\chi car(P=0.03)$	χtab
P ₁ (PCK-1)	10	-	-	-	-	-
P2(Lady Godiva)	-	10	-	-	-	-
F1(PCK-1×Lady Godiva)	10	-	-	-	-	-
F2 (PCK-1 × Lady Godiva)	113	33	109.5	36.5	0.446	3.84
$BC_1P_1(F_1 \times PCK-1)$	73	0	73	0	0	3.84
BC_1P_2 ($F_1 \times Lady Godiva$)	39	27	33	33	2.18	3.84

Table1: Goodness of fit test for hull-less seed trait in summer squash

Genetics of quantitative traits: The pooled analysis of variances for vine length (cm), inter-nodal length (cm), leaf length (cm), days to 50% flowering, peduncle length (cm), polar diameter (cm), equatorial diameter (cm), flesh thickness (cm), fruit yield per plant (kg), number of seeds per fruit, seed yield per fruit (g), and average seed weight revealed highly significant differences among the generation means of populations developed from a cross involving hull-less seeded summer squash (Table 2). However, the generation means of six-populations for all the other characters were non-significantly variable.

Occurrence of epistasis: The presence of epistasis for various quantitative traits was observed from the significance of A, B and C scaling test (Table 3). Significant value of B scale and highly significant value of A and C scales for leaf length (cm) and average seed weight (g) indicated the presence of all the three types of non-allelic interactions viz. additive x additive [i], additive x dominance [j] and dominance x dominance [1] for these characters. Also, significant values of A and B scales for vine length (cm), inter-nodal length (cm), days to 50% flowering, peduncle length (cm), polar diameter (cm), equatorial diameter (cm), flesh thickness (cm), fruit yield per plant (kg), number of seeds per fruit and seed yield per fruit (g) marked the presence of all type of epistasis. However, the insignificant A, B and C scales for node number of 1st female flower, node number of 1st male flower, number of primary branches, leaf width (cm), days to 1st harvest, number of fruits per plant, average fruit weight (kg), fruit shape index and petiole length (cm) was an indication for the absence of non-allelic interactions. The results of scaling tests were in accordance with findings of Mohan et al. (2012) in the ash gourd.

Additive dominance model: Additive dominance model given by Mather and Jinks (1952) explained the genetics of characters, where non-allelic interactions were absent. Therefore, three-parameter model elucidated the genetic behaviour of the traits mentioned in Table 4. Additive genetic variances for leaf width, petiole length and number of fruits per plant were high as compared with dominance genetic variances that expressed the presence of partial dominance for these traits. Therefore, further improvement of these traits should be made by accumulation of additive genetic variances through inbreeding and selection. However, other six characters, such as node number to first female flower, node number to first male flower, number of primary branches per vine, days to 1st harvest, average fruit weight, and fruit shape index, with the absence of non- allelic interactions, had significantly greater magnitude of dominant gene effects in the form of over-dominance. There was a substantial contribution of these effects in inheritance of above said characters. As the overdominance is predominates the expression of these traits,

Parameters	Source of variation					
	Years	Reps(year)	Generations	Gen×Year	Pooled error	-
Vine length (cm)	2	4	655	655	652	3547.81**
Inter-nodal length(cm)	2	4	655	655	652	13.25**
Days to 50% flowering	2	4	655	655	652	533.05**
Leaf length (cm)	2	4	655	655	652	49.67**
Equatorial diameter (cm)	2	4	655	655	652	95.15**
Polar diameter (cm)	2	4	655	655	652	53.50**
Flesh thickness (cm)	2	4	655	655	652	2.86*
Fruit yield per plant (kg)	2	4	655	655	652	205598.3**
Seed yield per fruit (g)	2	4	655	655	652	36.15*
Number of seeds per fruit	2	4	655	655	652	2095.75**
Average seed weight (g)	2	4	655	655	652	0.0043*

Table 2: Combined analysis for generation means showing source of variation and MS for different traits

*, ** Significant at 5% and 1% levels, respectively

Parameter	Scaling test					
	А	В	С			
Node number of 1 st female flower	-1.918±3.28	-2.3±1.91	4.5±7.45			
Node number of 1 st male flower	-0.95±3.21	-1.40 ± 1.86	6.20±6.65			
Days to 50% flowering	61.53±12.98**	46.40±7.54**	7.40±24.98			
Number of primary branches	-3.26±2.81	-3.30±1.74	1.90±5.37			
Leaf length (cm)	18.43±3.63**	9.30±2.31*	-1.30±7.92**			
Leaf width (cm)	-3.21±6.38	-2.40±3.93	-2.30±12.18			
Vine length (cm)	141.59±58.65*	122.0±40.19**	11.80±73.87			
Inter-nodal length(cm)	9.10±2.67**	4.60±1.66**	0.40±4.78			
Days to 1 st harvest	8.68±28.42	2.10±25.10	7.50±84.29			
Equatorial diameter (cm)	19.94±5.78**	24.70±3.43**	0.50±11.72			
Polar diameter (cm)	20.18±6.17**	10.80±4.10**	2.0±12.12			
Flesh thickness (cm)	4.04±1.87*	2.10±1.11	-0.90±2.65			
Fruit yield per plant (kg)	1156.61±609.14*	874.40±320.14**	165.8±1569.45			
Number of fruits per plant	0.21±2.63	0.20±1.56	1.0±5.45			
Average fruit weight (kg)	-89.94±188.05	-103.50±141.88	-134.30±323.47			
Seed yield per fruit (g)	45.28±14.14**	23.20±9.13*	8.00±14.77			
Number of seeds per fruit	168.27±65.22**	211.6±68.20**	61.4±188.54			
Average seed weight (g)	-0.24±0.07**	-0.1±0.05*	-0.5±0.16**			
Fruit shape index	-0.19±1.53	0.1±0.87	-0.2±2.89			
Petiole length (cm)	-1.47±12.48	2.60±8.94	-2.90±25.11			
Peduncle length (cm)	18.75±4.19**	20.9±2.71**	-2.90±7.23			

Table 3: Occurrence of epistasis for different quantitative traits in summer squash

*, ** Significant at 5% and 1% levels, respectively

the breeding objective should be set towards the development of hybrids for commercial purpose, because, the present cross cannot be exploited for simple selection in its advanced segregating generations with a selection pressure for more number of branches, earliness and bigger fruits. In contrast, Singh et al. (2002) in ash gourd, Ananthan (2002) in ridge gourd, Chandrakumar (2006) in pumpkin, Tewari et al. (1998)) in bitter gourd observed the additive gene effect in controlling the fruit weight and found predominantly dominant genes controlling the number of primary branches. The presence of significant additive genetic variances for fruit weight and fruit yield per plant and high dominant genetic variances for fruit traits has also been reported by Mohan et al (2012) in ash gourd.

Non-allelic interactions: The traits such as vine length (cm), leaf length (cm), inter-nodal length (cm), days to 50% flowering, peduncle length (cm), polar diameter (cm), equatorial diameter (cm), flesh thickness (cm), fruit yield per plant (kg), number of seeds per fruit, seed yield per fruit (g) and average seed weight (g) marked the presence of all type of epistasis (Table 4). Additive dominance model explained the variation among the generation means, but it was inadequate to explain the inter-allelic interactions for the expression of such traits. Therefore, six-parameter model was further used to elucidate the type of epistasis for each character. The estimation of genetic effects according to sixparameter model is given in Table 5. Dominant gene effects were higher as compared to the additive gene effects for all the characters having non-allelic

interactions. The pronounced epistasis and overdominance for all the traits, except number of branches per plant have also been reported by *Mohanty et al.* (1999). Epistasis with predominance of dominant gene effects was also reported by Sirohi and Ghoruri (1993) in pumpkin.

Although all the three type of genetic effects viz; dominance [h] effects, additive \times additive [i] and dominant \times dominant [l] were significant for days to 50% flowering, peduncle length (cm), and equatorial diameter (cm), but dominance and interactions of dominant genes had preponderance and additive ×additive [i] non-allelic interactions also play some role in the inheritance of these traits. The positive and negative estimates of dominance and dominant \times dominant [1] interactions clearly highlighted the presence of duplicate epistasis. On the other hand, the estimates of dominant [h] effects and dominant \times dominant [l]interactions were significant for vine length (cm), leaf length (cm), inter-nodal length(cm), polar diameter (cm), flesh thickness (cm) and average seed weight (g), which indicated that the small effects of many dominant genes with inter-allelic interactions were responsible for the inheritance of these traits. The presence of positive dominant gene effects [h] along with negative dominant \times dominant [*l*] interactions also indicated the involvement of duplicate type of epistasis in the inheritance of these characters. Significant variances for dominance [h] and additive x additive [i]inter-allelic interactions in fruit yield per plant (kg) and number of seeds per fruit explained highly significant

S. No.	Parameter	М	[d]	[h]	χ^2	Degree of dominance	Genetics effects
1.	Vine length (cm)	75.88±11.10*	3.24±12.18	11.56±19.24**	3.09	-	Epistasis
2.	Inter-nodal length(cm)	2.51±0.61*	0.49 ± 0.62	$0.01{\pm}1.01$	7.14	-	Epistasis
3.	Number of primary branches	1.96 ± 0.82	0.26 ± 0.82	3.16±1.42	1.07	3.49	Overdominance
4.	Leaf length (cm)	9.92±0.95*	$1.05 \pm 0.95*$	1.41±1.72*	11.79	-	Epistasis
5.	Leaf width (cm)	10.27±1.75	1.02 ± 1.75	-0.45 ± 3.24	0.13	0.66	Partial dominance
6.	Petiole length (cm)	15.62±2.67	4.29±2.69	1.22±4.71	0.11	0.53	Partial dominance
7.	Node number of 1 st female flower	2.56±0.94	0.22 ± 0.94	1.12±1.71	0.49	2.26	Overdominance
8.	Node number of 1 st male flower	2.04 ± 0.76	0.24 ± 0.76	1.00 ± 1.51	0.46	2.04	Overdominance
9.	Days to 50% flowering	22.82±2.10*	2.58 ± 2.10	12.35±5.97**	15.29	-	Epistasis
10.	Days to 1 st harvest	75.94±6.73	0.40 ± 6.74	7.39±14.46	0.05	4.30	Overdominance
11.	Peduncle length (cm)	9.96±1.22*	1.10±1.24*	$1.43 \pm 2.07*$	16.09	-	Epistasis
12.	Equatorial diameter (cm)	10.58±1.59**	0.53±1.60*	1.51±2.78*	11.10	-	Epistasis
13.	Polar diameter (cm)	9.33±1.65*	$1.06 \pm 1.66*$	1.70±3.01*	5.21	-	Epistasis
14.	Fruit shape index	1.03±0.36	0.08 ± 0.36	0.13±0.75	0.01	1.27	Overdominance
15.	Flesh thickness (cm)	2.07±0.45**	$0.20{\pm}0.45*$	0.19±0.83*	2.29	-	Epistasis
16.	Average fruit weight (kg)	179.22±81.54	-0.54 ± 83.10	-36.12±117.97	0.25	8.18	Overdominance
17.	Number of fruits per plant	1.80±0.57	0.07 ± 0.58	0.04±1.19	0.02	0.75	Partial dominance
18.	Fruit yield per plant (kg)	347.65±87.76**	15.07 ± 87.91	116.73±143.44*	2.04	-	Epistasis
19.	Number of seeds per fruit	119.32±5.49**	27.51±5.49	41.39±9.44*	3.59	-	Epistasis
20.	Average seed weight (g)	0.22±0.01*	$0.11 \pm 0.01*$	$-0.002 \pm 0.02*$	6.60	-	Epistasis
21.	Seed yield per fruit (g)	12.83±1.67*	2.45±1.68*	5.17±3.23*	4.34	-	Epistasis

Table 4: Estimation of genetic effects of quantitative traits using additive dominance model in summer squash

M= mean; d =additive variance; h=dominance variance. *, ** Significant at 5% and 1% levels, respectively

S. No.	Parameter	М	[d]	[h]	[i]	[j]	[1]	χ^2	Type of Epistasis
1.	Vine length (cm)	-179.0±191.91	3.8±12.39	777.1±512.13*	251.9±191.51	-	-515.5±326.42*	0.02	duplicate
2.	Inter-nodal length(cm)	-12.0±9.46	0.30±0.63	42.70±22.78*	14.10±9.44	-	-28.70±13.71*	0.93	duplicate
3.	Leaf length (cm)	-19.80±15.52	$0.70{\pm}0.98$	86.50±36.07*	29.01±15.48	-	-56.80±21.23**	1.25	duplicate
4.	Days to 50% flowering	-78.80±47.54	2.20±2.13	312.90±111.10**	100.50±47.50*	-	-208.40±66.12**	0.35	duplicate
5.	Peduncle length (cm)	-33.6±15.10	0.90±1.29	125.5±37.04**	42.50±15.04**	-	-82.20±22.66**	0.05	duplicate
6.	Equatorial diameter (cm)	-34.70±22.71	0.50±1.66	133.0±53.03*	44.1±22.65*	-	-88.6±31.34**	0.15	duplicate
7.	Polar diameter (cm)	-20.5±23.58	0.80 ± 1.71	89.8±55.59*	29.0±23.52	-	-60.0±33.14*	0.52	duplicate
8.	Flesh thickness (cm)	-5.10±5.96	$0.10{\pm}0.47$	20.20±15.22*	7.0±5.94	-	-13.10±9.54*	0.22	duplicate
9.	Fruit yield per plant (kg)	1533.60±3033.14	8.90±88.65	5869.0±6848.25*	1865.20±3031.84*	-	- 3896.20±3911.86	0.04	duplicate
10.	Number of seeds per fruit	-199.6±406.59	27.5±5.49	1057.4±982.42**	318.4±406.55*	-	-698.3±589.79	0.05	duplicate
11.	Average seed weight (g)	0.1±0.34	0.1±0.01	-0.2±0.82*	0.1±0.34		0.3±0.49*	0.44	duplicate
12.	Seed yield per fruit (g)	-48.0±45.58	2.1±1.70	194.0±125.61	60.4±45.55*	-	-128.9±81.14**	0.35	duplicate

Table 5: Estimates of non-allelic gene interactions for expression of quantitative traits in summer squash

M= mean; d =additive; h=dominance; i= additive ×additive; j= additive ×dominance; l= i= dominance×dominance. *, ** Significant at 5% and 1% level, respectively.

expression of dominant genes along with additive x additive [i] gene interactions for the inheritance of these traits. The opposite signs of dominance [h] and dominant \times dominant [l] interactions marked the presence of duplicate gene effects for these traits also. For seed

yield per fruit (g), additive x additive [i] as well as dominant × dominant [l] interactions were significant, but dominance and its interactions played major role in expression through duplicate gene interaction. The preponderance of dominant gene effects can be substantiated with findings of *Mohanty et al. (1999)*. The duplicate types of digenic non-allelic interactions were found by Mohan et al. (2012) in almost all the crosses for most of the traits except for vine length in ash gourd. The findings of equatorial diameter and polar diameter were in agreement with Bharathi et al. (2006) and Arvindkumar (2004) in muskmelon and Celine and Sirohi (1996) in bitter gourd, respectively. The earlier findings of Singh et al. (2000) in bottle gourd and Sharma and Bhutani (2001) in bitter gourd and Mohanty and Mishra (1999a and 1999b) and Chandrakumar (2006) in pumpkin are also in accord with the present investigation.

The genetic studies highlighted that hull-less seed trait is controlled by single recessive gene and can be identified in segregating generations. The preponderance of dominance and dominant \times dominant [l] gene interactions for most of the traits having epistasis in the present investigation revealed that the expression of these characters is controlled by many dominant genes with small and cumulative effects. The opposite effects of dominance [h] and the estimates of dominant \times dominant [1] interactions highlighted duplicate type of gene interactions. Due to dominance and epistatic interactions, the isolation of recombinant lines for these traits will not be possible. The results of present study explained that the parental cross involving bush type variety PCK-1 and vine type variety Lady Godiva (Hull-less) was useful source of favourable dominant genes and interallelic gene combinations for the expression of these traits in the form of hybrid vigour. Therefore, dominant variances and the epistasis with high magnitude of dominant interactions can only be exploited through heterosis breeding.

सारांश

छप्पन कद्दू में छः पीढ़ियाँ (पी., पी., एफ., एफ., बीसी, पी, (एफ, ग पी.सी.कं.–1) और प्रतीप संकरण पी. (एफ, ग लेडी गॉडिया) का विश्लेषण किया गया जिनमें पी.सी.के (छिलका युक्त बीज) ग लेडी गॉडिया (छिलका रहित बीज) के आपसी संकरण से प्राप्त हुआ विभिन्न संततियों का प्रयोग किया गया। विभिन्न संततियों की लता लम्बाई (मीटर), पत्ती की लम्बाई (सेन्टी मीटर), 50 प्रतिशत पुष्पन (दिनों में), अन्तर पार्श्व लम्बाई (सेन्टी मीटर), फल वष्त्त की लम्बाई (सेन्टी मीटर), व्यास (सेन्टी मीटर), फल वष्त्त की लम्बाई (सेन्टी मीटर), व्यास (सेन्टी मीटर), मध्य व्यास (सेन्टी मीटर), गूदा की मोटाई (सेन्टी मीटर), प्रति पौध फल उपज (किलोग्राम), प्रति फल बीजों की संख्या और बीज उपज प्रति फल (ग्राम) में सार्थक विविध् ता पाई गई। प्रथम मादा पुष्पन की पार्श्व गाँठ पर विकास, नर पुष्प की पार्श्व गाँठ संख्या, प्राथमिक शाखाओं की संख्या, पत्ती की चौड़ाई (सेन्टी मीटर), कटाई के दिन, प्रति पौध फलों की संख्या, फलों का औसत वजन (किलोग्राम), फल के आकार एवं पर्ण वष्ट्त की लम्बाई (सेन्टी मीटर) के लिए एपिस्टासिस सूचकांक अनुपस्थित पाया गया तथा पत्ती की चौडाई (सेन्टी मीटर), प्रति पौध फलों की संख्या और पर्ण वष्न्त की लम्बाई (सेन्टी मीटर) का अत्यधिक महत्वपूर्ण योगात्मक अनुवांशिक प्रसरण पाया गया और आंशिक प्रभाव के साथ अन्त प्रजनन अवनयन के लिए चयन प्रक्रिया के माध्यम से उन्नत किया जा सकता है। हालांकि प्रथम मादा पुष्प की पार्श्व गांठ संख्या, प्रथम नर पुष्प की पार्श्व गांठ संख्या, प्रति लता प्राथमिक शाखाओं की संख्या, प्रथम कटाई के दिन, फल का औसत वजन एवं फल के आकार पर प्रभाव के सूचकांक में उन्नयन के लिए प्रजनन ओज का उपयोग करने का सुझाव प्रस्तुत किया गया है। छः प्राचाल प्रतिमान ने अन्य लक्षणों के प्रभाव हेतू प्रभाविता और प्रभावी ग प्रभावी (एल) जीन के आपसी प्रक्रिया का अनावरण स्पष्ट होता है जिसमें छोटे और संचयी प्रभाव वाले कई प्रमुख वंशाणुओं की एकरूपता दिखती है। हालांकि प्रभाव के विपरीत प्रभाव (एच), प्रभावी ग प्रभावी (एल) क्रिया प्रभाव के अनुमानों में अनुलिपि प्रकार के वंशाणु का प्रभाव स्पष्ट होता है इसलिए पी.सी.के (छिलका युक्त बीज) x लेडी गॉडिया (छिलका रहित बीज) से युक्त छप्पत कद्दू के संकरण में उपज की अधिकता और सम्बन्धित लक्षणों के प्रमुख वंशाण् और वंशाण्ओं के आपसी प्रक्रिया संयोजन के स्रोत के रूप में उपयोग किया जा सकता है जिनमें ओज प्रजनन के माध्यम से संकर ओज की क्षमता प्राप्त की जा सकती है।

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