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Genetics of Inheritance of growth, yield and male sterility in *Capsicum annuum* L

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Abstract
Both Chilli and bell pepper comes under the species *Capsicum annuum* L. The present investigation entitled "Genetics of Inheritance of growth, yield and male sterility in Capsicum annuum L. were carried out at Research and Experimental Farm of Department of Vegetable Science, Dr. Y. S. Parmar University of Horticulture and Forestry, Nauni, Solan, H.P. The material included chilli genotypes DKC-12A and DKC-12ms which were male sterile and crossed with male fertile varieties of bell pepper i.e., California Wonder and HC-201. The characters studied were plant height, number of branches, leaf length (cm), leaf width (cm), days to 50% flowering, days to fruiting and fruit yield per plant (g). Analysis of variance showed significant variation among various crosses for leaf length, leaf width and yield/plant. F_1's performed in between the parental lines except for yield/plant. Generally F_2's showed inbreeding depression and B_1 and B_2 behaved as per expectations. Generation mean analysis revealed that selection will be effective in improvement of plant height, leaf length, leaf breadth, days to 50 per cent flowering and days to fruiting. Both selection and heterosis breeding will be effective in the improvement of number of branches at first node and yield per plant. There was dominance of male fertility over sterility and showed monogenic inheritance. On the basis of present findings, it appears that DKC-12A and DKC-12ms can be used to incorporate male sterility into bell pepper.

Keywords: Chilli, capsicum, genetics, yield, male sterility

Introduction
Bell pepper and chilli (*Capsicum annuum* L., 2n=2x=24) are important vegetable crops from several view points. Bell peppers are constituents of many foods, add flavour, colour, Vitamin C and pungency to world food industries. Pungent peppers also known as chillies are also widely cultivated species in the world where India is one of the leading countries in terms of area and production. Hybrids are gaining more popularity due to their productivity, improved quality, built in resistance, environment adaptation and earliness, which result into better monetary returns to the vegetable growers. Hybrids CH-1 (Hundal and Khurana, 1993) [5] and CH-3 (Hundal and Khurana, 2001) [6] released by the Punjab Agriculture University, Ludhiana have out yielded all the recommended chilli varieties by a margin of 80-100%. Both these hybrids used genetic male sterility (GMS) for hybrid seed production. In bell pepper, GMS lines are being used to a limited extent for hybrid seed production. Poulos (1994) [20] reported that genic male sterility was the first controlled pollination strategy adopted by the seed industry in the production of F_1 hybrid seeds after a long history of hand pollination and emasculation. Although, much hybrid seed is produced by hand emasculation and pollination, sterile lines are being used to reduce the labour cost and to improve hybrid purity. Therefore, use of male sterility for production of F_1 hybrids has been reported (Singh and Kaur, 1986) [28] as it facilitates natural pollination and cost involved in emasculation is lowered. Hence, the present investigation was undertaken to identify male sterility and its incorporation into the parental lines. The nature of the genetic variation of the economic characters is important in any crop improvement which greatly helps breeders in formulating efficient breeding programmes. So the nature of the genetics of inheritance / variation for growth and yield was also studied.

Material and methods
The present investigations were carried out at research and experimental farm of Department of Vegetable Science, Dr. Y. S. Parmar University of Horticulture and Forestry, Nauni, Solan, H.P. The material consists of four genotypes, consisting of two male sterile lines (DKC-12A and DKC-12ms) as identified from hot pepper and two male fertile lines (HC-201 and California Wonder) of bell pepper. These were crossed to generate four crosses namely DKC-12A x California Wonder (C1), DKC-12A x HC-201(C2), DKC-12ms x and California

Wonder (C3) and DKC-12ms x HC 201 (C4) during the Ist year of investigation. Each F_1 was raised and selfed to obtain F_2 generation as well as back crosses (B_1 and B_2) during the 2nd year. Thus, the experimental materials finally consisted of six generations *viz.,* P_1, P_2, F_1, F_2, B_1 and B_2 of all these crosses which were evaluated during the third year.The experimental material was planted in the compact family block design where all the generations of a cross were considered as a single family and generation within a cross as progenies. The whole material was replicated thrice with four blocks of four crosses in each replication. Each block consisted of 17 lines (10 plants per line), 2 lines each of parents and F1, 3 lines each of back crosses and 5 lines each of F2. Spacing was maintained at 60 x 45 cm. The data were recorded on 15 plants in the parents and F1's, 30 plants in backcrosses and 50 plants in F2's replication wise for the male sterility, plant height, number of branches at first node, leaf length, leaf breadth, days to 50% flowering, days to fruiting and yield/plant. Scaling tests were used for the detection of digenic interaction components. The detection of the digenic interaction were carried out using scaling tests given by Mather (1949) and Hayman and Mather (1955). The estimates of gene effects were derived from the generation mean analysis of joint scaling tests (Cavalli, 1952) and perfect fit solution of Hayman (1958).

Results and Discussion

The experimental results with respect to generation means, genetic parameters and gene action for the quantitative traits studied in four crosses of chilli and capsicum have been described below for Analysis of variance and Gene action

Analysis of variance

Analysis of variance for the experimental design (compact family block design) was carried out for all the traits studied. In this design various crosses as well as the generations within crosses were compared. The analysis of variance showed that there were significant differences among crosses for leaf length, leaf width and yield per plant,(Table 1), while non-significant differences for plant height, number of branches at primary node, days to 50% flowering and days to fruiting. DKC-12A x HC-201 gave comparatively higher mean values for yield/ plant where as leaf width were significantly higher for cross DKC-12ms x CW. The mean values of leaf length and leaf width were observed highest in cross DKC-12ms x HC-201. The analysis of variance among various generations within cross and the results of each character for different generations are presented cross wise.

Table 1: Estimates of mean values for various crosses with respect to traits studied

CROSSES	Plant Height (cm)	Number of branches at first node	Leaf Length (cm)	Leaf Width (cm)	Days to 50 flowering	Days to fruiting	Yield/ Plant (g)
DKC-12AxCW	73.64	1.46	9.86	4.82	54.88	61.88	884.79
DKC-12AxHC-201	74.36	1.31	10.43	4.93	53.66	60.55	973.81
DKC-12ms x CW	73.73	1.39	10.06	5.34	52.22	60.55	857.00
DKC-12ms x HC-201	70.90	1.18	10.76	5.28	54.55	61.50	887.17
CD (5%)	**NS**	**NS**	**0.30**	**0.24**	**NS**	**NS**	27.39

Table 2: Estimates of generation means in various crosses for the characters studied

	Plant height				**Number of branches at 1st node**			
Crosses/ generations	**DKC-12A x CW**	**DKC-12A x HC-201**	**DKC-12ms x CW**	**DKC-12ms x HC-201**	**DKC-12A x CW**	**DKC-12A x HC-201**	**DKC-12ms x CW**	**DKC-12ms x HC-201**
P1	86.53±1.45	86.83±1.45	84.83±310	84.83±3.10	2.03±0.05	2.03±0.05	1.98±0.07	1.98±0.07
P2	61.17±2.53	61.08±1.45	61.17±2.53	61.08±1.45	1.13±0.03	0.74±0.06	1.13±0.03	0.74±0.06
F1	79.80±4.28	75.53±1.41	70.17±2.53	70.78±1.05	1.09±0.02	1.59±0.39	1.33±0.29	1.35±0.18
F2	77.54±1.35	73.77±3.83	66.10±1.22	67.57±0.65	1.05±0.01	0.94±0.14	1.09±0.07	0.83±0.13
B1	72.28±1.71	80.50±1.09	80.63±3.66	80.02±4.15	1.98±0.08	1.88±0.16	1.83±0.05	1.85±0.24
B2	64.19±3.36	68.42±1.66	69.50±1.30	66.83±1.10	1.04±0.14	0.68±0.01	1.01±0.08	0.69±0.03
CD(5%)	8.83	5.85	6.67	7.49	0.21	0.46	0.33	0.41
	Leaf length				**Leaf width**			
P1	7.86±0.18	7.86±0.18	9.43±0.17	9.43±0.17	3.74±0.10	3.74±0.10	5.07±0.16	5.07±0.16
P2	11.51±0.24	13.19±0.28	11.51±0.24	13.19±0.28	6.07±0.15	5.98±0.10	6.07±0.15	5.98±0.10
F1	8.97±0.15	9.32±0.16	9.95±0.20	10.85±0.25	4.71±0.12	4.56±0.13	5.34±0.04	5.11±0.12
F2	10.97±0.34	11.35±0.41	9.78±0.06	10.28±0.15	4.81±0.24 5	17±0.03	4.79±0.11	5.08±0.03
B1	9.27±0.10	9.69±0.15	8.86±0.22	8.70±0.09	4.46±0.09	4.53±0.18	4.34±0.13	4.74±0.10
B2	10.61±0.29	11.17±0.09	10.83±0.07	11.04±0.23	5.18±0.13	5.38±0.06	6.04±0.08	5.66±0.15
CD(5%)	0.74	0.82	0.57	0.66	0.48	0.38	0.34	0.35
	Days to 50% flowering				**Days to fruiting**			
P1	54.67±1.20	54.67±1.20	56.00±1.00	56.00±1.00	63.00±0.58	63.00±0.58	64.33±1.45	64.33±1.45
P2	52.00±2.52	51.00±0.58	52.00±2.52	51.00±0.58	59.67±0.88	57.67±0.33	59.67±0.88	57.67±0.33
F1	54.00±3.79	53.00±0.58	55.00±1.15	54.33±0.67	60.00±0.58	57.83±0.44	62.00±2.52	61.33±0.88
F2	58.67±0.88	55.66±1.76	57.33±0.33	57.33±0.33	62.00±0.58	60.00±0.58	63.33±0.88	62.00±2.08
B1	56.67±1.67	55.00±0.58	56.33±1.20	57.00±0.58	65.00±0.58	64.33±0.33	65.33±0.88	65.00±1.15
B2	53.33±1.20	52.67±0.33	54.67±0.88	54.00±0.58	62.33±0.88	60.33±0.88	60.67±0.88	59.33±0.33
CD(5%)	NS	NS	NS	2.15	2.08	1.77	NS	3.54
	Yield/plant							
P1	631.51±8.69	630.51±8.69	706.59±3.67	706.59±3.67				
P2	1049.33±22.69	1057.11±14.76	1049.33±22.69	1057.11±14.76				

F1	1058.69±29.25	1569.99±11.10	891.80±6.67	1102.71±6.51				
F2	912.34±11.46	944.09±6.79	758.55±55.64	738.61±9.64				
B1	624.91±8.54	624.40±8.50	659.76±16.18	703.37±16.72				
B2	1032.97±11.55	1016.80±20.52	1040.02±22.63	1014.66±18.52				
CD (5%)	56.52	42.40	81.02	43.77				

Table 3: Estimates of scaling test and genetic parameters for the characters studied

	Plant height				Number of primary branches at first node			
Parameters	**DKC-12A x CW**	**DKC-12A x HC-201**	**DKC-12ms x CW**	**DKC-12ms x HC-201**	**DKC-12A x CW**	**DKC-12A x HC-201**	**DKC-12ms x CW**	**DKC-12ms x HC-201**
A	-22.08** ± 5.67	-1.36 ± 2.98	6.27 ± 8.40	4.42 ± 8.92	0.83*± 0.19	0.14± 0.51	0.34± 0.32	0.38± 0.53
B	-12.58 ± 8.36	0.22 ± 3.89	7.67 ± 4.61	1.80 ± 2.84	-0.14± 0.30	-0.97± 0.39	-0.44± 0.33	-0.71**± 0.20
C	2.54 ± 10.54	-3.91± 15.71	-21.93**± 8.29	-17.21**± 4.78	-0.36± 0.28	-2.19± 0.97	-1.40*± 0.66	-2.09**± 0.66
α^2_{3df}	31.89**	NS	35.59**	20.03**	178.69**	54.13**	259.06**	65.08**
M	77.54**±1.35	73.82**± 0.94	66.10**± 1.22	67.57**± 0.65	1.25**± 0.06	0.94**± 0.14	1.09*± 0.07	0.83**± 0.13
[d]	8.08** ± 3.77	-12.67**± 0.90	11.13**± 3.91	13.18**± 4.29	0.94**± 0.17	1.20**± 0.16	0.81**± 0.09	1.16**± 0.24
[h]	-31.40**±10.32	1.41±1.71	33.03**±9.81	21.26**±9.19	0.56± 0.44	1.56*± 0.76	1.07*±0.46	1.74* ± 0.76
[i]	-37.21**±9.27	_	35.87**±9.22	23.43**±8.97	1.05**± 0.44	1.36*± 0.65	1.3**± 0.36	1.76*± 0.74
[j]	-4.75±4.04	_	-0.70±4.40	1.31±4.62	0.48**±0.17	0.55**± 0.16	0.39**± 0.10	0.54* ± 0.25
[1]	71.87**±18.40	_	-49.80**±17.71	-29.66±17.83	-1.74± 0.75	-0.53± 1.16	-1.19± 0.77	-1.43± 1.19
Type of Epistasis	Duplicate	_	Duplicate		-	_	-	-
Parameters	Leaf length				Leaf width			
A	1.71**± 0.32	2.21**± 0.40	-1.66**± 0.51	-2.88**± 0.35	0.46*± 0.22	0.76± 0.39	-1.72**± 0.31	-0.68*± 0.27
B	0.73± 0.65	-0.17± 0.37	0.19± 0.35	-1.95**± 0.61	-0.41± 0.31	0.21± 0.20	0.66**± 0.21	0.24± 0.34
C	6.56**± 1.46	5.71**± 1.71	-1.72**± 0.57	-3.19**± 0.87	0.003± 1.00	1.84**± 0.32	-2.65**± 0.51	-0.94*± 0.31
α^2_{3df}	42.54**	18.40**	330.87**	433.98**	27.84**	159.11**	177.11**	913.48**
M	10.97**± 0.34	11.35**± 0.41	9.78**± 0.06	10.28**± 0.15	4.81**± 0.24	5.17**± 0.03	4.79**± 0.11	5.08*± 0.02
[d]	-1.33**± 0.30	-1.47**± 0.18	-1.97**± 0.23	-2.34**± 0.25	-0.72**± 0.15	-0.84**± 0.18	-1.69*± 0.15	-0.92*± 0.18
[h]	-4.82**± 1.54	-4.88**± 1.70	-0.26± 0.59	-2.10*± 0.86	-0.14± 1.02	-1.16**± 0.42	1.37*± 0.56	0.07± 0.40
[i]	-4.11*± 1.52	-3.68*± 1.68	0.24± 0.53	-1.65*± 0.80	0.04± 1.01	-0.86*± 0.39	1.59*± 0.55	0.49± 0.37
[j]	0.48± 0.34	1.19**± 0.25	-0.93**± 0.27	-0.46± 0.30	0.44*± 0.18	0.27± 0.20	-1.19**± 0.18	-0.46*± 0.20
[1]	1.66± 1.92	1.64± 1.86	1.22± 1.09	6.49*± 1.34	-0.09± 1.18	-0.12± 0.81	-0.53± 0.80	-0.04± 0.79
Type of Epistasis	_	_	_	Duplicate	Duplicate	_	Duplicate	_
	Days to 50% flowering	Days to fruiting			Yield/plant			
Parameters	DKC-12A x HC-201	DKC-12A x CW	DKC-12A x HC-201	DKC-12ms x HC-201	DKC-12A x CW	DKC-12A x HC-201	DKC-12ms x CW	DKC-12ms x HC-201
A	3.66**± 1.66	7.00**± 1.41	7.83**± 0.98	4.33± 2.86	-439.37**± 34.97	-951.69**± 22.07	-206.87**± 33.24	-402.56**± 39.98
B	-1.33± 1.45	5.66*± 2.86	5.16**± 1.84	-0.33± 1.15	-42.07± 43.63	-593.49**± 45.00	138.92± 57.06	-130.49**± 40.39
C	13.66**± 2.21	5.33± 2.78	3.66± 2.56	3.33± 8.64	-147.84± 78.19	-1051.24**± 39.04	-505.31*± 224.14	-1014.68**± 48.07
α^2_{3df}	51.87**	18.89**	51.95**	N.S	294.49**	2157.08**	36.89**	240.48**
M	57.33**± 0.33	62.00**± 0.57	60.00**± 0.57	61.60± 0.64	912.34**± 11.45	944.09**± 6.79	758.55**± 55.64	738.61**± 9.36
[d]	5.00**± 0.81	2.33± 1.45	4.00**± 0.94	-4.00**± 0.62	-408.06**± 14.36	-392.40**± 22.20	-344.26**± 27.81	-311.29**± 24.94
[h]	-10.5**± 2.28	6.00± 3.79	6.83**± 3.03	-0.26± 0.93	-114.83± 62.68	232.24**± 53.92	451.20*± 229.79	702.48**± 64.66
[i]	-11.33**± 2.10	7.33*± 3.71	9.33**± 2.98	-	-333.60**± 54.09	-493.94**± 52.06	437.36± 229.40	481.62**± 63.04
[j]	2.5*± 1.00	0.66± 1.54	1.33± 1.00	-	-198.65**± 18.81	-179.10**± 23.80	-172.82**± 30.09	-136.03**± 28.04
[1]	9.00*± 3.94	-20.00**± 6.44	-22.33**± 4.55	-	815.05**± 97.03	2039.13**± 97.03	-369.41± 250.24	51.42± 110.76
Type of Epistasis	D	_	D	-	-	Complimentary	-	-

Plant height (cm)

The perusal of data in Table 2 indicated significant difference among various generations of these crosses. The parental lines used in the studies showed significant differences for plant height

The mean values of F1 generation of all the crosses were significant over male parental lines and were in between the two parents. The mean values of F2 generation were statistically at par with F1. The mean values of backcross-1 generation in all crosses were lower than P1 whereas in backcross-2 the values were higher than P2 but both showed tendency towards respective parental values. The genotypes exhibited variation in the plant height wherein DKC-12A was the tallest and HC-201 the shortest among the parents. The F1's performances were in between the parental values indicating additive effects.The estimates of gene effects have shown that the additive gene effects made significant contribution in the inheritance of plant height (Table 3).

Moreover, additive x additive [i] components were also significant in all the crosses except for DKC-12A x HC-201. As dominance [h] and dominance x dominance [l] effects were having higher magnitude than additive [d] and additive x additive [i] gene effects but being of opposite signs resulted in duplicate epistasis. This suggests preponderance of additive gene action in the inheritance of plant height. Earlier workers like Sharma and Saini (1972), Singh and Singh (1976) [27], Ahmed *et al.* (1982) [1], Milkova (1984) [16], Khadi (1986) [10]

and Saritha *et al.* (2005) [23] have reported the importance of both additive and non additive gene effects for this character.

2) Number of branches at 1st node

The analysis of data in Table 2 regarding the number of branches at 1stnode revealed significant differences among various generations.The parents showed significant differences for number of branches at 1st node (Table-2). The mean values of F1 generation in all the four crosses were significantly less than P1 while in two crosses (DKC-12A x HC-201 and DKC-12ms x HC-201) significantly higher than P2. In all the crosses, except DKC-12ms x HC-201 it deviated from mid parental mean values. The mean values of F2 were significantly less than their corresponding F1 values in DKC-12A x HC-201and DKC-12ms x HC-201 whereas at par in DKC-12A x CW and DKC-12ms x CW. However, the mean performance of backcrosses was statistically at par with their parental means with tendency towards corresponding parental means. In general, the chilli genotypes had more number of primary branches at first node than the bell pepper genotypes. The F1's, in general showed tendency towards more branches whereas F2's showed inbreeding depression for the trait. The estimates of the six parameters from generation means showed that both additive and dominance gene effects were significant in all the crosses (Table-3). However, the magnitude of dominance gene effects was higher than additive. Except one cross (DKC-12A x CW), where dominance [h] and dominance x dominance [I] effects showed opposite signs, the other crosses showed the possibility of heterosis breeding. Epistatic effects were also significant in most cases. The results revealed that additive and non-additive gene effects with preponderance of non-additive gene action controls this trait as earlier reported by Sahoo *et al.* (1989) [22] and Pandian and Shanmugavelu (1992) [18].

3) Leaf length (cm)

The analysis of variance in Table 2 for the character leaf length revealed significant differences among various generations in all the crosses. The parental lines used in the studies showed significant difference for leaf length (Table 2). The mean values of F1 were significant over both the parents except for DKC-12ms x CW and showed tendency towards lower parental means. F2 's gave leaf length significantly higher than their corresponding F1 's in two crosses where DKC-12A was used as female parents where as at par in other two crosses where DKC-12ms was used as female parent. Backcross generations gave mean values towards their corresponding parents. In general, the pungent peppers had narrow, small leaves while sweet peppers had broad and large leaves. The F1's showed additive effect as their mean values were quite near to mid parental values. As such F2's also didn't show inbreeding depression. The estimates of the six parameters from generation means showed the importance of additive and dominance gene affects both being significant in majority of the crosses. Further, the additive x additive gene effects were also significant in all the crosses except for DKC-12ms x CW, suggesting that additive variance played a major role in the inheritance of this trait. The dominance x dominance gene effects was also quite high and significant in DKC-12A x HC-201, but gave duplicate type of epistasis and could not result in heterotic effects. Prasath and Ponnuswami (2008) [21] had also reported predominance of additive gene action than non-additive for this trait while evaluating hybrids utilizing six diverse genotypes.

4) Leaf width (cm)

The data regarding the generation mean values of different crosses for leaf width is presented in Table 2. The data revealed that P2 has significantly larger leaf width than P1. F1 values lied within the range of parental means and was significant over both the parents in two crosses i.e. DKC-12A x CW and DKC-12A x HC-201while over one parent in the remaining two crosses i.e. DKC-12ms x CW and DKC-12ms x HC-201. The mean values of F2 were significantly higher than F1 in DKC-12A x HC-201 while lower in DKC-12ms x CW. It was at par with DKC-12A x CW and DKC-12 ms x HC-201. Mean values of B1 and B2 tended towards their corresponding recurrent parent. Parental genotypes used in the study showed significant diversity for leaf breadth. The F1's performed around mid parental values indicating the absence of dominance. The F2's mean values were statistically similar to the F1's except in DKC-12A x HC-201 and DKC-12ms x CW whereas there was no inbreeding depression in DKC-12A x CW and DKC-12A x HC-201. The results of gene effects also suggest additive effects being significant in all the crosses (Table 3). The dominance gene effects were found significant in DKC-12A x HC-201 and DKC-12ms x CW. The epistatic (additive x additive) gene effects also showed significant contribution in two of the crosses but none of the crosses showed dominance x dominance gene effects supporting the absence of dominance. Since, additive gene effects are predominant for the leaf breadth, the selection will be effective in the improvement of this character. Prasath and Ponnuswami (2008) [21] had also reported predominance of additive gene action than non- additive for this trait.

5) Days to 50% flowering

Early flowering is the desirable trait as it results in early fruit formation and consequently fetching lucrative returns from the crop. In the present studies, the parental lines did not differ significantly. Consequently, there were non-significant differences among various crosses and three out of four crosses showed non-significant differences among various generations. One cross DKC-12ms x HC-201 was found significant for various generations (Table 2). The F1's of this cross showed performance around mid parental mean indicating the absence of dominance. The segregating generations also performed as per expected values, revealing no dominance. Gene effect studies showed that additive as well as dominance gene effects were significant, however, significance of additive x additive [i] gene effects showed the preponderance of additive gene action thus suggesting that selection will be effective in the improvement of this character (Table-3). Singh and Singh (1976) [27] produced F1, F2, B1 and B2 generations using eight parents of chilli to study genetic variances and degree of dominance for eight quantitative characters. They reported the importance of both additive and non additive gene affects for this trait. Joshi and Singh (1987) [7] also got the similar results. Kamble *et al.,* (2009) [9] however reported the predominance of non-additive gene action for the inheritance of this character.

6) Days to fruiting

The analysis of variance showed non-significant differences among various crosses for this trait whereas generations within cross were significant in all the crosses except for DKC-12ms x HC-201. The data is presented in Table 2.The parental mean values were significantly different from each other. The mean values of F1 were in between the parents but at par with P2. The F2 's were higher than F1 's but at par

with them except for the cross DKC-12A x HC-201. Likewise, B1 was at par with P1 but B2 was significantly different from P2 except for DKC-12ms x HC-201. Early flowering is the desirable trait as it results in early fruit formation and consequently fetching lucrative returns from the crop. In the present studies, the parental lines did not differ significantly. Consequently, there were non-significant differences among various crosses and three out of four crosses showed non-significant differences among various generations. One cross DKC-12ms x HC-201 was found significant for various generations. The F1's of this cross showed performance around mid parental mean indicating the absence of dominance. The segregating generations also performed as per expected values, revealing no dominance. Gene effect studies showed that additive as well as dominance gene effects were significant, however, significance of additive x additive [i] gene effects showed the preponderance of additive gene action thus suggesting that selection will be effective in the improvement of this character (Table-3). Singh and Singh (1976) [27] produced F1,F2, B1 and B2 generations using eight parents of chilli to study genetic variances and degree of dominance for eight quantitative characters. They reported the importance of both additive and non additive gene affects for this trait. Joshi and Singh (1987) [7] also got the similar results. Kamble *et al.,* (2009) [9] however reported the predominance of non-additive gene action for the inheritance of this character.

12) Yield per plant (g)

The analysis of variance showed significant differences among crosses for yield/plant. Likewise generations also showed significant differences within crosses. The results obtained are shown in Table 2.In perusal of the given data, it was indicated that mean fruit yield in P2 (bell type) were significantly higher than P1 (chilli type).In F1 generation mean values were significantly higher than the better parent in crosses involving HC-201 as male parent whereas it was at par in DKC-12A x CW and significantly less in DKC-12ms x CW. In all the crosses, the mean yield of F2 's were significantly lower than their corresponding F1 's. In backcross generations, mean value of B1 and B2 tends towards their recurrent parent with non-significant differences. Significant differences among genotypes for yield per plant suggest genetic diversity in the material. Yield per plant among parents varied from 630.50g (DKC-12A) to 1057.10g (HC-201). The F_1's performance showed overdominance over better parent in three crosses (DKC-12A x CW, DKC-12A x HC-201 and DKC-12ms x HC-201) while no dominance in DKC-12ms x CW. The positive increase in yield in pepper has also been reported by Angeli (1957, 1967) [2, 3], Scossiroli *et al.* (1972) [24], Pandey *et al.* (1981) [17], Balakrishnan *et al.* (1983) [4] and Uzo (1984) [32]. Both the additive and dominance gene effects were found to contribute in the inheritance of yield per plant in all the crosses. The magnitude of additive gene effects were more where DKC-12A was used as female parent where as dominance gene effects were more in those crosses where DKC-12ms was used as a female parent (Table 3). Dominance x dominance gene effects were found significant in both these crosses viz., DKC-12A x CW and DKC-12A x HC-201.All the crosses except DKC-12ms x CW showed significant additive x additive gene effects. Highly heterotic cross DKC-12A x HC-201 also gave complementary type of epistasis thus suggested its exploitation as F1 hybrid. In the other crosses especially DKC-12A x CW hybridization followed by selection in later generations will be advantageous. The additive and non-additive gene effects controlling fruit yield with predominance of non-additive gene effects have been reported by Khalf-Allah *et al.* (1975a) [11] while studying inheritance and gene action for yield in peppers. Later Sharma and Saini (1977) [25] carried a diallel analysis using ten parental lines and revealed that sca variances were high for fruit yield thereby signifying the importance of non additive gene effects for this character. Milkova (1977) [15], Thakur (1987) [30], Joshi (1990) [8], Szwadrak and Kardus (1991) [29], Pandian and Shanmugavelu (1992) [18] and Khereba *et al.* (2008) [12] also obtained the similar results.

4.2.1. Male sterility

The descriptive characters of the genotypes involved in the crosses for the present study and their behaviour are given in Table 32. Forty five F1 plants in each cross viz., DKC-12A x CW, DKC-12A x HC-201, DKC-12ms x CW and DKC-12ms x HC-201 were studied. All the F1's exhibited only fertile plants thereby showing the complete dominance of male fertility over male sterility.

Table 4: Behaviour of parents and F1's for male sterility.

S. No.	Parents and crosses	Phenotype
1	DKC-12A	male sterile
2	DKC-12ms	male sterile
3	CW	male fertile
4	HC-201	male fertile
5	DKC-12A x CW	male fertile
6	DKC-12A x HC-201	male fertile
7	DKC-12ms x CW	male fertile
8	DKC-12ms x HC-201	male fertile

All the F1's were selfed and backcrossed to raise the F2, B1 and B2 generations in which the number of male fertile and male sterile plants were identified. The results obtained in F1, F2, B1 and B2 indicated that male fertility is controlled by single dominant gene. The designation of gene for the same is given as

MsMs- male fertile

msms- male sterile

Table 5: Segregation of plants for male sterility in F2

S.No.	Cross	Number of		Expected ratio	χ 2calculated	Probability
		Male fertile plants	Male sterile plants			
1	DKC-12A x CW	116	34	3:1	0.42	0.75-0.50
2	DKC-12A x HC-201	113	37	3:1	0.008	0.90-0.75
3	DKC-12ms x CW	109	41	3:1	0.42	0.75-0.50
4	DKC-12ms x HC-201	115	35	3:1	0.21	0.90
	Summed	453	147	3:1	0.08	0.90-0.75

Keeping in view, the phenotypic classes and their frequencies in F2, male fertile and male sterile plants segregated in 3:1 ratio in all the crosses. Considering the total population, there were 453 fertile and 147 sterile plants, indicating a good fit on

expected 3:1 ratio which indicated that single dominant gene is responsible for male sterility. In order to confirm the active results, back crosses to both the parents were attempted. Segregation of plants in back crosses are presented in Table 6.

Table 6: Segregation of plants for male sterility in backcrosses

S. No.	Cross	Number of		Expected ratio	χ 2 calculated	Probability
		Male Fertile plants	Male Sterile plants			
1	DKC-12A x (DKC-12A x CW)	52	38	1:1	2.16	0.25-0.10
2	CW x (DKC-12A x CW)	90	0	1:0		
3	DKC-12A x (DKC-12Ax HC-201)	50	49	1:1	1.10	0.50-0.25
4	HC-201 x (DKC-12Ax HC-201)	90	0	1:0		
5	DKC-12msx(DKC-12ms x CW)	53	37	1:1	2.84	0.1-0.05
6	CW x (DKC-12ms x CW)	90	0	1:0		
7	DKC-12msx (DKC-12ms x HC-201)	49	41	1:1	0.70	0.50-0.25
8	HC-201 x (DKC-12ms x HC-201)	90	0	1:0		
	Summed	204	156	1:1	6.4	0.02-0.01

The results showed that the segregation of plants in back crosses with male sterile recurrent parent were in 1:1 ratio (male fertile: male sterile) and in the back crosses with fertile recurrent parent were in 1:0 ratio (all male fertile). The homogeneity test of F2 and back crosses also indicated that the crosses individually and collectively behaved as per expectation and as reported. In F1, male fertility was observed to be dominant over male sterility and further studies in F2 and backcrosses suggested that this trait is under one gene control, male fertility beingdominant over male sterility. The male sterility is governed by single recessive gene 'ms'. The results are in accordance with earlier findings of Shifriss (1973) [26], Meshram *et al.* (1982) [13, 14], Meshram and Narkhede (1982) [13, 14], Patel *et al.* (1998) [19] and Thiruvelavan *et al.* (2002) [31]. The designation of the gene for the same is given as:

MsMs: male fertile
msms: male sterile

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