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Short Communication

Genetical analysis and heterosis for green pod yield and its components in pea

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Information on gene action for yield and its components is pre-requisite for planning of an effective breeding strategy. Yield is the end product of the action and interaction of a number of quantitative components. Such characters are often controlled by large number of genes which individually have small effects. The environmental contribution to the variation of these characters is also appreciable. The study of the gene action of quantitative characters of economic value is essential to improve the yield potential. The heterosis on the other hand plays a significant role in improving any character of economic value. In self-pollinated crops like peas, its exploitation is most important as the crop is significant both as grain and vegetables for the country like India. Thus in the present investigation, an attempt has been made to study the genetics and extent of heterosis of green pod yield and yield traits to isolate desirable recombinants involving field and table pea genotypes.

The material comprising four field pea varieties/strains i.e. 'Rachna', 'KPMR-65', 'KPMR-184', mutant of 'P-43' and six table pea varieties/strains i.e. 'KS-136', 'KS-195', 'KS-225', 'KS-226', 'Azad P-1' and 'Azad P-3', was raised in crossing block and all possible combinations were made to obtain 45 crosses. The final experiment comprising of 45 genotypes, F_1s and F_2s alongwith their parents were sown in a Randomized Block Design in three replications at Vegetable Research Farm of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur during *rabi* 2003-04.Each plot consisted of five meter row length with spacing of 45 x 15 cm between rows and plants. All recommended practices were followed to raise a good crop. Ten random plants in each of parents and F_1s and 20 plants from each F_2 per replications were scored for nine characters. The components analysis of diallel cross were carried out following Hayman (1954).

The analysis of variance indicated appreciable genetic variability among the parents and hybrids for almost all the traits under study. Over dominance of consistent nature was observed by component analysis $(H_1/D)^{1/2}$ for all the characters in both the generations except for days to flowering in F_1 and F_2 and days to maturity and pod length in F_1 only (Table 1). The presence of over dominance might be due to linkage in F_2 which caused an upward estimation of dominance from F_2 population (Moll *et al.* 1964), while (Mather 1955) pointed out that over dominance might be attributed due to epistatic interaction. Complete to over dominance was also reported for grain yield and its components by (Kumar *et al.* 2006, Singh *et al.* 2006).

Conversion of partial dominance into over dominance might be attributed to gene combination, like positive allele, negative allele complementary gene action or simply correlated gene distribution (Hayman 1954). Partial dominance was also reported by Srivastava *et al.* (1986) for days to flowering, node number up to the first pod and seed yield, (Singh *et al.* 1986) for pods per plant, seeds per pod in F_2 and for pod number, seed number per plant, 100-seed weight and seed yield per plant (Singh *et al.* 2006).

The estimates of F were positive and significant based on both the generations for days to flowering and days to maturity and for pod length in F_2. The estimate of h^2 was positive for all the traits except days to flowering in F_1 and green pod yield in F_2 generation. The significant and positive values of F and h^2 indicated that dominant genes exhibited significant role in the control of these characters *viz.*, days to flowering and maturity in F_2, plant height, number of pods per plant, pod length and harvest index in both F_1 and F_2 and node number of first pod formed, number of productive branches and green pod yield in F_1 and days to flowering and maturity in F_2 only (for h^2). The above findings for these traits are in accordance with earlier reports of Koranne and Singh (1974), Sharma *et al.* (1977) and Verma (1978).

The proportion of positive and negative alleles in the parents $(H_2/4H_1)$ was not equal to the theoretical values of 0.25 in all the characters in both F_1 and F_2 generations which indicated that positive and negative genes were distributed asymmetrically as also reported by Srivastava (1982).

In the present study, the ratio of $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$ indicated that the dominant alleles were more frequent than recessive ones for all the characters except for plant height, number of pods per plant and harvest index in both F_1 and F_2 generations. Similar findings were also recorded for most of the characters studied in pea (Koranne and Singh 1974, Srivastava *et al.* 1986)

The ratio of (h^2/H_2) was less than unity for all the

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Table 1. Estimates of genetic components of variation in F_1 and F_2 progenies for nine characters in pea

Genetic parameters	Days to flowering		Days to maturity (edible pods)		Plant height (cm)		Productive branches/plant (no)	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
D	147.07**	147.22**	172.95**	172.78**	3167.50**	3165.93**	0.19**	0.19**
	±2.25	± 2.34	± 4.11	± 3.34	± 304.18	± 142.30	±0.06	± 0.04
H_1	26.90**	130.14**	46.74**	201.62**	5133.79**	8775.41**	0.82**	1.12**
	± 4.78	± 19.88	± 8.75	± 28.47	647.48±	± 1211.56	± 0.13	± 0.31
H_2	19.86**	107.66**	31.71**	152.79**	4179.37**	6582.54**	0.58**	0.86**
	± 4.06	± 16.90	± 7.44	± 24.20	± 550.29	± 1029.69	± 0.11	± 0.26
h^2	-0.07	27.52**	0.00	52.53 **	5021.65**	2108.28**	1.00**	0.00
	± 2.72	± 2.83	± 4.98	± 4.05	± 368.34	± 172.31	± 0.07	± 0.04
F	52.32**	96.97**	70.22**	156.36**	-1962.85**	-1591.27*	0.24	0.19
	± 5.18	± 10.78	± 9.48	± 15.43	± 701.84	± 656.64	± 0.14	± 0.17
E	0.55	0.41	0.36	0.52	8.80	10.37	0.0.1	0.00
	± 0.68	± 0.70	± 1.24	± 1.01	± 91.71	± 42.90	± 0.02	± 0.01
$(H_1/D)^{1/2}$	0.43	0.94	0.52	1.08	1.27	1.66	2.11	2.40
$H_2/4H_1$	0.18	0.21	0.17	0.19	0.20	0.19	0.18	0.19
$(4DH_1)^{1/2}+F$ $/(4DH_1)^{1/2}-F$	2.42	2.08	2.28	2.44	0.61	0.74	1.87	1.53
h^2/H_2	0.00	0.26	0.00	0.34	1.20	0.32	1.73	0.00
‘r’	-0.45	0.33	-0.22	0.22	-0.91	-0.89	-0.63	-0.36
t^2 value	0.72	0.06	1.34	0.06	3.81	2.20	3.58	1.19

Table1. Contd…..

Genetic parameters	Pods/plant (no)		Pod length (cm)		Developed ovules/pod (no)		Harvest index (%)		Green pod yield/plant (no)	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
D	11.79	13.35**	1.79**	1.79**	0.80**	0.80**	26.82**	26.80**	1002.60**	1008.63**
	± 23.25	± 4.19	± 0.04	± 0.03	± 0.24	± 0.13	± 2.88	± 2.37	± 92.89	± 55.03
H_1	245.66**	120.23**	0.33**	1.47**	2.21**	5.63**	34.12**	146.52**	2376.43**	2185.69**
	± 49.49	± 35.71	± 0.08	± 0.29	± 0.52	± 1.14	± 6.14	± 20.20	± 197.73	± 468.54
H_2	200.94**	102.37**	0.29**	2.24**	1.65**	4.35**	30.86**	102.22**	2281.17**	2030.71**
	± 42.06	± 30.35	± 0.06	± 0.25	± 0.44	± 0.97	± 5.22	± 17.16	± 168.05	± 398.20
h^2	745.50**	29.80**	0.18**	0.38**	0.15	0.05	16.28**	11.63**	6919.85**	-2.68
	± 28.15	± 5.08	± 0.04	± 0.04	± 0.29	± 0.16	± 3.49	± 2.87	± 112.49	± 66.64
F	-5.25	-11.46	0.00	0.35*	0.23	0.43	-5.65	-2.83	189.78	184.81
	± 53.64	± 19.35	± 0.08	± 0.16	± 0.56	± 0.62	± 6.66	± 10.95	± 214.33	± 253.94
E	2.14	0.58	0.00	0.00	0.01	0.01	0.16	0.18	14.33	8.30
	± 7.01	± 1.26	± 0.01	± 0.01	± 0.07	± 0.04	± 0.87	± 0.72	± 28.01	±16.59
$(H_1/D)^{1/2}$	4.56	3.00	0.43	1.17	1.66	2.65	1.13	2.34	1.54	1.47
$H_2/4H_1$	0.20	0.21	0.22	0.23	0.19	0.19	0.23	0.17	0.24	0.23
$(4DH_1)^{1/2}+F$ $/(4DH_1)^{1/2}-F$	0.91	0.75	1.00	1.18	1.19	1.23	0.83	0.96	1.13	1.13
h^2/H_2	3.71	0.29	0.60	0.17	0.09	0.01	0.53	0.11	3.03	0.00
‘r’	-0.70	-0.84	-0.67	0.66	-0.13	-0.07	0.62	0.54	-0.80	0.32
t^2 value	6.56*	4.83*	0.72	1.19	2.79	6.19*	1.69	2.34	0.03	0.24

*, ** Significant at P = 0.05 and 0.01, respectively

character in both the generations except for plant height, number of productive branches, number of pods per plant and green pod yield per plant in F_1 generation only, which indicated that the inheritance of the characters was governed by one major gene group. The remaining characters in their respective generations having higher value than unity indicated that more than one gene group was involved in the inheritance of these characters. Complementary gene interaction also seems to depress the ratio (Liang and Walter 1968).

The genetic system controlling these important quantitative traits showed a role of dominance as well as additive gene action (Kumar *et al.* 2006, Singh *et al.* 1988).

Cross combinations ‘KS 226/Azad P-1’, ‘KPMR-184/KS-136’, ‘KS-225/Azad P-3’, ‘KS-195/KS-226’, ‘KS-195/Azad P-3’ and ‘KS-136/KS-225’ showed more than 50% (50.48 – 69.82%) economic heterosis over ‘Azad P-1’ for green pod yield (Table 2). The crosses showing high heterosis also showed high inbreeding depression in F_2 generations (25.78 to 48.39%. Gupta *et al.* (2003) and Singh *et al.* (2005) also reported similar results.

However, few cross combinations namely, ‘KS-226/Azad P-1’, ‘KS-195/KS-225’ and ‘KS-195/KS-226’ showed high economic heterosis for pod yield per plant with comparatively

Table 2. Top ten crosses for economic heterosis in pea

Name of the cross	Economic heterosis (%)	Inbreeding depression (%)	Characters exhibiting desirable significant economic heterosis
KS-226 × Azad P-1	69.82**	25.78**	IV, V, VI, VII
KPMR-184 × KS-136	66.90**	48.39**	IV, V, VII
KS-225 × Azad P-3	64.52**	38.11**	I, IV, V
KS-195 × KS-226	64.21**	29.96**	IV, V
KS-195 × Azad P-3	55.40**	34.71**	IV, V, VII
KS-136 × KS-225	50.48**	27.49**	IV, V, VI, VII
KPMR-65 × KS-225	49.31**	30.77**	IV, V
KS-225 × Azad P-1	42.12**	20.54**	IV, V, VI, VII,
Rachna × Azad P-3	39.93**	37.00**	IV, V
KS-195 × KS-225	39.07**	12.33**	IV, V

I: Days to flowering, II: Days to maturity, III: Plant height, IV: Number of productive branches/plant, V: Number of pods/plant, VI: Pod length, VII: Number of developed ovules/pod, VIII: Harvest index
**Significant at P = 0.01

low inbreeding depression. The increase in pod yield in these crosses might be due to gene interaction of which substantial part could be due to fixable gene effect i.e. additive type. Thus, these crosses may likely produce some desirable transgressive segregants in advance generations as was also suggested by Brim and Cockerham (1961) and Singh *et al.* (1993). Further, these crosses also showed significant heterosis for other attributes with low inbreeding depression reflecting that more emphasis could be placed on these attributes during selection (Kumar and Tewatia 2005) were in view of above results.

Cross combinations namely, 'KPMR-184/KS-136', 'KS-225/Azad P-3', 'KS-195/KS-226' and 'KS-195/Azad P-3' showed high economic heterosis and comparatively high inbreeding depression which might be due to non-allelic gene interactions as also reported by Jatasra and Paroda (1979) in wheat crop.

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