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Combining Ability and Heterosis for Grain Yield and Some Yield Components in Pea (*Pisum sativum* L.)

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Abstract: This study was conducted to determine the general and specific ability, the heterosis, heterobeltiosis for grain yield and some yield components in pea as a good source of plant protein. Grain yield and its inheritance were studied in four pea cultivar and three winter pea genotypes by crossing them in line x tester fashion. The General Combining Ability (GCA) and Specific Combining Ability (SCA) effects were highly significant, indicating the presence of both additive and non-additive type of gene action. The ratio of additive variance to dominance variance indicated the predominant role of non-additive gene action for all traits. Heterosis was determined as the superiority over the mid-parent (HMP) and also over the better parent (HBP). Hybrids generally showed a better yielding than their parental genotypes. Grain yield showed highly significant heterosis: 83.2% heterosis over mid-parent and 66.8% heterosis over better-parent, respectively. An estimate of heritability (narrow sense) was low due to the major role of environmental factors in expression of grain yield and yield components in pea. Thus, delay selection was suggested for breeding of stable yielding lines. Correlation studies showed that the grain yield was significant positive correlated with plant height, pod number, seeds of pod and pod yield. The highest direct effect was exhibited by pod yield, indirect effects, especially through the pod number in the parents and hybrids.

Key words: *Pisum sativum*, line x tester, grain yield, yield components

INTRODUCTION

One of the basic questions in genetic experimentation is the choice of the correct crossing system. This determines what kinds of genetic information can be obtained in a given experiments. Line x tester crosses are among the crossing systems that have been used most frequently[1]. The line x tester system permits the estimation of the effects of the General Combining Ability (GCA) of lines and tester and also the Specific Combining Ability (SCA) of pairs of parental genotypes. There are many univariate statistical methods for the proper genetic analysis of data from line x tester experiments[1]. In addition the line x tester cross system was reported to provide early information on the genetic behavior of these attributes in early generation.

Pea (*Pisum sativum* L.) is an important legume grown as a garden and field crop throughout the temperate regions of the world; it is also grown as a cool season crop. It ranks third in production among the grain legumes after soybean and beans in the world. Pea is valued primarily for the nutritional quality of its seeds-pea protein is low in sulphur-containing amino acids, cysteine and methionine, but rich in lysine and other essential amino acids. In Turkey, pea is mainly used for human consumption (generally through canning)[2].

Breeding for superior varieties requires selection of parents capable of transmitting their desirable qualities. A rational approach for breeding is to select parents based on their combining ability rather than on visual observation of their traits. Studies on combining ability provide useful information for the selection of parents to include in a hybridization programme by defining the parent of gene action in the expression of quantitative traits[3, 4]. General combining ability provides information on the importance of genes with largely additive effects while specific combining ability indicates the importance of non-additive effects.

Several genetic studies have been conducted to understand the genetic control of grain yield and its components in pea. Studies of Krarup and Davies[5], Singh and Singh[6] and Srivastava *et al.*[7] have shown that additive genes control the genetic direction of grain yield. In contrast, Kumar *et al.*[3], Sharma *et al.*[4] and Singh and Singh[8] reported that grain yield is controlled mainly by non-additive genes.

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Heterosis and the combining ability which identify the hybrids with high yield are the most important criteria in breeding programmes. High heterosis and high combining ability for grain yield and yield related components of pea were reported by many researchers earlier[4,9-12]. Lejeune-Henaut *et al.* [9]found that yield average heterosis over mid- parent is 40% and average heterosis over the better parent is 22%. Sarawat *et al.*[11] found that four F_1 high yielding hybrids had up to 26% yield advantage over the best parent.

Some of components such as yield controlled by many yield components have pleiotropic gene effects. They affect each other and caused genetic correlations. Hence, it is important determine the contribution of components related with grain yield by using path coefficient analysis. The breeders also wanted to know which character affects strongly or weekly the yield. Sarawat *et al.*[11] reported that there is significant positively correlation between grain yield with branches per plant, pods per plant and hundred seed weight in pea. Branches per plant and pods per plant were also reported to be positive correlated in pea. Grain yield was found to be more strongly correlated with seed number per plant than with seed size[12].

Cultivation of pea in Turkey is very limited mainly in Western Anatolia region, compared to beans, chickpea and lentils, which constitute about 95 % of grain legumes production. This study was conducted to determine the general and specific ability, the heterosis, heterobeltiosis for grain yield and some yield components in pea as a good source of plant protein. If high yield varieties can be selected and grown successfully, pea can be involved in crop rotation in Turkey.

MATERIALS AND METHODS

Three elite genotypes of winter pea line (B_1, B_6 and B_{12}) and four of commercial pea cultivars (Sprinter, Bolero, Manuel and Carina), showing good agronomic performance, were selected. In the first experiment, three diverse lines were used as tester. Four pea cultivars were crossed with the three testers in a line x tester mating design at the experimental site of Faculty of Agriculture, Selcuk University, in Konya (Turkey).

Seeds of F_1 hybrids and parental lines were sown in a randomized complete block design with three replications on 18 March 2002. Each plot consisted of 12 F_1 or parent plants on a single 2 m row which were 50 cm apart. Plant spacing was 10 cm apart. Total annual precipitation was 159.5 mm, which was more than in long years (139.3 mm) of the site. The experimental crops were irrigated two times (at the initiation of flowering and at the pod filling stage). Weeds were removed manually. The soil at the region had a pH 8.03 and soil phosphorous, potassium, iron, zinc, calcium and organic matter were 55.9, 17.9 kg ha^{-1}, 14.74, 0.32 ppm and 37.6, 2.25%, respectively. Plants were grown without fertilization and harvested on 10 July 2002.

Grain yield (g) data were collected on five plants in each plot. Pod yield (g) data were collected at the dry pod stage on five plants in the each plot. Plant height (cm), number of pods per plant, number of branches per plant were measured on 5 randomly plants per plot taken at maturity. Seeds per pod were obtained from the seed numbers of a pod. Hundred seed weight (g) was expressed as a mean of four separate 20 seed weights, multiplied by 5.

Regarding the statistical analysis, data recorded on parents and the F_1 hybrids were analyzed together as suggested by Singh and Chaudhary[1]. The combining ability analysis was done following Kempthonre[13]. Narrow sense heritabilities were calculated for each character by using the Falconer's[14] methods. Heterosis over mid-parent (HMP) or the better parent (HBP) of the observed characters were calculated according to Sarawat *et al.*[11] which statistical analysis was applied also give reference.

RESULTS AND DISCUSSION

Variability among genotypes was highly significant for these characters. No significant difference was observed among lines and among tester, except for branches number, while variability among line x testers was significant differences for all traits, expect for branches per plant. Crosses showed significant differences for all characters. High significant differences were observed among parents for the six characters (except for seeds per pod), while parents versus crosses showed significant differences for all traits (Table 1).

The ratio of σ^2 GCA to σ^2 SCA was less than one for the seven characters (Table 3) indicating the importance of non-additive gene action for these characters. This is indicative that the material used in the present study was heterozygous and that this heterozygosity contributes towards the non-additive component. Further the non-additive component of genetic variance is not fixable in the segregating generations; therefore, its exploitation is limited to hybrids only. Similar observations have also been reported Kumar *et al.*[3], Krarup and Davies[5], Singh and Singh[6] and Srivastava *et al.*[7].

Table 1: Analysis of variance and estimates of variance components for grain yield and its components of the parents and their F_1 generation of pea

Source of variation	df	Grain yield (g)	Plant height (cm)	Branches per plant (No.)	Pods per plant (No.)	Seeds per pod (No.)	Pod yield (g)	Hundred seed weight (g)
Replications	2	2.399	14.333	0.439	69.175	0.754	2.404	0.217
Treatments	18	127.150**	686.903**	7.218**	416.292**	1.310**	205.816**	24.501**
Parents	6	18.033*	666.873**	10.413**	176.079**	0.317	19.647*	46.037**
Parents vs crosses	1	1439.298**	5322.119**	5.148**	2096.120**	3.369**	2028.068**	109.871**
Crosses	11	67.382**	276.444**	5.664**	394.606**	1.664**	141.704**	4.994**
Lines	3	53.700	616.889	11.657*	426.148	0.546	174.256	7.850
Testers	2	117.873	130.861	9.694*	467.583	3.694	169.719	5.275
Lines x testers	6	57.393**	154.750**	1.324	354.509**	1.546**	116.091**	3.472**
Error	36	6.772	20.926	0.587	31.842	0.365	7.645	0.138
Variance component estimate								
GCA		0.43	5.25	0.19	1.73	0.01	1.11	0.07
SCA		16.87	44.61	0.25	3.46	0.39	36.15	1.11
GCA/SCA		0.03	0.12	0.76	0.50	0.01	0.03	0.06
h^2		0.04	0.11	0.20	0.03	0.02	0.05	0.08

* : $p < 0.05$, ** : $p < 0.01$

Table 2: Mean grain yield and its component in pea

Lines	Grain yield (g)	Plant height (cm)	Branches per plant (No.)	Pods per plant (No.)	Seeds per pod (No.)	Pod yield (g)	Hundred Seed weight (g)
Sprinter	9.2	45.7	3.7	25.7	5.7	15.4	9.6
Bolero	11.8	41.7	6.0	23.0	6.0	15.9	10.2
Manuel	16.4	29.7	2.0	25.7	5.3	20.4	16.3
Carina	14.9	30.7	3.3	24.0	6.0	21.4	19.3
Testers							
B_1	11.4	64.0	6.3	29.7	5.7	15.7	14.1
B_6	13.8	65.0	6.7	45.3	6.3	19.6	18.3
B_{12}	11.4	58.3	6.3	30.3	6.0	16.2	17.8
Hybrids							
SprinterxB_1	17.2	62.7	3.3	29.0	5.7	22.3	14.1
SprinterxB_6	21.6	85.7	6.3	38.7	6.3	27.3	13.8
SprinterxB_{12}	19.8	78.7	6.0	37.7	6.0	25.2	11.6
BoleroxB_1	17.2	74.3	5.0	24.0	5.3	19.6	10.4
BoleroxB_6	24.2	76.7	6.7	40.0	6.7	29.6	11.3
BoleroxB_{12}	29.4	72.0	6.3	60.3	7.7	35.8	12.3
ManuelxB_1	22.4	62.7	3.3	42.0	6.0	34.2	11.5
ManuelxB_6	32.4	58.3	4.3	46.7	7.7	44.7	12.3
ManuellxB_{12}	18.6	58.0	4.7	28.0	5.7	25.5	10.5
CarinaxB_1	23.2	56.7	6.3	43.0	6.0	31.8	13.8
CarinaxB_6	26.9	59.3	6.3	53.0	6.7	35.7	13.4
CarinaxB_{12}	24.4	69.7	7.7	57.7	6.7	30.5	11.4

Low heritability (narrow sense) was obtained for all traits (Table 2). Low heritability in case of all traits suggest nonfixable component of variation governing these traits and therefore, F_1 population should be exploited to utilize these components of variation. Thus, these traits can be improved by making selections among the recombinants obtained through segregating populations. The results are in conformity with earlier reports of Sharma *et al.*[4] and Singh and Singh[8].

There were significant differences between parents for all traits. Hybrid performance was generally better than parental performance for all characters excepting hundred seed weight (Table 2). This result was in agreement with Kumar *et al.*[3], Sharma *et al.*[4], Krarup and Davies[5], Lejeune-Heanut *et al.*[9], Sarawat *et al.*[11] and Srivastava *et al.*[7].

The estimated GCA effects of parents (Table 3) revealed considerable differences among the parents. The parents that proved to be good general combiners on the basis of their desirable GCA effects were B_6 for seeds of pod, pod yield and hundred seed weight, Carina for branches number, pods per plant and pod yield and Sprinter for plant height and hundred seed weight. Bolero exhibited positively significant GCA effects for plant height and branches number. B_{12} expressed significant GCA in branches per plant and pods per plant. Manuel had desirable GCA effects for pod yield. B_1 exhibited positively significant GCA effects for hundred seed weight. However, among the parents the highest positive effect for grain yield was exhibited by Carina and B_6 hence they should be considered as the best female and male combiners. Krarup and Davies[5] suggested that number of pods per plant, plant height, hundred seed weight, pod yield and number of seeds per pod are primarily yield components. Plant breeders routinely select for these parameters to increase grain yield. In this study, one of the seven lines showed significant, positive GCA effects for at least one of the seven parameters. The presence

Table 3: General combining ability and specific combining ability related to grain yield and its component in pea

Lines/ Tester	Grain yield (g)	Plant height (cm)	Branches per plant (No)	Pods per plant (No)	Seeds per Pod (No)	Pod yield (No)	Hundred seed weight (g)
Sprinter	-3.58**	7.78**	-0.31	-6.56**	-0.36*	-5.24**	0.93**
Bolero	0.47	6.44**	0.47*	-0.22	0.19	-1.83	-0.86**
Manuel	1.38	-8.22**	-1.42**	-2.78	0.08	4.65**	-0.75**
Carina	1.73*	-6.00**	1.25**	9.56**	0.08	2.47**	0.68**
B_1	-3.11**	-3.81**	-1.03**	-7.17**	-0.61**	-3.20**	0.26*
B_6	3.16**	2.11	0.39*	2.92	0.47**	4.14**	0.50**
B_{12}	-0.06	1.69	0.64**	4.25*	0.14	-0.94	-0.75**
Hybrids							
SprinterxB_1	0.75	-9.19**	-0.86*	1.06	0.28	0.55	0.68**
SprinterxB_6	-1.12	7.89**	0.72*	0.64	-0.14	-1.75	0.14
SprinterxB_{12}	0.37	1.31	0.14	-1.69	-0.14	1.20	-0.81**
BoleroxB_1	-3.29*	3.81	0.03	-10.28**	-0.61	-5.51**	-1.20**
BoleroxB_6	-2.56	0.22	0.28	-4.36	-0.36	-2.89	-0.51*
BoleroxB_{12}	5.85**	-4.03	-0.31	14.64**	0.97**	8.40**	1.71**
ManuelxB_1	1.05	6.81**	0.25	10.28**	0.17	2.61	-0.18
ManuelxB_6	4.76**	-3.44	-0.17	4.86	0.75*	5.75	0.38*
ManuellxB_{12}	-5.82**	-3.36	-0.08	-15.14**	-0.92**	-8.36**	-0.20
CarinaxB_1	1.49	-1.42	0.58	-1.06	0.17	2.35	0.70**
CarinaxB_6	-1.09	-4.67*	-0.83*	-1.14	-0.25	-1.10	-0.01
CarinaxB_{12}	-0.41	6.08*	0.25	2.19	0.08	-1.24	-0.69**

*: $p < 0.05$, ** : $p < 0.01$

of positive GCA effects indicates that continued progress should be possible though breeding for yield and yield components in pea with these presents. Similar conclusions were obtained Kumar *et al.*[3], Sharma *et al.*[4], Sarawat *et al.*[11], Gritton[15] and Venkateswarlu and Singh[16].

The SCA effects (Table 3) clearly revealed that it would be possible to isolate crosses where all traits are in the most desirable combinations. The SCA estimates of the crosses Bolero x B_{12} and Manuel x B_6 were highly significant for grain yield. Similarly, Sprinter x B_6, Manuel x B_1 and Carina x B_{12} showed significant positive SCA effects for plant height, Sprinter x B_6 for branches per plant, Bolero x B_{12} and Manuel x B_1 for pods per plant, Bolero x B_{12} and Manuel x B_6 for seeds per pod, Bolero x B_{12} for pod yield, while Sprinter x B_1, Bolero x B_{12}, Manuel x B_6 and Carina x B_1 had significant positive SCA effects for hundred seed weight (Table 3). Specific combining ability is a suitable index to determine the usefulness of a cross. In this study some crosses showed significant positive SCA effects for grain yield and yield components and others significant negative SCA effects, indicating non-additive gene action. Hence, it is suggested that in pea emphasis should be given to specific crosses followed by selection in progenies rather than pursuing GCA by mass selection. This study showed that SCA effects were important for grain yield and yield components. Specific combining ability has previously been shown in pea to be the major contributing factor for grain yield and yield components[3-,7,11].

Heterosis was evident in all traits (Table 4). In the F_1 generations, the HMP values ranged from 34.1 to 114.6% for grain yield. The range of HMP for other traits was 14.3 to 56.6% (plant height), -33.3 to 58.6% (branches per plant), -8.9 to 126.3% (pods per plant), -8.6 to 31.4% (seeds per pod), 24.4 to 123.1% (pod yield) and -38.4 to 18.9% (hundred seed weight). Similar reports have been made in the studies by Krarup and Davies[5], Lejeune-Henaut *et al.*[9], Mishra *et al.*[10], Sarawat *et al.*[11], Gritton[15] and Singh *et al.*[17].

Positive significant heterosis in the F_1 generation, particularly for grain yield (83.2%), pod yield (69.3%), pods per plant (41.0%), plant height (36.5%), branches per plant (8.9%) were most frequently associated with significant and positive heterosis for seeds of pod (8.2%) (Table 4). The crosses, Bolero x B_{12} and Manuel x B_6 for grain yield; Sprinter x B_6, Manuel x B_1 and Carina x B_{12} for plant height; Sprinter x B_6 for branches per plant; Bolero x B_{12} for pods per plant and Bolero x B_{12} and Manuel x B_6 for seeds per pod had significant estimates of both HMP and SCA effects suggesting predominance of non-additive gene action for these traits in those crosses. Thus, selection for those characters would not be effective in such crosses; rather this may suggest that development of hybrid variety might be a better choice.

The HBP values were positive for grain yield (13.6 to 149.7%), pods per plant (-14.7 to 98.9%), seeds per pod (-11.1 to 27.8%) and pod yield (23.7 to 120.7%) in the majority of the combinations, while they were negative for branches per plant (-47.4 to 21.1%) and hundred seed weight (-40.9 to -0.2%) in most of the crosses. Sprinter x B_6, Sprinter x B_{12}, Bolero x B_6, Bolero x B_{12}, Manuel x B_6, Carina x B_1, Carina x B_6 and Carina x B_{12} had high positive HBP for grain yield.

Table 4: Heterosis (%) values over MId-Parent (HMP) and Better-Parent (HBP) of grain yield and its component in pea hybrids

	Grain yield (g)		Plant height (cm)		Branches per plant (g)		Pods per plant (No.)		Seeds per (No.)		Pod yield (g)		Hundred seed weight (g)	
Hybrids	HMP	HBP	HMP	HBP	HMP	HBP	HMP	HBP	HMP	HBP	HMP	HBP	HMP	HBP
SprinterxB$_1$	66.9*	51.2*	14.3	-2.1	-33.3**	-47.4**	4.8	-2.3	0.0	0.0	43.3*	42.0*	18.9**	-0.2
SprinterxB$_6$	87.2*	56.0**	54.8**	31.8**	22.6**	-5.0	8.9	-14.7	5.6*	0.0	55.9*	39.1**	-1.3**	-24.9**
SprinterxB$_{12}$	92.7*	74.4**	51.3**	34.8**	20.0**	-5.3	34.5	24.2	2.9	0.0	59.2	55.2**	-15.4**	-34.9**
BoleroxB$_1$	48.6*	46.0*	40.7**	16.3**	-18.9**	-21.1*	-8.9	-19.1	-8.6**	-11.1	24.4	23.7-	14.4**-	26.2**
BoleroxB$_6$	89.0**	74.9**	43.8**	18.0**	5.3*	0.0	17.1	-11.8	8.1**	5.3	66.7**	50.6*	-20.6**	-38.2**
BoleroxB$_{12}$	153.8**	149.7**	44.0**	23.4**	2.7	0.0	126.3*	98.9**	27.8**	27.8**	123.1**	120.7**	-12.0**	-30.8**
ManuelxB$_1$	61.7*	37.0*	33.8*	-2.1	-20.0**	-47.4**	51.8	41.6**	9.1**	5.9	89.2**	67.3**	-24.2**	-29.4**
ManuelxB$_6$	114.6**	97.9**	23.2*	-10.3*	0.0	-35.0**	31.5	2.9	31.4**	21.1**	122.9**	118.6**	-28.9**	-32.7**
ManuellxB$_{12}$	34.1	13.6	31.8*	-0.6	12.0**	-26.3**	0.0	-7.7	0.0	-5.6	38.9*	24.6*	-38.4**	-40.9**
CarinaxB$_1$	77.1*	56.1**	19.7*	-11.5*	31.0**	0.0	60.3	44.9**	2.9	0.0	71.6**	48.9**	-17.1**	-28.2**
CarinaxB$_6$	87.5*	80.9**	24.0*	-8.7	26.7**	-5.0	52.9*	16.9	8.1**	5.3	74.1**	67.1**	-28.9**	-30.6**
CarinaxB$_{12}$	85.7*	63.9**	56.6**	19.4**	58.6**	21.1*	112.3*	90.1**	11.1**	11.1	62.1**	42.6**	-38.3**	-40.7**
Mean	83.2	66.8	36.5	9.0	8.9	-14.3	41.0	22.0	8.2	5.0	69.3	58.4	-18.4	-29.8*

Table 5: Correlations coefficients among grain yield and its components pea crosses

	Grain yield(g)	Plant height(cm)	Branches per plant (No.)	Pods per plant (No.)	Seeds per Pod (No.)	Pod yield (g)	Hundred seed weight (g)
Grain yield	--------	0.377***	0.191	0.728**	0.573**	0.941**	-0.225
Plant height		--------	0.577**	0.428**	0.241	0.279*	-0.316*
Branches per plant			--------	0.454**	0.289*	0.091	-0.085
Pods per plant				--------	0.560**	0.698**	-0.054
Seeds per pod					--------	0.607**	-0.042
Pod yield						--------	-0.203
Hundred seed weight							--------

Table 6: Path coefficient analysis between grain yield and other variables examined among different pea genotypes

		Indirect effects													
		Direct effects		Plant height		Branches per Plant		Pods per plant		Seeds per pod		Pod yield		Hundred seed weight	
Variables	Coef. of cor.	p	(%)	p	(%)	p	(%)	p	(%)	p	(%)	p	(%)	p	(%)
Plant height	0.377**	0.079	20.03	-----	----	0.019	4.97	0.039	9.95	-0.009	2.29	0.242	61.43	0.005	1.35
Branch. Per plant	0.191	0.034	15.95	0.046	21.41	-----	----	0.042	19.57	-0.011	5.08	0.080	37.33	0.001	0.67
Pods per plant	0.728**	0.092	11.92	0.034	4.39	0.015	2.00	-----	----	-0.021	2.72	0.607	78.85	0.001	0.12
Seeds per pod	0.573**	-0.037	5.78	0.019	2.94	0.010	1.51	0.52	7.94	-----	----	0.529	81.70	0.001	0.11
Pod yield	0.941**	0.871	88.30	0.022	2.23	0.003	0.32	0.064	6.50	-0.023	2.31	-----	----	0.003	0.35
H. Seed weight	-0.225	-0.017	7.39	-0.025	10.98	-0.003	1.27	-0.005	2.17	0.002	0.70	-0.177	77.50	----	-----

*: $p < 0.05$, **: $p < 0.01$

Positive values of HMP and HBP were found in all the characteristics except hundred seed weight. The positive HMP and HBP suggested that dominant or overdominant genes controlled the expression of this character. Crosses which give high levels of heterosis for grain yield HMP and HBP are the most desirable for plant breeders and almost all of the crosses showed a significant HMP and HBP. Heterosis were found to be significant for grain yield and yield components. The values reported in this study are in agreement with the values of HMP and HBP obtained by Krarup and Davies[5], Lejeune-Henaut *et al.*[9], Mishra *et al.*[10], Sarawat *et al.*[11] and Gritton[15] which is attributable to non-additive gene effects rather than overdominant ones.

Correlation coefficients were determined between grain yield and other variables. The indicate correlations coefficients were calculated for each variable (Table 5). Grain yield was significantly positive correlated with plant height, pods per plant, seeds per pod and pod yield. The same insignificant positive correlations were found between grain yield and branches per plant. Relationships between plant height and branches per plant, pods per plant and pod yield were significant positively correlated. Branches per plant correlated significant positively with pods per plant and seeds per pod. Pod number correlated significant positively with seeds per pod and pod yield. A positive significant correlation between seeds per pod and pod yield was found. Plant height correlated significant negatively with hundred seed weight. Other variables were unimportant; it could be positively and negatively correlation. Sarawat *et al.*[11] found significant positively correlation between grain yield with branches per plant, pods per plant and hundred seed weight in pea cultivars. Positive correlations between branches per plant and pods per plant were reported for pea. Grain yield is more strongly correlated with seed number per plant than with seed size[12]. These results shown that, for high grain yield, winter pea crosses should be moderately with pod yield, pods per plant and plant height. This means that in pea, grain yield is likely to be improved by selection for combined components of yield.

The highest direct positive effects on grain yield were exhibited by pod yield. Relation between grain yield and pod yield was positive and significant, with a direct effect of 88.30% and indirect effects of 6.50%, especially through the pods per plant. Similarly, the direct effects of plant height, branches number and hundred seed weight on grain yield were also positive and significant. In spite of the high positive correlation between grain yield and seeds per pod, latter had a negative direct effects. The negative direct effect of seeds per pod weight was compensated by the positive indirect effects of pod yield and pods per plant, respectively. Similarly, the negative direct effect of hundred seed weight was compensated by negative indirect effects of pod yield (Table 6).

The highest direct positive effects on grain yield were exhibited by pod yield. Relation between grain yield and pod yield was positive and significant, with a direct effect of 88.30% and indirect effects of 6.50%, especially through the pod number. These relations for hybrids were further studied using breeding programs. Selection in a breeding program based on pod yield was 87.27 % which is as effective as selection for grain yield directly. When selection for grain yield was based alone on pods per plant, genetic advance was 11.92%.

The negative direct effect of pod number was compensated by the positive indirect effects of pod yield. Seeds per pod had lowest direct effect on grain yield. The negative direct effect on grain yield was compensated by the positive indirect effects of pod yield and pod number. To improve grain yield, the breeding program should focus on increasing both pod yield and pods per plant. In pea, path analysis of yield components revealed that the components showing the highest correlations with yield also had the largest direct effect on yield[18,19]. From the results of the breeding program, we were able to improve some characters in pea cultivars. The hybrids were characterized by higher grain yield and components related with grain yield than the parents.

From the results of the breeding programme, we were able to improve some characters in pea cultivars. The hybrids were characterized by higher grain yield and yield components than the parents. In addition, new germplasm for useful morphological and agronomic traits to be used for combining different desirable traits in breeding programmes were improved.

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