

RESEARCH ARTICLE

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Breeding potential of the field pea (*Pisum sativum* L.) cultivars and their progenies**Authors' address:**

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ABSTRACT

The inheritance and gene effects structure were investigated for ten quantitative traits in field cultivars by a full diallel model of four parents – the cultivars Kerpo, Pleven 10, Mir and EFB33. Overdominance was prevalent for most of the traits in both hybrid generations (F_1 and F_2) except for 1000-seed weight. A non-additive gene action appeared to be more predominant for the inheritance of most traits studied. The fraction of h_2/H_2 indicated that at least one group of genes controlled dominance for all the traits, namely for seed weight per plant (6), seeds per pod (3). The $H_2/4H_1$ ratio was close to the expected value of 0.25 for seeds per plant and seed weight per plant, indicating a symmetrical distribution of dominant and recessive genes. Dominant alleles were more frequent in parental forms for the inheritance of most traits except seeds per pod in F_1 . In the case of seeds per pod (F_1) and 1000-seed weight (F_1 and F_2) a comparatively low difference was established between the coefficient of heritability in narrow and broad sense, indicating that the selection in early generations may be effective. The genotypes with exhibited dominant alleles were EFB33 for plant height, first pod height, internode distance and fertile nodes per plant, Mir for pods per plant, nodes per plant and 1000-seed weight and Pleven 10 for seeds per plant and seed weight per plant. Kerpo had recessive alleles for all the tested traits except seeds per pod.

Key words: breeding, field pea, gene effects, genetic analysis, inheritance

Introduction

Pea (*Pisum sativum* L.) is an important forage and vegetable crop grown in various regions worldwide. However, its productivity has become static over the years despite the fact that its total harvested area has increased tremendously. This can be attributed to the lack of suitable improved cultivars for different agroecological conditions. In order to increase the yield potential in pea to a greater extent, it is desirable to develop new genotypes through a recombination breeding for which it is necessary to know the mode of inheritance and the genetic background of the desirable traits. The structure of the gene effects is an indicator for assessing the selection value of the parental components and is used widely in breeding and applied genetic research. A diallel scheme of crossing based on the data of the F_1 hybrids is an accurate method for its determination (Csizmadia, 1994; Sharma et al., 1999;

Srivastava et al., 2000; Bourion et al., 2002). It is determined as the additive effects and the quantity of the effective factors at inheritance of the specific traits. Of a special importance is the choice of the parents used in developing novel, stable and heterotic lines. Many authors reported on the inheritance of yield-related traits in field pea. Number of days to flowering is said to be additive (Parmar & Godawat, 1990) and non-additive (Singh et al., 1986) for days to flowering, number of pods per plant additive (Rathore et al., 1995) and epistatic (Narsinghani et al., 1982), number of seeds per pod additive and non-additive (Singh & Singh, 1991), plant height additive (Kumar et al., 1996), both additive and non-additive (Dixit, 1999) and (Panda et al., 1996). All these findings were probably the major bottleneck towards the formulation of efficient breeding strategies (Sood & Kalia, 2006).

By this reason, four field pea cultivars were hybridised in a full diallel model in order to study the genetics components of the traits related to seed yield.

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Materials and Methods

An experimental study was conducted from 2009 to 2011 at the Second Experimental Field of the Institute of Forage Crops, Pleven. The following field pea (*Pisum sativum* L.) cultivars were used as the parental components: the spring-sown Kerpo and three autumn-sown ones, namely Plevan 10, Mir and EFB33. The hybridisation was done by hand in 2009. The experiment was set up as a complete block design with two replications during the winter of 2010/2011. The parental forms (P_1 and P_2) and the first and the second hybrid generations (12 F_1 and 12 F_2) were sown according to a scheme $P_1 F_1 F_2 P_2$, with a plot size of 2 m × 1 m, at a row spacing of 20 cm, a distance within row of 5 cm and a plot to plot distance of 0.70 m. The seeds were sown by hand at a depth of 5 cm. All the agronomy practices during the trial were ordinary and officially approved by the Institute of Forage Crops.

The hybridisation included all direct and reciprocals crosses, that is, a full diallel scheme. From each genotype in P_1 , P_2 , F_1 and F_2 , a sample of 40 plants was used for analysing the following quantitative traits: plant height (cm), first pod height (cm), number of pods per plant, number of seeds per plant, number of seeds per pod, number of nodes per plant, internode distance (cm), seed weight per plant (g), 1000-seed weight (g), and number of fertile nodes per plant. The obtained data were analysed according to Hayman (Hayman, 1954a), while the genetical properties of the parental components were determined by the graphical method by Hayman (Hayman, 1954a; Hayman, 1954b), using the software DIALL (Ukai, 1989). The diallel analysis of variance (ANOVA) graphical analysis (W_r/V_r ; W_r^2/V_r) by Hayman is based on the variance-covariance matrix ($V_r - W_r$), where: a is primarily additive effects; b is primarily dominance effects; b1 is mean deviation of F_1 's from their mid-parental value; b2 is variation of deviation of F_1 's from their mid-parent value over arrays; b3 is that part of dominance variation unique to each F_1 ; c is average maternal or cytoplasmic effect of each parental line; d is reciprocal differences not ascribable to c.

The mean square of casual deviations of initial data on ANOVA analysis of diallel crosses was used for estimating σ_e^2 . Estimating includes the values of the following genetical parameters: D are additive gene effects (additive variance); H_1 and H_2 are dominance gene effects (dominance variance 1 and dominance variance 2); F is covariance of additive and non-additive effects in all the arrays that has a positive or

negative sign depending on whether dominant genes or recessive genes were more. When $F > 0$ predominate dominant alleles, when $F < 0$ the recessive, when $F = 0$ alleles are equal representative. In addition, h_2 is dominance effect as the algebraic sum over all loci in heterozygous phases in all cases; H_b is heritability for diallel in a broad sense; H_{ns} is heritability for diallel in a narrow sense; H_1/D is average degree of dominance in experimental material; $H_2/4H_1$ is mean the value (p_i, q_i) on all polymorphic locuses show dominating ($d_i \neq 0$); h_2/H_2 is the number of groups of genes which controlled the character and exhibited dominance; and $[(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F]$ is proportion of dominant and recessive genes in the parents.

The conclusions from the W_r, V_r graph are: 1) W_r is related to V_r by a straight regression line of unit slope in the absence of non-allelic interaction and with independent distribution of genes among the parents; 2) The distance between the origin and the point where the regression line cuts the W_r -axis provides a measure of the average degree of dominance; 3) $D > H_1$ (partial dominance) when the intercept is positive; $D = H_1$ (complete dominance) when line passes through the origin; $D < H_1$ (over dominance) when intercept is negative; and no dominance when the regression line touches the parabola limit.

Results

One dealing with applied genetics and plant breeding needs to know the genetical structure of a specific trait, that is, what genetical effects prevail, number of the polymorphic locuses, how the alleles are shared, and so on. Such information gives opportunity of including novel cultivars in hybridisation designs and breeding programmes. The theoretical base on diallel analysis of the additive-dominant model according to Hayman is founded upon the following presumptions: the investigated genotypes are diploid and homozygous, every locus can be in two allelic positions, no exhibition of epistatic effects, no difference in inheritance in reciprocal crosses and independently distribution of the genes between the parents (Hayman, 1954a).

Diallel ANOVA. The components of the genetical variation were established with the dispersion analysis of the traits in the tested field pea genotypes (Table 1 and Table 2). The analysis of variance revealed highly significant differences among the progenies indicating that the parents were diverse for the studied traits. In the diallel ANOVA, all the genetic effects were significant without b3 and d in F_1 for

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1000 seed weight, c for height first pod, b2 for seeds per plant and a, b, b2 for seeds weight per plant in F_2 . Dominant gene effects prevailed in a majority of the traits in both F_1 and F_2 . The additive gene effects prevailed solely for 1000-seed weight in F_1 and seeds per pod and 1000 seed weight.

W_r/V_r analysis. The estimate of the components of genetical variation for the different quantitative traits in forage pea is given in Table 3.

Plant height. The line of regression intercepted the negative part of axis W_r , showing the importance of overdominance ($H_1/D > 1$; $F > 0$) in F_1 and F_2 (Figure 1 and Figure 2). The regression coefficient was different from zero in both generations, showing the absence of epistatic gene effects and that the genes are independently distributed between the parents. One is the number of the group of genes controlling this trait and exhibiting dominance (h_2/H_2) in both generations. The true value of H_2 in principle cannot be higher than H_1 . The ratio $H_2/4H_1$ can be done by concluding that plus and minus alleles are distributed in a non-uniform way between parental forms. The ratio of $(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F$ showed a prevalent dominant gene effect.

First pod height. A regression dotted line intercepted the positive part of vertical axis solely in F_1 . This was an indication that mean degree of dominance is partial and that one of the parents was rare genotype. A solid line in F_1 and F_2 intercepted the negative part indicating the importance of overdominance. The genetical parameter D was lower than H_1 ($H_1/D > 1$) in F_1 (1.18) and F_2 (1.27). The ratio h_2/H_2 was similar to the one in plant height (0.62 in F_1 and 0.84 in F_2) indicating that one group of genes had control over the trait as $H_2/4H_1$ (0.20) for both generations. The ratio of dominant and recessive genes was close or more than one, assuming the action of dominant genes. The heritability (H_{ns} and H_{bs}) could be estimated as medium to high. Number of pods per plant. Intercepting the regression line with the vertical axis (W_r) showed overdominance in both the generations (Figure 1 and Figure 2). The regression coefficient was near one and very different from zero in both generations, indicating the absence of non-allelic interactions.

Table 1. Analysis of variance for combining ability of the field pea hybrids traits in F_1 generation (by Hayman)

Source of variation	df	Mean square									
		Plant height (cm)	First pod height (cm)	Pod number per plant	Seed number per plant	Seed number per pod	Node number per plant	Internode distance (cm)	Seed weight per plant (g)	1000-seed weight (g)	Fertile node number per plant
Replication	3	31.25	4.27	0.89 **	28.79	0.18 *	1.18	0.13	3.06	57.58	1.18
a	3	8315.25 **	1760.96 **	186.61 **	6110.33 **	0.61 **	116.55 **	1.44 **	15.47 **	11933.3 3**	57.89 **
b	6	9279.99 **	2132.31 **	371.96 **	10593.63 **	1.61 **	234.26 **	9.32 **	333.68 **	3074.56 **	97.10 **
b1	1	2346.4 **	2662.63 **	1535.67 **	46376.33 **	1.88 **	923.13 **	27 **	1698.13 **	4116.26 **	376.88 **
b2	3	15374.7 **	2352.30 **	186.86 **	4134.69 **	1.70 **	114.80 **	8.77 **	91.55 **	4676.09 **	58.80 **
b3	2	3604.66 **	1537.17 **	67.75 **	2390.68 **	1.33 **	69.02 **	1.31 **	14.65 **	151.42 **	14.65 **
c	3	1319.19 **	283.06 **	156.88 **	2889.23 **	1.21 **	180.15 **	1.52 **	33.48 **	2017.15 **	43.52 **
d	3	2932.41 **	1203.06 **	294.25 **	2846.52 **	2.54 **	322.98 **	1.90 **	130.15 **	651.56 **	74.02 **
Error	45	43.88	25.62	3.84	113.14	0.16	3.67	0.14	2.68	392.25	0.87

* significant at 5% level, ** significant at 1% level

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Table 2. Analysis of variance for combining ability of the field pea hybrids traits in F_2 generation (by Hayman)

Source of variation	df	Mean square									
		Plant height (cm)	First pod height (cm)	Pod number per plant	Seed number per plant	Seed number per pod	Node number per plant	Internode distance (cm)	Seed weight per plant (g)	1000-seed weight (g)	Fertile node number per plant
Replication	3	3	367.92*	163.60	32.68	1939.71	0.18	34.89*	0.23	67.10**	4009.04**
a	3	3	8225.25**	1471.90**	83.09**	8806.50**	2.36**	62.39**	1.85**	6.28	17037.58**
b	6	6	9060.83**	2551.62**	524.35**	12229.00**	1.50**	339.85**	9.73**	402.54	2625.60**
b1	1	1	5676.75**	4265.76**	1782.42**	49987.2	1.51*	1097.30**	38.52**	1969.92**	1819.17**
b2	3	3	13821.4**	2607.30**	281.93**	1855.85	2.28**	213.89**	6.19**	29.95	3922.78**
b3	2	2	3612.00**	1632.01**	258.94**	8909.46**	0.33	150.06**	0.65**	177.75**	1083.06**
c	3	3	650.08**	66.15	135.40**	4906.10**	3.25**	88.77**	1.06**	51.25*	693.54**
d	3	3	3835.58**	276.98*	171.56**	8402.40**	1.08*	135.69**	1.10**	85.21**	691.88**
Error	45	45	95.56	95.91	13.99	824.63	0.26	8.69	0.12	12.42	64.41

* significant at 5% level, ** significant at 1% level

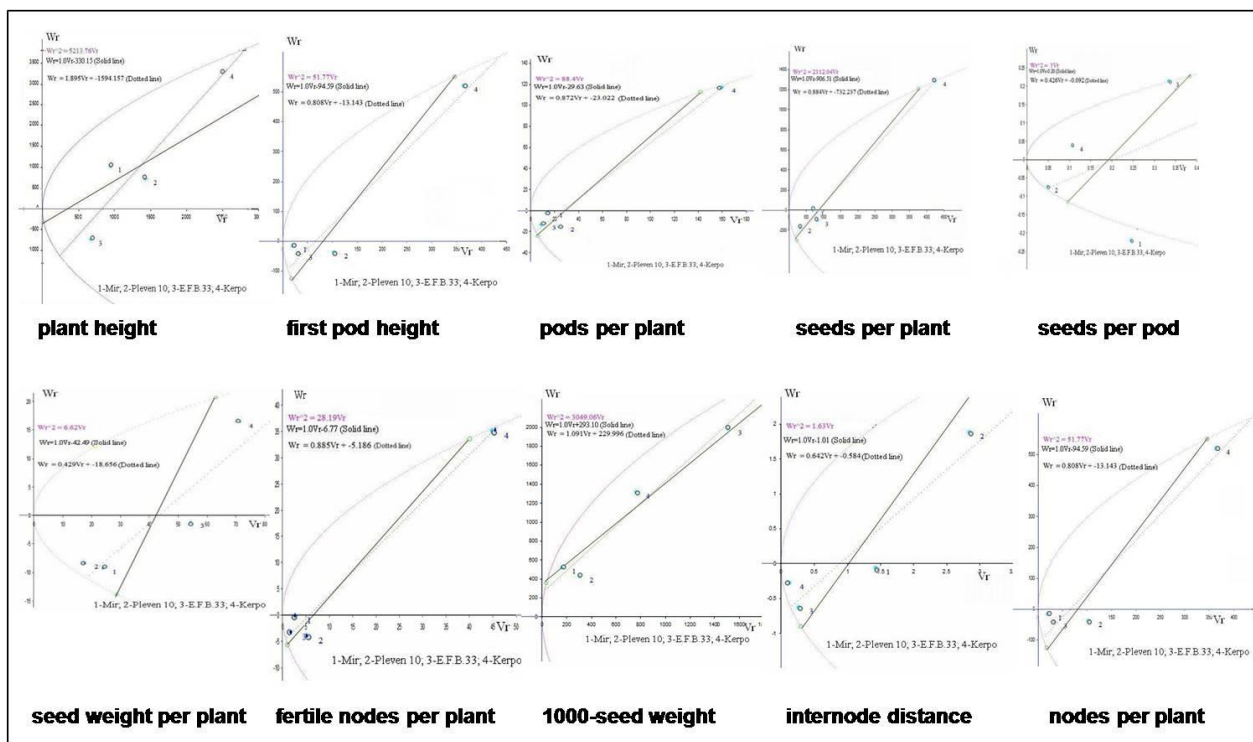


Figure 1. Graphical analysis of the field pea hybrids traits in F_1 generation.

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Table 3. Estimates of components of variation for different quantitative traits in field pea cultivars

Genetic parameters	Plant height (cm)		First pod height (cm)		Pod number per plant		Seed number per plant		Seed number per pod		Node number per plant		Internode distance (cm)		Seed weight per plant (g)		1000-seed weight (g)		Fertile node number per plant	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
D	5213.7	5203.38	965.81	951.62	88.39	78.18	2112.03	1555.80	0.10	0.17	51.76	50.51	1.63	1.63	6.62	4.18	3049.	766.45	28.18	22.92
H ₁	6534.3	6198.37	1344.17	1545.27	206.94	288.66	5738.10	5831.07	0.91	1.09	129.18	191.22	5.67	5.56	176.60	197.25	1876.	1762.8	55.27	68.64
H ₂	4619.3	4485.62	1054.14	1234.35	184.18	255.61	5240.15	5727.94	0.72	0.82	115.41	165.84	4.59	4.80	165.58	195.44	1353.	1282.6	48.08	58.56
F	6096.1	5902.90	1039.73	1093.55	88.42	103.04	1865.07	686.99	0.23	0.06	51.55	69.45	2.54	2.17	16.13	7.14	2141.	2727.1	28.30	30.23
D-H ₁	-1320	-994.99	-378.36	-593.65	-118.5	-210.4	-3626.1	-4275.2	-0.81	-0.92	-77.42	-140.7	-4.04	-3.93	-169.9	-193.1	1172.	-996.4	-27.09	-45.72
h ₁ /H ₁	0.12	0.31	0.62	0.84	2.07	1.73	2.20	2.15	0.59	0.84	1.99	1.64	1.46	1.99	2.56	2.50	0.69	0.34	1.95	1.73
H ₂ /H ₁	1.12	1.09	1.18	1.27	1.64	1.92	1.64	1.93	3.01	2.52	1.58	1.94	1.86	1.84	5.16	6.86	0.78	0.63	1.40	1.17
H ₂ /4H ₁	0.18	0.18	0.20	0.20	0.22	0.22	0.23	0.25	0.20	0.19	0.22	0.22	0.20	0.22	0.23	0.25	0.18	0.18	0.22	0.21
[(4DH ₁) ^{3/4} /F] [(4DH ₁) ^{1/2} -F]	1.0002	1.0002	1.0008	1.0007	1.0048	1.0046	1.0002	1.0001	8.583	1.3863	1.0077	1.0072	1.3186	1.2720	1.0139	1.0087	1.000	1.0020	1.0183	1.0194
H _{ms}	0.30	0.30	0.28	0.20	0.19	0.05	0.21	0.22	0.10	0.41	0.19	0.06	0.06	0.08	0.01	0.00	0.62	0.76	0.22	0.08
H _{bs}	0.99	0.98	0.98	0.94	0.98	0.95	0.98	0.90	0.83	0.87	0.97	0.95	0.97	0.97	0.98	0.94	0.91	0.98	0.98	0.98

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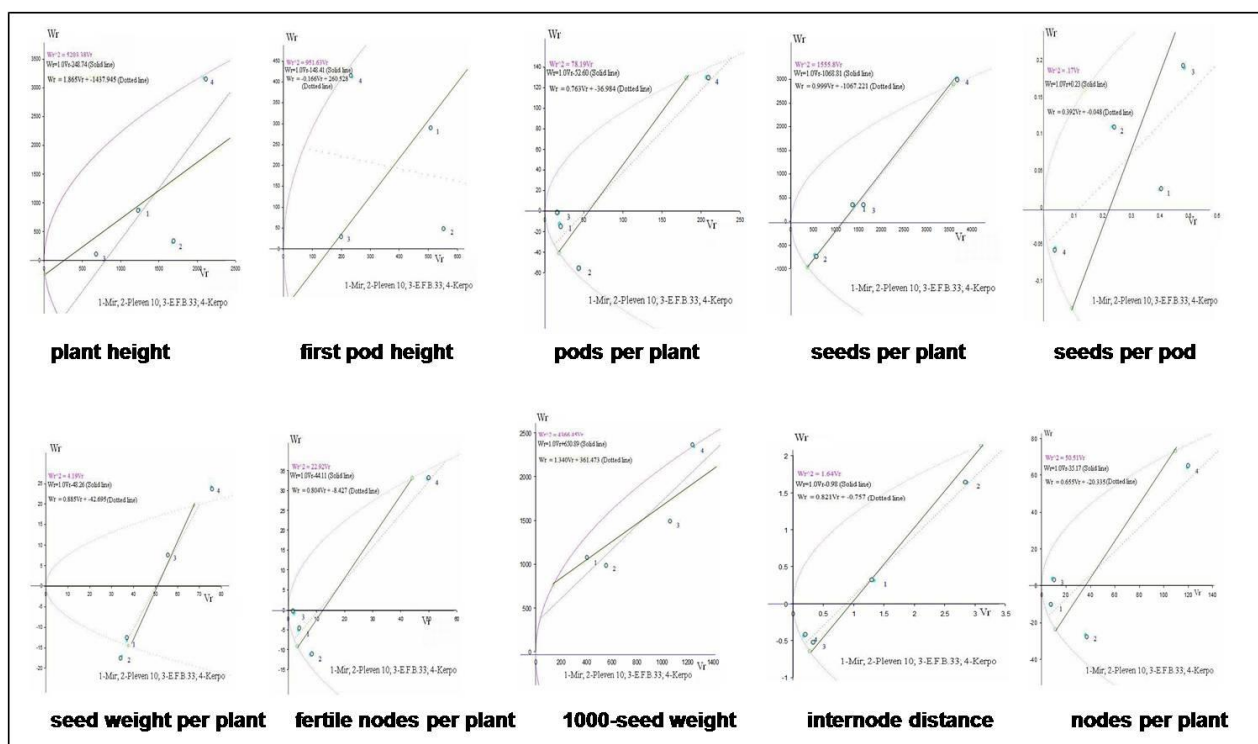


Figure 2. Graphical analysis of the field pea hybrids traits in F_2 generation

In the case of the component analysis, the dominance (b) and the additive (a) components were significant in both the generations. The magnitude of H_1 was higher than the D, ($H_1/D > 1$; $F > 0$) showing overdominance. One – two groups of genes controlled this trait and exhibited dominance. The positive and negative alleles were distributed almost uniformly between parental forms $H_2/4H_1$ (0.22) in both hybrid generations. The ratio between dominant and recessive genes favored the dominant genes. The estimate of narrow sense heritability was very low and broad sense high.

Number of seeds per plant. The regression line on Wr in the F_1 and F_2 is given in Figure 1 and Figure 2. The coefficient a of the regression equation was negative and $H_1/D > 1$ indicating overdominance. The coefficient b of the regression equation was close to unity indicating the absence of non-allelic interaction. The estimates of components of variation revealed high values for dominance (b) as compared to additive genetical components (a) in the F_1 and F_2 . The ratio h_2/H_2 (2.20 in F_1 and 2.15 in F_2) indicated that two or three groups of genes controlled number of seeds per plant. The ratio $H_2/4H_1$ in F_1 (0.23) and especially in F_2 (0.25) showed that the alleles were distributed uniformly between the parents and that the successful selection for increasing the

value of this trait was 50%. The values of the ratio between dominant and recessive genes prevailed to dominant genes. The coefficient of heritability could be estimated as medium (Hns) to high (Hbs) in both generations.

Number of seeds per pod. Intercepting the regression line with the vertical axis (Wr) below the beginning in both F_1 and F_2 indicated overdominance. The regression coefficient was different from unity in both generations indicating presence of non-allelic interaction. The additive (a) and dominance (b) components of variation were significant in both generations. The values of H_1/D for F_1 and F_2 suggest that the dominance component was more important than the additive component for the expression of this trait. The data for h_2/H_2 (0.59 for F_1 and 0.84 for F_2) showed that one group of genes controlled this trait. The alleles in each polymorphic locus showed dominance and a non-uniform distribution between the parents, since $H_2/4H_1$ for F_1 was 0.20, while for F_2 it was 0.19. The values of the ratio between dominant and recessive genes prevailed on recessive ones in F_1 and on dominant genes in F_2 . In F_1 , low narrow sense heritability was observed, while in F_2 a moderate heritability was found. As in previous cases, broad sense heritability was high in both hybrid generations. Simple progeny selection and search

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for better segregants in later generations may be followed as a procedure for the improvement of this trait.

Nodes per plant. The regression line intercepted W_r axis below the beginning, revealing overdominance in F_1 and in F_2 . The regression coefficient was different from zero and close to unity, indicating the absence of non-allelic interaction in both hybrid generations. The components of variation indicated that the additive (a) and dominance (b) components were significant in both F_1 and F_2 . The values of $H_1/D > 1$ and $F > 0$ suggested overdominance in both populations. According to the proportion h_2/H_2 (1.99 for F_1 and 1.64 for F_2) this trait is controlled by one or two groups of genes. The ratio $H_2/4H_1$ in both populations (0.22) showed that the selection for decreasing or increasing number of nodes per plant have identical chance. The ratio $(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F$ suggested a prevalence of dominant genes. Heritability in the broad sense was higher than the one in narrow sense in F_1 and in F_2 .

Internode distance. The regression line in both generations intercepted W_r below the the beginning, indicating that this trait was influenced by overdominance. The estimates of components of variation revealed higher values for dominance genetic components (H_1) than additive components (D) in F_1 and F_2 ($H_1/D > 1$). The ratio h_2/H_2 (1.46 for F_1 and 1.99 for F_2) indicated that this trait was under the oversight of two groups of genes. In F_1 (0.20) and F_2 (0.22), the ratio $H_2/4H_1$ showed that dominant alleles in the polymorphic loci are distributed almost uniformly between the parental forms. The coefficient of heritability in narrow sense was much lower than the one in broad sense.

Seed weight per plant. The regression line intercepted W_r axis in it the negative part in F_1 and F_2 . Non-significant were the additive and dominant genetic parameters b and b1 only in F_2 . In both generations, the coefficients of regression were close to unity, indicating the absence of non-allelic interaction. The value of the H_1/D is very much over unit as in F_1 (5.16) and F_2 (6.86), being an evidence for overdominance. This trait was controlled from two-three groups of genes h_2/H_2 (2.56 for F_1 and 2.50 for F_2). In this case, it is not possible to obtain rapid selection results on seed weight per plant since $H_2/4H_1$ was 0.23 in F_1 and 0.25 in F_2 . The values of the ratio between dominant and recessive genes showed a small prevailing on dominant genes toward the recessive ones. Heritability in the narrow sense of this trait was the lowest in comparison with all the others.

1000-seed weight. The regression line intercepted W_r axis in its positive part, depicting a partial dominance in F_1 and F_2 .

The regression coefficient (b) was close to unity and was highly different from zero, indicating the absence of non-allelic interaction. The coefficient of the regression equation was positive and $H_1/D < 1$, being an indication of the influence of additive genes actions. The obtained data for h_2/H_2 (0.69 for F_1 and 0.34 for F_2) indicated that 10000-seed weight was influenced by one group of genes. The value of the $H_2/4H_1$ (0.18) in both hybrid generations showed that dominant alleles in the polymorphic locuses were distributed non-uniformly between the parents. The heritability (H_{ns} and H_{bs}) was high in F_1 and F_2 . Comparatively low difference between the coefficient of heritability in narrow and broad sense probably indicated that the genetic diversity for this trait was strongly inheritable and that the selection by phenotype might be effective.

Number of fertile nodes per plant. The regression line in both generations intercepted W_r below the beginning, indicating that this trait was influenced by overdominance. The regression coefficient was different from zero indicating absence of non-allelic interactions. The estimates of genetic components showed that the dominance variation (H_1) was higher than additive (D) genetic, that is, $H_1/D > 1$. The ratio h_2/H_2 (1.95 in F_1 and 1.71 in F_2) indicated that one- two groups of genes controlled this trait and exhibited dominance. There were observed very high estimates for broad sense heritability in comparison with that in narrow sense.

Discussion

When the estimates of heritability (H_{ns} and H_{bs}) were fairly medium to high, thus suggesting that simple selection procedures like progeny selection may be opted for improvement of this trait. Similar gene actions for this trait were reported earlier (Kumar, 1976). Singh & Ram (1988), observed that additive and non-additive gene action predominated for 100 green pod weight, pod length, number node at which appear of first flower, primary branches per plant and plant height green pod yield in diallel analysis of garden pea. Genetic components of variation analysis supported these conclusions. Rastogi (1988) reported the presence of high non-additive genetic variance (H_1 and H_2) as compared to additive genetic variance (D) in a diallel analysis of ten parents for some traits of garden pea seed in F_1 generation. The role of additive, non-additive and both additive and dominance gene action may be attributed to the variable genetic material used by researchers in their studies (Raj al., 1998; Singh & Sharma, 2001). Sarawat et al. (1994)

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found that both additive and non-additive gene effects were important in the expression of branches per plant, pods per plant, seeds per pod and plant height. The dominance variance was higher for all the traits except pod length and seeds per pod. The degree of dominance indicated over-dominance for all the traits except pod length and seeds per pod. The distributions of genes in the parents were asymmetrical for all the variables. Kumar & Bal (1995) carried out graphical analysis and predicted over dominance for yield, number of pods per plant, 100 seed weight and partial dominance for other. The knowledge of gene action is very useful to a plant breeder in the selection of parents for hybridization, the estimation of some other genetic parameters and choice of breeding procedures for the genetic improvement of various quantitative characters (Sharma et al., 2013).

Prevalence of overdominance was observed for most of the traits in both hybrid generations (F_1 and F_2) except for 1000-seed weight. Non-additive gene action appeared to be more predominant for the inheritance of most the traits studied. The fraction of h_2/H_2 indicated that at least one group of genes controlled dominance for all the traits, namely 6 for seed weight per plant and 3 for number of seeds per pod. The $H_2/4H_1$ ratio was close to the expected value of 0.25 for number of seeds per plant and seed weight per plant, indicating symmetrical distribution of dominant and recessive genes. Dominant alleles were more frequent in parental forms for the inheritance of most of the traits except number of seeds per pod in F_1 . For number of seeds per pod (F_1) and 1000-seed weight (F_1 and F_2) there was established a comparatively low difference between the coefficient of heritability in narrow and broad sense, indicating that the selection in early generations might be effective. None one of the cultivars did not have only dominant or only recessive alleles. Exhibited dominant alleles were found in EFB33 for plant height, first pod height, internode distance and number of fertile nodes per plant, in Mir for number of pods per plant, number of nodes per plant and 1000-seed weight and in Pleveln 10 for number of seeds per plant and seed weight per plant. The cultivars Kerpo exhibited recessive alleles for all the traits except number of seeds per pod.

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