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Inheritance of seed yield and quality traits in peas (*Pisum sativum* L.)

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Summary. A half diallel analysis involving nine cultivars showed that additive as well as non-additive gene effects were important for the inheritance of seed yield per plant, 100-seed weights, protein content and potassium per cent. For remaining traits non-additive genetic components were important. Overdominance was observed for all traits except for 100-seed weight, which expressed partial dominance. Parents PMR-T10, EC21857, EC109182, T163 and EC109189 were good general combiners for seed yield, seed weight and quality traits. In general there was a good relationship between per se performance and the gca effects of the parents for all traits. Cross combinations such as LMR8 × EC109182, LMR8 × PMR-T10, LMR8 × EC21857, PMR-T10 × EC21857 and P23 × EC21857 were found promising. The seed yield was positively correlated with other quality traits. Protein had a positive correlation with methionine and phosphorus. All the values of correlation co-efficients were non-significant except for yield with potassium, 100-seed weight and protein with methionine, indicating that yield and quality attributes can be improved simultaneously by simple selection procedures.

Key words: Diallel analysis – *Pisum sativum* (L.) – Seed yield – Combining ability – Protein content

Introduction

The food legumes are an important source of protein, as well as of certain vitamins and minerals, essential to human nutrition in countries with cereal based diets. Thus, the only practical means of solving protein malnutrition is to increase production as well as quality of pulse crops. Pea is an important crop widely grown throughout the world for grain as well as for vegetable purposes. There is some information available on the genetics of yield, protein content and methionine in peas (Das and Kumar 1974; Pandey and Gritton 1975; Singh et al. 1980, 1981; Gupta et al. 1982), however, there is no information on the genetics of the chemical composition of pea seeds. With these considerations in mind, the present study was undertaken to estimate combining ability and genetic components controlling yield, seed weight and its chemical composition.

Materials and methods

The half diallel, involving nine genetically diverse cultivars (Table 1) and all possible F_1 crosses constituted the experimental material for the present study. One row plots of 3 meter lengths, spaces of 60 cm between rows and 15 cm within rows of all the resulting F_1s and their parents were raised in a randomized block design with three replications. Observations were recorded on five randomly selected plants in each replication for yield per plant and 100-seed weight. The quality traits – protein content, sulphur content, methionine content, potassium and phosphorus – were estimated from the bulk seed samples following the method outlined by Mackenzie and Wallace (1954) for protein content; Chensin and Yein (1951) for sulphur content; Horn et al. (1946) for methionine content; Wilde et al. (1964) for potassium and Dickman and Bray (1940) for phosphorus. The plot means were used for statistical analysis. The genetic components were determined according to the methods of Hayman (1954b) and Singh (1980). The combining ability analysis was done following Griffing (1956) method 2 and model 1. Heritability in the narrow sense was estimated as suggested by Crumpacker and Allard (1962).

Results and discussion

The mean performance of the genotypes indicated a considerable amount of genetic variability for yield,

Table 1. Mean values for seed yield, seed weight and its chemical composition traits in peas

Genotypes	Seed yield per plant (g)	100-seed wt (g)	Protein (%)	Sulphur (mg/100 g)	Methionine (mg/100 g)	Potassium (%)	Phosphorus (mg/100 g)
EC109189	7.35	4.77	21.13	563.35	99.00	1.49	588.33
T163	12.53	14.42	21.07	596.67	203.67	1.32	525.67
EC109196	5.78	13.85	21.90	533.33	181.67	1.35	575.33
LMR8	23.23	10.93	20.13	523.33	158.33	1.19	533.00
LMR200	11.05	8.81	22.23	476.67	208.00	1.20	499.00
EC109182	10.41	15.12	25.40	616.67	219.00	1.28	605.67
PMR-T10	21.20	16.80	23.23	586.67	385.67	1.18	529.33
P23	15.63	11.89	19.27	563.33	255.00	1.28	551.00
EC21857	15.21	28.59	20.00	513.33	258.33	1.27	625.33
Mean ± SEM	13.60 ± 0.14	13.91 ± 0.07	21.60 ± 0.16	522.59 ± 6.14	218.74 ± 28.33	1.27 ± 0.02	559.18 ± 17.36

Table 2. Analysis of variance for combining ability for yield, seed weight and its chemical composition traits in peas

Source of variation	d. f.	Seed yield per plant (g)	100-seed wt (g)	Protein (%)	Sulphur (mg/100 g)	Methionine (mg/100 g)	Potassium (%)	Phosphorus (mg/100 g)
G.C.A.	8	104.92**	111.72**	2.310**	2,704.09**	16,737.59**	0.0076**	5,291.48**
S.C.A.	36	30.02**	3.42**	1.843**	1,824.61**	10,572.11**	0.0036**	1,514.69**
Error	88	0.93	0.24	0.078	113.26	2,407.54	0.0013	904.07
σ^2S.C.A./ σ^2G.C.A.		3.15	0.34	8.699	7.266	6.267	3.833	1.531

** Significant $P = 0.01$

Table 3. Estimates of general combining ability effects for yield, seed weight and its chemical composition traits in peas*

Parents	Seed yield per plant (g)	100-seed wt (g)	Protein content (%)	Sulphur content (mg/100 g)	Methionine content (mg/100 g)	Potassium (%)	Phosphorus (mg/100 g)
EC109189	−6.92**	−5.42**	0.108	−1.495	49.815**	0.062**	5.445
T163	0.19	0.52**	−0.758**	25.778**	17.027	0.003	−11.283
EC109196	−0.78**	0.26	0.293**	−1.192	−53.973**	−0.005	10.020
LMR8	4.34**	−0.88**	−0.301**	−20.980**	−71.700**	−0.011	2.414
LMR200	−0.46	−3.03**	0.439**	−26.343**	11.360	−0.023*	−39.677**
EC109182	−0.69*	0.77**	0.424**	7.293*	−7.488	0.005	38.505**
PMR-T10	2.51**	1.67**	0.521**	8.505*	27.268*	−0.031**	−19.919*
P23	1.33**	−0.06	−0.437**	3.354	9.663	0.001	3.717
EC21857	0.49	6.18**	−0.289**	5.081	18.027	−0.002	10.778
SE (gi)	0.27	0.14	0.089	3.382	13.948	0.010	8.547
SE (gi−gi)	0.41	0.21	0.119	4.538	20.922	0.015	12.821

* Significant $P = 0.05$
** Significant $P = 0.01$

seed weight and various chemical constituents of seed in the peas (Table 1). The additive ($\hat{D}$) as well as the non-additive ($\hat{H}_1$) components of genetic variation were highly significant for seed yield per plant, 100-seed weight, protein content and potassium per cent. It showed the importance of both the additive as well as the non-additive component of genetic variance for determination of these traits. For methionine, sulphur and phosphorus content only non-additive ($\hat{H}_1$) was significant and indicated that the non-additive gene effects were important for the inheritance of these traits (Table 4). The mean squares due to gca and sca were also highly significant for all characters (Table 2). These results showed that additive as well as non-additive gene effects were important for all characters. However, the relative magnitude of the non-additive genetic component was more than the additive component as revealed by $\sigma^2 s\hat{c}a/\sigma^2 g\hat{c}a$ and $(\hat{H}_1/\hat{D})^{1/2}$ for all characters except 100-seed weight in which the additive component was higher.

Similar findings were reported in pea by Bhullar et al. (1975); Dahiya et al. (1977) and Singh et al. (1981) for yield and 100-seed weight, Das and Kumar (1974); Singh et al. (1980, 1981) for protein content, and Gupta et al. (1982) and Singh et al. (1981) for methionine. There is apparently no report on the genetics of sulphur, phosphorus and potassium contents.

The distribution of negative and positive alleles among parents was symmetrical for all characters except methionine and potassium content where asymmetry of gene distribution was observed. A preponderance of dominant alleles among the parents for all the traits except phosphorus was exhibited. In the latter case, recessive alleles were more frequent in the parents. The positive correlation between parental performance and Wr + Vr indicated that alleles for higher performances for yield, seed weight, sulphur, potassium and phosphorus were mostly recessive whereas the higher contents of protein and methionine were due to the presence of dominant alleles. High heritability estimates were obtained for 100-seed weight and potassium, medium ones for seed yield per plant, protein content and sulphur content and low for methionine and phosphorus contents.

In general, there was a fairly good relationship between the gca effect and per se performance of the parents (Table 3). Such parents as PMR-T10 and LMR8 were high yielding and also showed high gca effects for yield. Similarly, the parents PMR-T10, LMR200 and EC109182, which showed high gca effects, also had high protein content.

A similar trend was also observed for other characters. It suggested that in peas, the per se performance of the parents can be a reliable criterion for selecting parents for hybridization (Singh et al. 1980). Parents PMR-T10, EC21857, EC109182, T163 and EC109189 had desirable genes as they were good general combiners for yield, seed weight and its chemical composition. Obviously, these parents could be utilized in hybridization programmes for improving yield and quality traits in the pea.

The estimate of specific combining ability effects revealed that the cross combinations LMR8 × PMR-T10, LMR8 × EC21857, for yield; T163 × EC109182, T163 × EC21857 for 100-seed weight; EC109196 × PMR-T10 for protein content; T163 × EC109182, EC109182 × PMR-T10 for sulphur content; EC109189 × T163 for methionine content; EC109189 × EC109182, EC109189 × P23 for potassium and EC109189 × EC109196, EC109182 × EC21857 and EC109196 × EC21857 for phosphorus exhibited positive and significant sca effects. It is apparent from these crosses that specific cross combinations which were good for yield or quality characters, had both good general combining parents for those traits. Promising specific crosses, if they involve good combiners as parents, are likely to produce better segregants in the F_2 and future generations and thus provide better scope for selection of desirable types. However, cross combinations T163 × LMR8, EC109196 × LMR200, LMR8 × EC109182 and LMR200 × P23 had significant sca effects but parents involved in these crosses were not good combiners. These crosses may be utilized through intermating in segregating generations and simultaneous selection for desirable plant types for yield and quality traits.

To make the results more meaningful, correlations between yield and quality characters were also calculated (Table 5). All the correlations were non-significant except between yield and 100-seed weight, potassium, and between protein and methionine. However, the seed yield had a positive correlation with 100-seed weight and a negative association with the characters related to the chemical composition of seed, i.e., protein, sulphur, methionine, potassium and phosphorus contents. Hundred-seed weight had a positive association with sulphur and phosphorus content, but was negatively correlated with protein, methionine and potassium content.

Jarmyn and Slinkard (1976) and Singh et al. (1980) observed a negative correlation between protein and yield and the independence of protein and 100-seed weight was indicated. Protein content had a positive correlation with methionine and phosphorus while it was negatively associated with sulphur and potassium. Sulphur content was negatively correlated with methionine content whereas sulphur was negatively associated with phosphorus and potassium. The negative correlation was observed for methionine with phosphorus and potassium. Potassium was positively associated with phosphorus.

The observation on genetics and correlation indicated that yield and all quality attributes, though showing additivity, were strongly influenced by dominance. However, seed yield had positive correlation with 100-seed weight and 100-seed weight had positive association with phosphorus and sulphur content. Similar positive associations were observed between different characters of seed quality. The breeders of self-pollinated crops can utilize only a part of total genetic variance available, i.e. additive and epistatic additive gene interactions, which is transmitted to the progeny. In the present situation, it is suggested that isolation of progenies from advanced

Table 4. Estimates of the genetic components for yield seed weight and chemical composition attributes in peas

Component of variation	Seed yield per plant (g)	100-seed wt (g)	Protein content (%)	Sulphur content (mg/100 g)	Methionine content (mg/100 g)	Potassium (%)	Phosphorus (mg/100 t)
$\hat{D}$	34.15** ± 10.58	43.25** ± 2.38	1.6833** ± 0.7273	1,882.5800 ± 1,309.0730	3,899.0000 ± 4,302.0116	0.0084** ± 0.0012	850.4000 ± 772.0335
$\hat{H}_1$	125.80** ± 23.36	13.46** ± 5.26	8.0738** ± 1.6052	7,746.5000** ± 2,889.3476	42,240.0000** ± 9,495.2789	0.0125** ± 0.0027	3,926.0000** ± 1,704.0099
$\hat{H}_2$	105.25** ± 20.08	10.77** ± 4.52	6.5548** ± 1.3799	6,634.3600** ± 2,483.7915	29,790.0000** ± 8,162.4937	0.0091** ± 0.0023	3,684.0000** ± 1,464.8308
$\hat{h}^2$	20.08 ± 13.45	2.30 ± 3.03	0.7306 ± 0.9244	414.8836 ± 1,663.9174	21,060.1080** ± 5,468.1384	0.0002 ± 0.0015	1,632.851 ± 981.3052
$\hat{F}$	12.32 ± 24.69	5.53 ± 5.56	2.2968 ± 1.6966	2,044.4800 ± 3,053.8107	8,246.0000 ± 10,038.50	0.0101** ± 0.0028	−839.4000 ± 1,801.0030
$\hat{E}$	0.93 ± 3.35	0.24 ± 0.75	0.0781 ± 0.2300	113.82 ± 413.9652	2,408.0000 ± 1,360.4156	0.0013** ± 0.0004	904.1000** ± 244.1385
$(\hat{H}_1/\hat{D})^{1/2}$	1.92	0.36	2.1901	2.0285	3.2916	1.2225	2.1487
$\hat{H}_2/4\hat{H}_1$	0.21	0.20	0.2030	0.2141	0.1763	0.1818	0.2346
$K\hat{D}/K\hat{R}$	1.21	1.26	1.9049	1.7312	1.9468	2.9303	0.6264
Heritability (N.S.)	22.57	83.00	21.62	23.18	8.2037	52.31	9.21
r (Yr, Wr + Vr)	0.68	0.93	−0.6127	0.0471	−0.2839	0.6810	0.2556

** Significant $P = 0.01$

Table 5. Correlation coefficient between yield, seed weight and its chemical composition in peas

Characters	100-seed wt (g)	Protein content (%)	Sulphur content (mg/100 g)	Methionine content (mg/100 g)	Potassium (%)	Phosphorus (mg/100 g)
Seed yield per plant (g)	0.3538*	−0.2342	−0.0419	−0.2417	−0.4188**	−0.2147
100-seed wt (g)		−0.1709	−0.1591	−0.1575	−0.2169	0.2324
Protein content (%)			−0.2891	0.3317*	−0.1272	0.1610
Sulphur content (mg/100 g)				−0.0369	0.0419	0.0805
Methionine content (mg/100 g)					−0.1392	−0.1980
Potassium (%)						0.2893

* Significant $P = 0.05$
** Significant $P = 0.01$

generations of selected crosses (LMR8 × EC109182, LMR8 × PMR-T10, LMR8 × EC21857, PMR-T10 × EC21857 and P23 × EC21857) utilizing mostly fixable genetic components will result in an effective breeding programme. In advanced generations of these crosses, however, some kind of restricted selection model which accounts for the antagonistic association and maximizes the improvement of ultimate trait, in the present case yield and protein, without adversely affecting the desirable components, will be effective. The use of good combining parents is also advocated for the improvement of yield, seed weight and its chemical composition in peas.

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