J. Agric. Sci. Mansoura Univ., 32 (1): 297 - 307, 2007

STUDIES THE RELATION OF GENETIC BEHAVIOUR AND DIVERGENCE ANALYSIS FOR SOME QUALITY ATTRIBUTES FOR SOME CROSSES IN PEA (*Pisum sativum* L.)

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ABSTRACT

The present investigation was carried out to study gene effect and genetic divergence for nutritional quality attributes. Six parents of pea, named (P1) Master pea, (P2) Little marvel, (P3) Lincolen, (P4) Allepo, (P5) Alaska, (P6) Early perfection were randomly sampled among a large collection germplasm. The seeds of parents were introduced from different sources. The six parental genotypes were crossed according to half diallel crosses design. Total carbohydrates, total seed protein and amino acid compositions were determined for the studied pea genotypes.

The results revealed considerable variation for all studied quality attributes. The mean performances of F_1 hybrids for protein, carbohydrates and essential amino acids varied according to parental combinations and manifested heterotic effects. The results also revealed that cysteine content was low in Little marvel (P2) variety and controlled by recessive genes, while the high cysteine content of Alaska, (P6) was dominant in crosses.

In the analyzed set of pea genotypes, all essential amino acids contents except tryptophan were lower than those the recommended pattern of FAO/WHO reference protein. Based on nutritional quality attributes, the pea populations were grouped into five clusters. The data indicated that considerable genetic divergence was induced by hybridization and the F_1 hybrids were widely dispersed from their parents. The study revealed that there was no association between genetic divergence among parents and heterosis response of F_1 hybrids. It could be also regarded that non-additive gene effects were more important than those additive gene effects in determining the expression of all nutritional quality attributes. The average level of dominance for genes controlling these attributes was in the over dominance range. The association analysis revealed that total carbohydrate content was negatively correlated with seed protein content, while was positively correlated with total amino acids and all studied essential amino acids.

The obtained results suggested the possibility of development of high yielding and nutritionally superior pea genotypes through suitable breeding programs.

INTRODUCTION

Pea (*Pisum sativum*, L.) is widely grown as popular vegetable crop. Pea seeds is a rich source of protein, amino acids and carbohydrates. However, the nutritional value of protein of Pea, as well as, other legume proteins, is frequently less than ideal because of the deficiency in certain essential amino acids. The sulfur containing amino acids in legume proteins, although the levels of other essential amino acids such as lysine and tryptophan may be important (Deshpande, 1992), therefore, much attention must be directed to enhancing the nutritional qualities of Pea.

Basic informations on the relative proportion of additive and non-additive gene effects of complex traits in a population, the relationship between diversity as exhibited by parents and the heterosis effects of the

crosses and the interrelationships among different nutritional and anti-nutritional quality attributes could be used as tool in plant breeding. Many investigators studied important aspects for quality attributes in faba bean (Khare and Singh, 1992), lentil (Kumar *et al*., 1994) chickpea (Bala *et al*., 1994) dry beans (Elia *et al*., 1997) and mungbean (Oluwatosin, 1997). However, in pea the studies were on yield, yield related characters and seed protein content.

The available informations related to these important genetic aspects of nutritional quality attributes is very important in pea. Accordingly, the present study was undertaken to: (i) obtain information from a 6 x 6 diallel crosses mating design excluding reciprocal of pea on the type and relative magnitudes of gene effects influencing nutritional attributes, (ii) analyze genetic divergence for nutritional quality attributes in relation to heterosis and (iii) determine the extent of characteristics, these informations could be useful in developing breeding strategies for the production of high yielding pea genotypes with superior nutritional quality.

MATERIALS AND METHODS

The present study was carried out at Mansoura Vegetable Research Station at El-Baramoun, Dakhlia Governorate, Egypt during the two sucessive growing seasons 2003 and 2004.

The six pea (*Pisum sativum* L.) varieties namly (P1) Master pea, (P2) Little marvel, (P3) Lincolen, (P4) Allepo, (P5) Alaska, (P6) Early perfection were used. These varieties were solf-pollinated three times to increase the homozygosity level. The six parents were crossed according to a diallel crossed mating design excluding reciprocals to produce the seeds of 15 F_1 hybrids. All parental genotypes were also self pollinated to increase seeds from each one.

The six parental genotypes and their 15 F_1 hybrids were grown in a randomized complete block design with three replications. Each replicate contained 21 plots. Each plot consisted of two rows with 3.0 m. long and 70 cm apart between rows. All recommended cultural practices were applied for pea production at proper time. Data were recorded on the following traits. Total carbohydrates, total protein, total amino acids, cysteine, methioynine, lysine, tryptophan, phenylalanine, leucine.

The seeds were harvested from 10 plants of F_1 hybrids and parents were mixed and five randomly selected samples in each replication were used for biochemical analysis. Total carbohydrates content was determined according to Miller (1959). Nitrogen content was estimated by Micro-Kjeldahl methods and protein content was calculated (N x 6.25). Quantitative estimations of the contents of different essential amino acids assayed were expressed as g per 100-g protein (p per 16 g N) and compared with the FAO/WHO (1990) reference pattern.

The data were subjected to statistical analyses, using non-hierarchical euclidean cluster analyses (Spark, 1973) to assess genetic divergence in pea for nutritional quality attributes. Heterosis over the mid-parents was calculated. The diallel analysis was carried out using haymans approach

(Mather and Jinks, 1982). Phenotypic and genotypic correlation coefficients among pairs of studied traits were calculated from the variance and covariance components according to Kearsy and Pooni (1996).

The strienth of association between Euclidean distances and the other traits Total carbohybrates, Total protein, Total amino acids, Cysteine, Methionine, Lysine, Tryptophan, Phenylalanine and Leucine were obtained using correlation coefficients.

RESULTS AND DISCUSSION

The mean performances for the studied nutritional quality attributes are presented in Tables 1 and 2. The results illustrated the presence of differences in the contents of total carbohydrates, total seed protein, total amino acids and individual essential amino acids among the parental pea genotypes. The results also cleared that studied pea genotypes were high in protein content and had low levels of sulfur amino acids (cysteine and methionine), lysine, leucine and phenylalanine.

The mean performances of the F_1 hybrids for protein, carbohydrates and essential amino acids varied according to parental combination and manifested heterotic effects in either direction. Six essential amino acids, i.e. cysteine, methionine, lysine, tryptophan, phenylalanine and leucine in addition to the total of all amino acids were subjected to genetical analyses. The protein content in the F_1 hybrids, tended to be lower than the parents. Little marvel (P2) had the lowest cysteine content (Table 1).

Table 1: Mean values for total carbohydrates, total protein and total amino acids in different population of Pea.

Genotypes	Content (%)		
	T. carbohydrates	T. protein	T. amino acids
P1	51.15	32.51	16.38
P2	45.90	32.84	11.59
P3	57.96	28.98	12.51
P4	48.30	34.78	11.59
P5	58.81	19.25	19.32
P6	55.70	20.40	24.10
P1 x P2	58.76	22.17	18.18
P1 x P3	59.89	25.18	14.44
P1 x P4	58.74	23.32	17.39
P1 x P5	58.80	22.90	18.25
P1 x P6	59.69	17.39	24.90
P2 x P3	57.81	27.10	15.25
P2 x P4	53.80	26.04	20.05
P2 x P5	64.68	22.10	22.04
P2 x P6	58.68	22.10	18.17
P3 x P4	63.76	28.98	24.10
P3 x P5	55.20	25.90	20.05
P3 x P6	60.81	19.32	20.10
P4 x P5	60.68	24.10	18.25
P4 x P6	58.74	23.04	19.32
P5 x P6	59.60	27.83	17.39

All of the five crosses involved P2 had cysteine content above their mid-parent value, confirming that the low cysteine content of P2 was recessive in crosses. On the other hand, Alaska, (P6) had the highest cysteine content. All five crosses involving P6 had cysteine content above their mid-parent value, indicating that the high cysteine content of P6 was dominant in crosses (Table 2).

Table 2: The mean values for Cysteine, Methionine, lysine, tryptophan, Phenylalanine, and leucine in different Pea populations.

Genotype	Content (% of protein)					
	Cysteine	Methio-nine	Lysine	Trypto-phan	Phenyl-alanine	Leucine
P1	0.74	1.16	0.53	1.26	1.47	2.10
P2	0.53	0.84	0.63	1.36	1.57	1.68
P3	0.74	0.95	0.53	1.15	1.47	1.68
P4	0.84	0.84	0.68	1.15	1.47	1.57
P5	1.52	1.47	0.84	2.21	2.52	2.94
P6	1.58	1.58	1.26	2.42	2.73	3.57
P1 x P2	1.26	1.79	1.58	2.21	2.52	2.94
P1 x P3	0.42	0.95	1.26	1.58	1.37	2.10
P1 x P4	2.94	1.68	1.58	2.31	2.75	3.47
P1 x P5	1.26	1.37	0.84	1.79	2.31	2.83
P1 x P6	1.59	1.79	1.79	2.63	2.47	4.00
P2 x P3	2.31	1.58	1.89	1.79	2.73	2.84
P2 x P4	2.52	1.37	0.84	1.89	2.63	2.94
P2 x P5	1.79	1.26	1.37	1.68	2.21	2.73
P2 x P6	2.41	1.37	0.84	1.79	2.21	2.63
P3 x P4	1.79	1.79	0.84	1.79	3.57	2.52
P3 x P5	1.47	1.37	1.37	1.79	1.47	2.31
P3 x P6	1.89	1.58	0.74	2.31	2.47	2.94
P4 x P5	1.58	1.37	0.84	2.00	2.21	2.63
P4 x P6	1.89	1.05	0.84	1.79	2.10	2.63
P5 x P6	1.68	0.84	0.42	1.47	1.68	1.89

The analysis of variances for all studied nutritional quality attributes are presented in Table 3. The relatively large genetic variance component indicated that parent varieties and hybrids differed in their genetic potential and the presence of a high degree of genotypic variation in the control of these nutritional quality attributes. These results were in agreement with previous reports of Bishnoi and Khetarpaul (1993) in pea and Nielsen *et al*. (1993) and Oluwatosin *et al*. (1997) in cowpea. In the same time, the variance component due to parents VS. hybrids was highly significant for all studied nutritional quality attributes, indicating the presence of substantial amount of heterosis in the corsses.

Considering the variable distribution of parents and their hybrids, an attempt was made to determine association between genetic divergence among the parents and heterosis exhibited by their cross combination for nutritional quality attributes. Mid-parents heterosis of the 15 F_1 hybrids along with the Euclidean distances among parents of each F_1 hybrid are presented in Table 4. The number of hybrids showed significant heterosis differed for the nine nutritional quality traits. The direction and the magnitudes of heterosis varied from cross to cross.

T3-4

The majority of crosses exhibited moderate to high manifestations of mid-parents heterosis for nutritional quality attributes. The estimates of heterosis for total protein content were mostly in the negative direction. It is quite obvious, that all the crosses exhibited maximum estimates of heterosis for total amino acids and showed significant heterotic effects for the individual essential amino acids components. For example, the cross P2 x P3, having higher heterosis for total amino acids, also exhibited highly significant and positive heterotic effects for its components like cysteine, methionine and lysine. The magnitude and high incidence of heterosis in these crosses was an indicative of high degree of dominance and/or epistasis.

These analysis were based on the extent of relative dissimilarity among genotypes with regard to the traits that determine the nutritional quality of pea seeds, the 21 pea populations (six parents and their 15 F_1 hybrids) were grouped into five clusters. Cut off point at 10 Euclidean distance was fixed as minimum dissimilarity. The clustering pattern indicated that there was no relationship between the parental divergence and their hybrid performances. The parent varieties were distributed over four clusters. For nutritional quality attributes, the highest magnitude of Euclidean genetic distances among parents was observed between P4 and P6 and the minimum distance was between P1 and P2. Cluster I combined to hybrids P5 x P6 and none of their parents. It was also noticed that the parents P1, P2 and P4 were included in cluster I, while the hybrids among them were not included in this cluster. Cluster III consisted of fourteen F_1 hybrids and parent P5. These results indicated that considerable genetic divergence was induced by hybridization and that the F_1 hybrids were widely dispersed from their parents. Cluster II included P3 and P1 x P3. Cluster IV combined one parent, P6 and one F_1 hybrid, P1 x P6. The distribution of hybrids in all the five clusters revealed greater diversity in hybrids than their parents. The analysis of genetic divergence in pea based on yield and yield related characters was done (Singh and Tripathi, 1985). However, reports of genetic divergence based on nutritional quality attributes were not available in pea. Khare and Singh (1992) performed divergence analysis for nutritional and antinutritional attributes in faba beans.

The correlation coefficients Table 4 between genetic distance among the parents and heterosis exhibited by their cross combination for nutritional quality attributes were found nonsignificant. It appeared from these results that heterosis could not be a function of genetic divergence, rather it is a cross specific phenomenon, as heterotic hybrids with considerable heterosis e.g., P1 x P2, P1 x P4, P1 x P6 and P2 x P4 showed large differences for Euclidean distances among their parents. Significant association between heterosis and parental divergence would depend on several factors including availability of optimum environment for the expression of heterosis and the extent of internal cancellation or balancing of the various components of heterosis (Falconer, 1981). Furthermore, the heterosis expressed in a cross is a function of the allelic frequency differences among the parents. Rao and Narsinghani (1987) in Pea and Mian and Bahl (1989) in chickpea reported that there was no association between genetic divergence and heterosis for yield.

The basic assumptions underlying the diallel analysis were fulfilled as shown by non-significant t^2 values as mentioned previously in Table 3. However, the regression coefficient (b) of Wr and Vr for all nutritional quality attributes was itself non-significant, suggesting that the genetic system underlying control of these traits was complicated by non-allelic interactions arising from diversity in parental arrays. The estimates of variance components from a diallel analysis of the F_1 hybrids are shown in Table 5. The results cleared that the dominance components (H1 and H2) were highly significant for all nutritional quality attributes. Except for cysteine, the additive component (D) was also significant for all attributes and was lower than the dominance component. On the basis of these estimates, non-additive gene effects were shown to be more important that additive gene effects in determining the expression of all nutritional quality attributes. The estimates of H2 showed highly significance and positive for all studied essential amino acids. This finding indicated that dominance was unidirectional and the existence of many positive genes controlling the biosynthesis of these essential amino acids. The values of parameter F were significant and positive for all nutritional quality attributes except cysteine, indicating the excess of dominant genes among the parents. Similar findings were reported for protein content only in pea (Singh *et al*., 1987; Sirohi and Gupta, 1993 and Gupta *et al*., 1996) and in cowpea (Hazra *et al*., 1996).

The average degree of dominance over all loci estimated by $(H1/D)^{1/2}$ for genes controlling nutritional quality attributes was in the overdominance range. Symmetrical distribution of genes with postive and negative effects in the parents was not observed for any of the traits as the H2/4H1 ratio deviated from the expected 0.25. The ratio KD/KR for all nutritional quality attributes was greater than unity. These results indicated the possession of more dominant genes in the parents. Low estimates of heritability in narrow sense were obtained for all studied nutritional quality attributes, which were the consequence of lower proportion of the additive effects observed. Low estimates of heritability were also reported for seed protein and amino acid composition by many authors among them Gupta *et al*. (1982) in pea and in cowpea, Oluwatosin (1997). The preponderance of non-additive gene action observed in this study for nutritional quality attributes and the realization of high degree of heterosis suggested that biparental mating followed by recurrent selection would be the best method for the utilization of such gene action in the genetic improvement of nutritional quality attributes of pea seeds.

The calculated genotypic and phenotypic correlation coefficients among pairs of all nutritional quality attributes are given in Table 6. The association analysis revealed that total carbohydrate content was positively correlated with total amino acids and all studied essential amino acids, suggesting that selection for elevated levels of carbohydrate is likely to increase the contents of essential amino acids.

T5-6

Seed protein content showed strong negative correlation with total carbohydrates, total amino acids and all studied essential amino acids expressed as g per 16 g N. When amino acid concentrations are expressed as percent of dry matter, all of the amino acids assayed were also negatively correlated to seed protein content, though non-significant. These results indicated that selection for high protein content could decrease carbohydrate content and also decrease the content of essential amino acids, which will make the selected line nutritionally inferior. Such associations are consistent with those reported by Nielsen *et al*. (1993), Brunsgaard *et al*. (1994), Igbasan *et al*. (1996) and Oluwatosin (1997).

A desirable feature of the present study was that the containing of sulfur amino acids (cysteine and methionine) were positively associated to total carbohydrates (yield), lysine, tryptophan, phenylalanine and leucine. These results suggested that genetic improvement of the sulfur amino acid composition could be carried out simultaneously with an improvement in total carbohydrates (yield), lysine, tryptophan, phenylalanine and leucine. These results were important, since pea seed is mostly eaten alone as complete meals. Since the total protein content in pea is very high, its reduction due to increasing in carbohydrates content (yield) would not make much difference in overall nutritional quality. Therefore, the development of high yielding and nutritionally superior pea genotypes could be possible and should be given more priority in pea breeding programs.

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دراسة العلاقة بين (السلوك والتباعد الوراثى) لصفات الجودة الغذائية فى بعض هجن البسلة

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أجريت هذه الدراسة بمحطة بحوث البساتين بمحافظة الدقهلية خلال موسم ٢٠٠٣/٢٠٠٤م.

- اختيرت ستة أباء من بين مجموعة كبيرة من أصناف وسلالات البسلة والتى جمعت من أماكن مختلفة – الآباء هى ماستر B (P1) - لتلمارفل (P2) – لنكولن (P3) - البو (P4) - ايرلى بيرفيكش (P6) - ألاسكا (P6).
- تم التهجين بين الأباء الستة من نظام التزاوج النصف دائرى لدراسة العلاقة بين السلوك والتباعد الوراثى وصفات الجودة الغذائية لهذه الهجن.
- تم تقدير محتوى الكربوهيدرات والبروتين والأحماض الأمينية فى الآباء وهجين الجيل الأول.
- أظهرت الدراسة أن هناك اختلافات كبيرة لكل صفات الجودة الغذائية المدروسة ووضح أن صفات الجودة الغذائية فى الهجن قد اختلفت على حسب الآباء الداخلة فيها.
- وأظهرت بعض هجن الجيل الأول بعض تأثيرات قوة الهجين. أظهر التحليل أن المحتوى المنخفض للصنف (P2) لتلمارفل من الحامض الأمينى سيستين كان متنحى فى الهجن، بينما المحتوى العالى لنفس الحامض فى الصنف (P6) ألاسكا كان سائداً.
- وأظهرت الدراسة أن محتوى جميع الأحماض الأمينية الأساسية محل الدراسة ماعدا التربتوفان منخفض عن النسبة المعروفة.
- وبينت النتائج أن قدراً كبيراً من التباعد الوراثى قد تم استحداثه بواسطة التهجين وكانت هجن الجيل الأول موزعة بعيداً عن آبائها، وأظهرت النتائج أنه لا يوجد ارتباط معنوى بين مقدار التباعد الوراثى وتأثيرات قوة الهجين.
- أوضحت النتائج أن الفعل الجينى غير المضيف كان أكثر أهمية من الفعل الجينى المضيف فى تحديد تعبير صفات الجودة الغذائية.
- وأظهرت النتائج أن السيادة الفائقة كانت فعالة فى توارث صفات الجودة الغذائية، وأظهر محتوى الكربوهيدرات ارتباط معنوى سالب مع محتوى البروتين وموجب مع محتوى الأحماض الأمينية الكلى وجميع الأحماض الأمينية الأساسية المدروسة على المستوى الوراثى والمظهرى وتفيد النتائج إمكانية الحصول على تراكيب وراثية من البسلة عالية المحصول ومتنوعة فى صورتها الغذائية.

Table 3: Analysis of variances of diallel tests for all studied nutritional quality characteristics in pea crosses.

Source of variation	d.f	T. carbo-hydrates	Total protein	T. amino acids	Cysteine	Methio-nine	Lysine	Trypto-phan	Phenyl-alanine	Leucine
Replications	2	7.190	0.335	0.925	0.007	0.0001	0.0001	0.010	0.007	0.001
Genotypes	20	92.778**	80.332**	66.332**	1.779**	0.259**	0.368**	0.552**	0.826**	0.687**
Parents (P)	5	142.913**	166.014**	98.520**	0.389**	0.331**	0.188**	0.822**	1.501**	0.909**
Hybrids (H)	14	59.692**	58.426**	52.120**	1.884**	0.241**	0.380**	0.490**	0.643**	0.598**
P vs. H	1	453.685**	16.866**	157.395**	8.020**	0.182**	1.205**	0.159**	0.428**	1.130**
Error	40	2.709	0.294	0.703	0.012	0.005	0.004	0.009	0.009	0.009
t^2		-52736.5	-3329.1	-703.4	6.39*	1.915	0.270	0.064	0.126	0.130
b (Wr on Vr)		1.05 ± 0.6	-0.28± 0.5	0.46±0.68	0.14±0.18	0.24±0.25	0.48±0.30	-0.16±0.5	0.22±0.41	0.48±0.35
b-0/sb		1.587	-0.532	0.678	0.781	0.965	1.506	-0.205	0.536	1.369
1-b/sb		-0.080	2.419*	0.797	4.888**	3.021*	1.646	2.099	1.890	1.476

***, ** Significant at the 0.05 and 0.01 probability levels, respectively.**

Table 4: Heterosis values over mid-parents for all studied nutritional quality traits and the Euclidean distances among parents of F_1's in some Pea crosses.

F_1 Hybrids	Euclidean distances	T. carbo-hydrates	Total protein	T. amino acids	Cysteine	Methio-nine	Lysine	Trypto-phan	Phenyl-alanine	Leucine
P1 x P2	2.5	21.712**	-31.732**	70.535**	85.339**	72.122**	146.985**	74.691**	55.363**	57.046**
P1 x P3	6.4	12.044**	-5.490**	11.235**	-41.213**	-9.049	112.553**	18.660**	3.144**	0.693
P1 x P4	6.6	30.054**	-38.362**	86.348**	307.791**	59.287**	131.246**	97.659**	72.687**	84.089**
P1 x P5	16.6	11.542**	-8.148**	9.289**	14.094	-5.162	20.566**	11.177**	8.175**	15.716**
P1 x P6	24.3	11.419**	-32.747**	38.013**	30.273**	24.296**	97.367**	43.633**	39.872**	64.363**
P2 x P3	4.6	11.771**	-18.777**	108.330**	259.84**	74.873**	221.476**	46.426**	47.764**	74.091**
P2 x P4	7.6	21.812**	-24.126**	78.222**	293.51**	73.521**	52.595**	64.964**	57.812**	70.135**
P2 x P5	16.6	14.980**	-0.830	35.426**	93.956**	2.011	60.793**	-4.499	-5.733*	6.735
P2 x P6	24.3	9.568**	5.258**	6.834*	142.078**	-0.188	6.024	3.171	-1.028	5.958
P3 x P4	12.2	22.783**	-13.462**	49.998**	129.925**	103.85**	57.932**	43.293**	38.605**	57.427**
P3 x P5	13.9	1.785	10.582**	27.206**	42.303**	3.204	95.107**	-0.924	-5.417	7.015
P3 x P6	21.1	-3.011	-6.557	27.475**	53.812**	17.308**	7.176	23.366**	11.626**	13.271**
P4 x P5	22.7	18.758**	-12.291**	22.558**	54.878**	13.503**	2.388	8.772**	8.665**	9.376**
P4 x P6	30.6	10.524**	4.289**	7.409*	52.828**	-9.395*	-15.021**	-5.561	-3.686	-0.796
P5 x P6	8.2	-14.534**	86.604**	-35.825**	10.771	-40.370**	-50.752**	-41.100**	-43.786**	-37.414**
r^1	-	0.133	-0.185	-0.230	-0.058	-0.240	-0.336	-0.215	-0.167	-0.134

***, ** Significant at the 0.05 and 0.01 probability levels, respectively.**

r^1, is an indication of the power of association between Euclidean distances and each of the other traits estimated as correlation coefficients.

Table 5: The estimates of genetic components of variation for all studied nutritional quality attributes in pea.

Parameter	T. carbo-hydrates	Total protein	T. amino acids	Cysteine	Methio-nine	Lysine	Trypto-phan	Phenyl-alanine	Leucine
D	46.7**±14.0	55.4**±17.2	32.5**± 7.9	0.13 ± 0.26	0.11**±0.01	0.07 ± 0.03	0.30**±0.05	0.55**±0.15	0.33* ±0.14
H1	161.8**±33.6	153.3**±40.2	153.3**±40.2	2.77**±0.63	0.52**±0.04	0.66**±0.06	1.36**±0.12	2.08**±0.36	1.75**±0.35
H2	102.3**±29.7	93.5* ± 36.0	84.5**±16.8	2.20**±0.55	0.34**±0.04	0.43**±0.05	0.88**±0.11	1.34**±0.32	1.19**±0.31
h^2	36.3 ± 19.9	-7.1 ± 24.2	21.5 ±11.23	5.10**±0.41	0.75**±0.03	1.95**±0.04	0.88**±0.07	1.45**±0.21	2.11*±0.20
F	108.3**±33.6	109.2**±40.8	72.2**±19.0	0.45 ± 0.62	0.27**±0.04	0.22**±0.06	0.71**±0.12	1.14**±0.36	0.79*±0.35
E	0.95 ± 4.9	0.10 ± 6.07	0.20 ± 2.8	0.01 ± 0.09	0.002±0.006	0.001±0.01	0.002±0.01	0.003±0.05	0.003±0.05
	Proportions of genetic components								
$(H1/D)^{0.5}$	1.861	1.666	1.975	4.549	2.191	3.188	2.144	1.940	2.290
H2/4H1	0.158	0.152	0.166	0.194	0.166	0.162	0.163	0.161	0.170
h^2/H2	0.355	-0.077	0.255	2.372	2.122	4.535	0.995	1.084	1.776
r	-0.745	0.057	-0.614	-0.633	-0.446	-0.126	-0.444	-0.030	-0.372
r^2	0.555	0.003	0.377	0.401	0.199	0.016	0.197	0.001	0.139
KD/KR	3.964	3.915	3.552	2.190	3.547	3.349	3.510	3.268	3.130
Heritability	0.043	0.118	0.065	0.220	0.088	0.254	0.124	0.185	0.149

***, ** Significant at the 0.05 and 0.01 probability levels, respectively.**

Table 6: Genotypic (G) and phenotypic (P) corrleation coefficients among pairs of studied nutritional quality attributes in peas.

Attributes		T. carbo-hydrates	Total protein	T. amino acids	Cysteine	Methio-nine	Lysine	Trypto-phan	Phenyl-alanine	Leucine
Carbohydrates	G		-0.766**	0.730**	0.635**	0.506**	0.540**	0.585**	0.655**	0.695**
	P		-0.754**	0.715**	0.626**	0.490**	0.527**	0.569**	0.641**	0.675**
Total protein	G	-0.766**		-0.865**	-0.358**	-0.579**	-0.602**	-0.776**	-0.812**	-0.750**
	P	-0.754**		-0.861**	-0.357**	-0.577**	-0.598**	-0.771**	-0.810**	-0.747**
Amino acids	G	0.283**	-0.068		0.455**	0.594**	0.701**	0.763**	0.729**	0.749**
	P	0.274**	-0.066		0.455**	0.594**	0.696**	0.763**	0.728**	0.748**
Cysteine	G	0.440**	-0.069	0.447**		0.396**	0.393**	0.324**	0.482**	0.600**
	P	0.436**	-0.069	0.445**		0.395**	0.389**	0.323**	0.480**	0.599**
Methionine	G	0.104	-0.015	0.574**	0.108		0.637**	0.871**	0.885**	0.864**
	P	0.090	-0.018	0.569**	0.109		0.627**	0.869**	0.882**	0.862**
Lysine	G	0.193	-0.108	0.513**	0.235	0.222		0.610**	0.643**	0.692**
	P	0.185	-0.106	0.508**	0.232	0.211		0.603**	0.638**	0.687**
Tryptophan	G	0.176	-0.203	0.599**	-0.005	0.571**	0.084		0.922**	0.874**
	P	0.166	-0.199	0.602**	-0.001	0.572**	0.082		0.920**	0.870**
Phenylalanine	G	0.212	-0.113	0.627**	0.411*	0.642**	0.048	0.615**		0.964**
	P	0.196	-0.107	0.619**	0.393**	0.628**	0.053	0.613**		0.959**
Leucine	G	0.349**	-0.084	0.748**	0.646**	0.502*	0.295**	0.799**	0.457**	
	P	0.322**	-0.081	0.739**	0.636**	0.497**	0.292**	0.761**	0.458**	

***, ** Significant at the 0.05 and 0.01 probability levels, respectively.**

Values above diagonal for amino acids expresses as % of protein and below diagonal for amino acids expressed as % of dry matter.