GENETIC ANALYSIS OF SOME QUALITATIVE TRAITS IN PEA (*PISUM SATIVUM* L.) FOR F_4 GENERATION IMPLEMENTED BY HALF DIALLEL DESIGN SYSTEM.

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ABSTRACT

This study was carried out, to estimate some chemical components of fifteen genotypes of pea (*Pisum sativum* L.) (five parents+ ten crosses) produced using half diallel crossing system implemented by Randomized Complete Block Design (RCBD), repeated three times. The Least Significant Difference test (LSD) at 0.01 significant levels was used to compare means. The following is a summary of the study's findings:The mean squares of genotypes, GCA and SCA were highly significant for all studied traits except GCA mean squares of protein which was only significant. The cross (Avolla× Jeza) showed maximum protein and oil% reached 18.613 and 1.287% respectively, while maximum starch% was 58.403% showed by the cross (America× Jeza). Parent (America) showed the best performance for protein, oil and fiber% which recorded 19.793, 1.737 and 1.577% respectively. The cross (Avolla× Jeza) showed the best value for heterosis and heterobeltosis due to protein%, while the cross (America× Jeza) gave the highest values for heterosis and heterobeltosis for starch. The magnitude of σ^2_{sca} was larger than σ^2_{gca} for all studied traits confirming the importance of non-additive gene effect in controlling the inheritance of these traits. Heritability in broad sense was found to be high for all traits, while it was moderate for protein and ash and low for the other traits.

Key words: chemical components, heterosis, gene action, heritability.

التحليل الوراثي لبعض الصفات النوعية في الجيل الرابع لمحصول البازلاء بأستعمال تصميم التبادلي النصفي

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مدرس

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المستخلص

أجريت التحليل الكيميائى لخمس عشرة تركيب الوراثي (خمس أباء + عشرة هجن) من البازلاء والتي أنتجت الهجن بأستخدام تصميم التبادلي النصفي وطبقت التجربة بأستخدام تصميم القطاعات العشوائي الكامل RCBD وكررت ثلاث مرات. قورنت متوسطات التراكيب الوراثية بأستخدام أقل فرق معنوي LSD تحت مستوى (0.01). أشارت النتائج كالآتي: وجد بأن متوسط مربعات التراكيب الوراثية، القدرة العامة على الأئتلاف gca والقدرة الخاصة على الأئتلاف sca عالية المعنوية لجميع الصفات عدا متوسط مربعات gca للبروتين والتي كانت معنوية فقط. انتج الهجين (أظولا × جيزة) أعلى قيمة للبروتين والزيت 18.613 و 1.287% على الترتيب، في حين أعلى نسبة للنشأ كانت 58.403% من قبل الهجين (أميريكا × جيزة) . الأب أميريكا أظهر أداء جيد للبروتين، الزيت والألياف 19.791، 1.737 و 1.577% على الترتيب. وجد بأن الهجين (أظولا × جيزة) سجل أعلى قيمة لقوة الهجين بنوعيه لنسبة البروتين، بينما الهجين (أميريكا × جيزة) أعطى أعلى قيمة لقوة الهجين بنوعيه للنشأ. نسبة المشاركة σ^2_{sca} مقارنة بـ σ^2_{gca} كانت أعلي في توريث الصفات المدروسة، مؤشراً الى أهمية الفعل الجيني الغير الأضافي في توريث الصفات المدروسة. نسبة التوريث في معناها العام كانت عالية لجميع الصفات بينما كانت متوسطة في معناها الضيق بالنسبة للبروتين والرماد وكانت واطئة لبقية الصفات.

كلمات مفتاحية: المكونات الكيميائية, قوة الهجين, الفعل الجيني, نسبة التوريث.

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INTRODUCTION

Worldwide, millions of hectares are used for the cultivation of peas (Pisum sativum L.) (15). The Mediterranean and Near East are where peas first appeared. One of the oldest crops in the world, it was first grown for human use and animal feed 9,000 years ago (29). After soybeans, peanuts, and dry beans, peas are the world's largest crop and one of the four most significant cultivated legumes (37, 47). Due to its great nutritional value, especially in terms of proteins, peas are a pulse crop that is farmed all over the world and is economically beneficial. Its seeds contain a high percentage of protein (20–25%), 50% slowly digested starch, 50% soluble sugars by mass, and fiber (7). After dried beans, peas are the second most important legume crop in the world for seed production. High in protein, amino acids, minerals, and vitamins, Seed Pea is used in baking and canning. Due to its ability to supply the soil with organic matter and nitrogen, peas are also an important grain legume for crop rotation (4). Important leguminous crops, pulses are cultivated for their protein content as well as their carbs, minerals, and vitamins, particularly vitamin B complex (21). One of the most important pulses is the garden pea, which is cultivated in temperate regions of the world as a field and garden crop (19). Because its grain is high in protein (27.8%), complex carbohydrates (42.6%), vitamins, minerals, dietary fibers, and antioxidant components, the pea is a food rich in nutrients (42). Developments in pea breeding led to both increased yields and changes in the chemical makeup of the seeds (4,38). Mineral components abound in legume seeds (10). Pea seeds have an oil content ranging from 0.8 to 6.1% (32). It may have an important effect on pea flavor despite having little oil (23). In the diet, legumes provide an important source of dietary fiber, complex carbs, protein, vitamins and minerals. Nonetheless, they include several antinutritional components, including lectins, protease inhibitors, raffinose-series oligosaccharides, tannins, and phytic acid (16,44). Pea protein's economic value was estimated at US$32 million in 2017 and is expected to reach US$176 million by 2025 (31). The amount and quality of pea protein determine its nutritional value and functional characteristics (22). Numerous gene families are known to have an impact on the amount and makeup of pea protein (9), and the protein content is also indirectly influenced by various genes involved in starch biosynthesis (14). For two reasons, peas were selected as the second species. First, numerous genetic investigations have been conducted on this crop (8, 47). Another reason for selecting pea is that germplasm collections contain a number of apparently intermediate stages for pea domestication (48). In genetic research, diallel crossings have been used to find superior parents for the generation of hybrid cultivars and to ascertain which significant qualities are inherited by a group of genotypes. Traditional diallel analysis can only divide the whole data variance into the specific combining ability (sca) of each cross and the general combining ability (gca) of each genotype (46). Plant breeders find that understanding gene action is most useful when selecting parents for hybridization, estimating other genetic parameters, and selecting breeding techniques to increase the genetic makeup with various characteristics (40). This study was aimed to estimate some chemical components of fifteen genotypes of pea, general and specific combining abilities of parents and hybrids and to estimate the heterosis and heterobeltosis as compared with mid and best parents, using half diallel crossing system.

MATERIALS AND METHODS

This study was conducted to evaluate some qualitative traits of fifteen genotypes (five parents + ten crosses) of pea. The experiment was at Qlyasan Agricultural Research Station – College of Agricultural Engineering Science- University of Sulaimani. The parents were (Avolla, America, Jeza, Joneor and Wiled local arvena)

Table 1. Genotypes and crosses which used in this experiment

No.	Genotype and crosses	Half Diallel crosses, and parental No.
1	Avolla × America	1×2
2	Avolla× Jeza	1×3
3	Avolla× Joneor	1×4
4	Avolla× Wiled local arvena	1×5
5	America× Jeza	2×3
6	America× Joneor	2×4
7	America× Wiled local arvena	2×5
8	Jeza× Joneor	3×4
9	Jeza× Wiled local arvena	3×5
10	Joneor× Wiled local arvena	4×5
11	Avolla	1
12	America	2
13	Jeza	3
14	Joneor	4
15	Wiled local arvena	5

The following quality parameters will be conduct in the laboratory of Quality control of Razga Company during 20/4/2023 to 20/5/2023. The (Near-infrared/NIR spectroscopy Lab Analysis) and (Inductively coupled plasma atomic emission spectroscopy ICP-AES) will be used for determines the following study characters: Protein % 2- Starch % 3- Oil % 4- Fiber % 5- Moisture % 6- Ash %.

Statistical Analysis

Statistical analyses were performed based on Griffing's method II, and a fixed model I was conducted for each studied character (36); A Randomized Complete Block Design (RCBD) with three replications was implemented according to the following linear modeling, Each replicate consisted of 15 lines (5 parents and 10 crosses). Least significant difference (L.S.D) test was used to compare between the averages of the genotypes (5).

$$Y_{ij} = \mu + \tau_i + \rho_j + \varepsilon_{ij} \quad \begin{Bmatrix} i = 1,2,\ldots\ldots,t \\ j = 1,2,\ldots\ldots,r \end{Bmatrix}$$

Where:

Y_{ij}: The value of the observation belongs to the experimental unit designated as treatment (i) in the block (j).

μ: The general mean value

$Ʈ_i$: Effect of genotype (i).

ρ_j: Effect of block (j).

$\mathcal{E}_{ij}$: The value of the actual effect of the experimental error belongs to the observation designated as a treatment “i” in the block “j”.

$\mathcal{E}_{ij}$: ~ NID $(0, \sigma^2_e)$

Combining Ability Analysis

Combining ability analyses were performed according to the procedure of Griffing (1956a) using method II model I as elaborated by (36). General combining ability and Specific combining ability were estimated using the general linear model for the analysis which is represented by the following formula:

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + r_k + \varepsilon_{ijk}$$

Where,

Y_{ijk}: the observed value of the experimental unit

μ: populations mean

g_i: general combining ability (GCA) effect for the parent “i”

g_j: general combining ability (GCA) for the parent “j”

s_{ij}: specific combining ability (SCA) for the diallel the crosses involving parent i and j

r_k: replication (block) effect, and

$\mathcal{E}_{ijk}$: means error effect.

Estimation of general and specific combining ability effect

$$\hat{g}_{ii} = \frac{1}{p+2}\left[\sum\left(Y_{i.} - Y_{ij}\right) - \frac{2}{p} Y_{..}\right]$$

$$\hat{s}_{ij} = Y_{ij} - \frac{1}{p+2}\left[(Y_{i.} + Y_{ii}) + \left(Y_{.j} + Y_{jj}\right)\right] + \frac{2}{(p+1)(p+2)} Y_{..}$$

Where:

$\hat{g}_{ii}$: Effect of general combining ability for parent “i”

$\hat{s}_{ij}$: Effect of expected specific combining ability for single diallel the crosses ij when i = j

Y_{ij}: F_1s mean as a result of the crossing parent "i" with parent "j"

Y..: Sum of the means of all parents and F_1s the crosses non-reciprocal, and

p: Parent's number.

Estimation of components of variance for both general and specific combining abilities

$$\sigma^2_{\hat{g}_{ii}} = \sum \hat{g}^2_{ii} - \frac{r(n-1)}{r(n+2)} M\acute{S}_e$$

$$\sigma^2_{\hat{s}_{ij}} = \sum \hat{s}^2_{ij} - \frac{rn(n-1)}{(n+1)(n+2)} M\acute{S}_e$$

$\sigma^2_{\hat{g}_{ii}}$: Variance of the expected effect of the general combining ability of the parent i,

$\sigma^2_{\hat{s}_{ij}}$: Variance of the expected effect of the specific combining ability for diallel the crosses of parent i.

Estimation of standard error for the differences between the effects of the general combining ability of two parents

$$S.E._{(g_i - g_j)} = \sqrt{\frac{2M\acute{S}_e}{p+2}}$$

Estimation of standard error for the differences between the effects of two diallel

$$S.E._{(s_{ij} - s_{ik})} = \sqrt{\frac{2(p+1)M\acute{S}_e}{p+2}}$$

Heterosis: It will be estimated as the percentage deviation of F_1s the cross from mid parental value: (3).

$$Heterosis\ (H)\% = \frac{F_1' - M.P}{M.P} \times 100$$

Where:

F'_1: Mean of the cross,

M.P: Mid Parental value.

$$\text{M.P} = \frac{P_1 + P_2}{2}$$

P_1: Parent no. 1,

P_2: Parent no. 2.

Heritability: The variance of general and specific combining abilities as well as the variance of experimental error were used to evaluate heritability in both wide and narrow senses according to (36) follows:

$$h^2_{b.s} = \frac{\sigma^2_G}{\sigma^2_P} = \frac{\sigma^2_A + \sigma^2_D}{\sigma^2_A + \sigma^2_D + \sigma^2_e} = \frac{2\sigma^2_{gca} + \sigma^2_{sca}}{2\sigma^2_{gca} + \sigma^2_{sca} + \sigma^2_e}$$

$$h^2_{n.s} = \frac{\sigma^2_A}{\sigma^2_P} = \frac{\sigma^2_A}{\sigma^2_A + \sigma^2_D + \sigma^2_e} = \frac{2\sigma^2_{gca}}{2\sigma^2_{gca} + \sigma^2_{sca} + \sigma^2_e}$$

Where,

$h^2_{b.s}$: Heritability in the broad sense,

$h^2_{n.s}$: Heritability in a narrow sense,

σ^2_{gca}: The variance of general combining ability,

σ^2_{sca}: The variance of specific combining ability,

σ^2_e: The variance of experimental error i.e. environmental variance,

σ^2_A: Additive genetic variance,

σ^2_D: Non-additive (dominance and epitasis) genetic variance,

σ^2_G: Total genetic variance, and

σ^2_P: Phenotypic variance (genetic and environmental variance).

Average degree of dominance (ā)

The degree of dominance for the studied characters should be estimated as follows:

$$\bar{a} = \sqrt{\frac{\sigma^2_{sca}}{\sigma^2_{gca}}}$$

If ā = 0 indicates no dominance

If ā < 1 indicates partial dominance

If ā =1 indicates complete dominance

If ā >1 indicates over dominance

RESULTS AND DISCUSSIONS

Data in Table (2) illustrates the ANOVA Table of the studied traits, confirming that the mean squares of genotypes were highly significant for all traits, this signified the necessity of splitting mean square to gca and sca mean squares. Significant mean squares of genotypes for protein, starch, crude fiber, fat, and ash contents of peas were observed (43). The comparatively high component of genetic variance showed that parent varieties and hybrids have different genetic potential and a high level of genotypic diversity in the regulation of these characteristics of nutritional quality (6). The mean squares of gca were highly significant for all traits with the exception of protein% which was only significant, while the mean squares of sca was highly significant for all traits, this confirming The significance of both non-additive and additive gene effect in controlling the inheritance of these traits. Highest variations of the composition of field peas were (7,18,30 and 33) about high differences in the selection of varieties. For every attribute under study, the mean squares resulting from gca and sca were significant. (40).

Table 2. The mean squares of ANOVA components for studied traits

S.O.V	df	MS					
		Protein %	Starch %	Oil %	Fiber %	Moisture %	Ash %
Genotypes	**14**	**2.390****	**5.948****	**0.310****	**0.296****	**0.338****	**0.097****
GCA	**4**	**4.461***	**4.634****	**0.268****	**0.235****	**0.442****	**0.174****
SCA	**10**	**1.561****	**6.473****	**0.326****	**0.320****	**0.296****	**0.066****
Error	**30**	**0.066**	**1.695**	**0.010**	**0.016**	**0.036**	**0.010**

Data in Table (3) shows the performance of genotypes of studied traits. Maximum values for protein and oil% was 18.613% and 1.287% respectively recorded by the cross 1×3, Peas have a low lipid content, ranging from 0.8 to 6.1% for whole seeds (12), and (32) have shown that wrinkled peas contain between 4.5 and the total lipid content was 5.2% when round Only 2.8 to 3.1% are found in seeded varieties. Despite being minimal, the amount of crude oil may be importance in the flavor of peas (23). while the cross 2×3 exhibited maximum value for starch% reached 58.403%, Some reviews showed that starch content within the seeds varied from 18.6 to 54.5 g 100 g-1 (25,27, 28, 41 and 44). and the cross 1×4 showed maximum moisture% reached 8.799%. The highest value for fiber and ash% was 2.130 and 2.410% respectively. The dietary fiber content ranged from 190.7 to 223.1 g kg–1, and the values were slightly higher in the brown-seeded cultivars (17). In a study by (43) the content of ash in pea seeds depended on a study year, Location, and cultivar. In the referenced work, the ash content ranged from 2.57 to 2.79%. regarding to the performance of the parents it was noticed that the parent 2 produced maximum value for protein, oil and fiber% reached 19.793, 1.737 and 1.577% respectively. the highest moisture content was 8.740% showed by parent 4. Parent 5 recorded the highest value for starch and ash% reached 58.297 and 2.277% respectively. The research conducted by (43) demonstrated significant differences in the content of protein, starch, crude fiber, fat, ash, and phytates in pea seeds depending on a cultivation system and study site. The parents American and Jeza recorded maximum value for all studied characters (40).

Table 3. Mean performance of genotypes (crosses + parents) for studied traits

Genotypes	Protein%	Starch%	Oil%	Fiber%	Moisture%	Ash%
1×2	**18.107**	**56.497**	**0.983**	**0.757**	**8.647**	**1.897**
1×3	**18.613**	**55.970**	**1.287**	**0.927**	**7.643**	**1.900**
1×4	**17.010**	**58.327**	**0.647**	**1.187**	**8.797**	**1.893**
1×5	**17.540**	**57.410**	**1.280**	**1.480**	**8.347**	**2.120**
2×3	**18.610**	**58.403**	**1.217**	**1.353**	**8.160**	**2.213**
2×4	**18.303**	**57.750**	**1.243**	**1.270**	**8.107**	**2.233**
2×5	**17.797**	**58.000**	**0.550**	**1.483**	**8.693**	**2.030**
3×4	**16.023**	**57.393**	**1.163**	**1.533**	**8.430**	**1.910**
3×5	**17.807**	**53.303**	**0.837**	**2.130**	**7.900**	**2.410**
4×5	**16.697**	**58.107**	**0.790**	**1.187**	**8.530**	**1.890**
1	**17.577**	**57.417**	**1.207**	**1.393**	**8.267**	**1.853**
2	**19.793**	**55.153**	**1.737**	**1.577**	**8.207**	**2.267**
3	**17.690**	**56.340**	**1.380**	**1.487**	**8.223**	**2.170**
4	**17.767**	**57.540**	**0.833**	**1.210**	**8.740**	**2.077**
5	**18.453**	**58.297**	**1.393**	**1.203**	**7.943**	**2.277**
LSD	**0.209**	**1.063**	**0.082**	**0.104**	**0.155**	**0.082**

The heterosis and heterobeltosis values of studied traits present in Table (4). Positive and negative heterosis and heterobeltosis values were present for all traits except oil% in which all heterobeltosis values which was bearing a negative charge, maximum positive heterosis and heterobeltosis values for protein% were 5.558 and 5.220% respectively showed by the cross 1×3, while for starch% it was 4.766 and 3.662% respectively recorded by the cross 2×3. Maximum positive heterosis for oil% was 5.120%, whereas all heterobeltosis values for this trait showed negative value. Regarding to fiber and ash% the highest positive heterosis and heterobeltosis values were 58.364 and 43.241% for fiber%, while for ash% it was 8.369 and 5.841% respectively recorded by the cross 3×5. The cross 2×5 showed the highest positive heterosis and heterobeltosis values for moisture content reached 7.659 and 5.926% respectively.

Table 4. Estimates of heterosis and heterobeltosis of crosses for studied traits

Crosses	Protein%		Starch%		Oil%		Fiber%		Moisture%		Ash%	
	Hetero.	Heterobil.	Hetero.	Heterobil.	Hetero.	Heterobil.	Hetero.	Heterobil.	Hetero.	Heterobil.	Hetero.	Heterobil.
1×2	-3.095	-8.521	0.376	-1.603	-33.182	-43.389	-49.046	-52.019	4.978	4.593	-7.929	-16.336
1×3	5.558	5.220	-1.597	-2.520	-0.515	-6.763	-35.648	-37.682	-7.297	-7.544	-5.551	-12.442
1×4	-3.744	-4.261	1.476	1.367	-36.601	-46.424	-8.835	-14.812	3.450	0.648	-3.647	-8.843
1×5	-2.637	-4.948	-0.772	-1.522	-1.538	-8.112	13.992	6.246	2.982	0.964	2.663	-6.895
2×3	-0.703	-5.977	4.766	3.662	-21.925	-29.956	-11.643	-14.183	-0.670	-0.766	-0.225	-2.367
2×4	-2.538	-7.526	2.491	0.365	-3.243	-28.421	-8.852	-19.467	-4.327	-7.246	2.840	-1.485
2×5	-6.937	-10.086	2.248	-0.509	-64.856	-68.336	6.715	-5.940	7.657	5.926	-10.638	-10.848
3×4	-9.617	-9.814	0.796	-0.255	5.120	-15.700	13.721	3.116	-0.609	-3.547	-10.047	-11.982
3×5	-1.466	-3.503	-7.005	-8.566	-39.663	-39.938	58.364	43.241	-2.268	-3.928	8.396	5.841
4×5	-7.804	-9.518	0.325	-0.326	-29.042	-43.288	-1.657	-1.928	2.258	-2.403	-13.170	-16.996
SE	1.347	1.447	0.990	3.679	7.072	6.081	9.282	8.172	1.428	1.428	2.214	2.264

The gca effect of parents for studied traits present in Table (5). Parent 2 gave maximum positive gca effect for protein and oil% reached 0.756 and 0.121respectively, whereas parent 3 showed maximum positive effect of fiber% reached 0.121. parent 4 gave the highest positive gca effect for starch and moisture% reached 0.613 and 0.213 respectively, while parent 5 highest positive gca effect for ash% reached 0.078. maximum negative gca effect for fiber and ash% was -0.133 and -0.134 respectively produced by parent1, while parent 3 maximum negative and gca effect for starch and moisture% reached -0.659 and -0.182 respectively. the highest negative gca effect for protein and oil% was -0.57 and -0.158 respectively exhibited by parent 4.

Table 5. Estimates of gca effect of parents for studied traits

Parents	Protein%	Starch%	Oil%	Fiber%	Moisture%	Ash%
1	-0.099	0.096	-0.001	-0.133	0.016	-0.134
2	0.756	-0.201	0.121	-0.008	0.024	0.064
3	-0.097	-0.659	0.092	0.121	-0.182	0.045
4	-0.57	0.613	-0.158	-0.068	0.213	-0.054
5	-0.053	0.150	-0.054	0.088	-0.071	0.078
SE	0.050	0.331	0.024	0.039	0.056	0.030

The sca effect of crosses for qualities under study present in the Table (6). The cross 1×2 exhibited maximum negative fiber% reached -0.447, while the cross 1×3 had maximum positive sca effect for protein and maximum negative sca effect for moisture% reached 0.957 and -0.500 respectively. the cross 1×5 had the highest positive sca effect for oil% reached 0.232, while maximum positive sca effect for starch content was 2.203 showed by the cross 2×3. The cross 2×5 revealed maximum negative sca effect for oil% and maximum positive moisture% reached -0.621 and 0.432 respectively, while the cross 3×4 showed maximum negative sca effect for protein% reached -1.225. the cross 3×5 showed the highest negative sca effect for starch content and maximum positive sca effect for fiber and ash content reached -3.248, 0.578 and 0.210 respectively. the highest negative sca effect for ash content was -0.210 recorded by the cross 4×5.

Table 6. Estimates of sca effect of crosses for studied traits

Genotypes	Protein%	Starch%	Oil%	Fiber%	Moisture%	Ash%
1×2	-0.403	-0.459	-0.240	-0.447	0.298	-0.110
1×3	0.957	-0.528	0.093	-0.406	-0.500	-0.087
1×4	-0.237	0.557	-0.297	0.043	0.259	0.005
1×5	-0.161	0.103	0.232	0.180	0.093	0.100
2×3	0.099	2.203	-0.100	-0.105	0.009	0.028
2×4	0.202	0.277	0.177	0.000	-0.439	0.147
2×5	-0.759	0.990	-0.621	0.058	0.432	-0.189
3×4	-1.225	0.378	0.127	0.135	0.090	-0.158
3×5	0.104	-3.248	-0.305	0.576	-0.156	0.210
4×5	-0.596	0.283	-0.101	-0.179	0.079	-0.210
SE	0.113	0.739	0.053	0.086	0.125	0.068

The estimates of some genetic parameters due to studied traits present in Table (7). It was confirmed that the magnitude of $\boldsymbol{\sigma^2_{sca}}$ was larger than $\boldsymbol{\sigma^2_{gca}}$ for all studied traits, ratified that the ratio of $\boldsymbol{\sigma^2_{gca}/\sigma^2_{sca}}$ was less than one for all traits, while for every attribute, the average degree of dominance was more than one, demonstrating the significance of the non-additive gene effect in the inheritance of all characteristics. Heritability in broad sense was high for all characters, while in narrow sense it was reasonable for protein and ash%, and it was low for other traits. For the majority of the examined characters, the variance components caused by sca were greater than those caused by gca. (39). In determining the expression of every nutritional quality feature, it could also be argued that non-additive gene effects were more significant than additive gene effects. For the genes governing these characteristics, the average level of dominance in the over dominance range. (6). For every chemical component, cultivars differed significantly from one another. (2). For every character, significant genotypic differences were found. In both the F1 and F2 generations, specific combining ability variation was found to be higher than general combining ability variance, indicating the significance of non-additive gene action in the inheritance of these traits. (26). Earlier reports by (1, 12, 14, 22, 23, 26, 35 and 36) shown that the inheritance of pea seed yield and quality attributes in the F1 generation is influenced by both dominant and additive gene effect. The average degree of dominance for each character is greater than one, indicating the importance of the non-additive gene impact in controlling the inheritance of these features. (40).

Table 7. Estimates of some genetic parameters for studied traits

Genetic parameters	Protein%	Starch%	Oil%	Fiber%	Moisture%	Ash%
Mse	0.070	1.695	0.010	0.016	0.036	0.010
σ^2_{gca}	0.628	0.420	0.037	0.031	0.058	0.023
$\sigma^2_{sca} = \sigma^2_D$	1.496	4.778	0.316	0.304	0.260	0.056
$\sigma^2_{gca}/\sigma^2_{sca}$	0.420	0.088	0.117	0.103	0.223	0.419
σ^2_A	1.256	0.840	0.074	0.063	0.116	0.047
σ^2_D	1.496	4.778	0.316	0.304	0.260	0.056
σ^2_p	2.817	7.313	0.400	0.383	0.412	0.113
$\bar{a}$	1.543	3.374	2.926	3.116	2.117	1.546
$h^2_{b.s}$	0.977	0.768	0.975	0.958	0.912	0.911
$h^2_{n.s}$	0.446	0.115	0.185	0.164	0.282	0.415

CONCLUSION

Strong genetics control was noticed as genetic analysis showed high heritability for all traits. Non-additive gene action was predominant, through additive effect were also present. Starch% and protein% can be improved through selection, while ash%, oil% and fiber% are better enhanced through hybridization. Overall, both additive and non-additive effects influenced the studied quality traits. The high estimates of broad sense heritability (ranging from 0.768 to 0.977) suggest that most of the all typic variation is due to genetic factors, indicating good potential for genetic improvement.

CONFLICT OF INTEREST

The authors declare that they have no conflicts of interest.

DECLARATION OF FUND

The authors declare that they have not received a fund.

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