HALF DIALLEL ANALYSIS OF SEVEN PEA CULTIVARS FOR SEED YIELD AND ITS COMPONENTS FOR F_4 GENERATION UNDER SULAIMANI CONDITION

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ABSTRACT

The present study was carried out at Qlyasan locations, in Kurdistan Region-Iraq, Agricultural Research Station, College of Agricultural Engineering Sciences-University of Sulaimani, according to half diallel mating system using seven pea cultivars (1-Avolla, 2-Americana, 3-Jeza, 4-Joneor, 5-Pack land, 6-Arvena and 7-Samara) with 21 F_4 crosses. The genotypes were planted in a completely randomized block design with three replications. Highly significant mean squares due to genotypes were recorded indicating the presence of sufficient variability among genotypes for all traits. The mean squares due to gca and sca were significant for all the studied traits. The highest positive heterosis values estimated as the F_4s deviation from mid parental values recorded by the cross 2×6 and 4×5 for almost all traits. Maximum positive gca effect values for seed weight plant^{-1}, biological yield plant^{-1} and pods number plant^{-1} were recorded by parent 4, while parent 2 showed the best value for some components. The cross 4×5 was the best sca combiner for seed weight plant^{-1} and some its components including pods number plant^{-1}, pod weight plant^{-1} and seed number pod^{-1}. The type of gene action as controlled the inheritance of all characters was over dominance except 100-seed weight. Heritability in broad sense was found to be high for all treats except seed number pod^{-1} which was moderate, while at narrow sense it was high for average pod weight, pod length, seed weight pod^{-1} and 100-seed weight.

Key words: *Pisum sativum*, genetic analysis, combining ability, heterosis, heritability

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التهجين التبادلي النصفي لسبعة أصناف من البازلاء لحاصل البذور لكل نبات و مكوناته للجيل الرابع تحت ظروف منطقة السليمانية

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المستخلص

تم إجراء هذه التجربة في موقع قلياسان، إقليم كوردستان – العراق، محطة البحوث الزراعية، كلية علوم الهندسة الزراعية – جامعة السليمانية، وفقًا لنظام التهجينات التبادلية النصفية و بإستعمال سبعة أصناف من البازلاء (Avolla , Americana , Jeza , Joneor, Pack land , Arvena and Samara) مع هجنها 21 للجيل الرابع F_4. تم زراعة التراكيب الوراثية وفق تصميم القطاعات الكاملة المقساة بثلاث مكررات. كانت متوسطات مربعات التراكيب الوراثية عالية المعنوية، مما يشير إلى وجود اختلافات كبيرة بين التراكيب الوراثية لجميع الصفات. كانت متوسط المربعات gca عالية المعنوية لجميع الصفات باستثناء عدد البذور لكل قرنة ودليل الحصاد التي كانت معنوية فقط. كانت متوسط المربعات sca عالية المعنوية لجميع الصفات باستثناء عدد البذور لكل قرنة و وزن مائة بذرة التي لم تكن معنوية. أعلى قيمة موجبة لقوة الهجين المقدرة كمتوسط إنحراف الجيل الرابع عن معدل الآباء سجل بواسطة الهجين 2 × 6 و 4 × 5 لمعظم الصفات. سُجلَ أعلى قيم موجبة لتأثير gca للصفات وزن البذور لكل النبات، الحاصل البيولوجي، وعدد القرون لكل نبات عن طريق الأب 4، بينما أظهر الأب 2 أفضل قيمة لبعض المكونات. وجد بأن الهجين 4 × 5 له القابلية الجيدة للأئتلاف خاص لوزن البذور لكل نبات وبعض مكوناته، منها عدد و وزن القرنات لكل نبات، وعدد البذورلكل قرنة. و كان نوع الفعل الجيني الذي يسيطر على توريث جميع الصفات هي نوع الفعل الجيني التفوقي عدا وزن مائة بذرة. درجة التوريث في معناها العام كانت عالية لجميع الصفات عدا عدد البذور لكل قرنة و التي كانت متوسطة, بينما درجة التوريث في معناها الضيق كانت عالية لصفة معدل وزن القرنة, طول القرنة, وزن البذور لكل قرنة و وزن مائة بذرة.

كلمات مفتاحية: *Pisum sativum*, التحليلات الوراثية, التآلف, قوة الهجين, درجة التوريث

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INTRODUCTION

Pea (*Pisum sativum* L.) is a self-pollinated crop, diploid having 14 chromosome (2n=14). Pea is originated in Near East and Mediterranean regions. It is one of the most world oldest crops cultivated as early as 9,000 years ago for human foods and animals feed (5). A pea is one of the four of the most important cultivated legume and largest world's legume crop in the production after soybean, peanuts and dry beans (43 and 48). It has a prominent place among vegetables due to its high nutritive value, particularly proteins and other health building substances like carbohydrates vitamin A, vitamin C, calcium and phosphorus (29). The most powerful tool is diallel analysis for characterizing the genetic architecture, for plant materials and estimating the general combining ability of parent and the selection of high specific combining ability for the exploitation of heterosis (28). Diallel analysis is helpful for intersecting the suspect of the gca and sca. This analysis is very helpful to predict additive and dominance effects of a population which can then be used to predict the genetic variability and heritability (45). Diallel analysis (13 and 15) offers a potential means of obtaining information about parental combinations in terms of general and specific combining ability (gca and sca), direction and magnitude of dominance and over dominance and nature and extent of gene action. The estimation of gca and sca variances provide an appropriate diagnosis of the predominant role of additive or non-additive gene action. The gca and sca effects will help to locate the parents and their crosses that are responsible for bringing about particular type of gene action (24). Gca provides information about the importance of genes with additive effects, while sca indicates the importance of non-additive effects. Heterosis and combining ability which identify the hybrids with high performance are the most important criteria in breeding programs (8). Cross combinations displaying hybrid vigor can be utilized for developing high yielding lines of field pea. Heterosis or hybrid vigor in plants is the superior performance of the F_1 progeny with respect to the parental lines (36). Due to the complexity of heterosis, specific biochemical pathways have not been established to reveal a direct link to multi-genic heterosis (25). The present study was, undertaken to study the inheritance and exploit the elite parents and their potential combinations for some important pea seed traits among seven pea cultivars and their 21 half-diallel crosses.

MATERIALS AND METHODS

Seven pea cultivars (Avolla, Americana, Jeza, Joneor, Pack land, Arvena and Samara) were used with 21 F_4s generation. The genotypes (7+21 F_4) in (Table 1), were planted at Qlyasan locations, at Kurdistan Region-Iraq, Agricultural Research Station, College of Agricultural Engineering Sciences-University of Sulaimani, located (Lat 35° 34′ 307″; N, Long 45° 21′ 992″; E, 765 masl) 2 km North West of Sulaimani City, which produced according to half diallel mating system. The genotypes were planted using completely randomized block design with three replications implemented in field experiment, each replicate was consisted of 28 plots (7 parents and 21 crosses), each plot was consisted of one row of one material, 3 m long, 40cm between rows and 20cm with in row. LSD test was used to compare the genotype means (4). The statistical genetic analysis was based on half diallel mating system (41). At maturity 5 plants from each genotype were take randomly for recording the observations for the following treats (Pods number plant^{-1}, Pods weight plant^{-1} (g), Average pod weight (g), Pod length (cm), Seeds number pod^{-1}, Seeds weight pod^{-1}, 100-seed weight (g), Seeds weight plant^{-1} (g), Biological weight plant^{-1}(g) and Harvest index). Genetic parameters: General combining ability (gca), Specific combining ability (sca), Heterosis %, Heritability in Broad Sense, Heritability in narrow Sense and Average Degree of dominance (ā), were studied.

Table 1. Parents and crosses details

No.	Crosses, and parental no.	Parentage
1	1 × 2	Avolla × Americana
2	1 × 3	Avolla × Jeza
3	1 × 4	Avolla × Joneor
4	1 × 5	Avolla × Packland
5	1 × 6	Avolla × Arvena
6	1 × 7	Avolla × Samara
7	2 × 3	Americana × Jeza
8	2 × 4	Americana × Joneor
9	2 × 5	Americana × Packland
10	2 × 6	Americana × Arvena
11	2 × 7	Americana × Samara
12	3 × 4	Jeza × Joneor
13	3 × 5	Jeza × Packland
14	3 × 6	Jeza × Arvena
15	3 × 7	Jeza × Samara
16	4 × 5	Joneor × Packland
17	4 × 6	Joneor × Arvena
18	4 × 7	Joneor × Samara
19	5 × 6	Packland × Arvena
20	5 × 7	Packland × Samara
21	6 × 7	Arvena × Samara
22	1	Avolla
23	2	Americana
24	3	Jeza
25	4	Joneor
26	5	Packland
27	6	Arvena
28	7	Samara

RESULTS AND DISCUSSION

Data present in Table 2 shows the statistical analysis for studied characters as the mean squares variances. The mean squares due to genotypes were highly significant for all characters, while the mean squares due to gca were highly significant for all characters except seeds number pod^{-1} and harvest index which were significant only. Regarding to the mean squares for sca they were highly significant for all characters except seeds number pod^{-1} and 100-seed weight which did not significant. Al-Hamdany, (2) reported that the general combining ability was significant for seed yield, 100-seed weight and pods weight but non-significant for seeds pod^{-1}, while sca for most characters was significant in pea. Sharma *et al.*, (32) used combining ability analysis for diallel cross of pea cultivars and found that gca variance were significant for all characters. The performance of parents and crosses was usually associated with the combining ability effects (38). The general combining ability (gca) and specific combining ability (sca) were highly significant, indicating the presence of both additive and non-additive type of gene action. The ratio of additive variance to dominance variance indicated the predominant role of non-additive gene action for all traits (8). Significant gca and sca effects were reported for most of the yield components indicating importance of both additive and non-additive gene effects. The sca estimates were relatively greater than the corresponding estimates of gca, indicating preponderance of non-additive genetic variances. Similar results have been reported in field pea by several researchers (1, 10, 26, 39, and 46) and F_2 crosses with their parents (3).

Table 2. Mean squares of variance analysis for the studied characters

S.O.V.	d.f	M.S									
		Pods no. plant^{-1}	Pods weight plant^{-1} (g)	Average pod weight (g)	Pod length (cm)	Seeds no. pod^{-1}	Seeds weight pod^{-1} (g)	100-seed weight (g)	Seeds weight plant^{-1} (g)	Biological weight plant^{-1} (g)	Harvest Index
Blocks	2	5.892 n.s	7.578 *	0.017 n.s	0.098 n.s	1.853 *	0.002 n.s	0.455 n.s	3.583 n.s	4.018 n.s	0.014 n.s
Genotypes	27	258.194 **	131.515 **	0.274 **	7.362 **	1.765 **	0.107 **	69.315 **	108.440 **	442.8790 **	0.0465 **
gca	6	146.450 **	48.886 **	0.262 **	7.720 **	1.329 *	0.096 **	84.469 **	23.101 **	142.036 **	0.014 *
sca	21	68.812 **	42.396 **	0.043 **	0.949 **	0.377 n.s	0.018 **	5.572 n.s	39.874 **	149.224 **	0.016 **
Error	54	3.471	1.886	0.012	0.157	0.533	0.007	3.920	3.550	3.001	0.006

Data in Table 3 shows the means of studied characters for F$_4$ crosses and their parents. The cross 4×5 recorded maximum values for the character seeds weight plant^{-1} and some of its important components, pods number plant^{-1}, pod weight plant^{-1} and seed number pod^{-1} with 30.062g, 49.765, 40.468g and 7.567 respectively. Parent 6 recorded maximum value for pods number plant^{-1}, seeds weight plant^{-1} and biological weight plant^{-1} reached 39.578, 23.556g and 46.273g respectively. While parent 3 recorded the highest value for most important components seeds number pod^{-1} and seeds weight pod^{-1}reaching with 7.600 and 1.532g respectively. Several researchers (1, 3, 38 and 46) derived information on combining ability in garden pea involving twenty one crosses and seven parents.

Table 3. Means of some the studied characters for parents and their F$_4$ crosses

Crosses and parents	Pods no. plant^{-1}	Pods weight plant^{-1} (g)	Average pod weight (g)	Pod length (cm)	Seeds no. pod^{-1}	Seeds weight pod^{-1} (g)	100-seed weight (g)	Seeds weight plant^{-1} (g)	Biological weight plant^{-1} (g)	Harvest Index
1 x 2	22.629	32.500	1.701	7.667	5.133	1.414	23.500	19.991	45.118	0.350
1 x 3	19.803	23.537	1.394	7.500	6.567	1.142	17.513	15.342	30.413	0.424
1 x 4	35.562	27.461	1.295	6.000	6.600	1.155	16.920	18.556	41.269	0.442
1 x 5	26.828	30.404	1.373	6.667	5.467	1.127	16.643	14.888	36.247	0.402
1 x 6	36.398	26.701	1.183	6.167	5.300	0.867	15.260	16.835	45.381	0.329
1 x 7	30.203	26.625	1.329	6.933	5.833	1.113	17.874	16.430	22.886	0.700
2 x 3	15.574	21.409	1.656	9.833	5.567	1.237	21.687	9.037	26.264	0.314
2 x 4	35.262	36.189	1.509	6.800	5.100	1.177	24.103	26.293	32.216	0.644
2 x 5	25.114	24.943	1.803	7.667	6.100	1.314	25.870	16.978	35.220	0.452
2 x 6	19.974	29.818	2.215	10.833	6.267	1.494	24.007	12.499	44.112	0.238
2 x 7	26.464	32.506	2.112	8.933	5.033	1.386	24.997	18.368	51.144	0.349
3 x 4	27.514	24.435	1.262	6.467	5.767	1.034	15.757	15.441	35.556	0.425
3 x 5	32.488	31.393	1.726	8.200	7.033	1.380	18.463	21.581	44.712	0.570
3 x 6	18.322	21.867	1.620	9.000	7.500	1.305	15.460	12.384	30.241	0.403
3 x 7	14.495	16.975	1.083	8.500	6.600	1.157	16.367	10.759	31.723	0.297
4 x 5	49.765	40.468	1.539	8.500	7.567	1.249	16.243	30.062	60.478	0.440
4 x 6	26.652	17.275	1.137	5.400	5.667	0.946	5.617	12.079	42.981	0.254
4 x 7	46.056	34.555	1.206	5.600	5.600	1.048	15.313	26.871	71.942	0.347
5 x 6	21.314	17.967	1.407	6.000	6.267	1.178	18.317	9.817	19.864	0.454
5 x 7	37.695	38.546	1.584	6.933	5.733	1.344	22.410	27.361	44.586	0.636
6 x 7	37.891	31.310	1.328	6.167	6.100	1.123	11.947	20.098	36.448	0.521
1	28.985	26.874	1.414	6.633	6.167	1.227	16.560	17.441	21.443	0.654
2	17.103	25.723	1.955	10.133	5.067	1.364	28.193	11.958	36.201	0.317
3	30.375	22.750	1.837	9.333	7.600	1.532	18.133	14.642	30.548	0.443
4	31.437	23.357	1.074	5.067	5.433	0.792	14.690	14.679	37.490	0.315
5	13.702	13.502	1.409	6.933	5.200	1.215	22.523	4.825	15.258	0.294
6	39.578	24.885	1.136	4.933	6.400	0.812	13.930	23.556	46.273	0.483
7	30.916	32.683	1.360	6.633	5.333	1.110	20.043	13.342	29.148	0.451
LSD($p \leq 0.05$)	3.050	2.248	0.176	0.648	1.195	0.136	3.241	3.084	2.836	0.127

Data in Table 4 reveals heterosis % calculated as the F_4s deviated from mid parental values for the studied characters. The cross 4×5 recorded maximum positive heterosis values for seeds weight plant^{-1} (208.258%) and most important components such as pods number plant^{-1}, pod weight plant^{-1}, seeds number pod^{-1} and biological weight plant^{-1} reaching 120.495, 119.583, 42.320 and 129.308% respectively, while the cross 2×6 recorded the maximum positive heterosis values for average pod weight, pod length, seeds weight pod^{-1} and 100-seed weight reaching 43.282, 43.805, 37.328 and 13.984% respectively. The highest positive heterosis values indicate to the dominance gene effects for the parent with high value, while the negative heterosis values confirm the partial dominance gene effect for the parent with the low value. When a cross has high heterosis it is assumed that the two parents are more genetically diverse than the parents of crosses with low or no heterosis, (14). Kosev, (18) conducted a field study on breeding and genetic assessment of some quantitative characters in pea and showed the highest positive value of heterosis for seeds number pod^{-1}. Positive true heterosis for the investigated traits was found in all crosses of F_1 generations. All traits except some traits had epistatic gene effects (17). Borah, (7) and several researchers (1, 3, 6, 8, 9, 11, 12, 22, 27, 34 and 46), which reported for behavior of negative or feebly positive heterosis for traits of pea.

Table 4. % Heterosis values for F_4 crosses of the studied characters

Crosses	Pods no. plant^{-1}	Pods weight plant^{-1} (g)	Average pod weight (g)	Pod length (cm)	Seeds no. pod^{-1}	Seeds weight pod^{-1} (g)	100-seed weight (g)	Seeds weight plant^{-1} (g)	Biological weight plant^{-1} (g)	Harvest Index
1 x 2	-1.801	23.580	0.979	-8.549	-8.605	9.161	5.020	36.000	56.542	-28.027
1 x 3	-33.276	-5.140	-14.271	-6.054	-4.600	-17.241	0.961	-4.363	16.992	-22.698
1 x 4	17.712	9.338	4.100	2.564	13.793	14.427	8.288	15.544	40.056	-8.772
1 x 5	25.698	50.605	-2.763	-1.720	-3.812	-7.726	-14.832	33.726	97.526	-15.220
1 x 7	6.175	3.175	-7.202	6.628	-15.650	-14.912	0.098	-17.874	34.033	-42.087
1 x 7	0.843	-10.590	-4.206	4.523	1.449	-4.721	-2.339	6.747	-9.524	26.719
2 x 3	-34.395	-11.669	-12.648	1.027	-12.105	-14.539	-6.375	-32.054	-21.305	-17.281
2 x 4	45.293	47.470	-0.385	-10.526	-2.857	9.215	12.414	97.415	-12.563	103.903
2 x 5	63.051	27.176	7.163	-10.156	18.831	1.939	2.018	102.316	36.885	47.874
2 x 6	-29.519	17.837	43.282	43.805	9.302	37.328	13.984	-29.612	6.972	-40.441
2 x 7	10.226	11.309	27.441	6.561	-3.205	12.087	3.642	45.204	56.527	-9.067
3 x 4	-10.975	5.992	-13.262	-10.185	-11.509	-11.057	-3.991	5.324	4.517	12.148
3 x 5	47.413	73.190	6.346	0.820	9.896	0.498	-9.174	121.715	95.222	54.751
3 x 6	-47.615	-8.190	9.003	26.168	7.143	11.392	-3.566	-35.162	-21.269	-12.928
3 x 7	-52.702	-38.754	-32.242	6.472	2.062	-12.415	-14.258	-23.106	6.281	-33.458
4 x 5	120.495	119.583	23.980	41.667	42.320	24.410	-12.702	208.258	129.308	44.469
4 x 6	-24.939	-28.381	2.911	8.000	-4.225	17.914	-60.745	-36.820	2.624	-36.231
4 x 7	47.726	23.323	-0.904	-4.274	4.025	10.145	-11.823	91.794	115.921	-9.360
5 x 6	-19.991	-6.390	10.544	1.124	8.046	16.283	0.494	-30.824	-35.435	16.774
5 x 7	68.968	66.917	14.399	2.211	8.861	15.613	5.294	201.216	100.811	70.828
6 x 7	7.501	8.776	6.424	6.628	3.977	16.843	-29.670	8.936	-3.348	11.635
S.E	9.554	8.060	3.516	3.280	2.774	3.209	3.549	16.215	10.815	8.705

Table 5 represents the gca effect for the parents due to the studied characters. Parent 2 showed maximum positive gca effect values for the characters average pod weight, pod length and seeds weight pod^{-1} reaching 0.334, 1.478 and 0.139 respectively, while parent 4 recorded maximum positive gca effect values for pods number plant^{-1}, seeds weight plant^{-1} and biological weight plant^{-1} reaching 6.184, 2.641 and 6.756 respectively. Parent 2 showed maximum negative gca effect value for pods number plant^{-1} and harvest index with -5.423 and -0.048 respectively, while parent 3 gave maximum negative gca effect value for pods weight plant^{-1}, seeds weight plant^{-1} and biological weight plant^{-1} reaching -3.452, -2.340 and -4.290 respectively. Parents with high positive gca effect value signify their contribution in the inheritance of these characters to their crosses, while the parents with negative gca effect values express their contribution in the reduction of the values of these characters in some of their crosses. Singh *et al.*, (38) reported that the gca variances were highly significant for all the traits. Kumar and Jain (20) conducted field trial in pea and observed that variety Arka Ajeet showed highest gca effects for characters including pods number plant^{-1}. The cultivar had revealed Bonneville higher gca for earliness, pods number plant^{-1} and pod yield plant^{-1}. Singh *et al.,* (37) observed higher values of variance due to gca for pod length and pod yield plant^{-1} showed presence of additive gene action while it was non additive for pods number plant^{-1} based on both the generations. Similar results were observed perversely by (1 and 46) and F$_2$ crosses and their parents (3). The results indicated that Parent (Petit provencal) showed the best gca in the desirable direction for pods number plant^{-1}, seeds number plant^{-1}, seeds number pod^{-1}, seed yield plant^{-1} and seed yield plant^{-1} (6).

Table 5. Estimation of gca for the parents of the studied characters

Parents	Pods no. plant^{-1}	Pods weight plant^{-1} (g)	Average pod weight (g)	Pod length (cm)	Seeds no. pod^{-1}	Seeds weight pod^{-1} (g)	100-seed weight (g)	Seeds weight plant^{-1} (g)	Biological weight plant^{-1} (g)	Harvest Index
1	0.152	0.532	-0.088	-0.499	-0.085	-0.025	-0.807	0.226	-3.824	0.060
2	-5.423	1.402	0.334	1.478	-0.519	0.139	5.828	-0.867	0.873	-0.048
3	-4.343	-3.452	0.057	1.052	0.693	0.091	-0.732	-2.340	-4.290	-0.011
4	6.184	1.212	-0.200	-1.088	-0.093	-0.145	-2.752	2.641	6.756	-0.026
5	-0.824	-0.607	0.039	-0.096	0.063	0.058	1.655	-0.506	-2.999	0.014
6	1.298	-2.387	-0.082	-0.585	0.211	-0.107	-3.292	-0.452	1.439	-0.028
7	2.956	3.300	-0.060	-0.262	-0.270	-0.012	0.100	1.298	2.045	0.038
S.E	0.507	0.374	0.029	0.108	0.199	0.023	0.539	0.513	0.471	0.021

Table 6 represents the sca effect value for F$_4$ crosses due to the studied characters. The cross 2×6 recorded maximum positive sca effect values for average pod weight, pod length, seeds weight pod^{-1} and 100-seed weight with 0.475, 2.603, 0.274 and 2.959 respectively, while the cross 4×5 produced maximum positive sca effect value for pods number plant^{-1}, pods weight plant^{-1}, seeds number pod^{-1} and seeds weight plant^{-1} recording 15.902, 12.839, 1.596 and 11.066 respectively. The crosses with high positive sca effect values confirming their superiority values comparing to their parents in these characters. Singh *et al.,* (38) derived information on combining ability in garden pea involving twenty one crosses and seven parents. The sca variances were highly significant for all the traits. The sca variances were predominant in comparisons to gca variances for all the characters that indicated the greater contribution of non-additive gene action in the expression of these characters. The sca variance component was predominant indicating the importance of non-additive gene effects for all the characters except for peas pod^{-1} and pod yield which were influenced by additive gene action, suggesting their improvement through pure line selection (16). The cross combinations involving poor x poor, good x good and poor x good general combining parents with highest significant sca effects may be obtained for different horticultural traits. Crosses having both the parents as poor general combiners may involve dominance x dominance or epistatic interaction. Such crosses may not give good transgressive sergeants' in later generation. The crosses involving good x good general combiners and showing high sca effects could be utilized for the purpose of developing high yielding genotypes and obtaining transgressive sergeants' in F$_2$ generation (31). The variance components due to sca were larger than that of gca for most studied character (1, 3, 46 and 47). The cross (Thomas laxton x Petit provencal) exhibited significant sca effect in a desirable direction for pods weight plant^{-1}, pods number plant^{-1}, seeds number plant^{-1}, seed yield plant^{-1} and seed yield plant^{-1} (6).

Table 6. Estimation of sca for the F_4 crosses of the studied characters

Crosses	Pods no. plant^{-1}	Pods weight plant^{-1} (g)	Average pod weight (g)	Pod length (cm)	Seeds no. pod^{-1}	Seeds weight pod^{-1} (g)	100-seed weight (g)	Seeds weight plant^{-1} (g)	Biological weight plant^{-1} (g)	Harvest Index
1 x 2	-0.604	3.542	-0.032	-0.649	-0.263	0.113	-0.033	3.772	10.742	-0.089
1 x 3	-4.509	-0.566	-0.063	-0.390	-0.041	-0.112	0.540	0.595	1.200	-0.052
1 x 4	0.723	-1.307	0.096	0.251	0.778	0.138	1.967	-1.172	1.010	-0.019
1 x 5	-1.002	3.456	-0.065	-0.075	-0.511	-0.094	-2.716	-1.694	5.743	-0.099
1 x 6	6.445	1.532	-0.134	-0.086	-0.826	-0.188	0.847	0.199	10.438	-0.130
1 x 7	-1.409	-4.230	-0.011	0.358	0.189	-0.037	0.069	-1.955	-12.662	0.176
2 x 3	-3.164	-3.565	-0.223	-0.034	-0.607	-0.180	-1.922	-4.617	-7.646	-0.054
2 x 4	5.998	6.551	-0.112	-0.927	-0.289	-0.004	2.515	7.658	-12.740	0.291
2 x 5	2.858	-2.876	-0.058	-1.053	0.556	-0.070	-0.125	1.490	0.019	0.059
2 x 6	-4.404	3.778	0.475	2.603	0.574	0.274	2.959	-3.043	4.472	-0.113
2 x 7	0.427	0.780	0.351	0.381	-0.178	0.072	0.557	1.077	10.899	-0.067
3 x 4	-2.831	-0.348	-0.082	-0.834	-0.833	-0.100	0.728	-1.721	-4.237	0.034
3 x 5	9.151	8.429	0.142	-0.094	0.278	0.044	-0.972	7.566	14.675	0.140
3 x 6	-7.136	0.683	0.157	1.195	0.596	0.134	0.972	-1.686	-4.235	0.014
3 x 7	-12.623	-9.895	-0.402	0.373	0.178	-0.110	-1.514	-5.060	-3.359	-0.157
4 x 5	15.902	12.839	0.213	2.347	1.596	0.148	-1.172	11.066	19.394	0.025
4 x 6	-9.333	-8.574	-0.068	-0.264	-0.452	0.010	-6.851	-6.972	-2.542	-0.119
4 x 7	8.412	3.020	-0.021	-0.386	-0.037	0.017	-0.547	6.071	25.814	-0.092
5 x 6	-7.663	-6.063	-0.038	-0.656	-0.007	0.040	1.442	-6.087	-15.903	0.040
5 x 7	7.060	8.830	0.117	-0.045	-0.059	0.110	2.143	9.708	8.213	0.158
6 x 7	5.133	3.374	-0.018	-0.323	0.159	0.054	-3.373	2.390	-4.364	0.084
S.E	1.434	1.057	0.083	0.305	0.562	0.064	1.524	1.450	1.334	0.060

The estimation of $\sigma^2_{\hat{g}ii}$ for the parents illustrate in Table 7 due to studied characters. Parent 2 had the highest gca effect variance for average pod weight, pod length and 100-seed weight reaching 0.109, 2.151 and 33.096 respectively, while parent 4 showed maximum value for $\sigma^2_{\hat{g}ii}$ for pods number plant^{-1}, seeds weight pod^{-1}, seed weight plant^{-1} and biological weight plant^{-1} with 37.472, 0.019, 6.188 and 44.978 respectively. The parents posses high positive values for $\sigma^2_{\hat{g}ii}$ indicating their tendency to contribute the inheritance of these characters to their crosses.

Table 7. Estimation of ($\sigma^2_{\hat{g}ii}$) for the parents of the studied characters

Parents	Pods no. plant^{-1}	Pods weight plant^{-1} (g)	Average pod weight (g)	Pod length (cm)	Seeds no. pod^{-1}	Seeds weight pod^{-1} (g)	100-seed weight (g)	Seeds weight plant^{-1} (g)	Biological weight plant^{-1} (g)	Harvest Index
1	-0.748	-0.136	0.005	0.215	-0.111	-0.001	-0.219	-0.738	13.9578	0.0023
2	28.635	1.548	0.109	2.151	0.150	0.018	33.096	-0.037	0.0955	0.0010
3	18.086	11.501	0.001	1.073	0.361	0.007	-0.336	4.687	17.7392	-0.0012
4	37.472	1.050	0.038	1.150	-0.110	0.019	6.700	6.188	44.9785	-0.0007
5	-0.092	-0.050	-0.001	-0.026	-0.115	0.002	1.868	-0.533	8.3300	-0.0011
6	0.913	5.277	0.004	0.307	-0.074	0.010	9.968	-0.585	1.4051	-0.0006
7	7.968	10.468	0.001	0.034	-0.045	-0.001	-0.861	0.896	3.5160	0.0001

The estimation of $\sigma^2_{\hat{s}ij}$ for the parents of studied characters represent in Table 8. Parent 2 recorded maximum value for the variance of ŝij due to average pod weight, pod length and harvest index with 0.408, 9.218 and 0.113 respectively, while parent 4 showed maximum value for the variance of $\hat{s}_{ij}$ due to pods number plant^{-1}, seeds number pod^{-1} and biological weight plant^{-1} recording 453.217, 3.826 and 1228.478 respectively. Parents with maximum variance for $\hat{s}_{ij}$ effect confirming their abilities to transfer these characters to one or a few number of their crosses.

Table 8. Estimation of ($\sigma^2_{\hat{s}ij}$) for the parents of the studied characters

Parents	Pods no. plant^{-1}	Pods weight plant^{-1} (g)	Average pod weight (g)	Pod length (cm)	Seeds no. pod^{-1}	Seeds weight pod^{-1} (g)	100-seed weight (g)	Seeds weight plant^{-1} (g)	Biological weight plant^{-1} (g)	Harvest Index
1	63.725	45.656	0.030	0.686	1.344	0.086	9.977	20.613	418.373	0.0652
2	72.069	90.227	0.408	9.218	0.880	0.126	16.813	104.754	473.190	0.1131
3	330.334	181.477	0.260	2.335	1.218	0.083	6.409	108.249	320.674	0.0476
4	453.217	291.126	0.073	7.255	3.826	0.047	57.046	268.823	1228.478	0.1061
5	452.305	369.729	0.082	6.974	2.888	0.047	14.100	313.999	943.072	0.0564
6	282.013	137.638	0.268	8.724	1.286	0.129	68.524	101.445	423.572	0.0493
7	308.442	214.885	0.299	0.668	0.129	0.034	18.874	167.395	1043.244	0.1003

The estimation of some genetic parameters due to the studied characters represent in Table 9. It was reveal from this Table that the ration of σ^2_{gca} /σ^2_{sca} value are less than one for all characters except 100-seed weight which was more than one, and this reflected the average degree of dominance values due to the studied characters, in which they were more than one for all characters except 100-seed weight and the maximum value for average degree of dominance reached to 3.986 for seeds weight plant^{-1}. These results confirm the importance of non additive gene effect in controlling the inheritance of most characters. Heritability in broad sense was found to be highest for most characters except seeds number pod^{-1} and harvest index which recorded 0.460 and 0.736vrespectively they are found to be moderate. The highest value for heritability in broad sense recorded by biological weight plant^{-1} recording 0.984 and followed by pods number plant^{-1} with 0.966 and pods weight plant^{-1} with 0.965. Heritability in narrow sense for pods weight plant^{-1}, seeds number pod^{-1}, seeds weight pod^{-1}, biological weight plant and harvest index were found to be low, while for the other characters they are found to be moderate. According to these results hybridization method is found to be the best to improve these characters. Tawfiq and Abdulla (47) carried out genetic analysis between seven pea in a half diallel crosses and showed that the gca/sca variance ratio to be more than one in most studied traits, indicate the importance of additive gene effect in the inheritance of all characters. Sharma and Sharma (30) observed the prevalence of over dominance for most of the traits. However, additive and dominance genetic variance were highly significant for some studied characters. Sharma and Bora (33) reported higher values of heritability in broad sense and genetic gain indicating that the additive gene actions are important in determining the character pod yield. Sharma *et al.* (31) reported that additive genetic variance in pea was significant for seed yield plant^{-1}, while epistatic gene action was positive for pods number and seeds plant^{-1}. There was a positive additive, dominance and over dominance gene action for seeds plant^{-1}. For self-pollinated crop (as a pea *Pisum sativum* L.), is preferable to be used narrow sense heritability which reflects additive genetic contribution to phenotypic expression of traits, because only additive gene effects can be fixed to progeny. When traits have high values for narrow sense heritability, it is recommended to begin selection in F_2 and in these cases can be successful applied pedigree selection (23). The ratio of σ^2_{gca} to σ^2_{sca} was less than one for the seven characters indicating the importance of non-additive gene action for these characters. This is indicative that the material used in the present study was heterozygous and that this heterozygosity contributes towards the non-additive component. Further the non-additive component of genetic variance is not fixable in the segregating generations; therefore, its exploitation is limited to crosses only. Similar observations have also been reported by several researchers (19, 21, 42 and 44). Low heritability (narrow sense) was obtained for all traits, low heritability in case of all traits suggest no fixable component of variation governing these traits and therefore, F_1 population should be exploited to utilize these components of variation. Thus, these traits can be improved by making selections among the recombinants obtained through segregating populations. The results are in conformity with earlier report of (34 and 40). The heritability estimates were low in the present study therefore excepted genetic gains through mass, pedigree or family selection would not yield encouraging results (39). Shinde, (35), which reported for moderate to high inheritance of investigated from them quantitative traits. Recording the ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ to be more than one in these characters. The average degree of dominance was more than one in most studied characters, confirming the importance of non additive gene effect in the inheritance of these characters. Heritability in broad sense was found to be high in most studied characters. Heritability in narrow sense was high for some characters, while it was moderate for some other characters (47). An estimate of heritability (narrow sense) was low due to the major role of environmental factors in expression of grain yield and yield components in pea. Thus, delay selection was suggested for breeding of stable yielding lines. Correlation studies showed that the grain yield was significant positive correlated with pod number, seeds pod^{-1} and pod yield. The highest direct effect was exhibited by pod yield, indirect effects, especially through the pod number in the parents and crosses (8). Several genetic studies have been conducted to understand the genetic control of grain yield and its components in pea. Similar results recorded perversely by (1 and 46) and F_2 crosses and their parents (3). Studies of (19, 42 and 44) have shown that additive genes control the genetic direction of grain yield. In contrast, (21, 34 and 40) reported that grain yield is controlled mainly by non-additive genes.

Table 9. Estimation of some genetic parameters for the studied characters

Parameters	Pods no. plant^{-1}	Pods weight plant^{-1} (g)	Average pod weight (g)	Pod length (cm)	Seeds no. pod^{-1}	Seeds weight pod^{-1} (g)	100-seed weight (g)	Seeds weight plant^{-1} (g)	Biological weight plant^{-1} (g)	Harvest Index
Mse´	1.157	0.629	0.004	0.052	0.178	0.002	1.307	1.183	1.000	0.002
σ^2_{gca}	5.381	1.787	0.010	0.284	0.043	0.003	3.080	0.812	5.224	0.0004
$\sigma^2_{sca}=\sigma^2D$	22.552	13.922	0.013	0.299	0.066	0.005	1.422	12.897	49.408	0.004
$\sigma^2_{gca}/\sigma^2_{sca}$	0.239	0.128	0.739	0.950	0.643	0.660	2.166	0.063	0.106	0.092
σ^2A	10.762	3.575	0.019	0.568	0.085	0.007	6.160	1.624	10.447	0.001
$\bar{a}$	2.047	2.791	1.163	1.026	1.247	1.231	0.679	3.986	3.076	3.297
$h^2_{b.s}$	0.966	0.965	0.893	0.943	0.460	0.842	0.853	0.925	0.984	0.736
$h^2_{n.s}$	0.312	0.197	0.533	0.618	0.259	0.479	0.693	0.103	0.172	0.114

Recommendation

Continuous breeding programs are required to reveals pea varieties for high yielding crosses like Joneor×Packland and parent Arvena at autumn season. During this study, most of the growth yield and yield component traits showed the non additive genetic variance which can be exploited by adopting the heterosis breeding program. More investigation were required to evaluate more pea cultivars at both autumn and spring seasons which survival potential to the climatically conditions prevailing in Sulaimani region.

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