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GENETIC EVALUATION OF DEVELOPMENTAL AND YIELD CHARACTERS AND ISOZYMES POLYMORPHISM IN SOME PEA CROSSES

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ABSTRACT

This study was carried out during three successive seasons, 2001, 2002, and 2003 at the Experimental Farm of El-Kassasein Horticulture Research Station. The main objective of this work was to study the performance of developmental and yield characters of the three pea *(Pisum sativum)* parental genotypes and their F_1, F_2, BC_1 and BC_2 also to study the type of gene action and the polymorphism in the esterase and malate dehydrogenase molecular forms in each of root, stem, leaf and seed tissues. The six generations, P_1, P_2, F_1, F_2, Bc_1 and Bc_2 were grown in 2003 season and data were recorded on the means of all generations.

The F_1 "Atol X Mamoth" was higher than both parents for number of seeds per pod, weight of seeds per pod and diameter per pod. The BC_1 cross "Mammoth X Jurbo" had the highest mean values for all characters except for stem length and number of leaves per plant. The Bc_2 of the cross "Jurbo X Mammoth" had the highest mean values for all characters except for the stem length.

Significant values of the three scaling tests indicated the presence of non-allelic interaction in almost all characters of the four crosses.

Both positive and negative signifiant additive gene effects were observed in most characters of three out of the four crosses. Meanwhile, negtive significant additive gene effects were observed in four characters of the cross "Mammoth X Atol".

The dominance gene effects were significant for all characters over all crosses except for number of branches in all crosses, growth rate and weight of seeds per pod in the cross "Mammoth X Atol" indicating that the improvement of these characters could be achieved through recurrent selection.

Non-allelic interactions of the types "additive X additive", "additive X dominance" and "dominance X dominance" were found to be controlling the inheritance of most characters in all the four crosses.

Isozyme polymorphism showed both qualitative and quantitative changes in either isoesterase or malate dehydrogenase banding patterns. A total of twenty-two and thirteen molecular forms was observed for esterase and malate dehydrogenase isozymes, respectively.

Tissue specificity in segregated generations showed that the different molecular forms could be assigned to ten loci and five loci for the esterase and malate dehydrogenase isozymes, respectively.

These results indicated that both the developmental and yield characters under study are expressed through biochemical path ways which might not be affected directly by either esterase or malate dehydrogenase.

INTRODUCTION

Since yield is known to be a complex trait and highly affected by environmental conditions thus, direct selection for yield is not expected to be effective. Therefore, the breeder avoids selection for yield and prefers to

select for its components individually. The value of genotype is not an inherent absolute quality of the genotype but depends on the range of environments over which it has been tested. So, the estimates of genotypic variance would depend on the environment under which the material will be tested.

Many investigators worked on pea to study observed the inheritance of morphological, phsiological, yield characters and the three types of gene effects; additive, dominance and epistasis, (Oommen *et al.*,1999). In pea, the presence of additive, dominance gene effects and epistatic interaction in most crosses indicated the importance of both additive and non-additive gene action in the expression of most characters. However, the fixable gene effect additive x additive significantly contributed to the inheritance of days to flowering, days to maturity, seeds/pod, seed weight and harvest index, while the dominance gene effect mainly govened the inheritance of pods/plants. Both additive x additive dominance x dominance gene effects were important in the inheritance of plant height, seed yield and yield/plant. Duplicate type of epistasis was prevalent in most of the cases (Tyagi and Srivastava 2001; Vinay-Bhardwaj *et al.*, 2002 and Hooda *et al.*, 2003).

Electrophoretic variations are considered the direct result of genetic differences (Gottlieb, 1981). Variations in the level of enzyme molecular forms have provided a reasonably precise and quantitative measure of genetic identity and/or divergence between populations, subspecies, species, etc. Most studies have demonstrated high genetic identity between con-specific populations and between sub-specific taxa and generally between morphologically similar species (Gottlieb, 1981 and Crawford,1983).

Esterases, as a substrate non-specific enzymes, provide a larger number of molecular forms (Crawford, 1983) and controlled by many loci ranged from ten in maize (MacDonald and Brewbacker, 1975) to eighteen loci in pea by Guirgis *et al.* (2000).

Furthermore, malate dehydrogenase molecular forms are lower in their polymorphism and were found to be controlled by two loci which are controlling at least about nine isozymes with two alleles in each locus (Powling *et al.*, 1981), five loci in maize (Newton and Schwartz, 1980) and by six loci in pea (Guirgis *et al.*, 2000).

This investigation was conducted to estimate the performances, genic interaction, and the molecular forms of both esterase and malate dehydrogenase in four different tissues. The study extended to investigate the association among the scores of isozymes intensity and the performance of developmental and yield characters over the parental, F_1, F_2, Bc_1 and Bc_2 of the four crosses.

MATERIALS AND METHODS

This investigation was carried out at the Experimental Farm of El-Kassasein Hortiulture Research Station, during the seasons of 2001, 2002 and 2003, using three pea (*Pisum sativam* L.) parental genotypes; Jurbo as P_1, Atol as P_2 and Mammoth as P_3.

In the growing season 2001, the three parental genotypes were crossed as follows, cross 1(Atol X Mammoth), cross 2 (Mammoth, X Atol), cross 3

(Mammoth X Jurbo) and cross 4 (Jurbo X Mammoth) to produce the F_1 hybrid seeds. In October 2002, seeds of the parental and (F_1's) were sown. The F_1 hybrids were self-pollinated to produce F_2 population seeds. Each F_1 hybrid was also, crossed to both parents to produce Bc_1 (F_1 x P_1) and Bc_2 (F_1 x P_2). Self-pollination was also made for the parents to get parents' self seeds. Moreover, the parents were re-crossed to produce more F_1 hybrid seeds.

In October 2003 the parents, F_1, hybrids F_2 and backcrosses were planted in a randomized complete blocks design with four replications. Each replicate included two rows of each of the F_1, Bc_1, Bc_2 and the parents, in addition to eight rows of the F_2 populations. Two seeds per hill were sown in a single hill for each dripper. The drippers were 20 cm apart and the irrigation lines were 60 cm. in width. Each plot was 6 m^2. The agricultural treatments were similar for all entries under study.

Ten plants from each entry over all replications were randomly chosen for measuring all the developmental, and yield characters. The developmental characters recorded were stem length (cm), number of leaves per plant, number of branches per plant and growth rate which was measured as an average rate of the difference in stem length per day. The total yield characters were the weight of green pods per plant (g.) and number of pods per plant. The pod quality characters were measured as: number of seeds per pod, seeds weight per pod (g), pod length (cm.) and pod diameter (cm).

Isozyme electrophorsis:

Randomly samples were taken from each of the P_1, P_2, F_1, F_2, Bc_1 and Bc_2 for the four crosses. These samples were used to study the isoesterase (Est) and Malate dehydrogenase (Mdh) molecular forms in root, stem and leaf tissues after forty days of sowing date and from mature seeds as well.

Esterase (Est) and Malate dehydrogenase (Mdh) isozyme system were given the designations (Est, Ec 3.1.1.1) and Mdh, (Ec 1.1.1.37), respectively, in the report of commission of enzymes (International Union of Biochemists, 1978). Both enzymes were screened in all the plant materials at the Biotechnology Lab., El-Kassasein Horticulture Research Station.

1- Enzyme extraction, gel preparation, sample loading and electrophoresis:

Equal weight of fresh samples, representing four tissues collected from the marked plants of P_1, P_2, F_1, F_2, Bc_1 and Bc_2 generations and were crushed directly in an ice-cold (0-4°C) 1M tris buffer; pH7. The enzyme extraction buffer and procedures were applied according to Tanksley and Orton (1983). A 17.5% discontinuous non-dissociating, polyacrylamide gel mixture, using a stock of 30% acrylamide N', N', Bis-methylene acrylamide, was loaded in a 20x20 cm Bio-Rad PROTEAN-II vertical slab cell.

Sample volumes with equal protein concentrations were used for loading in gel after determining the concentration of protein in all samples according to Bradford (1976). The buffers used in preparing gels and samples as well as sample loading and electrophoretic conditions were discribed by Guirgis *et al.* (1996).

2- Staining and data collection:

Malate dehydrogenase isozymes were stained according to the procedures of Brown *et al.* (1978), meanwhile, the procedures of Kahler and Allard (1970) were applied with the modification suggested by Tanksley and Rick (1980) for detecting non-specific esterase isozymes. The traveled distances by isozyme bands were recorded directly on a graph paper as relative mobility values, RF, using a UVP fluorescent transilluminator. Then gels of the isozymes banding pattern were photographed.

C- Statistical Procedures:

Scaling tests which provide information regarding absence or presence of gene interactions were carried out according to Mather (1949). The three parameters A, B and C as well as their variances were calculated. Estimates of the types of gene effects were obtained using the relationships given by Jinks and Jones (1958).

Spearman's rank correlation coefficients (Spearman, 1904) were also computed to determine the association relationships between the mean performance of the studied populations and the isozymes intensity scores according to Nei (1971 and 1973) using the formula adopted by Brown and Weir (1983).

RESULTS AND DISCUSSION

The mean performance of the studied populations:

Tables 1 and 2 show the performance of the six populations for ten developmental and yield characters, in the four crosses. In Table 1, data showed that the means of the F_1 cross "Atol X Mammoth" were higher than both parental ones for number of seeds per pod, weight of seeds per pod parental ones and diameter per pod, but they had the second highest for stem length, number of leaves per plant and weight of pods per plant. Meanwhile, the Bc_2 was the highest for number of leaves per plant, weight of pods per plant, number of pods per plant and length of pod. Also, the mean of the Bc_2 were the second highest values for number of seeds per pod and pod diameter.

The cross "Mammoth X Atol" performance of Bc_1 had the highest values for number of branches per plant, growth rate, weight of pods per plant, number of pods per plant and number of seeds per pod. Meanwhile, it occupied the second order for stem length, number of leaves per plant, length of pod and diameter of pod.

The cross "Mammoth X Jurbo" in Table 2, showed that performance of Bc_1 had the highest mean values for all characters except for stem length and number of leaves per plant which were the second highest.

The Bc_2 of the cross "Jurbo X Mammoth" had the highest mean values for all the characters except the stem length per plant. Meanwhile, Bc_1 was the second one for number of branches per plant, weight of pods per plant, number of pods per plant, number of seeds per pod and weight of seeds per pod.

Table 1. Means of P_1, P_2, F_1, F_2, Bc_1 and Bc_2 and standard error for developmental and yield characters in two pea crosses.

Geno-types	Stem length (cm)	No. leaves/ plant	No. Branches/ plant	Growth Rate (cm/day)	Yield/plant		Pod characters			
					Pods wt. (g)	No. pods	No. seeds	Seeds wt. (g)	Length (cm)	Diameter (cm)
"Atol X Mammoth"										
P_1	81.00±4.55	73.75±2.06	4.50±0.65	0.63±0.01	102.66±7.41	-27.00±0.91	7.23±0.22	2.56±0.14	7.50±0.04	1.40±0.04
P_2	197.00±1.58	87.50±3.23	4.00±0.41	2.23±0.02	137.41±4.92	32.50±1.44	6.53±0.21	2.24±0.07	9.35±0.06	2.20±0.08
F_1	196.25±3.75	90.00±3.14	4.50±0.29	2.26±0.10	181.38±0.93	46.50±1.85	7.73±0.011	2.91±0.03	10.33±0.13	2.53±0.05
F_2	180.00±6.12	82.50±0.87	4.50±0.29	2.54±0.04	156.72±1.00	42.25±1.31	6.50±0.04	2.65±0.03	8.45±0.21	1.53±0.05
Bc_1	165.75±4.05	84.50±0.65	5.25±0.48	2.69±0.02	176.96±5.07	54.25±2.84	7.13±0.05	2.81±0.03	10.48±0.17	2.35±0.06
Bc_2	195.25±2.75	97.50±3.23	4.50±0.29	0.43±0.04	229.62±14.90	55.00±1.78	7.38±0.21	2.59±0.02	11.5±0.04	2.43±0.08
"Mammoth X Atol"										
P_1	197.00±1.58	87.5±3.23	4.00±0.41	2.23±0.02	137.41±4.92	32.50±1.44	6.50±0.21	2.24±0.07	9.35±0.06	2.20±0.08
P_2	81.00±4.55	73.75±2.06	4.50±0.29	0.64±0.02	102.66±7.41	27.00±0.91	7.23±0.22	2.56±0.14	7.50±0.04	1.40±0.04
F_1	97.25±4.40	97.00±1.47	5.00±0.41	2.43±0.02	141.36±0.58	47.25±1.31	7.60±0.04	2.94±0.01	9.75±0.06	2.43±0.09
F_2	87.75±0.9[illegible]	77.75±1.31	5.50±0.29	1.96±0.06	130.09±5.44	40.00±2.04	7.18±0.22	2.73±0.01	9.28±0.05	2.28±0.09
Bc_1	157.00±2.86	89.50±8.19	5.50±0.29	2.89±0.03	157.17±4.39	49.75±1.65	8.03±0.09	2.56±0.13	9.70±0.04	2.58±0.09
Bc_2	91.75±3.45	84.00±1.87	5.25±0.48	0.66±0.02	128.75±3.73	44.25±1.49	7.75±0.09	2.86±0.01	9.30±0.07	2.78±0.05

Table 2. Means of P_1, P_2, F_1, F_2, Bc_1 and Bc_2 and standard error for developmental and yield characters in two pea crosses.

Geno-types	Stem length (cm)	No. leaves/ plant	No. Branches/ plant	Growth Rate (cm/day)	Yield/plant		Pod characters			
					Pods wt. (g)	No. pods	No. seeds	Seeds wt. (g)	Length (cm)	Diameter (cm)
"Mammoth X Jurbo"										
P_1	197.00±1.58	87.50±3.23	4.00±0.41	2.23±0.02	137.41±4.92	32.50±1.44	6.53±0.21	2.21±0.09	9.35±0.06	2.20±0.08
P_2	77.50±2.10	50.75±2.17	3.5±0.29	0.88±0.04	62.42±1.56	19.50±0.48	5.98±0.27	2.14±0.06	8.03±0.19	1.83±0.06
F_1	95.75±1.38	96.00±2.27	3.5±0.29	2.36±0.19	164.59±1.07	42.50±1.04	7.43±0.15	2.50±0.03	9.58±0.05	2.48±0.08
F_2	157.50±3.23	87.00±3.24	5.00±0.41	1.87±0.05	139.76±2.30	41.00±1.08	6.70±0.07	2.28±0.03	9.28±0.18	2.25±0.06
Bc_1	157.50±2.10	94.00±2.61	5.00±0.41	2.36±0.05	234.02±6.30	53.00±1.78	7.50±0.19	2.96±0.02	10.15±0.06	2.63±0.05
Bc_2	95.75±2.21	89.75±2.06	4.00±0.65	1.76±0.03	183.44±5.73	50.25±1.93	6.60±0.11	2.95±0.02	9.55±0.11	2.55±0.06
"Jurbo X Mammoth"										
P_1	77.50±2.10	50.75±2.17	3.50±0.29	0.88±0.04	62.42±1.56	19.25±0.48	5.98±0.27	2.14±0.06	8.03±0.19	1.83±0.06
P_2	197.00±1.58	87.50±3.23	4.00±0.41	2.23±0.02	137.41±4.92	32.50±1.44	6.53±0.21	2.21±0.09	9.35±0.06	2.20±0.08
F_1	202.50±2.53	93.50±1.71	3.75±0.48	2.08±0.26	152.13±7.15	35.75±1.49	7.18±0.09	2.54±0.06	10.43±0.14	2.33±0.05
F_2	151.50±1.19	85.25±2.06	4.00±0.41	2.26±0.03	102.31±0.92	31.25±1.25	7.25±0.12	2.22±0.10	9.50±0.11	2.25±0.06
Bc_1	166.25±3.75	88.50±1.55	4.50±0.65	2.09±0.06	187.18±5.25	44.25±1.11	7.45±0.06	2.77±0.05	10.38±0.13	2.30±0.06
Bc_2	193.75±1.65	97.75±2.87	5.25±0.48	2.86±0.03	191.40±3.28	46.00±2.27	7.93±0.34	2.87±0.12	10.50±0.07	2.55±0.06

Scaling tests:

The results of scaling tests A, B and C are presented in Table 3. In cross "Atol X Mammoth", the A, B anc C tests were significant for growth rate, weight of pods per plant, number of pods per plant and length of pod. Only A and C were significant for stem length, number of seeds per pod and diameter of pod. In other words, these results indicated that the non-allelic interactions are governing these characters. The three scaling tests A, B and C did not significantly differ the zero indicating that the additive dominance model could be adequate to interpret the gene effects for number of branches per plant and weight of seeds per pod.

Cross "Mammoth X Atol" showed that the A, B and C tests were significant for length of pod. However, only A and B were significant for growth rate, number of pods per plant, length of pod and diameter of pod. But A and C were significant for stem length, number of branches per plant and number of seeds per pod. Meanwhile, A, B and C were not significant for weight of seeds per pod indicating the absence of non-allelic interaction in this character.

In cross "Mammoth X Jurbo" the A, B and C tests were significant for stem length weight of pods per plant and number of pods per plant. Both A and B were significant for weight of seeds per pod, length of pod and diameter of pod. But A and C were significant for number of branches per plant. These results indicated the presence of genic interaction for these characters. Also, the results indicated the presence of "dominance x dominance" non-allelic interaction for stem length and number of branches per plant.

Cross "Jurbo X Mammoth" showed that the A, B and C tests were significant for growth of rate, weight of pods per plant and number of seeds per pod. This indicated the presence of "dominance X dominance" genic interaction for these characters. Both A and B were significant for number of leaves per plant, number of pods per plant, weight of seeds per pod, length of pod and diameter of pod. For stem length, the three scaling tests A, B and C did not significantly differ from zero. This indicating the absence of genic interaction for stem length.

These results were in common agreement with those obtained, by Tyagi-MK; Srivastava-CP (2001), Oommen-A, *et al.* (1999), Raj-Kumar, *et al.* (2001) and Vinay-Bhardwaj, *et al.* (2002).

Types of gene action:

Data in Tables (4) and (5) showed the types of gene action and the epistatic effects using generation means for all characters for the four crosses. The mean (m) values were highly significant and positive for all studied characters in all crosses.

In the cross "Atol X Mammoth", the additive gene effects (d) were significantly negative for stem length, number of leaves, weight of pods per plant and length of pod or significantly positive for growth rate and weight of seeds per pod (Table 4).

In the cross "Mammoth X Atol", the additive gene effects (d) were significantly positive or negative for all studied characters except for number of leaves per plant and number of branches per plant.

Table 3. Scaling tests (A, B and C) and their standard errors for developmental and yield characters in four pea crosses.

	Stem length (cm)	No. leaves/ plant	No. Branches/ plant	Growth Rate (cm/day)	Yield/plant		Pod characters			
					Pods wt. (g)	No. pods	No. seeds	Seeds wt. (g)	Length (cm)	Diameter (cm)
"Atol X Mammoth"										
A	54.25±10.02**	5.25±3.97	1.50±1.19	2.50±0.11**	69.89±12.59**	35.00±6.04**	-0.70±0.26*	0.14±0.16	3.13±0.36**	0.78±0.14**
B	-2.75±6.84	17.50±7.87*	0.50±0.78	-3.64±0.13**	140.46±30.21**	31.00±4.26**	0.50±0.48	-0.04±0.09	3.33±0.16**	0.13±0.18
C	49.50±26.07	-11.25±8.12	0.50±1.50	2.77±0.26**	24.05±9.93*	16.50±6.65*	-3.20±0.41**	-0.01±0.21	-3.70±0.87**	-2.55±0.23**
"Mammoth X Atol"										
A	19.75±7.39*	-5.50±16.76	2.00±0.82*	1.11±0.07**	35.55±10.08**	19.75±3.84**	1.93±0.27**	-0.07±0.27	0.30±0.12*	0.52±0.21*
B	5.25±9.36	-2.75±4.52	1.00±1.08	-1.76±0.05**	13.48±10.54	14.25±3.39**	0.68±0.28*	0.21±0.14	1.35±0.16**	1.73±0.14**
C	-121.50±10.79**	-44.25±7.14**	3.50±1.50*	0.11±0.24	-2.44±23.54	6.00±8.75	-0.25±0.92	0.24±0.17	0.75±0.24**	0.65±0.40
"Mammoth X Jurbo"										
A	21.25±4.70**	4.50±6.55	2.50±0.96*	0.13±0.21	166.0[illegible]±13.57**	31.00±3.98**	1.05±0.45*	1.22±0.10**	1.38±0.15**	0.58±0.15**
B	17.25±5.09**	32.75±5.18**	2.00±1.35	0.28±0.20	139.88±11.61**	38.75±4.03**	-0.20±0.38	1.46±0.08**	1.51±0.29**	0.80±0.16**
C	160.00±13.46**	17.75±14.28	5.50±1.8**	-0.36±0.42	30.03±10.76**	27.25±5.03**	-0.55±0.54	-0.22±0.17	0.57±0.75	0.03±0.32
"Jurbo X Mammoth"										
A	52.50±8.19	32.75±4.16**	1.75±1.41	1.22±0.28**	159.80±12.80**	33.50±2.72**	1.75±0.31**	0.86±0.13**	2.30±0.36**	0.45±0.14**
B	-12.00±4.45	14.50±6.80*	2.75±1.15	1.41±0.27**	93.26±10.87**	23.75±5.00**	2.15±0.72*	1.00±0.26**	1.23±0.21**	0.57±0.16**
C	-73.50±7.43	14.75±9.72	1.00±1.96	1.77±0.53**	-94.85±15.61**	1.75±6.02	2.15±0.61*	-0.57±0.43	-0.23±0.56	0.32±0.29

Table 4. Mean estimation of six parameter model of gene effects for developmental and yield characters in two pea crosses.

paraneter	Stem length (cm)	No. leaves/ plant	No. Branches/ plant	Growth Rate (cm/day)	Yield/plant		Pod characters			
					Pods wt. (g)	No. pods	No. seeds	Seeds wt. (g)	Length (cm)	Diameter (cm)
					"Atol X Mammoth"					
m	180.00±6.12**	82.50±0.87**	4.50±0.29**	2.54±0.04**	156.72±1.00**	42.25±1.31**	6.50±0.04**	2.65±0.03**	8.45±0.21**	1.53±0.05**
d	-29.50±4.89**	-13.00±3.29**	0.75±0.56	2.27±0.04**	-52.66±15.74**	-0.75±3.35	-0.25±0.22	0.21±0.03**	-1.03±0.18**	-0.07±0.10
h	59.25±26.75*	43.38±8.30**	1.75±1.68	-3.08±0.21**	247.64±32.05**	66.25±8.78**	3.85±0.50**	0.70±0.16**	12.05±0.91**	4.18±0.28**
i	2.00±26.38	34.00±7.44**	1.50±1.61	-3.92±0.18**	186.30±31.73**	49.50±8.52**	3.00±0.46**	0.19±0.14	10.15±0.90**	3.45±0.28**
j	57.00±10.91**	-12.25±7.61	1.00±1.35	6.14±0.09**	-70.57±32.71*	4.00±6.92	-1.20±0.52*	0.10±0.17	-0.20±0.36	0.65±0.22**
l	-53.50±32.60	-56.75±15.47**	-3.50±2.69	5.06±0.31**	-396.64±63.73**	-115.50±14.96**	-2.80±0.95**	-0.36±0.25	-16.60±1.11**	-4.35±0.46**
					"Mammoth X Atol"					
m	87.75±0.95**	77.75±1.31**	5.50±0.29**	1.96±0.06**	130.09±5.44**	40.00±2.04**	7.18±0.22**	2.73±0.01**	9.28±0.05**	2.28±0.09**
d	65.25±4.48**	5.50±8.40	0.25±0.56	2.23±0.04**	28.42±5.76**	5.50±2.23*	0.27±0.12*	-0.30±0.13*	0.40±0.08**	-0.20±0.10*
h	104.75±10.94**	52.38±17.77**	0.25±1.68	0.24±0.25	72.81±25.03**	45.50±9.43**	3.58±0.92**	0.44±0.26	2.22±0.26**	2.23±0.41**
i	146.50±9.73**	36.00±17.61*	-0.50±1.61	-0.75±0.25**	51.48±24.63*	28.00±9.30**	2.85±0.90**	-0.10±0.26	0.90±0.25**	1.60±0.39**
j	14.50±10.17	-2.75±17.23	1.00±1.22	2.87±0.08**	22.07±14.56	5.50±4.77	1.25±0.39**	-0.28±0.30	-1.05±0.18**	-1.20±0.22**
l	-171.50±20.88**	-27.75±34.36	-2.50±2.69	1.40±0.08**	-100.52±32.94**	-62.00±12.48**	-5.45±1.04**	-0.04±0.54	-2.55±0.41**	-3.85±0.56**

Table 5. Mean estimation of six parameter model of gene effects for developmental and yield characters in two pea crosses.

paraneter	Stem length (cm)	No. leaves/ plant	No. Branches/ plant	Growth Rate (cm/day)	Yield/plant		Pod characters			
					Pods wt. (g)	No. pods	No. seeds	Seeds wt. (g)	Length (cm)	Diameter (cm)
" Mammoth x Jurbo"										
UR	157.50±3.23**	87.00±3.24**	5.00±0.41**	1.87±0.05**	139.76±2.30**	41.00±1.08**	6.70±0.07**	2.28±0.03**	9.28±0.18**	2.25±0.06**
d	61.75±3.05**	4.25±3.33	0.50±0.76	0.60±0.06**	50.58±8.52**	2.75±2.63	0.90±0.22**	-0.09±0.03*	0.60±0.12**	0.08±0.08
h	-164.00±14.41**	46.38±14.87**	-1.25±2.27	1.58±0.29**	340.55±19.56**	59.13±6.92**	2.58±0.56**	3.21±0.14**	3.19±0.77**	1.81±0.32**
i	-123.50±14.28**	19.50±14.57	-1.00±2.24	0.77±0.21**	275.88±19.36**	42.50±6.80**	1.40±0.56*	2.89±0.13**	2.31±0.76**	1.35±0.30**
j	4.00±6.65	-28.25±7.71**	0.50±1.61	-0.15±0.12	26.16±17.80	-7.75±5.47	1.25±0.55*	-0.24±0.12*	-0.13±0.32	-0.23±0.19
l	85.00±18.17**	-56.75±19.51**	-3.50±3.55	-0.19±0.48	-581.78±35.72**	-112.25±11.65**	-2.25±1.02*	-5.56±0.21**	-5.19±0.90**	-0.73±0.45**
"Jurbo X Mammoth "										
m	151.50±1.19**	85.25±2.06**	4.00±0.41**	2.26±0.03**	102.31±0.90**	31.25±1.25**	7.25±0.12**	2.22±0.10**	9.50±0.11**	2.25±0.06**
d	-27.50±4.10**	-9.25±3.26**	-0.75±0.80	-0.78±0.07**	-4.22±6.19	-1.75±2.53	-0.48±0.35	-0.11±0.13	-0.13±0.15	-0.25±0.09**
h	179.25±9.90**	55.88±10.81**	3.50±2.35	1.38±0.32**	400.13±14.96**	65.38±7.31**	2.68±0.86**	2.78±0.48**	5.49±0.55**	1.01±0.32**
i	114.00±9.48**	31.50±10.50**	3.50±2.29	0.88±0.18**	347.91±12.79**	55.50±7.11**	1.75±0.84*	2.42±0.48**	3.75±0.53**	0.70±0.31*
j	64.50±8.61**	18.25±7.60*	-1.00±1.68	-0.19±0.14	66.55±13.41**	9.75±5.28	-0.40±0.77	-0.14±0.28	1.08±0.36**	-0.13±0.20
l	-154.50±18.00**	-78.75±16.27**	-8.00±3.76*	-3.49±0.60**	-600.97±29.27**	-112.75±11.77**	-5.65±1.51**	-4.28±0.68**	-7.28±0.82**	-1.73±0.45**

In the cross "Mammoth X Jurbo", additive gene effects (d) were highly significant and positive for stem length, growth rate, weight of pods per plant, number of seeds per pod and length of pod. They were significantly negative for weight of seeds per pod. Meanwhile, in the cross "Jurbo X Mammoth" the gene effects (d) were significant and negative for stem length, number of leaves, growth rate, and pod diameter (Table 5).

The dominance gene effects (h) were significant for all characters for all crosses except for number of branches in the four cross and growth rate and weight of seeds per pod in the cross "Mammoth X Atol" as seen in Table 4. These results indicated that the improvement of these characters could be achieved through recurrent selection.

The additive x additive effects (i) were significant and positive for all studied characters in the four crosses. Meanwhile, they were highly significant and negative for growth rate in cross "Atol X Mammoth" (Table 4), and for stem length in cross "Mammoth X Jurbo" (Table 5). Non significant values were observed for number of branches in all crosses and for weight of seeds per pod in both the crosses "Atol X Mammoth" and "Mammoth X Atol" (Table 4).

Additive X dominance (j) type of digenic epistasis was found to have significant positive values for stem length, growth rate, diameter of pod in the cross "Atol X Mammoth" and for growth rate, weight of pods per plant and number of seeds per pod in cross "Mammoth X Atol" (Table 4), number of seeds per pod in the cross "Mammoth X Jurbo", stem length, number of leaves, weight of pods per plant and length of pod in the cross "Jurbo X Mammoth" (Table 5).

Meanwhile additive X dominance (j) type of digenic epistsis was found to have significant negative values for weight of pods per plant, number of seeds per pod in the cross "Atol X Mammoth", diameter of pod in the cross "Mammoth X Atol" (Table 4); number of leaves and weight of seeds per pod in cross "Mammoth X Jurbo" (Table 5).

The interaction "dominance X dominance" (L) was found to be highly significant negative for all studied characters in all crosses except for growth rate which had highly significant and positive value in the crosses "Atol X Mammoth" and "Mammoth X Atol" (Table 4). Meanwhile, number of branches in all crosses and number of leaves in the cross "Mammoth X Atol" had nonsignificant (L) values. Similar trends of genic interactions were obtained by Raj-Narayan *et al.* (1998), Raj-Narayan, *et al.* (1999), Oommen *et al.* (1999), Tyagi-MK; Srivastava-CR (2001), Raj-Kumar *et al.* (2001) Vinay-Bhardwaj *et al.* (2002) Ravider-Kaur *et al.* (2003) and Hooda-JS (2003).

Polymorphism of isozyme:

Isoesterase banding patterns in Figure (1) showed a total of twenty-two different molecular forms. These molecular forms were found to show qualitative changes in number of isozymes over different tissues. Moreover, quantitative changes which are expressed as changes in band intensity were also observed over different lanes in all genotypes. Similar results concerning differences in isozymes molecular forms were also observed by Guirgis *et al.*, (1993).

Tissue specificity expressed in parental, F_1, F_2, BC_1 and BC_2 over four crosses, were also demonstrated. Based on the presence and the absence of different isozymes over different tissues, the results in Fig.(1) suggest that esterase isozymes could be controlled by at least ten loci. The two bands at 10.2 and 10 cm anodal to origin could be assigned to the Est1 locus, the two bands at 9, 8.8cm for Est2, the two bands 5.8 and 6.1 cm for Est3, the three bands at 4.2, 4.5 and 4.8 cm for Est4, the common band at 3.9 cm for Est5, the two isozyme bands at 3.3 and 3.5 cm for Est6, the three bands at 2.1, 2.4 and 2.8 cm for Est7, the two bands at 1.6 and 1.8 cm for Est8, the common two bands at 1.0 and 1.3 cm for Est9 and the three isoforms at the positions 0.3, 0.5 and, 0.7 cm anodal to the origin were assigned to the locus Est10. In this concern, for example, loci Est1 and Est2 were only expressed in leaf tissues but they were found to be absent from the rest three tissues (Fig.1). Such tissue specificity was also reported by Guirgis *et al.* (2000).

Malate dehydrogenase isozymes appeared in Figure (2) showed a total of thirteen (13) molecular forms over all genotypes. Differences on the level of both the number of bands and band intensity were also observed in all tissues of either parental, F_1 and segregated generations.

Tissue specificity revealed that these thirteen isoforms could be assigned to five loci; Mdh1-Mdh5. The molecular form at 3.4cm anodal to the origin could be assigned to the locus Mdh1, the bands at 3.2, 2.9 and 2.7 cm for Mdh2, the single band at 2.5 cm for Mdh3, the four isoforms at 2.2, 2.0, 1.8 and 1.6 cm for Mdh4 and the four is forms at 1.3, 1.0, 0.5 and 0.3 cm for the locus Mdh5.Such tissue specificity was also observed by Gurgis *et al.*(2000).

Differential expression of isozymes necessary for the biochemical pathways in different cell types, tissues and organs is always associated with the different developmental stages of the plant. Moreover, Peirce and Brewbaker (1973) reported that isozymic variation often arises from allelic segragation at a single locus evidently representing more subtle changes in the enzyme molecule. Electrophoretic analysis clearly show that isozyme pattern and intensity are specific to the plant part or tissue and to maturity or developmental stage.

Results in Table 6 showed no significant Spearman's rank correlation coefficient between either Esterase or Malade dehydrogenase isozymes and the performance of developmental and yield characters in almost all crosses. These results indicate that both the developmental and yield characters under study are expressed through biochemical pathways which might not be directly affected by either esterase or malate dehydrogenase enzymes.

It is worthy to mention that considerable genetic variation either on the level of the performance of the ten developmental and yield characters or on the level of isozyme polymorphism were indicated in all generations among and within each cross. However, the non-allelic interaction was found in thirty-six out of forty studied character (ten for each cross), with the prevalence of both "additive x additive" and "dominance x dominance" types of genic interaction in these characters. Furthermore, the prevalence of dominance gene effects in nine out of the ten characters over each of the four crosses clearly suggest that the improvement of these characters could be achieved through recurrent selection.

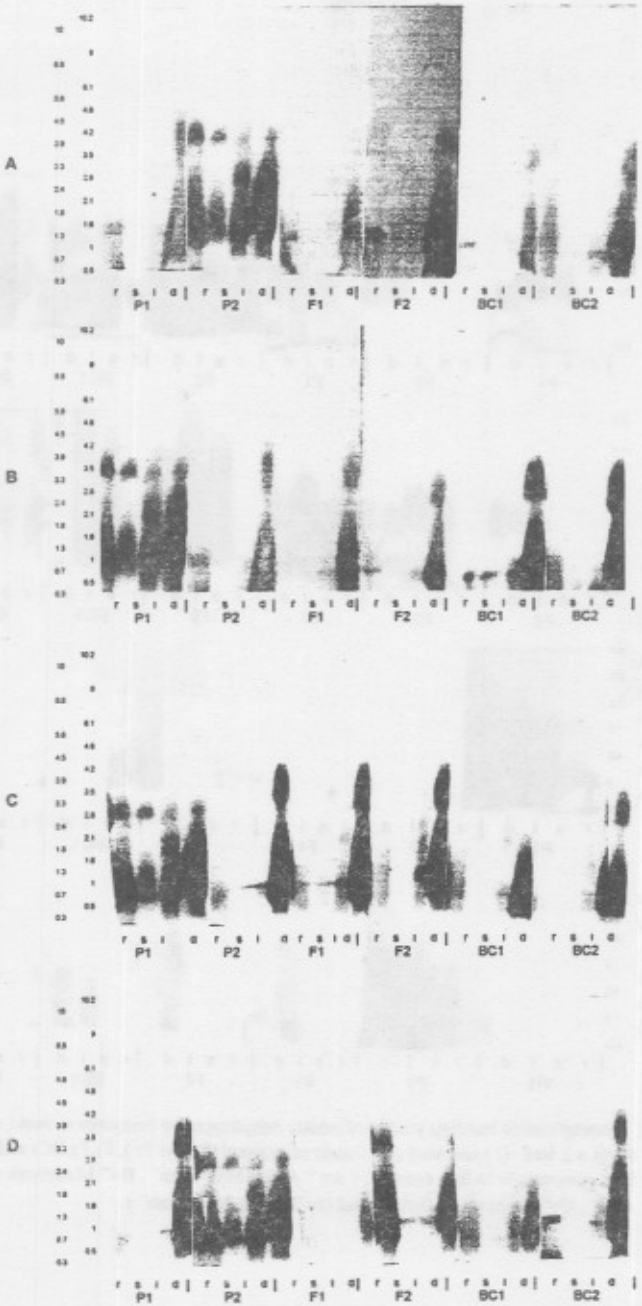

Fig.1: Electrophoretic banding pattren of esterase isozymes in root (r), stem(s), leaf (l) and seed (d) tissuse of parental (P_1 and P_2), F_1,F_2,BC_1 and BC_2 generations in four crosses ; (A= " Atol x Mammoth" , B=" Mammoth x Atol" , C="Mammoth x Jurbo " and D="Jurbo x Mammoth").

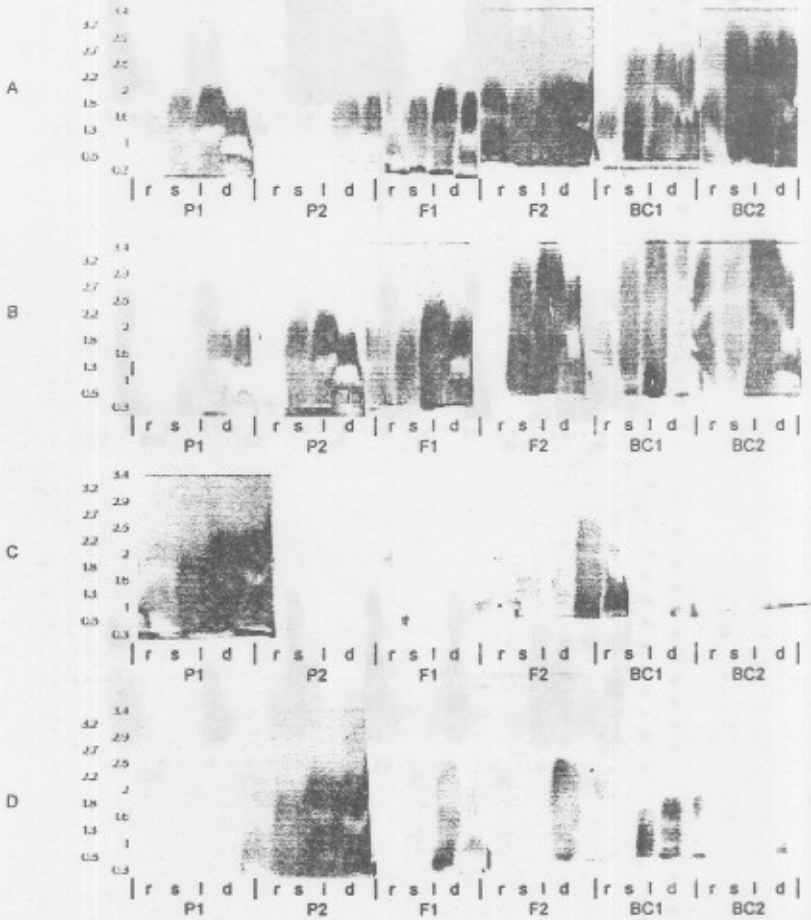

Fig.2: Electrophoretic banding pattren of malate dehydrogenase isozymes in root (r), stem(s), leaf (l) and seed (d) tissuse of parental (P_1 and P_2), F_1,F_2,BC_1 and BC_2 generations in four crosses ; (A= " Atol x Mammoth" , B=" Mammoth x Atol" , C="Mammoth x Jurbo " and D="Jurbo x Mammoth").

Table 6. Spearman's rank corelation coefficient (rs) between esterase (Est), Malete dehydrogenase (MDH) intensity scores in four pea tissues; root (r), stem(s) leaf (l) and seed (d), and the performance of P_1, P_2, F_1, F_2, Bc1 and Bc_2 for developmental and yield characters in four crosses.

Tissues	Stem length		No. leaves/ plant		No. Branches/ plant		Growth Rate		Yield/plant				Pod characters							
									Pod wt.gm		No. pods		No seeds		Seeds wt		Length		Diameter	
	Est	Mdh	Est	Mdh	Est	Mdh	Est	Mdh	Est	Mdh	Est	Mdh	Est	Mdh	Est	Mdh	Est	Mdh	Est	Mdh
"Atol X Mammoth"																				
R	0.23	-0.06	-0.35	-0.35	-0.96*	0.37	-0.41	0.81	-0.76	-0.06	-0.84	-0.12	-0.41	-0.32	-0.81	0.64	-0.73	-0.32	-0.64	-0.03
S	0.49	-0.53	0.15	0.12	-0.28	0.49	0.03	-0.19	-0.09	0.34	0.01	0.56	-0.73	0.28	0.49	0.03	0.06	0.56	-0.17	0.12
l	0.32	0.26	0.23	0.54	-0.15	-0.15	-0.06	-0.54	-0.03	0.26	0.17	0.37	-0.49	0.20	-0.55	-0.49	0.35	0.60	-0.06	0.26
D	0.37	0.62	0.14	0.77	-0.58	-0.06	-0.49	-0.29	-0.20	0.44	-0.14	0.50	-0.49	0.15	-0.83	-0.27	-0.03	0.74	-0.31	0.53
"Mammoth X Atol"																				
R	0.43	-0.21	0.15	-0.12	-0.84	0.75	0.08	-0.06	0.08	-0.06	-0.38	0.43	-0.30	0.53	-0.66	0.03	0.38	-0.28	-0.53	0.78
S	0.61	-0.33	0.23	-0.14	0.01	0.93	0.38	0.14	0.38	0.14	0.15	0.49	-0.06	0.06	-0.60	0.12	0.15	-0.26	0.23	0.49
l	-0.05	-0.03	-0.49	0.03	-0.26	0.85	-0.20	0.24	-0.20	0.24	-0.66	0.47	-0.77	0.21	-0.82	0.25	-0.55	-0.27	-0.66	0.59
d	0.38	0.39	0.26	0.18	0.38	0.01	0.26	0.44	0.26	0.44	0.49	-0.09	0.43	-0.65	-0.03	-0.37	0.14	-0.03	0.77	-0.38
"Mammoth X Jurbo"																				
r	0.25	-0.09	0.15	-0.66	-0.38	0.24	0.34	-0.38	-0.27	-0.31	-0.27	-0.31	-0.21	-0.26	-0.27	-0.31	0.15	-0.43	-0.27	-0.31
s	0.22	0.03	0.32	0.94*	-0.49	0.12	0.46	0.75	-0.23	0.83	-0.23	0.83	-0.12	0.98*	-0.23	0.83	0.23	0.89	-0.23	0.88
l	0.24	0.0	-0.54	0.58	0.01	-0.64	-0.58	0.49	-0.43	-0.30	-0.43	-0.03	-0.77	003	-0.43	-0.03	-0.49	0.40	-0.43	-0.03
d	-0.48	-0.15	-0.38	0.09	-0.36	-0.79	-0.16	0.09	-0.52	-0.55	-0.52	-0.55	-0.12	-0.35	-0.52	-0.55	-0.46	0.20	-0.52	-0.55
" Jurbo X Mammoth"																				
r	-0.35	0.03	-0.67	-0.23	-0.09	-0.72	0.29	-0.78	-0.58	-0.32	-0.64	-0.46	-0.41	-0.70	-0.64	-0.46	-0.73	-0.38	-0.26	-0.84
s	0.23	0.54	-0.23	0.71	0.09	0.38	0.29	-0.03	-0.17	0.77	-0.23	0.66	-0.12	0.43	-0.23	0.68	-0.29	0.60	-0.06	0.14
l	-0.37	0.49	-0.71	0.89	-0.17	0.67	0.20	0.37	-0.60	0.94*	-0.66	0.83	-0.43	0.66	-0.66	0.83	-0.77	0.77	-0.31	0.43
d	-0.54	0.31	-0.37	0.37	-0.06	0.20	0.14	0.43	-0.31	0.31	-0.37	0.09	-0.26	-0.03	-0.37	0.07	-0.43	0.14	-0.20	-0.09

*; Significant at 5% level.

REFERENCES

Bradford, M.M. (1976): A rapid and sensitive method for quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. Anal. Biochem., 72:248-254.

Brown, A.H.D. and B.S. Weir (1983): Measuring genetic variability in plant populations. In Tanksley S.D. and T.J. Orton (Ed.): Isozymes in Plant Genetics and Breeding. Part A, Elsevier Science Publishers B.V., Amsterdam.

Brown, A.H.D.; E. Nevo; D. Zohary, and O. Dagan (1978): Genetic variation in natural population of wild barley (Hordeum spontaneum). Gnetics, 49: 97-108.

Crawford, D.J. (1983): Phylogenetic and systematic inferences from electrophoretic studies. In Tanksley, S.D. and T.J. Orton (Ed.): Isozymes in Plant Genetics and Breeding. Part A, Elsevier Science Publishers, B.V., Amsterdam.

Gottlieb, L.D. (1981): Electrophoretic evidence and plant populations. Prog. In Phylochem. 7:1-46.

Guirgis, A.A.; A.A. Mahmoud and A.M. El-Fouly (1996): Molecular diversity, identity, genetic distance and heterozygosity in cucumber populations. Zagazig J. Agric. Res., 23(5): 763-772.

Guirgis, A.A.; Suzan, A. Swidan; A.H.M. El-Fouly and T.A. Ismail (2000): Malate dehydrogenase and esterase isozyme loci and alleles associated with high and low values of some quantitative traits in F_2 generations of pea. Zagazig J. Agric. Res., 27(1): 115-133.

Guirgis, A.A.; T.A. Ismail and M.A. Ismail (1993): Isoenzymic diversity index in relation to heterosis and combining ability for yield and fruit characters in tomato. Zagazig J. Agric. Res., 20(1A): 215-228.

Hooda-J.S.; Y.S. Tomer, B.P.S., Malik and R.S. Khatri (2003): Genetic analysis of seed and important traits in pigeon pea. Environment and Ecology, 21:(1), 37-40.

International Union of Biochemists (1978): Enzyme Nomenclature. Academic Press, New York, 606 pp.

Jinks, J.L. and R.M. Jones (1958): Estimation of the components of heterosis. Genetics 43:223-234.

Khaler, A.L. and R.W. Allard (1970): Genetics of isozyme variants in barley. I. Esterasses. Crop. Sci., 10:444-448.

MacDonald, T. and J.L. Brewbaker (1975): Isoenzyme polymorphism in flowering plants. V. The isoesterases of maize: Tissue and substrate specificities responses to chemical inhibitors. Hawaii Agric. Exp. Stn.Tech. Bull., 84, 24pp.

Mather, K. (1949): Biometrical Genetics. 1st ed. Methuem, London.

Nei, M. (1971): Identity of genes and genetic distance between populations. Genetics, 68:547.

Nei, M. (1973): Analysis of gene diversity in subdivided populations. Proc. Nat. Acad. Sci. U.S.A., 70:3321-3323.

Newton, K.J. and D. Schwartz (1980): Genetic bases of the major malate dehydrogenase isozymes in maize. Genetics, 95:425-442.

Oommen, A.; K.M.N. Namboodiri and V.K.G. Unnithan (1999): Genetic analysis of yield and yield components in pigeon pea. J. Tropical Agr. 37: 1-2, 12-16.

Peirce, L.C. and Brewbaker, J.L. (1973): Applications of isozyme analysis in horticultural science. HortScience, 8(1): 17-22.

Powling, A.; A.K.M.R. Islam, and K.W. Shepherd (1981): Isozymes in wheat-barley hybrid derivative lines. Biochem. Genet., 19:237-254.

Raj.Kumar; G. Kalloo, Singh-Major; R. Kumar and M. Singh (2001): Inhertance of growth traits in garden pea (*Pisum sativum* L.). Vegetable Sci. 28: (2): 113-116.

Raj-Narayan, K.B. Rastogi, B.S. Dogra and R. Narayan (1998): Genetics of yield and its components in garden pea. Vegetable Sci. 25: (1), 18-21.

Raj-Narayan, K.B. Rastogi, S.P. Kanaujia, Sumati-Narayan, R. Narayan and S. Narayan (1999): Genetics of yield and quality traits in garden pea. Vegetable Sci. 26(1):, 18-21.

Ravider-Kaur; Mohan-Singh; S.Kaur, P.S. Brar; T.S. Dhillon; R. Kaur and M. Singh (2003): Genetic control of economically important characters in garden pea. Environment and Ecology, 21: (1) 16-19.

Spearman, C. (1904): The proof and measurement of association between two things. Amer. J. Physiol., 15:72-101.

Tanksley, S.D. and C.M. Rick (1980): Isoenzyme gene linkage map of the tomato: Applications in genetics and breeding. Theor. Appl. Genet., 57:161-170.

Tanksley, S.D. and T.J. Orton (1983): Isozymes in Plant Genetics and Breeding. Part B. Elsevier, Amesterdam.

Tyagi, M.R and C.P. Srivastava (2001): Detection of epistasis and analysis of gene effects for yield and yield related traits in pea. Indian. J, of Pulses Res. 14:(1), 20-26.

Vinay-Bhardwaj, Raj. Narayan; S.P. Kanaujia; V. Bhardwaj and R. Narayan (2002): Genetics of yield and quality traits in garden pea. Applied Biological Res. (4): 1-2, 84-87.

التقييم الوراثي لصفات النمو والمحصول والتعدد المظهري لمشابهات الإنزيمات في بعض تلقيحات البسلة

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تمت هذه الدراسة أثناء المواسم الثلاثة المتتالية ٢٠٠١، ٢٠٠٢، ٢٠٠٣ في المزرعة التجريبية لمحطة بحوث البساتين بالقصاصين، وقد استهدفت دراسة أداء صفات النمو والمحصول لثلاث تراكيب وراثية أبوية لنبات البسلة والجيل الأول والثاني والتلقيحات الرجعية، وأيضا لدراسة نوع الفعل الجيني والتعدد المظهري للأشكال الجزئية لكل من الاستريز والماليت ديهيدروجينيز في أنسجة كلا من الجذر والساق والأوراق والبذور. تم زراعة الأجيال الستة الآباء والجيل الأول والجيل الثاني والأجيال الرجعية معا أثناء الموسم ٢٠٠٣، وقد سجلت البيانات على متوسطات كل الأجيال.

كان الجيل الأول Atol X Mammoth أعلى في متوسطاته عن كلا من الأبوين في صفات عدد بذور القرن، وزن بذور القرن، قطر القرن، ظهرت أعلى قيم متوسطات الجيل الرجعي BC_1 للتلقيح Mammoth X Jurbo في كل الصفات ماعدا طول الساق وعدد الأوراق في النبات، وقد سجلت أعلى قيم متوسطات في الجيل الرجعي BC_2 للتلقيح Jurbo X Mammoth وذلك في كل الصفات ماعدا صفة طول الساق.

أشارت القيم المعنوية لاختبارات نموذج توريث الصفات عن طريق الإضافة والسيادة إلى وجود تفاعل غير الليلي تقريبا في كل الصفات في الأربعة تلقيحات.

لوحظ تأثيرات الإضافة المعنوية السالبة والموجبة في معظم صفات ثلاث من الأربعة تلقيحات بينما لوحظت قيم التأثيرات الجينية الموجبة والسالبة في أربع صفات للتلقيح Mammoth X Atol. كانت التأثيرات الجينية السائدة معنوية في كل الصفات على مستوى الهجن الأربعة ماعدا صفة عدد الأفرع في كل التلقيحات وصفتي معدل النمو ووزن البذورللقرن في التلقيح Mammoth X Atol مما يشير أن تحسين تلك الصفات يمكن أن يتم من خلال الانتخاب المتكرر.

وقد وجد أن التفاعل الغير الليلي من الأنواع "مضيف × مضيف"، "مضيف × سائد، و"سائد × سائد" أنها جميعا تتحكم في وراثة معظم الصفات في كل التلقيحات الأربعة.

أظهر التعدد المظهري لمشابهات الإنزيمات وجود كلا من التغيرات الكمية والوصفية في نماذج حزم مشابهات الاستريز والماليت ديهيدروجينيز، وقد لوحظ مجموع كلي من ٢٢ شكل جزئي و١٣ شكل جزئي لكل من المشابهات الإنزيمية في الاستريز والماليت وهيدروجينيز على الترتيب.

وقد أوضح التخصص النسيجي في الأجيال الانعزالية أن الأشكال الجزئية المختلفة يمكن توزيعها على عشرة مواقع وراثية وعلى خمسة مواقع وراثية لكل من المشابهات الإنزيمية للاستريز والماليت ديهيدروجينيز على الترتيب.

أظهرت النتائج أن كل من صفات المحصول والنمو موضع الدراسة يتم التعبير عنها من خلال مسارات بيوكميائية والتي قد لا تتأثر بصورة مباشرة سواء بانزيم الاستريز أو الماليت ديهيدروجينيز.