

COMBINING ABILITY ANALYSIS, HERITABILITY AND HETEROSIS IN SOYBEAN

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ABSTRACT

Combining ability analysis , heritability and heterosis were studied for earliness, as well as maturity , yield and some of its components in five diverse soybean (*Glycine max* "L." Merrill) genotypes, which were crossed in a diallel mating pattern. Results revealed significant differences among the 25 genotypes, for all, the studied traits. General and specific combining abilities were also significant except for number of seeds/pod and 100-seed weight in g.c.a., indicating the importance of both additive and non-additive gene effects. The genotype MBB 80-133 was positively a high general combiner for all attributes except number of days to flowering and maturity. It was the best parent for seed yield /plot. The crosses (MBB 80-133 X H15 L4), (MBB 80-133 X H2L24) and (H2L24 X L35) were found to exhibit high positive specific combining ability effects for number of seeds/pod, seed filling period and seed yield/plot, in the same order. For seed yield/plot the cross (H2L24 X L35) showed positive significant reciprocal effect. The highest value for broad sense heritability was found for number of days to maturity . The mid-parent and better parent heterosis were significant for all the characters. For seed yield/plot, most of the crosses gave more yield than their mid-parent values. The cross (MBB 80-133 X H2L24) showed the highest heterosis over mid and better parents 47.99 and 29.12% , respectively.

INTRODUCTION

Soybean is one of the important field crops in Egypt. The seeds has high nutritional value and is used in manufacturing many human foods. In addition, for feeding livestock. Plant breeders and geneticists are becoming increasingly concerned at the rapidity with which long-established local varieties are being lost (Weiss, 2000) . A period of 45 to 60 days normally elapses between emergence and the beginning of flowering. Such early flowering reduces the height of the plants, and the yield. In addition, early maturing cultivars are influenced more by planting date than are full-season cultivars. If planted too early or too late for its area of adaptation, the yield of on early-maturing cultivar will be decreased due to premature flowering (Delorit, et al., 1984). Sharma and Phul (1994) reported that the choice of the parents in a hybridization programme is of immense importance for getting better segregants in crop like soybean where hybridization followed by pedigree method is most commonly used. They also found that both additive and non-additive gene effects were present. However, the ratio of non-additive/additive gene effects showed the preponderance of non-additive gene action for the expression of all the traits they studied. Chauhan (1983) found that both general and specific combining ability mean squares were highly significant for all the soybean studied characters, indicating the role of additive and non-additive gene effects in governing the inheritance of those traits. Gadag and Upadhyaya (1995) showed that heterosis was significant

and positive for yield in 6 hybrids over their mid-parents and in 9 hybrids over the better parents. In addition, heterosis for yield was generally accompanied by heterosis for yield components. Talwar and Singh (1983) observed that the highest heritability value was recorded for grain yield/plant (34%) followed by number of pods/plant (26%) and number of grains/plant (18%).

The present investigation was carried out to study combining ability, heritability and heterosis for earliness, maturity yield and some its components in five soybean genotypes.

MATERIALS AND METHODS

A five-soybean diverse parent diallel cross, including reciprocals was studied at El-Gemmeiza Agricultural Research Station, ARC. During the summer season of 1995 all crosses and reciprocals were made to make all possible F1's combinations between the parents. In 1996 the five parents and their 10 F1's were grown in a randomized complete block design with three replications. The parents and F1's were planted in three rows plots. The rows were 3m. long and 60 cm apart with interplant distance of 20 cm within the rows. Five equally spaced plants were randomly taken from each of the parental and F1 plots. Data were recorded on number of days to 50% flowering, number of days to maturity , 100-seeds weight (gm), number of seeds per pod, seed filling period (days) and seed yield/ plot (gm). Maturity group, parental code number, names and pedigree are presented in Table (1). The approximate zone for the 10 different maturity groupings, cultivars in group 00 are the earliest maturing and cultivars in group VIII are the latest maturing. The five soybean genotypes under study were belongs to III and IV maturity groups .

Table (1): Code numbers, names and pedigree of the five parental soybean genotypes.

Maturity group	Code number	Parental name	Pedigree
III	P1	MBB 80-133	Illinois USA
IV	P2	H5L21	D79-10426 X Lakata
IV	P3	H2L24	Crowford X celest
IV	P4	H15L4	Crowford X D79-10426
IV	P5	L35	Giza 35 (Crowford X celest)

Data were analysed as RCBD experiment according to Snedecor and Cockron (1967), differences between means were tested against the L.S.D. at 5% and 1% levels of probability. Combining ability analysis computed following Griffing's (1956) method II model I.

Heritability was estimated in broad sense according to Burton and Devon (1953) as follows : $h^2b = 6^2A + 6^2D / 6^2A + 6^2D + 6^2E$
Where : A, D and E stand, respectively for additive, dominance and environmental variances.

$$6^2A = 26^2g \qquad 6^2g = 1/P+2 (MS \text{ g.c.a.} - MS \text{ s.c.a.})$$

$$6^2D = 6^2s \qquad 6^2s = MS \text{ s.c.a.} - Ms \text{ e}$$

$$6^2E = Mse \qquad (\text{Poold error} = MSE/r).$$

Heterosis percentage relative to mid-parents (M.P) and high parents (H.P) performance was calculated as described by Bhatt (1971) as follows :
 Mid-parent heterosis (M.P) = $(F_1 - MP)/M.P \times 100$

“ “ “ L.S.D.= $t \sqrt{3MSE/2r}$

High parent heterosis (H.P.) = $(F_1 - H.P)/H.P \times 100$

“ “ “ L.S.D.= $t \sqrt{2MSE/r}$

where (t) is the tabular value at the stated level of probability for the degrees of freedom of the experimental error, MSE is the mean square for error, and (r) is the number of replicates.

RESULTS AND DISCUSSION

Analysis of variance (Table 2) showed significant differences among the 25 genotypes, (parents and their F₁'s) for all studied traits indicating the presence of genetic variability in the material under study.

Table (2) : Analysis of variance for different characters in a diallel of soybean.

Characters	d.f.	Mean squares					
		No. of days to flowering	No. of days to maturity	100-seeds weight (gm)	No. of seeds /pod	seed filling period (days)	seed yield/ plot (gm)
Replication	2	0.813	19.373	2.820	0.693	26.173	1568.39
Genotypes	24	59.953**	71.028**	19.726**	0.417*	56.047**	8100.38**
Error	48	0.813	0.859	1.075	0.402	1.465	239.51

*, ** Significant at 5% and 1% level of probability.

The mean performance of the five tested parental genotypes and their crosses presented in Table (3) . Results show that P3 (H2L24) has the lowest number of days to 50% flowering (31 days) while P1 (MBB 80-133) was the earliest in maturity from the other parents (87 days) and also showed the shortest seed filling period. Also, results revealed that P4 (H15L4) gave the highest values for 100-seed weight (15.20 gm) and seed yield/plot (420 gm). However, P5 (L35) had the highest number of seeds/pod (2.00).

Table (3) show that the hybrid (P2XP4) was the earliest regarding number of days to flowering and maturity. The hybrid (P3 X P2) had the heaviest seeds than other F₁'s crosses (17.67 gm). While (P2 X P3) had the lowest value for seed filling period (47 days). The hybrid (P1 X P3) yielded the highest seed yield/plot (520.18 gm), but it needed longer periods for flowering, maturity and seed filling period.

The variances due to general and specific combining abilities were highly significant for all the studied characters except number of seeds/pod and for both g.c.a and s.c.a 100-seed weight for g.c.a. (Table (4) indicating the importance of both additive and non-additive gene effects. However, g.c.a. variances were higher than s.c.a. variance only for seed yield/plot,

indicating the predominance of additive gene action in the expression of this character. While the variance due to s.c.a. was higher for number of days to flowering and maturity, 100-seeds weight and seed filling period indicating that non-addition effects was responsible in the inheritance of these traits. Similar results have also been reported by Alam, et al. (1984) and Ghassemi and Yazdi-Samadi (1987).

The estimation of g.c.a. effects for the parental genotypes are presented in Table (5) . The genotype MBB 80-133 was positively a high general combiner for all attributes except for number of days to flowering and maturity. The parental genotypes H5L21 and H2L24 , proved to be good general combining parents for number of days to flowering and maturity. L35 was a good general combiner for number of days to maturity, seed filling period and number of seeds/pod. It was also the best parent for last traits. On the other hand, the parent H15L4(P4) was a poor combiner because it gave negative g.c.a. effects for all the traits except 100-seeds weight.

Since more of the perents used was a good general combiner for all the traits studied , it would be desirable to have multiple crosses and practice selection in the advanced generations . For bringing together different desirable traits, diallel selective mating may be followed, as it might break linkage blocks and faster genetic recombination (Jenson 1970).

Specific combining-ability effects are given in Table 6. For number of days to 50% flowering and days to maturity the cross (P3 X P4) showed significant and high positive s.c.a. effects. The cross (P2 X P3) was the best specific combination for 100-seeds weight. The crosses (P1 X P4) , (P1 X P3) and (P3 X P5) were found to exhibit high positive s.c.a effects as well as the best combiners for number of seeds/pod, seed filling period and seed yield/plot respectively. These findings are in agreement with the observations of Chauhan, (1983) and Sharma and Phul (1994).

The reciprocal effects of the crosses for various characters are given in Table (7) . Significant and positive reciprocal values were observed. The cross (P3 X P1) is considered to have the highest r.e. values for number of days to flowering, number of days to maturity and seed yield/plot. Significant and positive reciprocal effects were found only in the cross (P5 X P4) for seed filling period. For seed yield/plot, the cross (P3 X P1) gave the best positive significant reciprocal effect (64.50 gm), followed by the crosses (P2 X P1) and (P5 X P1) . It could be noticed that reciprocal effects are significant indicating the existence of maternal effects for these characters which should be taken into consideration in the breeding programmes to improve soybean.

Table (3) : Mean values for the different characteristics of parents and their F1 crosses.

Characters genotypes	No. of days to 50% flowering	No. of days to maturity	100-seeds wdight (gm)	No. of seeds/ pod	Seed filling period (days)	Seed yield / plot (gm)
P1	33.33	87.00	11.41	1.66	53.66	402.85
P2	43.33	102.00	9.44	1.33	58.66	320.18
P3	31.00	96.00	10.98	1.66	65.00	300.16
P4	32.00	87.33	15.20	1.66	55.33	420.00
P5	34.33	92.33	14.21	2.00	58.00	370.71
P1 X P2	42.66	96.66	8.37	2.33	54.00	490.17
X P3	42.33	98.00	8.98	2.00	54.33	520.18
X P4	36.66	86.00	11.41	2.66	49.33	420.13
X P5	34.00	94.00	11.68	1.66	60.00	460.00
P2 X P3	36.33	83.33	12.60	1.66	47.00	370.85
X P4	30.33	80.66	11.49	1.66	50.33	380.00
X P5	41.33	96.00	8.55	1.66	54.66	340.74
P3 X P4	42.33	96.66	12.21	1.33	54.66	372.52
X P5	40.66	95.33	8.25	2.00	54.66	460.91
P4 X P5	34.00	91.33	9.86	2.33	57.33	355.61
P2 X P1	32.33	93.00	15.23	2.33	60.66	410.18
P3 X	31.00	93.66	13.88	2.33	62.66	390.60
P4 X	32.33	95.66	11.58	2.33	63.33	430.83
P5 X	33.33	89.60	16.83	1.66	56.33	419.60
P3 X P2	33.33	92.00	17.67	1.33	58.66	374.80
P4 X	40.00	96.66	12.15	1.33	56.66	360.70
P5 X	32.33	93.33	11.84	2.00	61.00	355.25
P4 X P3	43.00	96.00	12.10	1.66	52.66	424.82
P5 X	40.00	94.33	8.71	2.00	54.33	450.00
P5 X P4	35.00	91.33	10.95	2.00	56.33	425.00
L.S.D. 0.05	1.49	1.53	1.71	1.05	1.99	25.52
0.01	1.99	2.04	2.29	1.40	2.67	34.12

Table (4): Analysis of variance of combining abilities for the six characters of soybean in the diallel crosses.

Characters	d.f	No. of days to flowering	No. of days to maturity	100-seeds weight (gm)	No. of seeds /pod	seed filling period (days)	seed yield/ plot (gm)
S.O.V							
G.C.A.	5	7.88**	13.09**	0.75	0.164	5.19**	3974.6**
S.C.A.	15	14.68**	17.39**	5.74**	0.142	10.01**	1890.97**
R.effects	15	14.65**	16.14**	4.53**	0.025	18.15**	1104.43**
Error	70	0.271	0.286	0.36	0.134	0.488	79.84
Ratios		1:2	1:1	1:7	1:1	1:2	2:1
g.c.a/s.c.a		0.536	0.752	0.130	1.154	0.518	2.102

** Significant at 1% level of probability.

Table (5) : Estimates of g.c.a. effects of parents for different characters in five soybean genotypes

Parents	No. of days to flowering	No. of days to maturity	100-seeds weight (gm)	No. of seeds /pod	seed filling period (days)	seed yield/ plot (gm)
MBB 80-133	-1.161	-0.666	0.254	0.199	0.413	33.72
H5L21	1.239	0.833	-0.145	-0.167	-0.353	-28.78
H2L24	0.807	1.400	-0.187	-9.979	0.513	-4.68
H15L4	-0.526	-1.834	0.391	-8.000	-1.253	-0.18
L35	-0.359	0.266	-0.314	6.820	0.681	-0.08
S.E(gij)	0.147	0.151	0.169	0.104	0.198	2.53

Table (6) : Estimates of s.c.a. effects of F1 crosses for six characters studied in soybean.

Characters Crosses	No. of days to flowering	No. of days to maturity	100-seeds weight (gm)	No. of seeds /pod	seed filling period (days)	seed yield/ plot (gm)
P1 X P2	1.125	1.932	-0.133	0.434	0.887	43.98
X P3	0.727	2.365	-0.460	0.202	1.185	25.38
X P4	-0.109	0.600	-0.974	0.434	0.787	-9.12
XP5	-1.105	-0.500	2.491	-0.470	0.687	5.28
P2 X P3	-3.507	-7.299	3.644	-0.101	-3.712	5.38
X P4	-1.839	-3.069	-0.249	0.200	-1.280	-1.62
X P5	-0.340	0.834	-1.168	0.065	1.119	-24.22
P3 X P4	6.092	4.033	0.127	-0.267	-1.982	1.78
X P5	3.591	0.432	-2.841	0.168	-3.082	59.18
P4 X P5	-0.905	0.167	-1.495	0.234	1.019	-10.32
S.E. (Sij)	0.265	0.272	0.306	0.366	0.356	4.55

Table (7) : Estimates of reciprocal (r.e) effects for different characters in soybean crosses.

Characters Crosses	No. of days to flowering	No. of days to maturity	100-seeds weight (gm)	No. of seeds /pod	seed filling period (days)	seed yield/ plot (gm)
P2 X P1	5.165	1.830	-3.43	0.000	-3.33	40.00
P3 X	5.665	2.169	-2.45	-0.165	-4.164	64.50
P4 X	2.164	-4.830	-0.085	0.165	-7.000	-5.50
P5 X	0.334	2.169	-2.575	0.000	1.834	20.00
P3 X P2	1.500	-4.334	-2.535	0.165	-5.83	-2.00
P4 X	-4.835	-8.00	-0.329	0.165	-3.164	9.50
P5 X	4.500	1.334	-1.645	-0.170	-3.17	-7.00
P4 X P3	-0.334	0.330	0.054	-0.165	1.00	-27.00
P5 X	0.329	0.500	-0.230	0.000	0.165	5.50
P5 X P4	-0.500	0.00	-0.545	0.165	0.50	-34.50
S.E. (rij)	0.368	0.378	0.424	0.259	0.494	6.31

Negative reciprocal effects in all crosses except cross (P4 X P3) were found for 100-seeds weight. No significant effects in all reciprocal crosses were observed for number of seeds/pod.

Data presented in Table (8) show genetic components of variance and heritability. Both additive and dominance gene effects had positive estimates for number of seeds/pod and seed yield/plot, indicating that 6^2A and 6^2D are important in the inheritance of these traits. However, the additive genetic variances were negative for number of days to flowering, number of days to maturity, 100-seeds weight and seed filling period. This indicated that all the genetic variations were due to dominance effects of genes. Broad sense heritability varied, from 9.45% for number of seeds/pod to 98.23% for number of days to maturity. These results are in agreement with findings of Byth et al., (1969).

Table (8) : Estimates of additive (6^2A) and dominance (6^2D) types of gene action and heritability in broad (h^2b) sense for studied characters.

Parameters	6^2A	6^2D	6^2E	$h^2b\%$
Characters				
No.of day to flowering	-1.94	14.40	0.271	97.87
No. of days to maturity	-1.22	17.11	0.28	98.23
100-seeds weight (gm)	-1.42	5.38	0.36	91.66
No. of seeds/pod	0.006	0.008	0.13	9.45
Seed filling period (days)	-1.37	9.52	0.49	94.35
Seed yield /plot (gm)	595.32	1811.13	79.84	96.78

The mid-parent and high parent heterosis were significant for all the characters tested (Table 9) . The M.P. heterosis ranged from -19.48 to 36.50 for days to flowering and from -15.82 to 9.73 for days to maturity. These results are in agreements with Gadag and Npadhyaya (1995) .Mid-porent heterosis ranged from -34.52 to 73.06 for 100-seed weight, -19.87 to 60.24 for No. of seeds/pod, -23.98 to 16.22 for seed filling period and from -10.05 to 47.99 for seed yield /plot.

Heterosis relative to the high parent ranged from -30.00 to 34.37 for number of days to flowering , -20.92 to 12.64 for days to maturity -41.94 to 33.47 for 100-seeds weight, -19.87 to 60.24 for number of seeds/pod, -27.69 to 14.45 for seeds filling period and -14.11 to 29.12 for seed yield/plot.

Regarding days to flowering and maturity, many hybrids showed a desirable heterotic effect over mid and better parent, which were significant and negative values. Gadag and Upadhyaya (1995) found that same hybrid appears to be promising with Bp heterosis in desirable direction for days to flowering and maturity. Six hybrids (Table 9) showed significant useful heterosis over mid-parent and five over better parent for 100-seed weight. Most hybrids had more seeds per pod than mid-parent and their better parent.

Concerning seed yield/plot, all crosses yielded more than their thin mid-parents except three crosses which showed negative heterosis. Gadag and Npadhyaya (1995) reported that heterosis for yield and its component varied considerably. The cross (P1 X P3) expressed the highest heterosis over mid and better parents (47.99%) and (29.12%) , respectively. Kunta et al. (1985) found that the hybrids were more stable than their parents for seed yield. In general, the hybrids had better performance than their parents and differences between hybrids for the studied characters were mainly due to the gene constitution of the parental lines. Although, the parents did not vary too much in their maturity groups (Table 1) , there was considerable variation in earliness, maturity and seed filling period which could be considered in selection programs since some crosses earlier and of good yield.

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تحليل القدرة على التألف ، وتقدير درجة التوريث وقوة الهجين في فول الصويا

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** قسم البقوليات - محطة الجميزة - مركز البحوث الزراعية

بأستخدام خمسة تراكيب وراثية من فول الصويا لدراسة القدرة على التألف وتقدير درجة التوريث وقوة الهجين . وقد اجريت الدراسة خلال موسمي ١٩٩٥ ، ١٩٩٦ وذلك بمحطة الجميزة - مركز البحوث الزراعية وتم زراعة الآباء في الموسم الأول واجريت جميع التهجينات الممكنة بينها وخلال الموسم الثاني تم زراعة الآباء وهجن الجيل الأول في تصميم قطاعات كاملة العشوائية في ثلاث مكررات لدراسة صفات التبكير ، وزن ١٠٠ بذرة ، عدد البذور في القرن ، فترة امتلاء البذور ، محصول البذور للقطعة .
وأظهرت النتائج مايلي :

- وجود فروق معنوية بين ٢٥ تركيب وراثي وهي عبارة عن الآباء والهجن المستقيمة والهجين العكسية في جميع الصفات المدروسة .
- دلت النتائج على وجود فروق معنوية للقدرة العامة وكذلك القدرة الخاصة على التألف لجميع الصفات تحت الدراسة ماعدا صفة عدد البذور بالقرن ووزن ال ١٠٠ بذرة بالنسبة للقدرة العامة على التألف . وهذا دليل على اهمية التأثير الجيني المصنف وغير المضيف في دراسة الصفات . وقد اظهر الاب (MBB 80-133) قدرة عامة عالية على التألف لجميع الصفات المدروسة فيما عدا صفتي عدد الايام حتى ٥٠% تزهير وعدد الايام حتى النضج هذا بالإضافة انه كان اعلى الآباء في صفة محصول البذور للقطعة .
- كما اشارت النتائج ان الهجن (MBB 80-133 X H15 L4) و (MBB 80-133 X H2 L24) و (H2L24 X L35) كانت ذات قدرة خاصة على التألف عالية لصفات عدد البذور في القرن وفترة امتلاء البذور ومحصول البذور للقطعة على التوالي .
- أظهرت النتائج ان اعلى قيمة لدرجة التوريث بمعناها الواسع كانت لصفة عدد الايام حتى النضج . وكانت قوة الهجين على اساس متوسط الآباء وفضل الآباء لجميع الصفات المدروسة . وبالنسبة لصفة محصول البذور /قطعة فأن جميع الهجن قد اعطت اعلى من متوسط الآباء ماعدا ثلاثة هجن فقط وكان الهجين (MBB 80-133 X H2 L24) قد سجل اعلى قيمة لقوة الهجين بالنسبة لكل من متوسط الآباء . وأفضل الآباء

Table (9) : Estimates of heterosis (%) relative to mid-parents (m.p) and high parent (h.p) for characters studied.

Characters Crosses	No. of days to flowering		No. of days to maturity		100-seeds weight (gm)		No. of seeds/ pod		Seed filling period (days)		Seed yield / plot (gm)	
	m.p	h.p	m.p	h.p	m.p	h.p	m.p	h.p	m.p	h.p	m.p	h.p
P1 X P2	11.29	-1.54	2.28	-5.23	-19.75	-26.64	55.33	40.36	-3.84	-7.94	35.58	21.67
X P3	31.58	26.99	7.10	12.64	-19.82	-21.29	20.48	20.48	-8.42	-16.41	47.99	29.12
X P4	12.24	9.99	-0.19	-1.52	-14.21	-24.93	60.24	60.24	-9.46	-8.06	2.11	0.03
X P5	-11.29	-0.02	4.60	1.80	-8.82	-17.80	-9.28	-17.00	7.46	3.44	18.93	14.18
P2 X P3	-2.25	-16.15	-15.82	-18.30	23.40	14.75	10.66	0.00	-23.98	-27.69	19.56	15.82
X P4	-19.48	-30.00	-14.79	-20.92	-6.73	-24.40	10.66	0.00	-11.68	-14.20	2.67	-9.52
X P5	6.43	-4.61	-1.20	-5.88	-27.72	-39.83	-0.59	-17.00	-6.29	-6.81	-1.36	-8.08
P3 X P4	34.38	32.28	5.44	0.68	-6.72	-19.67	-19.87	-19.87	-7.87	-15.90	3.45	-11.30
X P5	24.49	18.43	-0.91	-0.69	-34.52	-41.94	9.28	0.00	-11.12	-15.90	37.40	24.33
P4 X P5	-9.74	-0.96	1.66	-1.08	32.97	-35.13	27.32	16.50	1.16	-1.15	-10.05	-4.07
P2 X P1	-15.65	-25.38	1.58	-8.82	46.02	33.47	35.62	40.36	8.01	3.40	13.46	1.82
P3 X	-3.63	-6.99	3.36	-2.43	23.92	21.64	40.36	40.36	5.61	-3.60	11.13	-3.04
P4 X	-1.01	-3.00	9.73	9.53	-12.93	-23.81	40.36	40.36	16.22	14.45	4.72	2.58
P5 X	-13.04	-2.91	-0.011	-2.89	31.38	18.43	-0.59	-17.00	0.89	-2.87	8.49	4.16
P3 X P2	-10.33	-23.07	-7.07	-9.80	73.06	25.47	-11.33	-19.87	-5.12	-9.75	20.83	17.06
P4 X	6.18	-7.68	2.10	-5.23	-1.37	-20.06	-11.33	-19.87	-0.57	-3.40	-2.54	-14.11
P5 X	-16.73	-25.38	-3.95	-8.50	0.88	-16.67	19.76	0.00	4.57	3.98	2.83	-4.17
P4 X P3	36.50	34.37	4.72	0.00	-7.56	-20.39	0.00	0.00	-11.24	-18.98	17.97	1.15
P5 X	22.47	16.51	0.16	-1.73	-30.87	-39.70	9.28	0.00	-11.65	-16.41	34.15	21.39
P5 X P4	-7.08	1.95	1.66	-1.08	-25.56	-27.96	9.28	0.00	0.58	-2.87	7.49	1.19
L.S.D. at 5%	1.29	1.48	1.32	1.53	1.48	1.71	0.91	1.05	1.73	1.99	22.11	25.52
1%	1.72	1.99	1.77	2.04	1.98	2.29	1.21	1.40	2.31	2.67	29.54	34.11