RESEARCH ARTICLE

HETEROSIS AND COMBINING ABILITY IN LATE MATURING QPM HYBRIDS IN MAIZE (*ZEA MAYS* L.)

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Abstract: Fifteen maize inbred were crossed as lines to three testers(HKI-193-1, CLQRCYQ-40-3-1 and HO6R-6136-68-1-1-6) in Line X Tester mating design to generate 45 F_1 crosses. The sixty seven genotypes including 45 F_1 hybrids along with their 18 parents and 4 checks were evaluated for five qualitative traits namely starch content, oil content, protein content, tryptophan content and lysine content in Randomized Block Design to estimate the General Combining Ability (GCA), Specific Combining Ability (SCA) and Heterosis of F_1 crosses.In the Line x Tester analysis, significant variability was observed among the genotypes for five traits. The hybrids L_3 x T_3 and L_5 x T_3 exhibited maximum mean values for oil content and hybrid L_{10} x T_1 exhibited maximum mean values for starch content. The maximum mean value for protein content was depicted by hybrid L_6 x T_2, whereas hybrid L_{10} x T_3 exhibited maximum mean value for tryptophan content. The hybrid L_7 x T_3 exhibited maximum mean values for lysine content.

Keywords: Combining ability, Grain yield, Heterosis, Quality protein maize

INTRODUCTION

Maize (*Zea mays* L.; 2n=20) is the third most important cereal crop among the cereals grown in India and is one of the promising crops for food, feed, fodder and industrial utilization. However, its protein is deficit in essential amino acids particularly, lysine and tryptophan. To overcome this deficiency, Quality Protein Maize (QPM) donors with sufficiently higher quantity of lysine and tryptophan have been developed at CIMMYT Mexico (Vasal, 1999).Maize protein is characterized by high level of glutamicacid and leucine. Lysine (1.2 per cent of protein) and tryptophan(0.4 per cent) are limiting amino acids in maize. This is due tothe fact that major storage protein is a prolamine fraction zein,which forms up to 50-60 per cent of the storage protein. Zeinconsists of a group of hydrophobic proteins, completely devoidof lysine and tryptophan (Inglett, 1970). Hence genetic manipulationfor improved nutritional value, particularly, protein qualitywas considered as a noble goal. This effort was stimulated bythe 1963 discovery that a little known mutant maize containedproteins that are nearly twice as nutritious as those found innormal maize called “opaque 2 maize”, its protein had a nutritivevalue about 90 per cent of that of proteins found in skim milk.The discovery of this mutant and subsequently its modifierwere considered remarkable and lead to the concept of “Breedingfor Quality Protein Maize (QPM)” (Vassal, 1999). The lysinelevels in normal and QPM maize average 2.0 per cent and 4.0 percent of total protein respectively, but range across genetic backgroundsfrom 1.6 - 2.6 per cent in normal maize and 2.7 - 4.5 percent in their o2 converted counterparts (Moro *et al*., 1996) Thelysine content of QPM in whole grain is about 0.33 per cent to0.54 per cent, with the average 0.38 per cent, and is 46 per centhigher than normal maize. The tryptophan content is 0.08 percent, 66 per cent higher than normal maize. (Ortega *et al*., 1986;Sproule *et al*., 1988; *Osei et al*., 1999). Normal maize contributesup to a third or more of the crude protein content of chicken diets.On the other hand, maize is low in protein in addition to itsgeneral deficiency in essential amino acids, particularly lysineand tryptophan. An understanding of the genetic architectureof parents and their mode of inheritance will greatly assist thebreeder to formulate appropriate breeding methodologies to incorporatethe traits in question into an otherwise desirable variety.Various biometrical approaches are available to access thebreeding value of the traits under transfer. Line X tester analysisis one of those employed by which the genetic architecture ofgiven character, the combining ability and heterosis could beunderstood.Most efficient use of such materials would be possibleonly when adequate information on the amount andtype of genetic variation, combining ability effects and heterotic effects in the materials is available. Inthis context, L × T analysis (Kempthorne, 1957) hasbeen widely used for evaluation of inbred lines bycrossing them with testers. The present investigationwas undertaken for estimation of combining ability andheterosis of normal inbred lines with QPM donors astester for initiating a successful quality protein maize conversion programme.

MATERIAL AND METHOD

The present investigation was carried out during the *Kharif* season of 2013-2014 at Instructional farm,Rajasthan College of Agriculture, Maharana

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Pratap University of Agriculture and Technology, Udaipur, India. The parental material for present investigation comprised of 15 inbred lines, 3 testers and 4 checks. These were selected on the basis of wide diversity for different metric traits. The inbred lines were developed and maintained at the Centre of AICRP on Maize, Udaipur, whereas, testers for investigation *viz.*,HKI-193 was collected from CCSHAU, Uchani, Karnal,CLQRCYQ-40-3-1 was collected from DMR, New Delhi and EIQ-102 from AICRP on Maize, Udaipur.The experimental material consisted of 45 crosses made during *Rabi* 2013, involving 15 lines, 3 testers along with 4 checks sown in a Randomized Block Design with three replications in *Kharif* 2013-2014. Each genotype was planted in a single row plot of 4 m length having a uniform inter and intra row spacing of 60 cms and 20 cms respectively. Two seeds per hill was planted and later on one plant was thinned (if necessary) from each hill to maintain the optimum plant population. Border rows were planted to avoid border effect.The data was subjected to the estimation of heterosis over better parent and standard variety (Fonseca and Patterson, 1968).

RESULT AND DISCUSSION

The analysis of variance revealed that mean squares due to parents and crosses were highly significant forall the characters (Table 1) .This reflected presence of adequate genetic variability in the experimentalmaterial included under study. Similarly, significant mean squares due to parents *vs.* crosses indicatedpresence of average heterosis for all the characters.Considerable amount of heterosis was observed for allthe characters under study, however the magnitude varied with characters (Table 2).

In the case of oil content, ten hybrids exhibited positive significant economic heterosis over the best check Pratap QPM hybrid-1.The maximum positive significant economic heterosis was depicted by the hybridL_5 x T_3 (20.38 per cent) followed by hybrid L_3 x T_3 (20.32 per cent) and hybrid L_1x T_3 (19.67 per cent). Poneleit and Bauman (1970), Oropeza *et al.* (1984), Joshi *et al*. (1985), Lico (1989), Ivanov (1990) reported economic heterosis for oil content. For starch content, only two hybrids *viz.*, L_9 x T_1 (2.67 per cent) and L_4 x T_2 (2.56 per cent) exhibited positive significant economic heterosis over the best check PMH-4(Table 2). Dubey *et al*. (2009), Premlatha and Kalamani (2010), Pavan *et al*.(2011), Abuali *et al*.(2012), Singh *et al*.(2013) reported economic heterosis for seed oil content and starch content in maize.

The significant economic heterosis in positive direction was observed in ten hybrids for protein content with the magnitude ranged from 2.21 (L_{13} xT_1) to 14.47per cent (L_6 xT_2). The maximum positive significant economic heterosis was expressed by hybrid L_6xT_2 (14.47 per cent) followed by hybrid L_5 xT_1 (13.97 per cent) and hybrid L_6 x T_3 and L_9 x T_3 (6.37 per cent). The best check for this trait was PMH-4. In the case of tryptophan content, three hybrids *viz.*, L_{10} x T_3 (10.59 per cent), L_{13} x T_1 (9.75 per cent) and L_5 x T_1 (3.39 per cent) exhibited positive significant economic heterosis over the best check Pratap QPM hybrid-1. For lysine content, only one hybrid L_7 x T_3 (11.20 per cent) exhibited positive significant economic heterosis over the best check HQPM-7(Table 3). Theestimates of gca effects revealed that inbred line L_6has been found good general combiner for majority of traits *viz*., protein content, tryptophan content, lysine content and oil content.

Table 1. Analysis of variance for combining ability for fourteen traits in maize

Source of Variation	d.f.	Oil content	Starch content	Protein content	Tryptophan content	Lysine content
Replication	2	0.0017915	1.11136	0.019464	0.00086**	0.00138955
Genotype	66	1.15901**	11.2226**	2.85890**	0.02228**	0.148883**
Parents	17	0.38630**	11.4575**	0.655283**	0.01862**	0.114285**
Parent v/s Crosses	1	0.23489**	26.1513**	63.1113**	0.00583**	0.012038**
Crosses	44	1.5540**	11.3381**	2.51028**	0.02581**	0.174887**
Lines	14	1.01664**	6.47167**	3.16054**	0.02883**	0.126802**
Tester	2	4.51353**	28.9602**	0.22196**	0.05651**	0.059644**
Line x Tester	28	1.61137**	12.5127**	2.34860**	0.02211**	0.207161**
Error	88	0.0009633	0.742169	0.016409	0.0001430	0.0005053
Variance						
σ^2_L		-0.066082	0.67123	0.090216	0.0007461	-0.0089287
σ^2_t		0.064492	0.3655	-0.047259	0.0007644	-0.0032782
σ^2_{GCA}		-0.002918	-0.059814	0.0082337	0.0001884	-0.0016436
σ^2_{SCA}		0.5368	3.9235	0.7774	0.0073242	0.068885
$\sigma^2_{SCA/GCA}$		183.9616	65.595011	94.4168	38.875796	41.911049

*,** Significant at 5 % and 1 % level of significance respectively.

Table 2. Extent of heterosis for oil content (%) and starch content (%)

SN.	Crosses	Oil content (%)			Starch content (%)		
		Het	Hb	EH	Het	Hb	EH
1.	L1 x T1	10.19**	3.27**	1.88**	1.58	1.09	-
2.	L2 x T1	-3.56**	-	-	5.03**	2.12	-
3.	L3 x T1	-1.74**	-	-	3.52**	3.18**	0.70
4.	L4 x T1	15.22**	14.16**	-	1.57	0.32	-
5.	L5 x T1	2.75**	0.34	-	2.24*	2.16	-
6.	L6 x T1	8.99**	2.46**	0.41	-1.68	-	-
7.	L7 x T1	-13.47**	-	-	0.94	0.69	-
8.	L8 x T1	-8.64**	-	-	2.63**	2.55*	-
9.	L9 x T1	8.33**	3.81**	-	2.28*	2.12	-
10.	L10 x T1	13.87**	13.75**	-	4.69**	3.51**	2.67**
11.	L11 x T1	7.58**	1.51**	-	-1.51	-	-
12.	L12 x T1	-9.52**	-	-	1.61	1.34	-
13.	L13 x T1	10.43**	4.43**	1.06*	2.55*	-	-
14.	L14 x T1	13.42**	13.34**	-	-1.21	-	-
15.	L15 x T1	-3.29**	-	-	0.80	0.12	-
16.	L1 x T2	-22.98**	-	-	1.32	-	-
17.	L2 x T2	12.76**	4.68**	1.17**	2.50*	-	-
18.	L3 x T2	20.03**	18.13**	1.00*	2.63**	1.40	1.40
19.	L4 x T2	-5.75**	-	-	5.42**	2.56**	2.56**
20.	L5 x T2	3.84**	3.48**	-	-1.25	-	-
21.	L6 x T2	1.33**	-	-	1.14	-	-
22.	L7 x T2	-15.19**	-	-	-2.26*	-	-
23.	L8 x T2	7.29**	-	-	-0.07	-	-
24.	L9 x T2	11.32**	4.62**	-	-0.84	-	-
25.	L10 x T2	-3.34**	-	-	-4.87**	-	-
26.	L11 x T2	-23.87**	-	-	-0.98	-	-
27.	L12 x T2	31.54**	28.34**	11.69**	0.24	-	-
28.	L13 x T2	-3.27**	-	-	3.19**	-	-
29.	L14 x T2	-14.77**	-	-	-6.13**	-	-
30.	L15 x T2	-7.00**	-	-	0.62	-	-
31.	L1 x T3	29.81**	21.31**	19.67**	-5.37**	-	-
32.	L2 x T3	9.27**	3.10**	-	2.09*	1.09	-
33.	L3 x T3	40.53**	40.34**	20.32**	-2.19*	-	-
34.	L4 x T3	20.40**	19.66**	2.58**	1.06	0.44	-
35.	L5 x T3	43.36**	40.41**	20.38**	6.09**	4.07**	1.06
36.	L6 x T3	7.13**	0.42	-	2.83**	0.59	-
37.	L7 x T3	0.42	-	-	2.75**	1.11	-
38.	L8 x T3	-8.00**	-	-	1.27	-	-
39.	L9 x T3	1.21**	-	-	-2.20*	-	-
40.	L10 x T3	22.42**	22.17**	5.17**	-8.01**	-	-
41.	L11 x T3	6.93**	0.60	-	7.35**	6.09**	1.50
42.	L12 x T3	-11.49**	-	-	3.65**	2.03	-
43.	L13 x T3	6.89**	0.79	-	10.29**	6.38**	-
44.	L14 x T3	1.40**	1.16*	-	-2.07*	-	-
45.	L15 x T3	-13.48**	-	-	2.14*	0.96	-

*,** Significant at 5 % and 1 % level of significance respectively.

Table 3. Extent of heterosis for protein content (%), tryptophan content (%) and lysine content (%)

SN.	Crosses	Protein %			Tryptophan %			Lysine %		
		Het	Hb	EH	Het	Hb	EH	Het	Hb	EH
1.	L1 x T1	26.20**	20.52**	-	-7.20**	-	-	-8.04**	-	-
2.	L2 x T1	0.29	-	-	8.83**	0.00	-	3.66**	-	-
3.	L3 x T1	28.53**	25.20**	2.98**	9.55**	-	-	4.85**	-	-
4.	L4 x T1	23.43**	20.77**	-	19.52**	15.03**	-	17.93**	16.64**	-
5.	L5 x T1	37.13**	35.74**	13.97**	26.10**	7.49**	3.39**	5.96**	-	-
6.	L6 x T1	10.16**	6.46**	-	0.27	-	-	-4.24**	-	-
7.	L7 x T1	25.21**	24.86**	3.28**	16.57**	10.67**	-	-5.54**	-	-
8.	L8 x T1	9.14**	6.78**	-	34.46**	24.38**	-	-7.82**	-	-
9.	L9 x T1	7.49**	3.99**	-	19.03**	15.20**	-	16.98**	15.14**	-
10.	L10 x T1	10.95**	9.33**	-	21.14**	11.58**	-	15.43**	11.27**	-
11.	L11 x T1	5.00**	-	-	17.51**	7.22**	-	12.54**	7.44**	-
12.	L12 x T1	11.08**	9.41**	-	7.07**	-	-	3.51**	-	-
13.	L13 x T1	27.46**	24.27**	2.21*	30.81**	9.75**	9.75**	-9.76**	-	-

14.	L14 x T1	-7.28**	-	-	17.26**	4.39**	-	14.38**	8.44**	-
15.	L15 x T1	2.63*	0.43	-	9.83**	2.15	-	2.92**	-	-
16.	L1 x T2	48.37**	44.92**	13.76**	-11.23**	-	-	-10.06**	-	-
17.	L2 x T2	10.03**	3.99**	-	0.26	-	-	0.50	-	-
18.	L3 x T2	20.14**	19.75**	-	14.80**	14.80**	-	-5.37**	-	-
19.	L4 x T2	9.67**	9.53**	-	3.52*	-	-	4.06**	-	-
20.	L5 x T2	15.11**	11.37**	-	-22.93**	-	-	-5.58**	-	-
21.	L6 x T2	37.35**	29.81**	14.47**	7.02**	1.84	-	7.68**	2.46**	0.77
22.	L7 x T2	12.26**	9.39**	-	2.14	-	-	3.18**	-	-
23.	L8 x T2	27.39**	21.85**	4.76**	-10.24**	-	-	4.64**	1.73*	-
24.	L9 x T2	22.11**	20.86**	-	-10.08**	-	-	-9.55**	-	-
25.	L10 x T2	8.21**	4.23**	-	-3.63**	-	-	-4.07**	-	-
26.	L11 x T2	7.35**	-	-	20.00**	19.39**	-	8.24**	8.03**	-
27.	L12 x T2	9.86**	8.98**	-	-19.31**	-	-	-17.94**	-	-
28.	L13 x T2	18.20**	17.92**	-	-15.74**	-	-	-10.63**	-	-
29.	L14 x T2	30.60**	30.02**	2.98**	-31.67**	-	-	-0.55	-	-
30.	L15 x T2	4.73**	0.19	-	-10.47**	-	-	-13.07**	-	-
31.	L1 x T3	17.14**	13.02**	-	0.54	0.00	-	0.78	0.13	-
32.	L2 x T3	9.47**	4.71**	-	-12.77**	-	-	-12.27**	-	-
33.	L3 x T3	21.06**	19.18**	-	-13.39**	-	-	3.81**	0.62	-
34.	L4 x T3	5.85**	4.66**	-	3.35*	0.00	-	3.18**	0.13	-
35.	L5 x T3	15.13**	12.76**	-	-18.93**	-	-	-15.96**	-	-
36.	L6 x T3	34.92**	29.05**	13.80**	3.98**	-	-	-13.03**	-	-
37.	L7 x T3	20.64**	19.03**	-	28.37**	25.95**	-	35.79**	32.94**	11.20**
38.	L8 x T3	20.02**	16.21**	-	16.51**	1.08	-	14.02**	13.87**	-
39.	L9 x T3	44.60**	41.35**	13.80**	0.56	-	-	13.45**	9.58**	-
40.	L10 x T3	11.80**	9.01**	-	39.20**	37.37**	10.59**	5.28**	3.42**	-
41.	L11 x T3	10.78**	3.62**	-	17.68**	14.95**	-	-4.08**	-	-
42.	L12 x T3	-0.71	-	-	-5.85**	-	-	1.66**	-	-
43.	L13 x T3	18.13**	16.39**	-	7.36**	-	-	-7.56**	-	-
44.	L14 x T3	8.16**	7.28**	-	14.36**	8.78**	-	9.49**	5.75**	-
45.	L15 x T3	17.99**	14.26**	-	-9.43**	-	-	-1.15	-	-

*,** Significant at 5 % and 1 % level of significance respectively.

In thepresent study, parents were classified as high, averageand low combiners based on their effects. Parents withdesirable GCA effect (significantly different from zero)were considered as high combiners, while parentsshowing insignificant estimates were classified as averagecombiners. Low or poor combiners had significant butnegative (undesirable) GCA effects.Theestimates of gca effects revealed that inbred line L_6has been found good general combiner for majority of traits *viz*., protein content, tryptophan content, lysine content and oil content. Ivy and hawlader (2000) and Hussain *et al.*(2003) alsoobserved the similar phenomenon.

The SCAeffects of the crosses for yield and different yieldcontributing characters are presented in Table 4. The significant positive sca effects for tryptophan content were observed in eighteen hybrids with the magnitude ranged from 0.02 (L_{12} x T_1, L_{15} x T_2 and L_8 x T_3) to 1.15 (L_5 x T_1). The maximum positive significant sca effects was recorded in hybrid L_5 x T_1 (1.15) followed by hybrid L_3 x T_2(1.14) and hybrid L_{10} x T_3 (1.13).

In the case of lysine content, the significant positive sca effects were observed in twenty-two hybrids with the magnitude ranged from 0.04 (L_{15} x T_3) to 0.58 (L_7 x T_3). The maximum positive significant sca effects was recorded in hybrid L_7 x T_3 (0.58) followed by hybrid L_6 x T_2(0.41) and hybrid L_5 x T_1 and L_8 x T_3 (0.23).Positive SCA indicate thatlines are in opposite heterotic groups, while negative SCAeffects indicate lines are in the same heterotic group.

In general, the GCA effects of the parents were notreflected in the SCA effects of the crosses in most of thestudied traits. This is corroborated with the results of Debnath and Sarker (1987), Paul and Daura (1991), Debnath (1992) andHussain *et al*. (2003). Besides, Deitos *et al.*(2000) reportedthat good general combining parent does not alwaysshow high sca effects in their hybrid combinations.

Table 4. GCA and SCA effects for Protein content (%), Tryptophan content (%), Lysine content (%), Oil content (%) and starch content (%)

SN	Genotype	Protein %	Tryptophan %	Lysine %	Oil content (%)	starch content %
1	T1	-0.08**	0.03**	0.02**	-0.01*	0.48**
2	T2	0.05*	-0.04**	-0.04**	-0.31**	0.44**
3	T3	0.03	0.01**	0.02**	0.32**	-0.93**
4	L1	0.63**	-0.07**	-0.22**	0.27**	-1.02**
5	L2	-0.52**	-0.04**	-0.11**	0.22**	-0.02

SN	Genotype	Protein %	Tryptophan %	Lysine %	Oil content (%)	starch content %
6	L3	0.26**	0.00	0.02*	0.54**	0.82**
7	L4	-0.51**	-0.01*	0.04**	0.05**	0.67*
8	L5	0.57**	-0.01**	0.01	0.29**	1.27**
9	L6	1.23**	0.04**	0.05**	0.25**	0.47
10	L7	0.24**	0.04**	0.13**	-0.55**	-0.11
11	L8	0.38**	-0.05**	0.01	-0.16**	0.51
12	L9	0.30**	-0.05**	-0.01	0.19**	-0.29
13	L10	-0.39**	0.08**	0.10**	0.15**	-1.23**
14	L11	-0.19**	0.09**	0.13**	-0.23**	0.33
15	L12	-0.95**	-0.04**	-0.04**	-0.20**	0.73*
16	L13	0.11*	0.09**	-0.17**	0.16**	-0.38
17	L14	-0.69**	-0.01**	0.20**	-0.38**	-1.84**
18	L15	-0.48**	-0.06**	-0.12**	-0.61**	0.07
19	L1 x T1	-0.13	-0.07**	-0.14**	0.28**	1.05
20	L2 x T1	-0.35**	-0.00	0.08**	-0.45**	0.69
21	L3 x T1	0.61**	-0.03**	0.02	-0.98**	0.94
22	L4 x T1	1.02**	-0.01	0.15**	0.30**	-1.13
23	L5 x T1	1.40**	0.15**	0.23**	-0.61**	-0.48
24	L6 x T1	-1.26**	-0.09**	-0.11**	0.22**	-1.96**
25	L7 x T1	0.67**	-0.06**	-0.50**	-0.17**	-0.12
26	L8 x T1	-0.62**	0.04**	-0.37**	-0.24**	0.43
27	L9 x T1	-1.17**	0.03**	0.16**	0.12**	1.16
28	L10 x T1	0.23**	-0.06**	0.17**	0.19**	4.27**
29	L11 x T1	-0.06	-0.08**	0.09**	0.60**	-2.35**
30	L12 x T1	0.53**	0.02*	0.13**	-0.58**	-0.56
31	L13 x T1	0.68**	0.09**	-0.09**	0.35**	-2.07**
32	L14 x T1	-1.23**	0.05**	0.09**	0.70**	0.80
33	L15 x T1	-0.31**	0.02	0.09**	0.28**	-0.66
34	L1 x T2	1.19**	0.03**	-0.01	-1.24**	1.93**
35	L2 x T2	0.14	0.08**	0.19**	0.59**	0.19
36	L3 x T2	-0.41**	0.14**	-0.06**	0.26**	1.43*
37	L4 x T2	-0.42**	0.04**	0.01	-0.51**	2.34**
38	L5 x T2	-0.77**	-0.06**	0.10**	-0.36**	-1.66**
39	L6 x T2	0.66**	0.09**	0.41**	0.02	0.85
40	L7 x T2	-0.74**	-0.01	-0.09**	-0.04	-1.12
41	L8 x T2	0.54**	-0.06**	0.14**	0.80**	-0.24
42	L9 x T2	-0.37**	-0.01	-0.30**	0.47**	0.21
43	L10 x T2	-0.33**	-0.07**	-0.14**	-0.45**	-0.82
44	L11 x T2	-0.18*	0.08**	0.19**	-0.81**	-1.01
45	L12 x T2	0.10	-0.02**	-0.27**	1.61**	-0.38
46	L13 x T2	-0.41**	-0.10**	0.07**	-0.16**	-0.62
47	L14 x T2	1.44**	-0.14**	-0.11**	-0.46**	-1.35*
48	L15 x T2	-0.46**	0.02*	-0.14**	0.30**	0.25
49	L1 x T3	-1.06**	0.04**	0.14**	0.96**	-2.98**
50	L2 x T3	0.22*	-0.07**	-0.28**	-0.13**	-0.87
51	L3 x T3	-0.20*	-0.11**	0.05**	0.72**	-2.37**
52	L4 x T3	-0.60**	-0.03**	-0.15**	0.20**	-1.20*
53	L5 x T3	-0.63**	-0.09**	-0.33**	0.97**	2.13**
54	L6 x T3	0.61**	-0.00	-0.30**	-0.23**	1.11
55	L7 x T3	0.07	0.08**	0.58**	0.21**	1.24*
56	L8 x T3	0.07	0.02*	0.23**	-0.55**	-0.18
57	L9 x T3	1.53**	-0.01	0.14**	-0.59**	-1.37*
58	L10 x T3	0.09	0.13**	-0.03*	0.26**	-3.45**
59	L11 x T3	0.24**	-0.01	-0.28**	0.22**	3.36**
60	L12 x T3	-0.62**	0.00	0.14**	-1.03**	0.94
61	L13 x T3	-0.28**	0.00	0.02	-0.19**	2.69**
62	L14 x T3	-0.20*	0.10**	0.02	-0.24**	0.54
63	L15 x T3	0.76**	-0.04**	0.04**	-0.58**	0.41
	Standard error					
	Ti	0.02	0.00	0.00	0.01	0.15

SN	Genotype	Protein %	Tryptophan %	Lysine %	Oil content (%)	starch content %
	Lj	0.04	0.00	0.01	0.01	0.30
	Sij	0.09	0.01	0.02	0.02	0.59
	Ti-j	0.03	0.00	0.00	0.01	0.18
	Li-j	0.06	0.01	0.01	0.01	0.41
	Ti-Lj	0.05	0.00	0.01	0.01	0.31
	STi-Tj	0.11	0.01	0.02	0.03	0.73
	SiL-jL	0.12	0.01	0.02	0.03	0.81
	Sij-kl	0.12	0.01	0.02	0.03	0.83

*,** Significant at 5 % and 1 % level of significance respectively.

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