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General and specific combining ability in dual purpose sorghum [Sorghum bicolor (L.) Moench]

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Abstract
The aim of this study was to evaluate the general combining ability of sorghum lines and the specific combining ability of the hybrids for yield and its related traits. Three fertility restorer lines, ten male-sterile lines, and their hybrids from line x tester mating design crosses were evaluated in RBD with three replications in four environments. Analysis was performed using the Griffing's method of diallel (1956) for individual environments and Daljit Singh (1979) for over the environments. There was a significant effect of GCA and SCA for most of the traits evaluated, indicating the participation of additive or dominant genes in inheritance. The restorer line SPV 1822 and five male sterile lines ICSA 29003, ICSA 29004, ICSA 29011, ICSA 29014 and ICSA 29016 show potential for use as parents in sorghum breeding programs. Crosses ICSA 29004 × SPV 1822 and ICSA 29012 × SPV 1822 were identified for multilocation testing.

Keywords: Sorghum bicolor, parent selection, line x tester, hybrid breeding.

Introduction
Sorghum bicolor (L.) Moench (2n = 20), family poaceae is one of the most important crops in the world because of its adaptation to a wide range of ecological conditions, suitability for low input cultivation and diverse uses (Doggett, 1988) [8]. Sorghum occupies fifth position after wheat, rice, maize and barley at world level, both in area and production. The crop is widely grown for food, feed, fodder, forage and fuel in the semi-arid tropics (SAT) of Asia, Africa, America and Australia. It occupies 42.14 m ha area in the world with an annual grain production of 59.34 m tones and productivity of 1408 kg/ha (FAO, 2018) [1]. In India, it covers about 4.96 m ha with an annual grain production of 5.80 m tonnes and productivity of 967 kg/ha (FAO, 2018) [1]. India is largest producer of sorghum in the world (FAO, 2018) [1]. Sorghum green fodder is one of the cheapest sources of feed for milch, meat and draft animals. Among the cereals, sorghum plays an important role being grain cum fodder crop. Some idea about the usefulness of parents may be obtained from their *per se* performance, but the knowledge of nature of inheritance is essential for success of breeding programme. Breeding for wide adaption is another important aspect in genetic improvement of crop plants. It is well known that a specific genotype may not exhibit the same performance in all the environments nor all the genotypes respond alike to a specific environment. Such differential response of genotypes to varying environmental conditions reduces the agricultural production. Therefore, knowledge about behavior of genotypes in different environment is essential for their recommendation and their further use in breeding programme. For this, it is desirable to see the impact of various environments on the sorghum genotypes in order to identify the parents and /or crosses for further utilization in breeding programme. L x T for combining ability is most appropriate mating design for the type of genetic material used in present investigation and information to be derived. Maintenance of plant population in per unit area is very difficult. Buffering ability of the genotypes is the only way to cope up with the available space. Therefore, breeding for buffering ability is another important aspect in genetic improvement of crop plants. Development of such a hybrid/variety, which gives a constant and desirable performance over wide range of spacing, is needed. For this, it is desirable to see the impact of various spacing on the yield of sorghum genotypes and identification of genotypes having buffering ability. The purpose of the present study was to evaluate the general combining ability of elite lines of sorghum and the specific combining ability of the hybrid combinations for yield and yield related components.

Material and method
Lines and hybrids evaluated and experimental design
The experimental material comprised of 10 male sterile lines *viz.*, ICSA 29003(L_1), ICSA 29004 (L_2), ICSA 29006 (L_3), ICSA 29010 (L_4), ICSA 29011(L_5), ICSA 29012 (L_6), ICSA

29013 (L_7), ICSA 29014 (L_8), ICSA 29015 (L_9) and ICSA 29016 (L_{10}), three restorer testers viz., SPV 245 (T_1), SPV 1430 (T_2) and SPV 1822 (T_3) and three checks *viz.* CSV 23, CSV 27, and CSH 25. These 10 lines and three testers were crossed in factorial fashion to obtain the 30 hybrids. The crossing programme was attempted at RCA, MPUAT, Udaipur, India during kharif 2014 and at IIMR off season nursery Warangal, India during rabi 2015.

Sites and conduction of field experiments

Geographically Instructional Farm is situated at 24° - 35' North latitude and 73° - 42' East longitude. The elevation of institution farm is 582.17 meters above mean sea level. The climatic conditions of the area represent subtropical condition with humid climate. The soil of experimental fields was clay loam, deep, well drained, alluvial in origin and having fairly good moisture holding capacity. The experiments were conducted in a randomized block design with three replications in four different environments created by using different spacing viz., 22.5 x 5 cm (E_1), 30 x 10 cm (E_2), 45 x 10 cm (E_3) and 60 x 10 cm (E_4) at Instructional farm RCA, Udaipur, Rajasthan, India. Basal fertilization consisted of 405 kg per ha of the 80:40:40 NPK formulation in the planting furrow. At 35 days after planting, 87 kg per ha urea was applied in top-dressing.

Traits measured

Following phenological, fodder and quality traits were measured. Days to 50 % flowering, plant height (cm), grain yield (q ha^{-1}), green fodder yield (q ha^{-1}), protein content in grain (%), protein content in fodder (%), seed index and harvest index (%),

Analysis of variance

The plot means of each character were subjected to analysis of variance for individual environment as well as over the environment where error variance in different environment were homogeneous using least square technique of Fisher (1932). The linear model of analysis of variance for individual environment was as under:

$Y_{ij} = \mu + G_i + R_j + \sigma_{ij}$

Where,

Y_{ij} = Value of i^{th} genotype in j^{th} replication,

μ = Population mean,

G_i = An effect of i^{th} genotype which were further partitioned in Parents, Checks, Crosses, Lines, Testers and Line x Tester

R_j = An effect of j^{th} replication and

σ_{ij} = An uncontrolled variation associated with i^{th}genotype and j^{th} replication.

The statistical model for pooled analysis of variance was as under

$Y_{ijk} = \mu + G_i + R_j + E_k + GE_{jk} + \sigma_{ijk}$

Where,

Y_{ijk} = Yield of the i^{th} genotype in j^{th} replication of k^{th} environment,

μ = General mean,

G_i = An effect of i^{th} genotype where genotypes were further partitioned into checks, parents, hybrids, parent v/s checks and parent's vs hybrids.
Parents were further partitioned between testers, lines and testers' v/s lines. Hybrids were partitioned into effects of testers (GCA tester), effects of lines (GCA line) and their interactions line x tester (SCA).

R_j = An effect of j^{th} replication,

E_k = An effect of k^{th} environment,

$(GE)_{ik}$ = An interaction effect of i^{th} genotype with k^{th} environment. This effect was further partitioned into the interaction of environment with checks, parents (testers, lines and testers v/s lines) parents v/s checks, parents v/s hybrids and hybrids (GCA tester, GCA line and SCA)

σ_{ijk} = An uncontrolled variation associated with i^{th} genotype in j^{th} replication and k^{th} environment.

Line x tester mating design

Griffing's method of diallel (1956) [10] for individual environments and Daljit Singh (1973, 1979) [5] for over the environments were extended for Line x Tester mating design. Details of method followed were as follows:

Combining ability effects for individual environment

$$\mu = \frac{\sum_{i=1}^{t}\sum_{j=1}^{l}\sum_{k=1}^{r} X_{ijk}}{ltr} \qquad GCA\ tester = \frac{\sum_{i=1}^{l}\sum_{k=1}^{r} X_{ijk}}{lr} - \mu$$

$$GCA\ line = \frac{\sum_{i=1}^{t}\sum_{k=1}^{r} X_{ijk}}{tr} - \mu \quad SCA = \frac{\sum_{k=1}^{r} X_{ijk}}{r} - \frac{\sum_{j=1}^{t}\sum_{k=1}^{r} X_{ijk}}{tr} - \frac{\sum_{j=1}^{l}\sum_{k=1}^{r} X_{ijk}}{lr} + \mu$$

Standard error of combining ability effects

S.E. (GCA line)	=	$(MSE/rt)^{1/2}$	Where,		
S.E. (GCA tester)	=	$(MSE/rl)^{1/2}$	X_{ijk}	=	Value of hybrid between i^{th} line and j^{th} tester in k^{th} replication
S.E. (SCA)	=	$(MSE/r)^{1/2}$	t	=	Number of testers
S.E. (GCA_i - GCA_j) line	=	$(2 \times MSE/rt)^{1/2}$	l	=	Number of lines
S.E. (GCA_i - GCA_j) tester	=	$(2 \times MSE/rl)^{1/2}$	r	=	Number of replications
S.E. (SCA_{ij} - SCA_{kl})	=	$(2 \times MSE/r)^{1/2}$	MSE	=	Error mean square *i.e.* M_{14}

II. Combining ability effects for over the environments

Over the environments general combining ability effects of parents and specific combining ability effects of hybrids were calculated for all the character's same manner as for individual environments except the number of environments was an additional divisor.

$$\mu = \frac{\sum_{m=1}^{s}\sum_{i=1}^{t}\sum_{j=1}^{l}\sum_{k=1}^{r} X_{ijkm}}{sltr}$$

$$GCA\ tester = \frac{\sum_{m=1}^{s}\sum_{i=1}^{l}\sum_{k=1}^{r} X_{ijkm}}{slr} - \mu$$

$$GCA\ line = \frac{\sum_{m=1}^{s}\sum_{i=1}^{t}\sum_{k=1}^{r} X_{ijkm}}{str} - \mu$$

$$SCA = \frac{\sum_{m=1}^{s}\sum_{k=1}^{r} X_{ijkm}}{sr} - \frac{\sum_{m=1}^{s}\sum_{j=1}^{t}\sum_{k=1}^{r} X_{ijkm}}{str} - \frac{\sum_{m=1}^{s}\sum_{j=1}^{l}\sum_{k=1}^{r} X_{ijkm}}{slr} + \mu$$

The effects of individual environments were subtracted from above effects to estimates of the deviation of effects in individual environments from effects of over the environments. The standard error of effects was worked out as follows:

S.E. (GCA line)	=	$(MSE/rts)^{1/2}$	Where,		
S.E. (GCA tester)	=	$(MSE/rls)^{1/2}$	X_{ijkm}	=	Value of hybrid between i^{th} lines and j^{th} tester in k^{th} replication and m^{th} environment.
S.E. (SCA)	=	$(MSE/rs)^{1/2}$	t	=	Number of testers
S.E. (GCA_i - GCA_j) line	=	$(2 \times MSE/rts)^{1/2}$	l	=	Number of lines
S.E. (GCA_i - GCA_j) tester	=	$(2 \times MSE/rls)^{1/2}$	r	=	Number of replications
S.E. (SCA_{ij} - SCA_{kl})	=	$(2 \times MSE/rs)^{1/2}$	s	=	Number of environments
S.E. (GCA_{ij} – GCA_i) line	=	$[(1+s)\ MSE/rts]^{1/2}$	MSE	=	Error mean square
S.E. (GCA_{ij} – GCA_i) tester	=	$[(1+s)\ MSE/rls]^{1/2}$			
S.E. (SCA_{ijk} – SCA_{ij})	=	$[(1+s)\ MSE/rs]^{1/2}$			

Results and discussion

Analysis of variance revealed significant difference among the crosses for all the characters in all the environment except harvest index in E_1 and E_2 (Table 1). Partitioning of this variance in lines, testers and line x testers revealed significant different among GCA of lines for all the characters except harvest index in E_1 and E_2. GCA of tester for all the characters except seed index in E_1 and harvest index in E_1 and E_2. General combining ability is very important tool for identification of the parents for any breeding programme. Good GCA indicates presence of dominant genes along with additive effects. Frequency of good combiner parents was more or less equal in all the characters considering all the environments together. Significant difference for SCA was observed for all the characters in all the environments except days to 50% flowering in E_1 and harvest index in E_1 and E_2. The GCA effect due to lines and testers and SCA effect due to crosses were calculated only where mean square due to lines, testers and line x testers, respectively were significant.

The early flowering was important therefore negative GCA and SCA effects were considered desirable for days to 50% flowering. GCA effects was significant and desirable for 2 (E_1), 4 (E_2), 4 (E_3) and 1 (E_4) lines while among **t**esters T_2 in E_1, E_2 and E_3. The estimates of SCA was significant and negative for Crosses *viz*., L_9 xT_1 (-5.13) in E_2, L_5 x T_2 (-3.71), L_6 x T_2 (-3.93), L_{10} x T_2 (-3.60) in E_3 and L_3 x T_2 (-6.01), L_{10} x T_2 (-5.57) in E_4. (Table 4.2). The plant height was important for fodder yield therefore positive GCA and SCA effects were considered desirable for plant height. The estimates of GCA effects was significant and positive for 3 lines and 1 tester viz., 16.44 (L_5), 6.75 (L_6) and 6.11 (L_7), T_3 (32.25) in pool. Crosses *viz*., L_4 x T_1, L_{10} x T_1, L_5 x T_2, L_9 x T_2, L_1 x T_3, L_3 x T_3 and L_7 x T_3 exhibited significant and positive SCA effects over the environments (Table 4.2). For plant height GCA was estimated only in pool and in individual environment deviation from pool GCA was estimated where for plant height L_2 was having significantly higher GCA in E_2 then pool. So L_5, L_6 and L_7 were good general combiners for trait. For grain yield lines L_1, L_2, L_5, L_6, L_8 and L_{10} having significant and positive GCA effects in more than one environment and T_3 in E_2 and E_4. The SCA effects was significant and positive for 8, 10, 9 and 11 crosses in E_1, E_2, E_3 and E_4, respectively. Crosses *viz*., L_3 x T_1, L_8 x T_2 and L_9 x T_2 exhibited significant and positive SCA effects in more than two environments (Table 4.2). With reference to green fodder yield the GCA effects among lines and tester was significant and desirable for 3(E_1), 4(E_2), 3(E_3) and 4(E_4) lines and L_5, T_3 **(**in E_2, E_3 and E_4). The estimates of SCA effects was significant and positive for Crosses *viz*., L_9 x T_1, L_2 x T_2, L_6 x T_2, L_8 x T_2, L_9 x T_2, L_3 x T_3, L_5 x T_3 and L_7 x T_3 in more than one environments (Table 4.2). As regard the protein content in grain the estimates GCA effects among lines and tester was significant and positive for 3, 4, 4 and 4 lines in E_1, E_2, E_3 and E_4, respectively**.** L_1, L_2 and L_{10} having significant and positive GCA effects in more than two environments and T_1 in E_1, E_2 and E_4. The SCA effects was significant and positive for crosses *viz.*, L_3 x T_1, L_1 x T_2 and L_2 x T_3 in all the four environments (Table 4.3). Combining ability in positive direction was desirable for protein content in fodder. GCA effects of L_2, L_7 and T_1 having significant and positive GCA effects in all the four environments. The SCA was significant and positive for crosses *viz.*, L_1 x T_2, L_8 x T_1, L_1 x T_2, L_6 x T_2, L_8 x T_2 and L_2 x T_3 exhibited significant and positive SCA effects in all the four environments (Table 4.3). For the Seed index the GCA effects of L_3 and L_5 having significant and positive GCA effects in more than two environments and T_3 in E_2, E_3 and E_4. The estimates of SCA effects was significant and positive for crosses L_6 x T_1 and L_5 x T_3. in more than two environments. (Table 4.3). For the harvest index GCA effects of L_5 and L_{10} in E_3 and L_4 and L_8 in E_4, T_1 in E_3 and E_4 was significant and positive The SCA was significant and positive for L_{10} x L_1, L_1 x L_3 and L_9 x L_3 in E_3 and L_2 x L_1 in E_4 (Table 4.3). Tester T_1 was good general combiner for green fodder yield (E_1), seed index (E_2), harvest index (E_3 and E_4), grain yield (E_3), protein content in grain (E_1, E_2 and E_4) and protein content in fodder (E_1, E_2, E_3 and E_4). Tester T_2 was good general combiner for dry fodder yield (E_1 and E_2), protein content in fodder (E_3 and E_4) and protein content in grain (E_2 and E_4). Tester T_3 was good general combiner for plant height (pool), green fodder yield (E_2, E_3 and E_4), seed index (E_2, E_3 and E_4) and grain yield (E_2 and E_4). Lines L_1, L_2, L_5, L_8 and L_{10} and tester T_3 were good general combiner for grain yield and most of the yield contributing characters. Therefore, these parents were noted as good sources of favourable genes for increasing grain yield through various yield contributing characters and use of these parental lines would be more rewarding for boosting grain yield in sorghum. It was further noted that involvement of these parents had resulted into hybrids expressing useful heterosis for various traits. Therefore, developing dual purpose and early genotypes tester T_3 could be identified. Similar results were found by Indhubala *et al.*, (2010) [12] Salunke and Deore (2000) [23], Ravindrababu *et al.*, (2001) [22] Bahadure *et al.*, (2015) [2], Meena *et al.*, (2017) [17] and Iyanar *et al.*, (2001) [11], Leonilo *et al.*, (2020) [15], also identified lines with good GCA effects for grain yield along with other attributes. SCA along with GCA is essential for taking the decision about breeding methodology. SCA was estimated for six characters in all the four environments and for harvest index in E_3 and E_4 and for plant height SCA effects were estimated over the environments and deviation from pool were estimated in individual environments. For 7 characters including harvest index the SCA effects were significant in 196 combinations considering 30 crosses and four environments. Frequency of good SCA effects in E_1, E_2, E_3 and E_4 were 44, 56, 68 and 28, respectively. Frequency of good SCA effects were maximum in protein content in fodder (51) followed by protein content in grain (40) and grain yield (39). Cross L_2 x T_2 was also having good SCA effects for seed index. For grain yield in E_1 nine crosses had good SCA effects, L_5 x T_1 was also having good SCA for protein content in grain and protein content in fodder. Maximum frequency of good SCA effects was observed in the crosses between G x P GCA parents it was followed P x P, G x A, A x P and A x A this indicate that good SCA less frequent in crosses between average general combiner parents. In E_2 ten crosses had good SCA for grain yield. Cross L_{10} x T_2 having good SCA for protein content in grain, protein content in fodder and seed index L_2 x T_3 for protein content in grain, protein content in fodder and seed index along with grain yield. In E_3, 9 crosses having good SCA effects for grain yield. Out of these cross L_3 x T_1 also having good SCA effects for seed index and protein content in grain, cross L_1 x T_3 for protein content in grain and seed index and L_{10} x T_1 for harvest index. For seed index SCA was good in L_9 x T_2 and for green fodder yield and protein content in fodder in L_8 x T_3. In E_4, 11 crosses having good SCA for grain yield. Among these one or other cross also having good SCA for seed index, protein content in fodder, protein content in grain, green fodder yield and days to 50 % flowering. Cross L_{10} x T_2 having good SCA for protein content in grain, protein content in fodder, seed index, days to 50 % flowering and days to maturity along with grain yield followed by L_2 x T_3 for green fodder yield, protein content in grain, protein content in fodder and seed index. Cross L_5 x T_3 for protein content in fodder and seed index. Across the environments cross L_3 x T_1, L_9 x T_1, L_4 x T_2 and L_9 x T_2 were having good SCA for grain yield in E_1, E_2 and E_3 where as cross L_8 x T_2 having good SCA in E_2, E_3 and E_4. There were nine crosses which had good SCA in all the four environments but for different characters. Remaining 12 crosses having good SCA in single environment only, that too varies from cross to cross. For plant height SCA was significant in seven crosses over the environments. Presence of good SCA indicates that the above crosses having role of non additive gene action in inheritance of these characters in respective environments. Similar results were found by Govil and Murty (1973), Rao *et al.* 1976), Singhania (1980), Pillai *et al.* (1995), Karale *et al.* (1998) [13], Bhavsar and Borikar (2002) [6], Rafiq *et al.* (2002) [21], Bunphan et al (2015) [4], Thakare et al (2014) [24], Meena *et al.*, (2018) [18] and Kaul *et al.* (2003) [14] also reported importance of SCA in inheritance of one or other characters. Out of 45 combinations of 24 crosses having economic heterosis for different characters in different environments good SGA effect were observed in 26 combinations. In remaining 19 SCA effect were none significant. All the 45 combinations involving at least one good general combiner parent except two crosses L_5 x T_2 (A x A) and L_{10} x T_2 (P x A) for days to flowering in E_2. The frequency of G x G (15), G x A (15) and G x P (13) were almost equal. Cross L_2 x T_3 and L_6 x T_3 having economic heterosis for grain yield and L_1 x T_3 for grain yield having good SCA effects and involving at least one good general combiner in E_2 parent may be utilized as hybrid for medium spacing i.e. 30 x 10 cm after testing at multi locations. Such hybrids having good SCA and involving at least one good general combiner parent were also identified by Reddy and Joshi (1993), Patel *et al.* (2006) [20], Senthil and Palamisamy (1994), Bhadouriya and Saxena (1997) [3], Chaudhary *et al.* (2004) [7] and Yadhav and Pahuja (2007) [25], Sally *et al.*, (2017), Meena *et al.*, (2018) [18], Mara *et al.*, (2018) [16]. In a specific environmental conditions. Two crosses L_2 x T_3 and L_6 x T_3 having economic heterosis more than 15 per cent for grain yield, good SCA, involving one good GCA parents, nicking in flowering in normal spacing environment and male parent taller than the female parent are identified to contribute in the coordinated trials for multilocation testing. If perform well these crosses will serve the purpose of dual purpose sorghum. Cross L_1 x T_3 is also identified for contribution in coordinated trials for grain purposes as it has very high economic heterosis for grain yield (56.65%) in medium spacing environment *i.e.30 x 10 cm* along with good nicking in flowering and taller male parent. Selection may also be exercised for transgressive segregants in segregating generations of ICSA 29003 B × SPV 1822 as this cross having high heterosis, good SCA and involving both good general combiner parents.

Table 1: Mean square for different characters in individual environment

S. No.	Characters	Env	Rep	Genotype	Checks	P Vs Chk	Parents	Tester	Lines	L Vs T	P Vs C	Crosses	Tester	Lines	L X T	Error
			[2]	[45]	[2]	[1]	[12]	[2]	[9]	[1]	[1]	[29]	[2]	[9]	[18]	[90]
1	Days to 5% flowering	1	26.81	66.02	5.44	32.59	29.17	21.78	29.94	36.98	165.55**	80.04**	270.00**	128.93**	34.48	23.60
		2	47.44**	56.87**	104.11**	3.59	40.73**	2.78	53.66**	0.25	259.47**	52.91**	153.68**	62.04**	37.15**	6.62
		3	24.93*	58.85	0.33	38.94*	3.97	1.44	4.89	0.72	642.40**	58.09**	51.73**	120.94**	27.36**	6.05
		4	12.53	63.23*	37.33*	22.89	87.69**	18.11	100.24**	113.87**	81.51**	53.88**	112.90**	78.85**	34.84**	11.55
2	Plant height	1	228.38	4664.01**	5502.78**	7116.72**	5575.03**	5875.11**	5262.23**	7790.05**	19602.69**	3829.78**	21578.80**	3368.44**	2088.34**	244.59
		2	367.75	4622.98**	2000.44**	20733.39**	1592.25**	2890.11**	837.29**	5791.12**	34104.20**	4964.34**	37406.34**	4636.55**	1523.57**	199.05
		3	1213.36**	2775.89*	1119.44*	15204.18**	1417.53**	1058.33*	1242.02**	3715.58**	37223.73**	2246.41**	15802.50**	523.61*	1601.57**	244.42
		4	1767.07**	4656.56**	4381.00**	30724.92**	2012.15**	4999.00**	1026.33**	4910.78**	38078.42**	4342.94**	26938.84**	1495.11**	3256.19**	329.84
3	Green fodder yield	1	1613.83	101741.42**	71415.11**	199062.19**	142641.08**	9216.33*	183051.48**	45796.92**	37.91	86105.58**	126505.54**	91646.25**	78846.36**	2013.91
		2	456.96	72389.61*	5140.11*	404832.18**	53678.03**	26850.33**	23243.63**	381243.08**	72638.53**	75741.33**	404461.48**	68137.56**	43018.75**	1117.98
		3	80.92	22701.12**	29206.33**	956.33	30842.35**	3814.78*	25020.87**	137290.83**	17983.43**	19578.89**	72515.88**	22224.17**	12374.36**	1171.12
		4	3483.25	28495.85**	49284.78**	59073.85**	13472.35**	23713.44**	9134.24**	32033.23**	39687.14**	32715.42**	38902.81**	42038.61**	27366.34**	2109.41
4	Grain yield	1	74.62**	461.03**	280.44**	1198.72**	457.80**	252.11**	553.64**	6.62	254.61**	464.81**	150.10**	468.08**	498.15**	14.56
		2	106.44**	1274.01**	411.11**	4959.51**	707.15**	187.44**	523.61**	3398.32**	3088.38**	1448.98**	8072.43**	1266.35**	804.36**	19.75
		3	3.62	367.96**	835.44**	1252.12**	223.58**	42.33**	277.20**	103.51**	1520.08**	350.45**	1496.70**	359.36**	218.64**	6.38
		4	2.11	411.15**	53.44**	1532.93**	410.45**	995.44**	65.94**	2341.05**	742.28**	404.81**	339.70**	133.73**	547.59**	4.39
5	Protein content in grain	1	0.85**	5.12**	3.43**	17.06**	6.91**	0.14	9.09**	0.82*	18.02**	3.95**	0.81**	3.92**	4.32**	0.16
		2	0.01	11.31**	2.78**	6.43**	14.24**	0.87**	15.21**	32.27**	21.34**	10.70**	7.01**	21.36**	5.79**	0.06
		3	0.37	8.42**	4.48**	10.72**	9.75**	2.20**	6.92**	50.36**	6.82**	8.27**	4.29**	11.67**	7.02**	0.31
		4	0.01	9.15**	6.37**	10.46**	14.49**	1.73**	14.98**	35.63**	21.93**	6.92**	0.83**	13.23**	4.44**	0.01
6	Protein content in fodder	1	0.07	3.68**	1.24**	9.52**	1.59**	0.22**	1.84**	2.04**	1.77**	4.65**	1.51**	1.52**	6.56**	0.02
		2	0.07**	3.40**	1.53**	3.95**	3.03**	0.97**	3.77**	0.49**	5.06**	3.69**	4.74**	4.86**	2.99**	0.01
		3	0.01	3.13**	1.37**	2.84**	2.97**	0.87**	3.65**	0.98**	4.02**	3.35**	4.85**	4.39**	2.67**	0.01
		4	1.60**	3.14**	1.79**	3.88**	2.80**	0.47**	3.45**	1.56**	4.87**	3.37**	4.99**	4.65**	2.55**	0.01
7	Seed index	1	0.31**	0.20**	0.30**	0.06	0.27**	0.74**	0.18**	0.16**	0.35**	0.17**	0.04	0.19**	0.17**	0.02
		2	0.03*	0.59**	0.13**	4.41**	0.55**	0.83**	0.55**	0.02	0.17**	0.52**	0.89**	0.32**	0.57**	0.01
		3	0.12	0.61**	0.48**	2.67**	0.33**	0.40**	0.35**	0.05	2.28**	0.65**	0.89**	1.04**	0.43**	0.06
		4	0.04**	0.46**	0.33**	1.08**	0.34**	0.60**	0.32**	0.01	2.61**	0.46**	0.43**	0.54**	0.42**	0.01
8	Harvest index	1	0.30	12.72	0.88	192.53**	6.25	2.89	7.42	2.41	12.70	10.37	32.92	9.73	8.19	11.80
		2	6.05	8.18	7.66	1.58	8.96	3.24	10.16	9.55	0.46	8.40	3.59	5.59	10.35	6.79
		3	21.20	134.33**	90.78**	63.35	121.25**	171.38**	111.56**	108.21*	0.00	149.51**	119.97**	229.20**	112.95**	16.49
		4	22.49	40.41	3.67	52.22**	68.98**	3.74	82.48**	78.01**	25.85	31.86**	74.08**	49.64**	18.28**	7.57

*, ** Significant at 5 and 1 percent level of significance

Table 2: GCA and SCA effects for days to 50% flowering, grain yield, plant height and green fodder yield

S. No.	Genotype	Days to 50% flowering				Plant height					Grain yield				Green fodder yield			
		E1	E2	E3	E4	E1	E2	E3	E4	Pool	E1	E2	E3	E4	E1	E2	E3	E4
1	T1	0.00	-0.76	-1.07*	-1.27	3.62	-6.66	3.18	-0.14	-9.68**	1.53	-10.53**	7.30**	0.37	72.62**	-113.86**	-20.79**	-11.72
2	T2	-3.00**	-1.79**	-0.40	2.23**	-0.70	-1.61	3.57	-1.26	-22.57**	1.03	-8.37**	-6.80**	-3.53**	-52.48**	-4.39	-35.36**	-28.69**
3	T3	3.00**	2.54**	1.47**	-0.97	-2.92	8.27	-6.75	1.39	32.25**	-2.57**	18.90**	-0.50	3.17**	-20.14*	118.24**	56.14**	40.41**
4	L1	3.80*	1.34	4.39**	1.06	-17.92	-6.21	9.78	14.36	-16.72**	6.63**	15.72**	-3.61**	1.26	176.03**	-64.04**	9.59	93.24**
5	L2	3.02	2.01*	0.83	-0.17	-12.39	31.65*	-4.81	-14.45	0.08	-4.37**	-1.94	5.06**	3.37**	-46.08**	-103.60**	65.59**	82.80**
6	L3	1.13	2.23*	4.72**	1.28	23.99	5.59	-12.31	-17.28	5.36	11.30**	14.06**	-11.28**	-6.86**	124.14**	65.62**	9.81	-32.76*
7	L4	-5.98**	-2.32*	-2.72**	-1.17	14.86	-30.32*	0.78	14.69	-7.72**	1.97	-14.61**	-1.39	-3.08**	-35.86*	-53.16**	-38.19**	-9.76
8	L5	1.24	-2.21*	0.28	-0.39	-0.64	11.29	-11.17	0.52	16.44**	-3.59**	6.39**	4.94**	-2.30**	-99.52**	156.07**	46.37**	63.24**
9	L6	-0.42	-1.88*	-2.83**	2.39*	10.16	9.65	2.97	-22.78	6.75*	-11.81**	1.61	5.72**	3.81**	-114.08**	-36.93**	-110.52**	-55.53**
10	L7	1.91	-1.88*	-1.94*	-1.61	1.36	-3.04	-1.39	3.08	6.11*	-7.14**	-5.72**	7.39**	2.59**	-64.74**	72.29**	21.48	-66.09**
11	L8	-7.64**	-3.66**	-7.06**	-6.61**	-15.76	-6.16	5.61	16.30	-0.89	3.63**	-3.39*	4.17**	-2.52**	-53.52**	0.62	27.81*	61.02**
12	L9	1.80	3.57**	2.50**	4.72**	-0.78	-6.52	5.25	2.05	-14.42**	-3.37*	-20.94**	-4.50**	5.37**	4.81	-103.71**	-25.08*	-88.98**
13	L10	1.13	2.79**	1.83*	0.50	-2.87	-5.93	5.28	3.52	5.00	6.74**	8.83**	-6.50**	-1.63*	108.81**	66.84**	-6.86	-47.20**
14	L1 x T1	-1.00	-1.24	-0.82	-1.29	8.44	-3.51	-3.46	-1.47	-13.93*	-2.20	-10.69**	-9.86**	2.08	-14.73	-3.92	-43.32	-12.94

15	L2 x T1	1.78	1.42	-2.60	-1.73	-33.51	25.22	-5.29	13.58	5.68	-15.53**	-10.69**	7.48**	-19.37**	-217.29**	38.63	-74.66**	-61.83
16	L3 x T1	1.67	0.20	0.51	2.16	11.61	-20.56	18.71	-9.75	-6.09	8.13**	6.98*	4.14*	-10.81**	-2.18	-144.26**	-53.54*	53.72
17	L4 x T1	3.78	0.09	-1.04	-0.07	-1.59	-11.98	13.29	0.28	14.32*	1.13	6.98*	-1.08	-1.59	120.82**	18.86	14.46	86.39**
18	L5 x T1	-2.11	-1.36	-0.38	-2.84	-15.51	-6.34	4.15	17.69	4.57	18.02**	4.64	-2.41	4.63**	-27.51	6.63	115.57**	-27.28
19	L6 x T1	-0.44	-0.69	3.73*	-1.29	-10.39	7.22	-13.74	16.92	-1.98	-5.09	-10.58**	12.14**	24.19**	-163.96**	4.97	22.46	91.50**
20	L7 x T1	4.89	-0.36	-1.16	1.04	-10.42	0.41	4.79	5.22	-8.84	-15.76**	2.42	-2.52	18.74**	-205.96**	54.41*	4.12	-24.28
21	L8 x T1	-3.89	6.76**	0.62	1.38	0.52	8.02	2.96	-11.50	-13.68*	3.13	0.42	-13.97**	-4.48**	168.16**	12.08	-66.21**	-63.06
22	L9 x T1	-0.67	-5.13**	-2.27	0.04	7.97	9.47	-21.93	4.50	0.10	10.13**	12.31**	-2.97	-1.03	255.49**	66.41**	60.34*	30.28
23	L10 x T1	-4.00	0.31	3.40	2.60	42.88	-7.95	0.54	-35.47	19.85**	-1.98	-1.80	9.03**	-12.37**	87.16**	-53.81*	20.79	-72.50*
24	L1 x T2	2.67	-1.88	0.84	3.88	5.76	11.44	-5.51	-11.69	-2.71	-1.03	-19.52**	-3.42	-2.36	-87.63**	39.28	25.24	63.36
25	L2 x T2	1.44	-0.21	0.73	2.77	4.14	-13.83	-4.01	13.70	1.90	13.30**	-9.19**	-9.42**	15.87**	186.14**	-29.50	58.24*	-7.53
26	L3 x T2	-0.67	-3.43	-1.16	-6.01*	10.84	-0.03	-3.43	-7.38	-14.79**	-2.03	-5.86	-1.09	7.76**	2.92	-37.39	0.69	-92.31**
27	L4 x T2	-6.22	1.79	3.96*	1.10	-13.27	35.31	-7.76	-14.27	-20.46**	5.97*	7.81*	1.69	-11.02**	-70.41*	-35.28	-35.64	-103.98**
28	L5 x T2	0.22	1.34	-3.71*	4.99*	-3.52	-27.72	2.10	29.14	14.12*	-26.48**	-7.86*	7.69**	-8.47**	-72.08*	-136.17**	-70.20**	-2.64
29	L6 x T2	-0.44	-1.32	-3.93*	0.88	3.59	-5.83	-7.79	10.03	2.90	3.41	-9.08**	-0.76	-2.24	198.14**	73.50**	37.69	49.13
30	L7 x T2	-4.11	2.68	4.18*	0.88	4.81	-15.06	15.99	-5.74	-2.54	-0.59	3.59	-0.76	-16.69**	-36.52	-42.06	-25.98	-62.64
31	L8 x T2	0.78	-3.88*	0.29	0.21	3.67	-6.19	0.07	2.45	8.37	5.30	10.59**	5.80**	3.42*	-42.41	208.28**	12.02	139.91**
32	L9 x T2	2.67	6.90**	2.40	-3.12	-22.80	-4.67	27.27	0.20	20.07**	7.97**	9.81**	5.13**	0.87	-87.41**	49.28*	44.91	75.24*
33	L10 x T2	3.67	-1.99	-3.60*	-5.57*	6.78	26.58	-16.93	-16.44	-6.85	-5.81*	19.70**	-4.87**	12.87**	9.26	-89.94**	-46.98	-58.53
34	L1 x T3	-1.67	3.12	-0.02	-2.59	-14.19	-7.94	8.97	13.16	16.64**	3.23	30.21**	13.28**	0.28	102.37**	-35.36	18.08	-50.41
35	L2 x T3	-3.22	-1.21	1.87	-1.03	29.36	-11.38	9.31	-27.28	-7.58	2.23	19.88**	1.94	3.50*	31.14	-9.13	16.41	69.37*
36	L3 x T3	-1.00	3.23	0.64	3.86	-22.44	20.59	-15.28	17.13	20.89**	-6.10*	-1.12	-3.06	3.06*	-0.74	181.64**	52.86*	38.59
37	L4 x T3	2.44	-1.88	-2.91	-1.03	14.86	-23.33	-5.53	13.99	6.14	-7.10**	-14.79**	-0.61	12.61**	-50.41	16.42	21.19	17.59
38	L5 x T3	1.89	0.01	4.09*	-2.14	19.03	34.06	-6.25	-46.84	-18.69**	8.46**	3.21	-5.28**	3.83*	99.59**	129.53**	-45.37	29.92
39	L6 x T3	0.89	2.01	0.20	0.41	6.81	-1.38	21.53	-26.95	-0.92	1.68	19.66**	-11.39**	-21.94**	-34.19	-78.47**	-60.14*	-140.63**
40	L7 x T3	-0.78	-2.32	-3.02	-1.92	5.61	14.64	-20.78	0.52	11.39*	16.34**	-6.01	3.28	-2.06	242.48**	-12.36	21.86	86.92**
41	L8 x T3	3.11	-2.88	-0.91	-1.59	-4.19	-1.83	-3.03	9.05	5.31	-8.43**	-11.01**	8.17**	1.06	-125.74**	-220.36**	54.19*	-76.86*
42	L9 x T3	-2.00	-1.77	-0.13	3.08	14.83	-4.80	-5.33	-4.70	-20.17**	-18.10**	-22.12**	-2.17	0.17	-168.08**	-115.69**	-105.26**	-105.52**
43	L10 x T3	0.33	1.68	0.20	2.97	-49.67*	-18.63	16.39	51.91*	-13.00*	7.79**	-17.90**	-4.17*	-0.50	-96.41**	143.76**	26.19	131.03**
	Standard error																	
	Ti	1.02	0.54	0.52	0.72	7.52	7.52	7.52	7.52	1.68	0.80	0.94	0.53	0.44	9.46	7.05	7.21	9.68
	Lj	1.70	0.90	0.86	1.19	12.47	12.47	12.47	12.47	2.79	1.33	1.55	0.88	0.73	15.69	11.69	11.96	16.06
	Sij	3.40	1.80	1.72	2.38	24.94	24.94	24.94	24.94	5.58	2.67	3.11	1.77	1.47	31.38	23.38	23.93	32.11
	Ti-j	1.25	0.66	0.63	0.88	9.21	9.21	9.21	9.21	2.06	0.99	1.15	0.65	0.54	11.59	8.63	8.84	11.86
	Li-j	2.29	1.21	1.16	1.60	16.82	16.82	16.82	16.82	3.76	1.80	2.09	1.19	0.99	21.16	15.76	16.13	21.65
	Ti-Lj	1.85	0.98	0.93	1.29	13.56	13.56	13.56	13.56	3.03	1.45	1.69	0.96	0.80	17.06	12.71	13.01	17.46
	STi-Tj	4.16	2.20	2.11	2.91	30.55	30.55	30.55	30.55	6.83	3.27	3.81	2.16	1.79	38.43	28.63	29.31	39.33
	SiL-jL	4.58	2.43	2.32	3.20	33.63	33.63	33.63	33.63	7.52	3.60	4.19	2.38	1.98	42.31	31.52	32.26	43.30
	Sij-kl	4.75	2.52	2.40	3.32	34.87	34.87	34.87	34.87	7.80	3.73	4.34	2.47	2.05	43.87	32.68	33.45	44.90

*, ** Significant at 5 and 1 percent level of significance

Table 3: GCA and SCA effects for Protein content in fodder, protein content in grain, seed index and harvest index

S. No.	Genotype	Protein content in grain				Protein content in fodder				Seed index				Harvest index			
		E1	**E2**	**E3**	**E4**	**E1**	**E2**	**E3**	**E4**	**E1**	**E2**	**E3**	**E4**	**E1**	**E2**	**E3**	**E4**
1	T1	0.19*	0.51**	-0.04	0.14**	0.23**	0.36**	0.39**	0.38**	0.01	0.14**	0.05	-0.06**	-1.20	0.40	2.15*	1.40*
2	T2	-0.11	-0.07	0.40**	0.05*	-0.01	0.07**	0.03	0.04*	-0.04	-0.19**	-0.19**	-0.08**	0.70	-0.21	-1.80*	0.30
3	T3	-0.07	-0.45**	-0.36**	-0.18**	-0.22**	-0.43**	-0.42**	-0.43**	0.03	0.05*	0.14**	0.14**	0.51	-0.19	-0.35	-1.70**
4	L1	0.84**	2.47**	2.21**	2.12**	0.09	-0.28**	-0.35**	-0.34**	-0.04	0.13**	0.32**	0.03	-1.84	-0.41	-4.04**	-3.69**
5	L2	1.06**	0.97**	0.46*	0.42**	0.47**	0.67**	0.63**	0.64**	0.01	0.17**	0.19*	-0.13**	1.62	1.00	2.30	0.44
6	L3	0.16	1.87**	0.84**	1.33**	-0.39**	0.74**	0.65**	0.69**	-0.24**	0.19**	0.55**	0.56**	-0.64	0.55	-11.36**	-4.18**
7	L4	-0.49**	-0.89**	-0.93**	-0.73**	0.28**	-0.13**	-0.08*	-0.18**	-0.23**	-0.23**	0.28**	-0.02	-0.78	0.10	1.25	2.88**
8	L5	-0.60**	-1.54**	-0.73**	-1.56**	-0.51**	-0.86**	-0.85**	-0.82**	0.14**	0.20**	-0.19*	0.16**	1.21	-1.78	7.48**	0.11
9	L6	-0.64**	-1.05**	-0.07	-1.01**	-0.62**	-1.25**	-1.17**	-1.22**	0.09	-0.02	-0.40**	-0.26**	0.75	0.80	2.18	0.98
10	L7	-0.13	-0.66**	-0.81**	-0.55**	0.29**	1.17**	1.12**	1.18**	0.21**	-0.22**	-0.48**	-0.01	-0.51	0.37	-0.14	1.58
11	L8	-0.03	-1.95**	-1.56**	-1.05**	0.13*	0.23**	0.25**	0.25**	0.07	-0.04	-0.25**	0.02	0.57	-0.13	0.33	2.51*

12	L9	-0.79**	-0.61**	-0.47*	-0.13**	-0.24**	-0.17**	-0.13**	-0.16**	0.03	-0.30**	-0.13	-0.03	-0.28	-0.40	-1.66	-0.14
13	L10	0.63**	1.39**	1.06**	1.17**	0.49**	-0.11**	-0.06	-0.04	-0.04	0.11**	0.13	-0.33**	-0.10	-0.11	3.65*	-0.49
14	L1 x T1	-0.57*	0.06	0.63	0.47**	0.58**	1.00**	0.94**	0.88**	0.10	-0.04	0.10	0.12*	-1.88	-0.13	-4.83	-1.25
15	L2 x T1	-1.18**	-0.16	0.50	0.36**	-0.61**	-0.13	-0.21**	-0.16**	-0.31**	-0.57**	0.31	-0.06	1.23	0.30	3.47	4.10*
16	L3 x T1	0.85**	0.87**	0.98*	1.51**	0.25*	-0.30**	-0.28**	-0.30**	-0.22*	-0.54**	0.47**	0.14**	-1.61	1.54	3.63	-2.59
17	L4 x T1	-1.25**	-0.51**	-0.13	-0.46**	-2.03**	0.08	0.16*	0.26**	0.13	0.07	-0.34	0.13*	-1.64	-1.86	-2.77	-1.37
18	L5 x T1	1.00**	0.73**	0.05	-0.22**	0.95**	0.07	-0.02	0.04	0.18	0.36**	-0.38*	0.34**	-0.31	0.54	-1.63	1.93
19	L6 x T1	-0.07	-1.05**	-2.31**	-1.15**	-0.20	-0.85**	-0.64**	-0.89**	0.33**	0.53**	0.08	0.37**	1.45	1.21	-1.42	0.55
20	L7 x T1	0.94**	-0.52**	-0.18	-0.27**	0.44**	-0.10	-0.13	-0.09	-0.30**	0.08	0.27	-0.15**	2.84	-3.08	5.04	-2.49
21	L8 x T1	0.15	-0.24	-0.40	-0.65**	0.78**	0.61**	0.67**	0.73**	0.20*	-0.15*	-0.29	-0.44**	1.74	0.29	-4.04	-0.26
22	L9 x T1	-0.52	0.23	0.21	-0.18*	-1.29**	0.02	-0.05	-0.04	-0.19	0.11	-0.35*	-0.25**	-0.50	1.57	-5.22	1.65
23	L10 x T1	0.66*	0.59**	0.64	0.59**	1.12**	-0.38**	-0.44**	-0.42**	0.07	0.15*	0.13	-0.20**	-1.33	-0.39	7.76**	-0.27
24	L1 x T2	1.71**	2.43**	1.83**	1.91**	0.54**	0.19*	0.18*	0.23**	-0.06	-0.39**	-0.25	-0.21**	-0.82	-1.23	-5.30	-1.07
25	L2 x T2	-1.47**	-1.60**	-1.72**	-1.12**	-1.58**	-0.86**	-0.78**	-0.76**	0.21*	0.50**	-0.20	-0.32**	-0.14	0.35	-0.17	-1.45
26	L3 x T2	-0.53	-1.62**	-2.38**	-2.22**	1.22**	-0.43**	-0.36**	-0.33**	-0.13	0.48**	-0.53**	0.10	0.90	-0.02	5.12	2.91
27	L4 x T2	0.35	0.63**	0.19	0.40**	-0.19	1.33**	1.22**	1.01**	0.12	-0.29**	0.02	-0.18**	0.83	2.91	2.51	-0.86
28	L5 x T2	-0.86**	-1.14**	0.81*	0.11	-1.10**	-0.26**	-0.18*	-0.21**	-0.02	-0.57**	0.01	-0.56**	-0.17	-0.65	0.83	-1.14
29	L6 x T2	0.37	-0.10	2.51**	0.36**	0.91**	0.86**	0.71**	0.89**	-0.01	-0.20**	0.21	0.28**	0.04	0.57	5.42	2.60
30	L7 x T2	-1.09**	0.34	-0.36	0.27**	-1.59**	-0.47**	-0.46**	-0.45**	0.12	-0.01	-0.05	-0.00	-1.26	1.60	-3.62	-1.16
31	L8 x T2	0.50	0.16	-0.89*	-0.45**	0.68**	0.73**	0.57**	0.52**	-0.21*	0.66**	0.07	0.20**	-0.90	-1.57	3.48	-0.24
32	L9 x T2	1.00**	-0.59**	-0.58	-0.03	1.63**	-1.44**	-1.36**	-1.32**	0.12	0.11	0.76**	0.12*	1.30	-3.09	-5.07	-1.21
33	L10 x T2	0.02	1.48**	0.58	0.78**	-0.53**	0.34**	0.47**	0.43**	-0.13	-0.28**	-0.04	0.58**	0.22	1.13	-3.22	1.63
34	L1 x T3	-1.14**	-2.49**	-2.46**	-2.38**	-1.12**	-1.19**	-1.12**	-1.11**	-0.04	0.43**	0.15	0.09	2.70	1.36	10.13**	2.32
35	L2 x T3	2.65**	1.76**	1.22**	0.76**	2.18**	0.99**	0.99**	0.92**	0.10	0.07	-0.11	0.38**	-1.09	-0.65	-3.30	-2.65
36	L3 x T3	-0.32	0.75**	1.41**	0.71**	-1.48**	0.73**	0.64**	0.64**	0.35**	0.06	0.06	-0.24**	0.71	-1.53	-8.75**	-0.31
37	L4 x T3	0.90**	-0.12	-0.07	0.05	2.22**	-1.41**	-1.38**	-1.27**	-0.25*	0.22**	0.32	0.05	0.80	-1.05	0.27	2.23
38	L5 x T3	-0.14	0.41*	-0.86*	0.11	0.15	0.19*	0.21**	0.17**	-0.16	0.21**	0.37*	0.22**	0.48	0.12	0.80	-0.79
39	L6 x T3	-0.30	1.14**	-0.21	0.79**	-0.71**	-0.01	-0.07	0.00	-0.32**	-0.33**	-0.29	-0.64**	-1.49	-1.78	-4.01	-3.15
40	L7 x T3	0.15	0.18	0.54	0.00	1.15**	0.57**	0.59**	0.54**	0.18	-0.07	-0.22	0.15**	-1.58	1.48	-1.42	3.65
41	L8 x T3	-0.65*	0.09	1.29**	1.10**	-1.45**	-1.34**	-1.24**	-1.26**	0.01	-0.51**	0.22	0.23**	-0.84	1.28	0.55	0.50
42	L9 x T3	-0.48	0.36*	0.37	0.22**	-0.35**	1.43**	1.42**	1.36**	0.07	-0.22**	-0.41*	0.13**	-0.79	1.52	10.28**	-0.43
43	L10 x T3	-0.67*	-2.07**	-1.22**	-1.37**	-0.59**	0.05	-0.02	-0.01	0.07	0.13	-0.10	-0.38**	1.10	-0.75	-4.54	-1.36
	Standard error																
	Ti	0.08	0.05	0.12	0.02	0.03	0.02	0.02	0.02	0.03	0.02	0.05	0.01	0.72	0.55	0.86	0.58
	Lj	0.14	0.09	0.19	0.04	0.05	0.04	0.04	0.03	0.05	0.04	0.09	0.02	1.20	0.91	1.42	0.96
	Sij	0.28	0.18	0.39	0.08	0.11	0.07	0.08	0.06	0.10	0.07	0.18	0.05	2.40	1.82	2.84	1.92
	Ti-j	0.10	0.07	0.14	0.03	0.04	0.03	0.03	0.02	0.04	0.03	0.07	0.02	0.89	0.67	1.05	0.71
	Li-j	0.19	0.12	0.26	0.05	0.07	0.05	0.05	0.04	0.07	0.05	0.12	0.03	1.62	1.23	1.91	1.30
	Ti-Lj	0.15	0.10	0.21	0.04	0.06	0.04	0.04	0.03	0.06	0.04	0.10	0.03	1.31	0.99	1.54	1.05
	STi-Tj	0.34	0.22	0.48	0.09	0.13	0.09	0.09	0.07	0.12	0.09	0.22	0.06	2.94	2.23	3.48	2.36
	SiL-jL	0.37	0.24	0.53	0.10	0.15	0.10	0.10	0.08	0.14	0.10	0.24	0.07	3.24	2.46	3.83	2.59
	Sij-kl	0.39	0.25	0.54	0.11	0.15	0.10	0.11	0.08	0.14	0.10	0.25	0.07	3.36	2.55	3.97	2.69

*, ** Significant at 5 and 1 percent level of significance

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