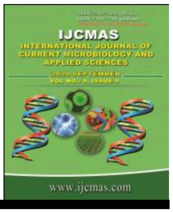
Int.J.Curr.Microbiol.App.Sci (2020) *9*(9): 360-376

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 9 Number 9 (2020)**
Journal homepage: http://www.ijcmas.com



Original Research Article https://doi.org/10.20546/ijcmas.2020.909.046

Combining Ability Analysis for Yield and Yield Attributes in Dual Purpose Sorghum [*Sorghum bicolor* (L.) Moench]

B. L. Meena[1*], B. R. Ranwah[2], H. S. Meena[1], S. K. Meena and R. K. Meena

[1]ICAR-DRMR, Bharatpur Rajasthan-321303, India
[2]MPUAT, Rajasthan College of Agriculture, Udaipur Rajasthan -313001, India

**Corresponding author*

A B S T R A C T

Keywords

Line x tester, General combining ability, Specific combining ability, Sorghum bicolor, Parent selection, Hybrid breeding

Article Info

Accepted:
04 August 2020
Available Online:
10 September 2020

Combining ability analysis (GCA) enables plant breeders to select parental lines for crossing and provides the opportunity to understand the nature of gene actions involved in the inheritance of desired traits. In this study, we used a line x tester mating design to generate 30 hybrid crosses using three restorer (R) and ten cytoplasmic male sterile (CMS; A) lines. Field performance of the hybrids, parents and standard checks were evaluated for grain yield and important phenological, fodder and quality traits. There were 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.

Introduction

Sorghum bicolor (L.) Moench (2n = 20) is an 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). 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 58.20 m ha area in the world with an annual grain production of 68.87 m tones and productivity of 1535 kg/ha (FAO, 2015). In India, it covers about 5.82 m ha with an annual grain production of 5.39 m tonnes and productivity of 926 kg/ha (FAO, 2015). India is largest producer of sorghum in the world (FAO, 2015). The major sorghum growing states in India are Maharashtra, Karnataka, Madhya Pradesh, Andhra Pradesh, Rajasthan, Tamil Nadu, Uttar Pradesh and Gujarat. In Rajasthan, it is grown for dual purpose with high emphasis on fodder, mainly it is grown under sub-marginal agro-climatic and edaphic conditions which, is characterized by low soil fertility and recurring moisture stress. It occupies an area of about 6.61 lakh hectares with 5.05 lakh tones production in the year 2015. The productivity of sorghum in the state is 763 kg/ha (Anonymous, 2015). Low productivity is due to cultivation of sorghum on marginal soil, low inputs and more emphasis on fodder. Being C_4 sorghum has great potentiality. Its grain yield productivity in rice fellow fields is up to 80 q ha^{-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. Mainly three type of sorghum is cultivated i.e. grain, fodder and multicut sorghum. Sorghum is predominantly self-pollinated crop endowed with a wide range of genetic variability due to its wide range of adaption and free gene exchange among various races. Careful selection of parents for hybridization is a key of success in any breeding programme. 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 is most appropriate mating design for the type of genetic material used in present investigation and information to be derived.

Materials and Methods

The present investigation entitled Combining ability analysis for yield and yield attributes in dual purpose sorghum [*Sorghum bicolor* (L.) Moench] was conducted at Instructional farm, Rajasthan College of Agriculture, Udaipur during kharif 2014 and *kharif* 2015.

Experimental material

On the basis of days to flowering and suitability for dual purpose 36 lines were received from ICRISAT. After evaluation at this station 10 lines were identified on the basis of nicking of flowering. Three testers were identified on the basis of availability of restorer gene and past performance. Checks CSV 23, CSV 27 and CSH 25 were national checks in coordinated trials.

Line x Tester

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 Udaipur during *kharif* 2014 and at Warangal during *rabi* 2014-15.

Experimental design

Line x Tester mating design

In this experiment total 46 genotypes (10 lines, 3 testers, 30 crosses and 3 checks) were grown in a randomized block design with three replications in four different environments during *kharif* 2015 at Instructional farm, Rajasthan College of Agriculture, Udaipur (Rajasthan). Each genotype was sown in a single row plot of 2 meter length maintaining a separate crop geometry (spacing) for each environments. The row to row and plant to plant spacing was 22.5 cm x 5 cm, 30 cm x 10 cm, 45 cm x 10 cm and 60 cm x 10 cm in $E_{1,}$ $E_{2,}$ E_3 and $E_{4,}$ respectively.

Traits under investigation

In the experiments observations were recorded on days to 50 % flowering, days to maturity, dry fodder yield (q ha^{-1}), ear head length (cm), number of primaries per plant, number of seeds per primaries, grain yield (q ha^{-1}) and protein content in grain

Statistical analysis

Plot means of all the characters were subjected to various statistical analyses.

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 was homogeneous using least square technique of Fisher (1932).

Analysis of variance for individual environment

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 mean, general mean, standard error, critical difference and coefficient of variation were calculated as:

$$\text{Mean } (\bar{X}_{\mathbf{i}}) = \sum_{i=1}^{r} X_{ij} \ /r$$

$$\text{General Mean } (\bar{X}) = \sum_{i=1}^{g} \sum_{j=1}^{r} X_{ij} \ /rg$$

If mean square due to genotype was significant then CD was calculated as follow:

CD = SE (Diff.) x T $_{[(r-1)\ (g-1)]}$ at 5% or 1% level of significance

$$CV\ \% = \frac{\sqrt{MSE}}{\bar{X}} \times 100$$

Where,

$\bar{X}_{\mathbf{i}}$ = mean of the i^{th} genotype
$\bar{X}$ = mean over genotypes and replications
$\bar{X}_{\mathbf{ij}}$ = value of i^{th} genotypes in j^{th} replication
r, g = number of replications and genotypes, respectively

$$SE\ (Diff.) = \sqrt{\frac{2\ MSE}{r}}$$

MSE = Error mean square (M_{14}) from table 3 and

Analysis of variance over environments

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 parents 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.

Bartlett's test: Before doing the pool analysis of variance homogeneity of error variance was tested using the Bartlet test. Pool analysis was performed only when error variance was homogeneous in different environments.

$$Corrected\ \chi^2 = \frac{\chi^2}{CF}$$

Where

$$\chi^2 = (\textstyle\sum_{i=1}^{l} df_i) \times loge\ EMSP - \textstyle\sum_{i=1}^{l}(df_i.loge\ EMS_i)$$

$$CF = 1 + \frac{1}{3(l-1)} \times [\sum_{i=1}^{l} \frac{1}{df_i} - \frac{1}{\sum_{i=1}^{l} df_i}]$$

df_i = Error degrees of freedom in i^th environment

l = Number of environments

EMSP = Pool error mean square, and

EMS_i = Error mean square in i^th environment.

Combining ability effects

Griffing's method of diallel (1956) for individual environments and Daljit Singh (1973, 1979) 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

$$\mu = \frac{\sum_{i=1}^{t} \sum_{j=1}^{l} \sum_{k=1}^{r} X_{ijk}}{ltr}$$

$$GCA\ \ line = \frac{\sum_{i=1}^{t} \sum_{k=1}^{r} X_{ijk}}{tr} - \mu$$

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

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

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 characters same manner as for individual environments except the number of environments was an additional divisor.

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

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

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

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

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.

Results and Discussion

Analysis of variance for experimental design and mean values

The analysis of variance for experimental design in individual environment (Table 1) revealed significant differences among genotypes for all the characters in all the four environments except for days to 50% flowering in E_1 and E_3, days to maturity in all the four environments, dry fodder yield in $E_{3,}$ number of primaries per plant in $E_{3,}$ number of seeds per primaries in E_1 and E_4. Partitioning of genotypic variance into parents, crosses and parents v/s crosses revealed that for all the characters under study there were significant difference in all the environments except mean squares due to parents for days to 50 % flowering in E_1 and $E_{3,}$ ear head length in E_1, mean squares due to parents v/s crosses for number of primaries in $E_{1.}$

The Bartllet test (Table 2) revealed that error variance was homogeneous for ear head length only. Therefore pooled analysis was carried out for this character only.The pooled analysis revealed significant differences between the environments for ear head length. The mean squares due to genotypes including parents, crosses and parents vs. crosses were also significant for the ear head length. Mean squares due to genotypes x environments interactions were significant for this characters. The cross x environments and parents x environments was significant for the character.The interaction of checks, parent vs. checks, tester, tester vs lines, parent vs crosses with environment were non significant for ear head length (Table 3).

Combining ability

Kempthorne (1957) suggested the analysis of variance for L x T factorial mating design using random effect model. But later on it was extended by various workers for using fixed effect model. Singh and Singh (1976 &1979) suggested the method of diallel analysis over the environments. The same principles were used in present investigation to analyze the data over the environments. In past also so many plant breeders used the same. 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 ear head length in E_1 and $E_{3,}$ number of seeds per primary and seed index in E_1 and harvest index in E_1 and $E_{2.}$ Significant difference for SCA was observed for all the characters in all the environments except days to 50% flowering in E_1, ear head length in E_4 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 character wise finding of GCA effects of tester and line and SCA effect of crosses were as follows (Table 4 to 5).

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). 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).

The mean square due to lines, testers and L x T were significant in all the four environments. The early maturity was important therefore negative GCA and SCA effects were considered desirable for this character. The estimates GCA effects among lines ranged from -1.79 (L_7) to 3.99 (L_9) in E_1, -1.60 (L_7) to 3.18 (L_9) in E_2, -1.59 (L_5 and L_7) to 3.08 (L_9) in E_3 and -1.98 (L_7) to 3.02 (L_9) in E_4. It was negative and significant for 1, 3, 3 and 3 lines in E_1, E_2, E_3 and E_4 respectively**.** L_7 having significant and negative GCA effects in all the four environments. Among the testers T_3 having significant and negative GCA effects in E_2, E_3 and E_4. The estimates of SCA effects ranged from -8.99 (L_{10} x L_2) to 5.14 (L_{10} x T_1) in E_1, -8.47 (L_{10} x T_2) to 4.50 (L_{10} x T_3) in E_2, -8.34 (L_{10} x T_2) to 4.69 (L_{10} x T_3) in E_3 and -8.02 (L_{10} x T_2) to 4.14 (L_{10} x T_3) in E_4. It was significant and negative for 8, 8, 8 and 7 crosses in E_1, E_2, E_3 and E_4, respectively. Cross *viz*., L_2 x T_1, L_5 x T_1, L_8 x T_1, L_3 x T_2, L_{10} x T_2, L_4 x T_3 exhibited significant and negative (desirable) SCA effects in all the four environments (Table 4). For dry fodder yield the estimates GCA effects among lines ranged from -36.71 (L_6) to 50.29 (L_1) in E_1, -51.84 (L_1) to 53.60 (L_{10}) in E_2, -32.83 (L_4) to 29.06 (L_1) in E_3 and -28.60 (L_7) to 36.07 (L_1) in E_4. It was significant and potential for 3, 4, 2 and 4 lines in E_1, E_2, E_3 and E_4 respectively**.** L_1 having significant and positive GCA effects in E_1, E_3 and E_4. Among the testers T_3 having significant and positive GCA effects in E_2, E_3 and E_4.The estimates of SCA effects ranged from -98.87 (L_3 x L_1) to 92.13 (L_9 x L_1) in E_1, -87.62 (L_9 x L_3) to 113.27 (L_6 x L_3) in E_2, -72.14 (L_9 x L_3) to 74.32 (L_9 x L_2) in E_3 and -47.71 (L_{10} x L_1) to 36.62 (L_8 x L_2) in E_4. It was significant and positive for 12, 10, 7 and 9 crosses in E_1, E_2, E_3 and E_4 respectively. Cross *viz*., L_5 x T_1, L_9 x T_1, L_2 x T_3, L_4 x T_1, L_7 x T_1, L_{10} x T_1 and L_2 x T_2 exhibited significant and positive (desirable) SCA effects in more than one environments (Table 4).

With regards to Ear head length the mean square due to lines, testers and L x T were significant in all the four environments and over the environments. Interaction of lines, testers and L x T with environments were also significant (Table 4). Combining ability in positive direction was considered desirable.

The estimates GCA effects among lines ranged from -1.57 (L_{10}) to 1.09 (L_5) over the environment. It was significant and positive for 3 lines viz., L_2 (.98), L_5 (1.09) and L_7 (1.51) over the environment**.** Among the testers T_2 having significant and positive GCA effects over the environment.

Table.1 Mean square for different characters in individual environment

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]
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
Days to maturity	1	3.98	52.30	1.00	48.08**	88.47**	18.11**	111.19**	24.70**	162.24**	38.68**	18.34**	23.07**	48.74**	2.62
	2	2.89	46.51	0.44	42.78**	81.30**	16.33**	102.55**	20.01**	153.39**	33.04**	39.70**	19.44**	39.11**	1.66
	3	0.90	44.15	1.33	45.24**	76.92**	8.78**	97.29**	29.89**	109.86**	32.45**	42.34**	21.36**	36.90**	1.62
	4	1.62	43.18	2.33	43.39**	77.08**	21.78**	95.65**	20.53**	164.41**	29.12**	17.21**	19.38**	35.32**	1.61
Dry fodder yield	1	17.07	9575.48**	14802.78**	22051.62**	6866.19**	5584.00**	7877.41**	329.61	1234.86**	10222.36**	4421.01**	7012.23**	12472.02**	122.78
	2	245.42	19555.94**	7159.11**	51838.78**	17175.53**	3073.78**	8013.19**	127840.09**	17213.42**	20862.36**	131459.38**	12450.87**	12779.55**	323.84
	3	179.01	4576.05	261.44	14135.01**	5163.40**	490.78	5950.70**	7422.91**	5959.24**	4412.35**	9663.68**	2616.82**	4726.63**	278.96
	4	83.96	3219.74**	2989.00**	15079.04**	2492.90**	1026.33**	2926.54**	1523.27**	6878.04**	3179.63**	2049.38**	4888.25**	2450.90**	125.49
Ear head length	1	8.90	15.66*	21.78*	63.95**	8.42	19.44*	6.91	0.02	37.14**	16.70**	9.38	26.92**	12.40**	5.26
	2	0.66	19.43**	44.78**	17.12	16.47**	30.11**	15.24**	0.22	41.91**	18.68**	70.63**	14.70**	14.89**	5.44
	3	3.14	26.87**	55.11**	5.67	32.97**	67.00**	25.00**	36.62**	19.52*	23.56**	5.91	30.30**	22.15**	3.61
	4	30.49**	18.93**	57.33**	6.58	26.77**	34.78**	26.50**	13.14	49.49**	12.63**	45.30**	17.71**	6.46	5.98
Number of primaries per plant	1	1.59	473.69**	421.44**	2029.17**	433.80**	318.78**	502.40**	46.40	25.88	438.36**	211.68**	638.64**	363.41**	23.58
	2	8.67	645.40*	140.78*	6961.59**	883.68**	1312.11**	303.04**	5252.51**	1332.93**	384.48**	392.74**	626.35**	262.62**	34.27
	3	35.66	351.62	81.33	2275.69**	454.97**	204.33*	431.89**	1164.01**	795.69**	268.51**	444.90**	446.97**	159.68**	50.43
	4	9.94	557.37**	388.00**	1878.00**	914.80**	1228.44**	751.74**	1755.12**	2243.90**	354.97**	499.08**	679.39**	176.74**	43.53
Number of seeds per primary	1	441.42**	3396.21	136.11	222.93	2527.18**	3403.11**	2178.00**	3917.85**	3192.81**	4103.56**	682.98**	4133.01**	4468.90**	73.53
	2	136.36*	690.02*	129.78*	1804.62**	370.76**	86.33	302.85**	1550.78**	237.96**	808.51**	1093.34**	760.00**	801.12**	29.84
	3	58.79	1250.89**	430.78**	1435.00**	740.47**	684.33**	747.14**	792.62**	2494.68**	1503.32**	563.41**	3067.79**	825.52**	62.53
	4	21.96	512.69	30.11	1395.01**	624.29**	17.33	533.02**	2659.57**	411.68*	485.23**	109.43	551.98**	493.61**	66.75
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
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

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

Table.2 Test of homogeneity of error mean square (Bartlet test)

S. No.	Character	Bartlet value [3]
1.	Days to 5% flowering	56.41**
2.	Days to maturity	8.26*
3.	Dry fodder yield	34.82**
4.	Ear head length	6.23
5.	Number of primaries per plant	14.10**
6.	Number of seeds per primary	20.05**
7.	Grain yield	62.52**
8.	Protein content in grain	200.69**

*, ** Significant at 5 and 1 percent level of significance
[ ] Degrees of freedom

Table.3 Mean square over the environment ear head length

S. No.	Source	df	Ear head length
1.	Environment	3	148.40**
2.	Rep./Env	8	10.80*
3.	Genotype	45	42.91**
	Check	2	160.19**
	P vs Chk	1	72.93**
	Parent	12	51.04**
	Tester	2	136.69**
	Line	9	35.39**
	T v/s L	1	20.53**
	P v/s C	1	144.26**
	Cross	29	28.74**
	Tester	2	60.43**
	Line	9	45.46**
	L x T	18	16.87**
4.	G x E	135	12.66**
	Check x E	6	6.27
	Chk Vs P x E	3	6.79
	P x E	36	11.20**
	T x E	6	4.88
	L x E	27	12.75**
	T v/s L x E	3	9.82
	P v/s C x E	3	1.27
	Cross x E	87	14.27**
	T x E	6	23.60**
	L x E	27	14.72**
	L x T x E	54	13.01**
5.	Pooled Error	360	5.07

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

Table.4 GCA and SCA effects for days to 50% flowering, days to maturity dry fodder yield and ear head length

S. No.	Genotype	Days to 50% flowering				Days to maturity				Dry fodder yield				Ear head length				
		E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4	Pool
1	T1	0.00	-0.76	-1.07*	-1.27	-0.26	0.03	0.12	0.12	13.42**	-58.31**	1.51	3.04	0.18	-1.10	-0.04	0.97	-0.47
2	T2	-3.00**	-1.79**	-0.40	2.23**	0.88*	1.13**	1.12**	0.69*	-3.21	-13.64**	-18.66**	-9.36**	-0.17	0.68	-0.59	0.08	0.82**
3	T3	3.00**	2.54**	1.47**	-0.97	-0.62	-1.17**	-1.24**	-0.81**	-10.21**	71.96**	17.14**	6.31**	-0.01	0.42	0.64	-1.05	-0.35
4	L1	3.80*	1.34	4.39**	1.06	0.10	-0.04	-0.37	0.69	50.29**	-51.84**	29.06**	36.07**	0.08	0.58	-0.23	-0.44	-0.41
5	L2	3.02	2.01*	0.83	-0.17	-1.12	-1.49**	-1.26**	-1.20**	-0.93	4.60	-11.72*	32.96**	-2.64	0.53	2.05	0.06	0.98*
6	L3	1.13	2.23*	4.72**	1.28	0.99	1.51**	2.19**	1.13*	-16.27**	16.82**	0.72	16.40**	1.94	-0.44	-0.48	-1.02	-0.38
7	L4	-5.98**	-2.32*	-2.72**	-1.17	-0.12	0.40	0.19	0.47	-0.27	-44.96**	-32.83**	10.18*	-0.53	-0.58	-0.62	1.73	-0.35
8	L5	1.24	-2.21*	0.28	-0.39	-1.01	-0.71	-1.59**	-1.64**	-11.16**	35.82**	19.50**	-5.93	-1.08	0.86	-0.06	0.28	1.09**
9	L6	-0.42	-1.88*	-2.83**	2.39*	-0.46	-1.04*	-0.48	0.13	-36.71**	36.60**	-0.06	-20.49**	1.44	-2.28	0.13	0.70	0.23
10	L7	1.91	-1.88*	-1.94*	-1.61	-1.79**	-1.60**	-1.59**	-1.98**	-23.27**	-10.07	0.06	-28.60**	1.72	-1.22	1.08	-1.58	1.51**
11	L8	-7.64**	-3.66**	-7.06**	-6.61**	0.10	0.40	0.08	-0.31	-16.82**	2.27	8.39	-27.71**	-0.50	0.44	-0.59	0.64	0.73
12	L9	1.80	3.57**	2.50**	4.72**	3.99**	3.18**	3.08**	3.02**	13.40**	-42.84**	-9.72	-8.04*	0.08	0.69	-0.45	-0.33	-1.85**
13	L10	1.13	2.79**	1.83*	0.50	-0.68	-0.60	-0.26	-0.31	41.73**	53.60**	-3.39	-4.82	-0.53	1.42	-0.84	-0.05	-1.57**
14	L1 x T1	-1.00	-1.24	-0.82	-1.29	0.03	-0.92	-0.90	0.54	18.58*	23.31	-27.62*	-18.27*	-0.15	1.35	-1.37	0.17	-2.23**
15	L2 x T1	1.78	1.42	-2.60	-1.73	-2.41*	-2.48**	-2.34**	-1.90*	-69.87**	-36.47**	-28.18*	-13.49	-1.43	-1.59	3.02	0.01	0.38
16	L3 x T1	1.67	0.20	0.51	2.16	2.14	2.19*	2.88**	1.77*	-98.87**	-47.02**	29.04*	-1.93	1.16	-2.12	-0.29	1.26	-1.76*
17	L4 x T1	3.78	0.09	-1.04	-0.07	2.59*	1.63	1.88*	1.77*	-20.53**	49.42**	21.60	32.62**	0.63	-1.32	-0.15	0.84	0.88
18	L5 x T1	-2.11	-1.36	-0.38	-2.84	-3.19**	-2.59**	-2.01*	-1.79*	74.36**	52.98**	23.60*	-16.93*	0.68	-0.26	0.79	-1.22	1.61*
19	L6 x T1	-0.44	-0.69	3.73*	-1.29	-0.74	-0.59	-1.12	-1.23	5.58	-56.80**	-40.18**	36.62**	0.24	0.96	-2.32	1.12	0.38
20	L7 x T1	4.89	-0.36	-1.16	1.04	0.59	0.97	1.32	0.88	-64.53**	28.53*	-20.62	34.40**	-3.04	2.91	-1.26	1.39	-0.56
21	L8 x T1	-3.89	6.76**	0.62	1.38	-4.63**	-2.70**	-3.34**	-3.46**	47.02**	-4.80	3.38	-26.82**	1.10	0.82	-1.34	-0.58	-0.70
22	L9 x T1	-0.67	-5.13**	-2.27	0.04	0.48	0.52	-0.01	-0.46	92.13**	27.64*	-2.18	21.51**	-1.07	0.66	2.93	-2.52	1.47
23	L10 x T1	-4.00	0.31	3.40	2.60	5.14**	3.97**	3.66**	3.88**	16.13*	-36.80**	41.16**	-47.71**	1.88	-1.40	-0.01	-0.47	0.52
24	L1 x T2	2.67	-1.88	0.84	3.88	3.90**	3.98**	3.43**	2.98**	1.21	-6.02	3.88	16.80*	-0.55	-0.85	1.09	0.31	0.57
25	L2 x T2	1.44	-0.21	0.73	2.77	3.46**	3.42**	3.66**	3.53**	36.10**	-48.47**	45.99**	-2.76	0.76	-0.21	-1.60	1.06	0.27
26	L3 x T2	-0.67	-3.43	-1.16	-6.01*	-3.32**	-2.91**	-2.79**	-3.13**	46.43**	-7.69	-17.79	8.80	-1.24	4.68	-1.82	-1.61	0.71
27	L4 x T2	-6.22	1.79	3.96*	1.10	1.79	1.87*	1.21	1.87*	60.77**	-4.58	-23.57*	-35.64**	-0.19	-0.27	1.90	-1.44	-0.57
28	L5 x T2	0.22	1.34	-3.71*	4.99*	3.68**	3.31**	2.99**	2.31*	-97.68**	-61.69**	-36.23**	-7.87	-1.88	0.37	1.09	0.42	-1.09
29	L6 x T2	-0.44	-1.32	-3.93*	0.88	1.79	1.98*	1.88*	1.87*	3.54	-56.47**	14.99	0.02	-0.33	-2.07	2.65	-0.25	-0.65
30	L7 x T2	-4.11	2.68	4.18*	0.88	-1.54	-1.13	-1.34	-1.02	6.77	-13.80	2.88	-24.87**	3.23	-0.29	-0.79	-2.14	0.57
31	L8 x T2	0.78	-3.88*	0.29	0.21	1.57	0.53	0.99	0.98	-40.01**	60.87**	-5.79	15.24	-0.72	-1.46	1.71	0.47	0.85
32	L9 x T2	2.67	6.90**	2.40	-3.12	-2.32*	-2.58**	-1.68	-1.36	6.77	59.98**	74.32**	3.58	1.03	-0.38	-2.77	2.11	-0.23
33	L10 x T2	3.67	-1.99	-3.60*	-5.57*	-8.99**	-8.47**	-8.34**	-8.02**	-23.90**	77.87**	-58.68**	26.69**	-0.11	0.48	-1.46	1.08	-0.43
34	L1 x T3	-1.67	3.12	-0.02	-2.59	-3.93**	-3.06**	-2.53**	-3.52**	-19.79*	-17.29	23.74*	1.47	0.70	-0.50	0.28	-0.48	1.66*
35	L2 x T3	-3.22	-1.21	1.87	-1.03	-1.04	-0.94	-1.31	-1.63	33.77**	84.93**	-17.81	16.24*	0.67	1.81	-1.42	-1.06	-0.65

36	L3 x T3	-1.00	3.23	0.64	3.86	1.18	0.72	-0.09	1.37	52.43**	54.71**	-11.26	-6.87	0.09	-2.56	2.11	0.36	1.04
37	L4 x T3	2.44	-1.88	-2.91	-1.03	-4.38**	-3.50**	-3.09**	-3.63**	-40.23**	-44.84**	1.97	3.02	-0.44	1.58	-1.75	0.61	-0.32
38	L5 x T3	1.89	0.01	4.09*	-2.14	-0.49	-0.72	-0.98	-0.52	23.32**	8.71	12.63	24.80**	1.20	-0.11	-1.89	0.80	-0.51
39	L6 x T3	0.89	2.01	0.20	0.41	-1.04	-1.39	-0.76	-0.63	-9.12	113.27**	25.19*	-36.64**	0.09	1.11	-0.33	-0.87	0.27
40	L7 x T3	-0.78	-2.32	-3.02	-1.92	0.96	0.17	0.02	0.14	57.77**	-14.73	17.74	-9.53	-0.19	-2.61	2.06	0.74	-0.01
41	L8 x T3	3.11	-2.88	-0.91	-1.59	3.07**	2.17*	2.36**	2.48**	-7.01	-56.07**	2.41	11.58	-0.38	0.64	-0.36	0.11	-0.15
42	L9 x T3	-2.00	-1.77	-0.13	3.08	1.84	2.06*	1.69	1.81*	-98.90**	-87.62**	-72.14**	-25.09**	0.03	-0.28	-0.17	0.41	-1.23
43	L10 x T3	0.33	1.68	0.20	2.97	3.84**	4.50**	4.69**	4.14**	7.77	-41.07**	17.52	21.02**	-1.77	0.92	1.47	-0.62	-0.09
	Standard error																	
	Ti	1.02	0.54	0.52	0.72	0.34	0.27	0.27	0.27	2.34	3.79	3.52	2.36	1.06	1.06	1.06	1.06	0.24
	Lj	1.70	0.90	0.86	1.19	0.57	0.45	0.44	0.44	3.87	6.29	5.84	3.92	1.76	1.76	1.76	1.76	0.39
	Sij	3.40	1.80	1.72	2.38	1.13	0.90	0.89	0.89	7.75	12.58	11.68	7.83	3.52	3.52	3.52	3.52	0.79
	Ti-j	1.25	0.66	0.63	0.88	0.42	0.33	0.33	0.33	2.86	4.65	4.31	2.89	1.30	1.30	1.30	1.30	0.29
	Li-j	2.29	1.21	1.16	1.60	0.76	0.61	0.60	0.60	5.22	8.48	7.87	5.28	2.37	2.37	2.37	2.37	0.53
	Ti-Lj	1.85	0.98	0.93	1.29	0.62	0.49	0.48	0.48	4.21	6.84	6.35	4.26	1.91	1.91	1.91	1.91	0.43
	STi-Tj	4.16	2.20	2.11	2.91	1.39	1.10	1.09	1.09	9.49	15.41	14.30	9.59	4.31	4.31	4.31	4.31	0.96
	SiL-jL	4.58	2.43	2.32	3.20	1.53	1.22	1.20	1.20	10.45	16.97	15.75	10.56	4.75	4.75	4.75	4.75	1.06
	Sij-kl	4.75	2.52	2.40	3.32	1.58	1.26	1.24	1.24	10.83	17.59	16.33	10.95	4.92	4.92	4.92	4.92	1.10

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

Table.5 GCA and SCA effects for number of primaries per plant and number of seeds per primary, grain yield and protein content in grain

S. No.	**Genotype**	**Number of primaries per plant**				**Number of seeds per primary**				**Grain yield**				**Protein content in grain**			
		E1	**E2**	**E3**	**E4**	**E1**	**E2**	**E3**	**E4**	**E1**	**E2**	**E3**	**E4**	**E1**	**E2**	**E3**	**E4**
1	T1	2.54*	3.68**	-0.10	2.94*	0.24	-6.88**	-4.61**	2.10	1.53	-10.53**	7.30**	0.37	0.19*	0.51**	-0.04	0.14**
2	T2	0.21	-3.56**	-3.80*	-4.66**	4.64*	4.42**	3.99*	-1.63	1.03	-8.37**	-6.80**	-3.53**	-0.11	-0.07	0.40**	0.05*
3	T3	-2.76**	-0.12	3.90*	1.71	-4.89**	2.46*	0.62	-0.47	-2.57**	18.90**	-0.50	3.17**	-0.07	-0.45**	-0.36**	-0.18**
4	L1	12.08**	7.74**	-1.32	3.72	-27.64**	-0.11	-18.68**	10.19**	6.63**	15.72**	-3.61**	1.26	0.84**	2.47**	2.21**	2.12**
5	L2	-2.92	-4.59*	-11.21**	2.50	-18.87**	-3.56	25.99**	5.63	-4.37**	-1.94	5.06**	3.37**	1.06**	0.97**	0.46*	0.42**
6	L3	3.08	-6.48**	-4.66	-1.28	2.58	-6.44**	-23.79**	-16.48**	11.30**	14.06**	-11.28**	-6.86**	0.16	1.87**	0.84**	1.33**
7	L4	4.86**	13.08**	3.34	3.17	40.47**	-6.89**	24.10**	2.97	1.97	-14.61**	-1.39	-3.08**	-0.49**	-0.89**	-0.93**	-0.73**
8	L5	-8.37**	5.74**	14.12**	18.17**	-23.64**	-7.78**	10.21**	2.97	-3.59**	6.39**	4.94**	-2.30**	-0.60**	-1.54**	-0.73**	-1.56**
9	L6	11.19**	-4.70*	1.01	3.06	1.91	-2.11	11.54**	-2.81	-11.81**	1.61	5.72**	3.81**	-0.64**	-1.05**	-0.07	-1.01**
10	L7	-9.81**	-7.59**	1.68	-14.50**	14.91**	17.11**	10.88**	-1.81	-7.14**	-5.72**	7.39**	2.59**	-0.13	-0.66**	-0.81**	-0.55**
11	L8	5.30**	-0.59	3.68	-1.28	16.47**	16.22**	-12.79**	8.30**	3.63**	-3.39*	4.17**	-2.52**	-0.03	-1.95**	-1.56**	-1.05**
12	L9	-5.14**	-11.70**	1.57	-8.28**	9.02**	-6.11**	-14.01**	-6.37*	-3.37*	-20.94**	-4.50**	5.37**	-0.79**	-0.61**	-0.47*	-0.13**
13	L10	-10.26**	9.08**	-8.21**	-5.28*	-15.20**	-0.33	-13.46**	-2.59	6.74**	8.83**	-6.50**	-1.63*	0.63**	1.39**	1.06**	1.17**
14	L1 x T1	-5.54	1.32	1.99	7.94	16.98**	20.21**	15.28**	-0.32	-2.20	-10.69**	-9.86**	2.08	-0.57*	0.06	0.63	0.47**
15	L2 x T1	-22.54**	5.32	-0.12	2.17	-26.13**	-19.68**	10.94	0.57	-15.53**	-10.69**	7.48**	-19.37**	-1.18**	-0.16	0.50	0.36**
16	L3 x T1	-3.88	-2.46	-11.68*	2.61	-10.58	-15.12**	10.06	1.01	8.13**	6.98*	4.14*	-10.81**	0.85**	0.87**	0.98*	1.51**

17	L4 x T1	9.34**	-0.34	7.99		-2.50	-65.13**	16.99**	-38.50**	-8.10	1.13	6.98*	-1.08	-1.59	-1.25**	-0.51**	-0.13	-0.46**
18	L5 x T1	6.90*	-11.34**	1.88		-2.17	-6.69	-4.79	-7.94	6.23	18.02**	4.64	-2.41	4.63**	1.00**	0.73**	0.05	-0.22**
19	L6 x T1	-11.66**	-7.57	-2.34		3.94	-14.58*	-1.12	6.72	6.34	-5.09	-10.58**	12.14**	24.19**	-0.07	-1.05**	-2.31**	-1.15**
20	L7 x T1	-2.99	5.32	-4.68		-2.83	-36.58**	4.32	-0.28	-15.32**	-15.76**	2.42	-2.52	18.74**	0.94**	-0.52**	-0.18	-0.27**
21	L8 x T1	9.90**	-2.34	1.99		-5.06	49.20**	7.88*	-12.61*	4.57	3.13	0.42	-13.97**	-4.48**	0.15	-0.24	-0.40	-0.65**
22	L9 x T1	14.34**	9.10*	2.10		0.28	43.64**	-6.46	-2.39	0.23	10.13**	12.31**	-2.97	-1.03	-0.52	0.23	0.21	-0.18*
23	L10 x T1	6.12	2.99	2.88		-4.39	49.87**	-2.23	18.72**	4.79	-1.98	-1.80	9.03**	-12.37**	0.66*	0.59**	0.64	0.59**
24	L1 x T2	0.79	-11.78**	0.36		3.54	-21.42**	-18.09**	-20.66**	-12.26*	-1.03	-19.52**	-3.42	-2.36	1.71**	2.43**	1.83**	1.91**
25	L2 x T2	18.79**	-3.44	-1.09		-5.57	43.47**	1.02	-13.32*	-1.37	13.30**	-9.19**	-9.42**	15.87**	-1.47**	-1.60**	-1.72**	-1.12**
26	L3 x T2	-6.21	-6.56	1.36		1.54	4.69	12.24**	2.46	-4.59	-2.03	-5.86	-1.09	7.76**	-0.53	-1.62**	-2.38**	-2.22**
27	L4 x T2	-2.66	1.89	-4.64		-6.23	41.80**	-17.31**	16.57**	-10.37	5.97*	7.81*	1.69	-11.02**	0.35	0.63**	0.19	0.40**
28	L5 x T2	-7.10*	3.56	-3.42		11.77*	-9.76	-7.42	5.79	-1.03	-26.48**	-7.86*	7.69**	-8.47**	-0.86**	-1.14**	0.81*	0.11
29	L6 x T2	3.68	-1.33	0.02		-2.12	18.02**	11.24**	7.12	8.74	3.41	-9.08**	-0.76	-2.24	0.37	-0.10	2.51**	0.36**
30	L7 x T2	8.68*	1.56	4.36		-10.23*	-18.98**	25.02**	10.46	-2.26	-0.59	3.59	-0.76	-16.69**	-1.09**	0.34	-0.36	0.27**
31	L8 x T2	-4.77	2.22	-4.98		1.21	-8.87	-10.09**	2.12	3.63	5.30	10.59**	5.80**	3.42*	0.50	0.16	-0.89*	-0.45**
32	L9 x T2	-5.66	-1.33	13.80**		-0.79	-24.42**	-3.42	3.34	22.30**	7.97**	9.81**	5.13**	0.87	1.00**	-0.59**	-0.58	-0.03
33	L10 x T2	-5.54	15.22**	-5.76		6.88	-24.53**	6.80	-13.88*	-2.81	-5.81*	19.70**	-4.87**	12.87**	0.02	1.48**	0.58	0.78**
34	L1 x T3	4.76	10.46*	-2.34		-11.49*	4.44	-2.12	5.38	12.58*	3.23	30.21**	13.28**	0.28	-1.14**	-2.49**	-2.46**	-2.38**
35	L2 x T3	3.76	-1.88	1.21		3.40	-17.33**	18.66**	2.38	0.80	2.23	19.88**	1.94	3.50*	2.65**	1.76**	1.22**	0.76**
36	L3 x T3	10.09**	9.01*	10.32*		-4.16	5.89	2.88	-12.51*	3.58	-6.10*	-1.12	-3.06	3.06*	-0.32	0.75**	1.41**	0.71**
37	L4 x T3	-6.69	-1.54	-3.34		8.73	23.33**	0.32	21.93**	18.47**	-7.10**	-14.79**	-0.61	12.61**	0.90**	-0.12	-0.07	0.05
38	L5 x T3	0.20	7.79	1.54		-9.60*	16.44**	12.21**	2.16	-5.20	8.46**	3.21	-5.28**	3.83*	-0.14	0.41*	-0.86*	0.11
39	L6 x T3	7.98*	8.90*	2.32		-1.82	-3.44	-10.12**	-13.84*	-15.09**	1.68	19.66**	-11.39**	-21.94**	-0.30	1.14**	-0.21	0.79**
40	L7 x T3	-5.69	-6.88	0.32		13.07**	55.56**	-29.34**	-10.18	17.58**	16.34**	-6.01	3.28	-2.06	0.15	0.18	0.54	0.00
41	L8 x T3	-5.13	0.12	2.99		3.84	-40.33**	2.21	10.49	-8.20	-8.43**	-11.01**	8.17**	1.06	-0.65*	0.09	1.29**	1.10**
42	L9 x T3	-8.69*	-7.77	-15.90**		0.51	-19.22**	9.88*	-0.96	-22.53**	-18.10**	-22.12**	-2.17	0.17	-0.48	0.36*	0.37	0.22**
43	L10 x T3	-0.58	-18.21**	2.88		-2.49	-25.33**	-4.57	-4.84	-1.98	7.79**	-17.90**	-4.17*	-0.50	-0.67*	-2.07**	-1.22**	-1.37**
	Standard error																	
	Ti	1.02		1.23	1.50	1.39	1.81	1.15	1.67	1.72	0.80	0.94	0.53	0.44	0.08	0.05	0.12	0.02
	Lj	1.70		2.05	2.48	2.31	3.00	1.91	2.76	2.86	1.33	1.55	0.88	0.73	0.14	0.09	0.19	0.04
	Sij	3.40		4.09	4.97	4.61	6.00	3.82	5.53	5.71	2.67	3.11	1.77	1.47	0.28	0.18	0.39	0.08
	Ti-j	1.25		1.51	1.83	1.70	2.21	1.41	2.04	2.11	0.99	1.15	0.65	0.54	0.10	0.07	0.14	0.03
	Li-j	2.29		2.76	3.35	3.11	4.04	2.58	3.73	3.85	1.80	2.09	1.19	0.99	0.19	0.12	0.26	0.05
	Ti-Lj	1.85		2.22	2.70	2.51	3.26	2.08	3.01	3.11	1.45	1.69	0.96	0.80	0.15	0.10	0.21	0.04
	STi-Tj	4.16		5.01	6.08	5.65	7.34	4.68	6.77	7.00	3.27	3.81	2.16	1.79	0.34	0.22	0.48	0.09
	SiL-jL	4.58		5.52	6.70	6.22	8.08	5.15	7.46	7.70	3.60	4.19	2.38	1.98	0.37	0.24	0.53	0.10
	Sij-kl	4.75		5.72	6.94	6.45	8.38	5.34	7.73	7.99	3.73	4.34	2.47	2.05	0.39	0.25	0.54	0.11

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

The estimates of SCA effects over the environment were ranged from -2.23 (L_1 x T_1) to 1.66 (L_1 x T_3). It was significant and positive for 2 crosses over the environments. Crosses *viz*., L_5 x T_1 and L_1 x T_3 (Table 4) for number of primaries per plant the mean square due to lines, testers and L x T were significant in all the four environments. Combining ability in positive direction was calculated desirable for this character.

The GCA effects among lines ranged from -9.81 (L_7) to 12.80 (L_1) in E_1, -11.70 (L_9) to 13.08 (L_4) in E_2, -11.21 (L_2) to 14.12 (L_5) in E_3 and -14.50 (L_7) to 18.17 (L_5) in E_4.It was significant and positive for 4, 3, 1 and 1 lines in E_1, E_2, E_3 and E_4 respectively**.** L_5 having significant and positive GCA effects in E_2, E_3 and E_4 and T_1 in E_1, E_2, and E_4. The estimates of SCA effects ranged from -22.54 (L_2 x L_1) to 18.79 (L_2 x L_2) in E_1, -18.21 (L_{10} x L_3) to 15.22 (L_7 x L_2) in E_2, -15.90 (L_9 x L_3) to 13.80 (L_9 x L_2) in E_3 and -10.23 (L_7 x L_2) to 13.07 (L_7 x L_3) in E_4. It was significant and positive for 8, 6, 2 and 2 crosses in E_1, E_2, E_3 and E_4, respectively. Crosses L_9 x T_1, L_3 x T_3 and L_6 x T_3 exhibited significant and positive SCA effects in more than one environments (Table 5). With reference to grain yield the mean square due to lines, testers and L x T were significant in all the four environments. Combining ability in positive direction was desirable the estimates GCA effects among lines ranged from -11.81 (L_6) to 11.30 (L_3) in E_1, -20.94 (L_9) to 15.72 (L_1) in E_2, -11.28 (L_3) to 7.39 (L_7) in E_3 and -6.86 (L_3) to 5.37 (L_9) in E_4. It was significant and positive for 4, 4, 5 and 4 lines in E_1, E_2, E_3 and E_4, respectively**.** 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 ranged from -26.48 (L_5 x L_2) to 18.02 (L_5 x L_1) in E_1, -22.12 (L_9 x L_3) to 30.21 (L_1 x L_3) in E_2, -13.97 (L_8 x L_1) to 13.28 (L_1 x L_3) in E_3, and -21.94 (L_6 x L_3) to 24.19 (L_6 x L_1) in E_4. It 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 5). For number of seeds per primary the mean square due to lines, testers and L x T were significant in all the four environments. Combining ability in positive direction was desirable for this character. The GCA effects among lines ranged from -27.64 (L_1) to 40.47 (L_4) in E_1, -6.44 (L_3) to 17.11 (L_7) in E_2, -18.68 (L_1) to 25.99 (L_2) in E_3 and -16.48 (L_3) to 10.18 (L_3) in E_4. It was significant and desirable for 4, 2, 5 and 2 lines in E_1, E_2, E_3 and E_4, respectively**.** L_4, L_7 and L_8 having significant and positive GCA effects in more than one environments and T_2 having significant and positive GCA effects in E_1, E_2, and E_3.The estimates of SCA effects ranged from -22.54 (L_2 x L_1) to 18.79 (L_2 x L_2) in E_1, -18.21 (L_{10} x L_3) to 15.22 (L_{10} x L_2) in E_2, -38.50 (L_4 x L_1) to 16.57 (L_4 x L_2) in E_3, and -22.53 (L_9 x L_3) to 22.30 (L_9 x L_2) in E_4. It was significant and positive for 10, 8, 3 and 4 crosses in E_1, E_2, E_3 and E_4, respectively. Crosses L_1 x T_1, L_8 x T_1, L_{10} x T_1, L_4 x T_2, L_6 x T_2, L_2 x T_3, L_5 x T_3 and L_7 x T_3 exhibited significant and positive SCA effects in more than one environments. (Table 5)

The analysis of variance for experimental design in individual environment revealed significant differences between genotypes for all the characters in all the four environments except for days to 50 % flowering in E_1 and E_3, days to maturity in all the four environments, dry fodder yield in E_3, number of primaries per plant in E_3, number of seeds per primary in E_1 and E_4. This indicated significant variation between genotypes for all the characters in all the environments except above. Partitioning of genotypic variance into parents, crosses and parents vs crosses revealed that for all the characters under study there were significant difference between parents in all the environments except for days to 50 % flowering in E_1 and E_3 and ear head length in E_1. Difference between crosses was also significant for all the characters in all the environments. Difference between parents and crosses was also significant in most of the cross which indicates existence of average heterosis for these characters in different environments. The error variance was homogeneous for ear head length therefore, pooled analysis was carried out only for this character. The differences between genotypes, parents, cross and parents vs crosses were significant for ear head length over the environments. This indicates variation among parents and crosses and existence of average heterosis for these two characters. The significance of G x E interaction for the character indicated that different genotypes influenced by the environment differentially. Non-significant parents vs cross x environment interaction mean square indicated that the difference between mean of parents and hybrids was constant and in same direction for ear head length.Analysis of variance for combining ability revealed that both additive as well as non additive variance were important in the inheritance of various traits as evident from significance of lines, testers and lines x testers mean square for all the characters in all the four environments except ear head length in E_1 and $E_{3,}$ number of seeds per primary in $E_{4.}$ 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. For ear head length GCA was estimated only in pool and in individual environment deviation from pool GCA was estimated for ear head length L_2, L_6 and L_8 were good general combiners over the environments. For all the characters at least one line was found good general combiner in each environment. Maximum number of lines for a character in an environment was five for grain yield in E_3, number of seeds per primary in E_3. Similarly all the lines were having good GCA for one to five characters in E_1, two to six characters in E_2, two to seven characters in E_3 and one to six characters in E_4 except L_9 which was having good GCA for grain yield in E_4 and dry fodder yield and number of seeds per primary in E_1 only. For grain yield all the ten lines were good general combiner in one or other environment. There were seven lines viz., L_1, L_3 and L_{10} in E_1 and $E_{2,}$ L_2 and L_6 in E_3 and E_4, L_5 in E_2 and E_3 and L_8 in E_1 and E_3 having significant GCA in more than one environments. The line L_4 in $E_{3,}$ and L_7 and L_9 in E_4 were having good GCA for grain yield. All these lines were also good general combiner for one or other phenological, fodder and quality characters. Testers were also having the similar trend. In general one tester was good general combiner for one character in one environment except number of seeds per primary in E_2, protein content in grain in E_4 where two testers were found good general combiners. Tester T_1 was good general combiner for dry fodder yield (E_1), number of primaries per plant ($E_{1,}$ E_2 and E_4), grain yield (E_3) and protein content in grain ($E_{1,}$ E_2 and E_4). Tester T_2 was good general combiner for dry fodder yield (E_1 and E_2), ear head length (pool), number of seeds per primary ($E_{1,}$ E_2 and E_3) and protein content in grain (E_2 and E_4). Tester T_3 was good general combiner for days to maturity ($E_{2,}$ E_3 and E_4), dry fodder yield ($E_{2,}$ E_3 and E_4), number of primaries per plant (E_3), number of seeds per primary (E_2) and grain yield (E_2 and E_4). Therefore developing dual purpose and early genotypes tester T_3 could be identified. Kukadia *et al.*, (1983), Pillai *et al.*, (1995), Bhadouriya and sexena (1997), Patil (2000), Salunke and Deore (2000), Ravindrababu *et al.*, (2001), Pahuja *et al.*, (2003) and Iyanar and Fazllullah (2005) also identified lines with good GCA effects for grain yield along with other attributes. 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. SCA along with GCA is essential for taking the decision about breeding methodology. SCA was estimated for seven characters in all the four environments and for ear head length the SCA effects were estimated over the environments and deviation from pool were estimated in individual environments. SCA was estimated for seven characters in all the four environments and for ear head length SCA effects was estimated over the environments and deviation from pool were estimated in individual environments. For 7 characters the SCA effects were significant in 198 combinations considering 30 crosses and four environments. Frequency of good SCA effects in E_1, E_2, E_3 and E_4 were 55, 54, 38 and 51 respectively. This indicated that frequency of crosses with good SCA effects were almost same in all the four environments. Frequency of good SCA effects were maximum in by protein content in grain (40) followed grain yield (39), dry fodder yield (38), days to maturity (30) and number of seeds per primary (25). For number of primaries per plant and days to 50 % flowering the good SCA effects were 17 and 7 crosses, respectively. Apart from these, five other crosses also had good SCA effects for number of primaries per plant and days to 50 % flowering in two and two crosses, respectively. For grain yield in E_1 nine crosses had good SCA effects. Among them L_5 x T_1 was also having good SCA for dry fodder yield, protein content in grain and days to maturity. 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 dry fodder yield, days to maturity and protein content in grain, L_2 x T_3 for dry fodder yield and protein content in grain 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 dry fodder yield and protein content in grain, cross L_1 x T_3 for dry fodder yield, protein content in grain and L_{10} x T_1 for dry fodder yield and number of seeds per primary. For days to maturity SCA was good in L_9 x T_2. In E_4, 11 crosses having good SCA for grain yield. Among these one or other cross also having good SCA for dry fodder yield, days to maturity, protein content in grain and days to 50 % flowering. Cross L_{10} x T_2 having good SCA for dry fodder yield, protein content in grain, days to 50 % flowering, days to maturity along with grain yield followed by L_2 x T_3 for dry fodder yield and protein content in grain. Cross L_5 x T_3 for dry fodder yield. 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 ear head length the SCA was significant only in two crosses. Presence of good SCA indicates that the above crosses having role of non additive gene action in inheritance of these characters in respective environments. In past Govil and Murty (1973), Rao *et al.*, (1976), Singhania (1980), Amsalu and Bapat (1990), Pillai *et al.*, (1995), Karale *et al.,* (1998), Bhavsar and Borikar (2002), Rafiq *et al.*, (2002) and Kaul *et al.*, (2003) 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 dry fodder 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 (Table 5.1). 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.*, (1993), Senthil and Palamisamy (1994), Bhadouriya and Saxena (1997), Chaudhary *et al.,* (2006) and Yadhav and Pahuja (2007). 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 and dry fodder 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. Apart from above, 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.

Acknowledgements

Indian Council of Agricultural Research (ICAR), is sincerely acknowledged for financial support of the study, Maharana Pratap University of Agriculture and Technology (MPUAT) is sincerely acknowledged for providing facility and support for the study.

References

Anonymous 2015. FAOSTAT, Food and Agriculture Organization of the United Nations Statistics Division, Rome.

Bahadure DM, Marker S, Umakanth AV, Prabhakar, Ramteke PW, Patil JV and Rana BS (2015) Combining ability and heterosis on millable stalk and sugar concentration for bioethanol production across environments in sweet sorghum (*Sorghum bicolor* (L.) Moench). Electronic Journal of Plant Breeding 6: 58-65.

Bhadouriya, N. S. and Saxena, M. K. (1997). Combining ability studies in sorghum through diallel analysis. Crop Res., 14(2): 253-256.

Bunphan D, Jaisil P, Sanitchon J, Knoll JE and Anderson WF (2015) Heterosis and combining ability of F1 hybrid sweet sorghum in Thailand. Crop Science 55: 178-187.

Daljit Singh. 1979. Diallel analysis for combining ability over environments. *Indian J. Genet., 39*(3): 383-386.

Bhavsar, V. V. and Borikar, S. T. (2002). Combining ability studies in sorghum involving diverse cytosteriles. J. Maharashtra Agric. Univ., 27(1): 35-38.

Chaudhary, S.B., Patil, J.V., Thombare, B.B. and Kulkarni, V.M. (2004). Selection of parents based on combining ability in sorghum [*Sorghum bicolor* L. Moench]. Annals of Plant Physiology 20 (1): 95-97.

Doggett H, 1988. Sorghum. Longman Scientific & Technical, London. Cereal Sci 44: 236-251

Fisher, R. A. (1932). The Genetical Theory of Natural Selection. Clarendon, Oxford.

Griffing, B. (1956). Concept of general and specific combining ability in relation to diallel crossing system. Aust. J. Biol. Sci., 9: 463-493.

Iyanar, K., Gopalan, A. and Ramasamy, P. (2001). Combining ability analysis in sorghum [*Sorghum bicolor* (L.) Moench]. Annals of Agriculture Research New Series, 22 (3): 341-345.

Indhubala M, Ganesamurthy K and Punitha D (2010) Combining ability studies for quality traits in Sweet Sorghum (*Sorghum bicolor* (L.) Moench). The Madras Agricultural Journal 97: 17-20.

Karale, M. U, Suryavanshi, Y. B. and Mehtre, S. S. (1998). Combining ability studies in sorghum (Sorghum bicolor (L.) Moench). Andhra Agric. J., 45: 42-46.

Kaul, S. L., Rafiq, F. M. and Singh, K. (2003). Heterobeltiosis and combining ability for grain yield components in post rainy season sorghum. International Sorghum and Millets News Letter, 44: 21-23.

Leonilo V. Gramaje. Joanne D. Caguiat . John Oscar S. Enriquez .Quirino D. dela Cruz . Reneth A. Millas. Jake E. Carampatana .Dindo Agustin A. Tabanao. (2020).Heterosis and combining ability analysis in CMS hybrid rice. Euphytica 216:14.

Mara Jane da Rocha1, José Airton Rodrigues Nunes, Rafael Augusto da Costa Parrella, Pakizza Sherma da Silva Leite, Gabrielle Maria Romeiro Lombardi, Mayra Luiza Costa Moura, Robert Eugene Schaffert and Adriano Teodoro Bruzi (2018). General and specific combining ability in sweet sorghum. Crop Breeding and Applied Biotechnology,18:365-372.

Meena B.L., B.R. Ranwah, S.P. Das, S.K. Meena, R. Kumari, Rumana Khan, V.K. Bhagasara and A. Gangarani Devi (2017). Estimation of Heterosis, Heterobeltiosis and Economic Heterosis in Dual Purpose Sorghum [*Sorghum bicolor* (L.) Moench]. Int.J.Curr.Microbiol.App.Sci. 6(5): 990-1014.

Meena B.L., Ranwah, B.R., Meena, H S, Meena, M.D., Meena, K N and Rai, P K (2020). Stability Analysis in Dual Purpose Sorghum [*Sorghum bicolor* (L.) Moench] . Int.J.Curr.Microbiol. App.Sci 9(3):2521-2530.

Meena B.L., Ranwah, B.R., Das S.P., Meena H S, Meena, S.K.,Kumari R. and Nath, Anamika (2018). Assessment of Economic Heterosis in Dual Purpose Sorghum [*Sorghum bicolor* (L.) Moench] . Int.J.Curr.Microbiol.App.Sci 7(7):3196-3205.

Pillai, M.A., Rangaswamy, P., Nadarjan, N., Vannirajan, C and Ramalingam, J. (1995). Combining ability analysis for ear head characters in sorghum. Indian Journal of Agricultural Research, 29 (2): 98-102.

Patel, S. D., Patel, A. I., Patel, R. H., Mali, S. C., Patel, V. S. and Kshirsagar, R.M. (2006). Study of heterosis in sorghum. Crop Prot. Prod., 2(2): 59-63.

Rafiq, S. M., Thete, R. Y., Madhusudhana, R. and Umakanth, A. V. (2002). Combining ability studies for grain yield and its components in post rainy season where sorghum grown in medium deep and shallow soils. International Sorghum and Millet News

Letter, 43: 33-37.

Ravindrababu, Y., Pathak, A. R. and Tank, C. J. (2001). Studies on combining ability for yield and yield attributes in sorghum (*Sorghum bicolor* (L.) Moench). Crop Res., 22(2): 274-277.

Salunke, C. B. and Deore, G. N. (2000). Combining ability studies for physiological traits, harvest index and grain yield in rabi sorghum. Ann. Plant Physiol., 14 (2): 190-195.

Thakare, D.P., Ghorade, R.B and Bagade A.B. (2014). Combining ability studies in Grain Sorghum using line X tester analysis. Int.J.Curr.Microbiol.App.Sci 3(10) 594-603.

Yadav, R .and Pahuja, S.K. (2007). Combining ability for fodder yield and its components in forage sorghum. Forage Research, 32(4): 220-223.

How to cite this article:

Meena, B. L., B. R. Ranwah, H. S. Meena, S. K. Meena and Meena, R. K. 2020. Combining Ability Analysis for Yield and Yield Attributes in Dual Purpose Sorghum [*Sorghum bicolor* (L.) Moench]. *Int.J.Curr.Microbiol.App.Sci.* 9(09): 360-376.
doi: https://doi.org/10.20546/ijcmas.2020.909.046