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COMBINING ABILITY AND GENE ACTION STUDIES IN GRAIN YIELD AND AGRONOMIC TRAITS FOR DEVELOPMENT OF MARKETABLE HYBRIDS IN MAIZE (*ZEA MAYS* L.)

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Abstract

Farmers are always on the lookout for better maize hybrids in the competitive seed market. Combining ability in association with standard heterosis and gene actions in private sector germplasm were not much investigated in maize (*Zea mays* L.). In present study, 15 newly developed inbred lines and 4 proven tester inbreds were crossed in line × tester fashion to investigate combining ability, gene actions and yield potentiality in maize. The hybrids and their parents along with popular check hybrids were evaluated at four locations, which represent important maize growing districts in Southern India, during rainy season of 2015. Grain yield, yield components and agronomic traits like maturity, plant height, ear placement and lodging tolerance were studied. Best general combiners and specific combinations for grain yield and other traits were identified. Suggested the involvement of at least one good general combiner in a cross to obtain desirable *SCA* effects and higher standard heterosis for grain yield. Both additive and non-additive gene actions were important in the expression of grain yield with preponderance of additive gene actions for crop duration, plant height, ear placement, ear size and kernel number and non-additive gene actions for test weight, shelling percent and lodging tolerance. Found that *SCA* effects were not stable across locations for complex character like grain yield where as stable *GCA* effects was noticed for other traits. Multiple breeding strategies *viz*., *GCA* improvement in parental lines, line development from high *GCA* × high *GCA* (elite × elite) crosses, exploitation of heterosis by maximizing *SCA* effects, optimizing best agronomic traits with gran yield, multi-location testing of hybrids, utilization of high frequent lines, prediction of three way crosses based on single cross data may be adopted for commercial success of maize hybrids.

Key words : Maize, line × tester, *GCA*, *SCA*, additive gene action, non-additive gene action, grain yield.

Introduction

Maize (*Zea mays* L.) is the world's most widely grown cereal. It is the key crop for food and food security and income generation for millions of farmers (Prasanna, 2014). Globally, 167 countries produced 1021 million tons (mt) of maize from the area of 183 million hectares (m.ha) in 2014 (FAOSTAT). India is the second and sixth largest producer of maize in Asia and World respectively, with an area of 8.6 m. ha and production of 23.6 mt. In India, demand of hybrid maize seed is majorly being met by private seed industry which is supplying around one lakh tons per year accounting over Rs. 1500 crore (Economic times, 9/4/2014). Farmers are always on the lookout for new varieties and replace their existing hybrids with better ones whenever available in the market. Development of new and better hybrids on continuous basis is big and difficult challenge (Vassal, 1998). One must prevent yield plateau and this will require focus on development and identification of inbred lines with good per se performance and good general combing ability. Good combining lines should also have the ability to produce best specific combinations with high grain yield by exploiting heterosis along with best agronomic features like lodging tolerance. Combining ability can be defined as the ability of a genotype to inherit its required economic performance to its crosses. The concept of general and specific combining ability was introduced by Sprague and Tatum (1942). Estimation of combining ability and genetic variance components are important in the breeding programs for hybridization (Fehr, 1993). The line × tester design has

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been widely used for estimating *GCA* and *SCA* of grain yield, and other genetic parameters (Hallauer and Miranda, 1988; Menikir *et al*., 2004; Barata and Carena, 2006; Fan *et al*., 2007). This method was suggested by Kempthorne (1957) and is used for estimating favourable parents, crosses and their general and specific combining ability effects. Equally important is the nature of gene action involved in expression of both quantitative and qualitative traits of economic importance. Falconer (1989) observed that *GCA* is directly related to the breeding value of the parent and is associated with additive genetic effects, while *SCA* is associated with non-additive genetic effects predominantly contributed by dominance, or epistatic interaction effects and is important to provide information on hybrid performance. (Rojas and Sprague, 1952). These two components of variance *viz*., additive and non-additive, which are important to decide upon parents and crosses to be selected for eventual success. Choice of best parents based on average *GCA* effects across the mult-locations can be done if there is interest in single cross hybrids adapted to all environments (Luciano Lourenco Nass, 2000). Paying due consideration to genotype × environment interaction during studies on combining ability may be helpful in identifying desirable genotypes and in understanding the precise nature of inheritance of economic traits (Chandra *et al*., 2011). Accordingly, the present investigation was undertaken to have an idea on nature of gene action involved in the inheritance of important quantitative traits and to select the parents with good *GCA* and crosses with good *SCA* effects, to identify superior crosses with acceptable features, through line × tester analysis over locations in Maize.

Materials and Methods

Fifteen inbred lines *viz*., NM 121, NM 161, NM 183, NM 562, NM 617, NM 720, NM 530, NM 414, NM 421, NM 502, NM 945, NM 141, NM 749, NM 235 and NM 818 and four testers NTP 21, NTP 44, NTP 51 and 82 were planted during *Rabi*-2014 at Nuziveedu Seeds Research Station, Medchal, Hyderabad and crossing was performed in line × tester fashion to produce 60 hybrids. During *Kharif*-2015, the 60 hybrids along with nineteen parents and three popular check hybrids *viz*., NK 6240, PHI-30V92 and 900M Gold were evaluated in RCBD with three replications per location at four locations *viz*., Medak, Aurangabad, Dindigul and Davanagere which represent commercial maize belts in Telangana, Maharashtra, Tamilnadu and Karnataka states, respectively. Each experiment unit (plot) consisted of four rows of 4-meter length, with 60 cm and 25 cm spacing between and within rows respectively. Plant density was 66, 666 plants per ha. Observations on agronomic characters like days to 50% silking (D50%S), days to maturity (DM), plant height (PH), Ear height (EH), root and stalk lodging (LODG%), grain yield (GY) and yield contributing traits like number of kernel rows per ear (ROWS/ER), number of kernels per row (KN/R), Ear length (EL), Ear girth (EG), thousand kernel weight (TKW), Shelling percent (SH%) were collected on individual plant as well as whole plot basis in each entry per replication. The total grain yield from all the ears of each plot was recorded and adjusted to 15% moisture content and later converted into t/ha. Both root and stalk lodged plants were counted together in each plot and estimated the lodging percentage. Data obtained were subjected to line × tester analysis (Kempthorne, 1957) to estimate general and specific combining ability effects and their respective variances. The result of pooled analysis over locations is presented. Data analysis was performed using the statistical package of Indostat services, Hyderabad.

Results and Discussion

Mean performances of crosses

Mean performances of the 60 and three checks for all studied traits combined over four locations in during kharif-2015 are shown in table 1. Results showed that crosses ranged from 49.2 days for test cross L7 × T3 to 57.67 days for test cross L10 × T1 for D50%S trait. Generally, out of 60 test crosses 17 were significantly earlier than the earliest check hybrid 900M Gold. As for the PH trait, test crosses ranged from 196.00 cm (L13 × T3) to 241.17 (L9 × T1) and found that 17 test crosses were significantly taller than the tallest check hybrid 900M Gold. As for the EH trait, test crosses ranged from 85.67 cm (L13 × T4) to 124.83 (L9 × T1) and found that 20 test crosses had lower ear placement (<45% of plant height) 34 had medium ear placement (45% to 50% of the plant height) and remaining six test crosses had higher ear placement (>50% of the PH). As for the ROWS/ER trait, test crosses ranged from 13.83 (L13 × T1) to 19.37 (L7 × T4) and found that 26 test crosses were significantly superior to the best check of this trait 900M Gold. As for the KN/R trait, test crosses ranged from 34.25 (L5 × T1) to 48.00 (L2 × T4). Only 5 test crosses had shown significantly higher number of kernels per row over the best check 30V92. As for the EG trait, test crosses ranged from 15.12 cm (L8 × T1) to 17.64 cm (L10 × T2) and found that 28 test crosses had significantly girthed cob over the best check of this trait NK-6240. As for the TKW trait, test crosses ranged from 324.62 grams (L11

Table 1 : Mean performance of crosses, lines, testers and checks for twelve traits combined over four locations during *Kharif*-2015.

S. no.	Pedigree	Code	D50%S	DM	PH	EH	ROWS/ER	KN/R	EL	EG	TKW	SH%	LODG%	GY
1.	NM 121 × NTP-21	L1 × T1	54.92	108.67	234.67	109.83	14.36	36.10	19.15	15.60	375.74	79.22	14.33	7.48
2.	NM 121 xNTP-44	L1 × T2	53.67	106.58	222.83	108.33	15.38	40.72	20.73	15.80	352.83	80.10	1.50	8.62
3.	NM 121 × NTP-51	L1 × T3	52.25	102.92	211.17	103.25	14.97	37.26	18.72	15.90	380.76	80.94	1.50	8.01
4.	NM 121 × NTP-82	L1 × T4	54.83	107.00	224.08	99.42	16.27	39.88	21.32	16.29	351.67	81.62	6.00	9.12
5.	NM 161 × NTP-21	L2 × T1	55.17	109.50	223.83	111.17	15.93	41.55	22.45	16.70	380.83	79.28	4.42	11.09
6.	NM 161 × NTP-44	L2 × T2	53.67	106.92	223.42	107.92	16.70	42.71	22.08	16.27	355.33	80.76	5.75	10.74
7.	NM 161 × NTP-51	L2 × T3	53.00	104.92	217.08	112.17	16.38	39.51	20.09	16.32	359.73	80.03	7.25	9.97
8.	NM 161 × NTP-82	L2 × T4	54.58	108.25	235.42	103.50	18.16	48.00	23.55	16.88	380.47	82.02	4.60	12.68
9.	NM 183 × NTP-21	L3 × T1	56.83	113.17	234.75	102.92	14.23	36.79	18.27	15.94	359.35	79.46	11.32	7.29
10.	NM 183 × NTP-44	L3 × T2	55.17	109.25	221.67	98.75	15.16	39.28	20.70	16.23	338.17	81.83	4.42	8.26
11.	NM 183 × NTP-51	L3 × T3	54.83	107.92	207.83	94.50	14.97	35.90	18.58	16.32	364.48	79.07	1.17	7.45
12.	NM 183 × NTP-82	L3 × T4	55.75	110.92	222.00	90.42	16.56	41.63	20.66	16.61	344.34	81.13	2.08	9.15
13.	NM 562 × NTP-21	L4 × T1	55.00	110.33	227.67	109.58	16.38	38.64	21.39	15.93	364.83	80.63	8.25	10.10
14.	NM 562 × NTP-44	L4 × T2	53.00	105.25	222.92	105.33	17.27	40.97	24.52	16.79	370.48	81.06	4.58	11.26
15.	NM 562 × NTP-51	L4 × T3	52.92	105.00	211.00	98.25	16.73	38.85	21.65	15.81	360.73	79.19	0.83	10.01
16.	NM 562 × NTP-82	L4 × T4	54.33	106.25	232.83	99.75	18.52	42.28	24.70	17.18	377.13	80.28	4.33	11.69
17.	NM 617 × NTP-21	L5 × T1	55.75	110.50	238.42	107.83	15.35	34.25	18.71	16.21	374.20	78.30	7.25	7.42
18.	NM 617 × NTP-44	L5 × T2	54.33	108.25	217.75	110.83	16.19	42.33	24.15	17.13	389.00	80.24	4.75	12.30
19.	NM 617 × NTP-51	L5 × T3	53.33	106.92	202.42	96.75	15.88	35.47	19.05	16.45	365.60	81.03	4.00	7.96
20.	NM 617 xNTP-82	L5 × T4	55.33	109.92	223.17	98.08	16.90	41.17	21.55	16.79	370.72	79.43	4.50	10.11
21.	NM 720 × NTP-21	L6 × T1	55.75	110.92	237.83	104.50	16.48	39.66	21.64	16.48	354.49	79.91	9.33	9.93
22.	NM 720 × NTP-44	L6 × T2	54.83	109.25	237.33	100.42	17.39	41.08	23.19	16.59	360.20	80.13	9.08	10.89
23.	NM 720 × NTP-51	L6 × T3	54.17	107.92	212.75	98.00	16.96	39.11	21.86	16.23	357.35	81.32	0.42	10.61
24.	NM 720 × NTP-82	L6 × T4	55.92	110.92	233.75	87.42	18.83	44.91	24.42	17.39	374.59	80.65	0.58	12.61
25.	NM 530 × NTP-21	L7 × T1	53.00	105.58	214.17	103.50	17.08	37.70	22.24	16.44	346.82	81.85	0.00	10.02
26.	NM 530 × NTP-44	L7 × T2	50.67	97.58	217.00	98.75	18.00	42.04	24.34	17.20	376.32	78.99	0.08	12.00
27.	NM 530 × NTP-51	L7 × T3	49.42	96.92	215.33	95.58	17.89	39.70	23.37	17.33	367.88	80.67	0.00	11.36
28.	NM 530 × NTP-82	L7 × T4	53.67	106.00	219.92	88.67	19.37	42.76	24.52	16.83	372.62	80.13	1.00	12.62
29.	NM 414 × NTP-21	L8 × T1	55.17	110.58	226.08	113.67	14.13	37.78	18.90	15.12	367.17	80.47	11.67	7.92
30.	NM 414 × NTP-44	L8 × T2	53.67	105.58	227.83	108.50	14.51	38.53	21.30	15.49	334.35	77.42	6.33	7.57
31.	NM 414 × NTP-51	L8 × T3	54.25	108.00	218.17	104.92	14.32	35.64	18.88	15.55	361.20	76.34	0.75	7.30
32.	NM 414 × NTP-82	L8 × T4	54.67	108.58	232.58	87.33	15.73	39.65	20.57	15.76	344.70	77.48	2.17	8.69
33.	NM 421 × NTP-21	L9 × T1	55.67	110.92	241.17	124.83	14.33	35.78	18.71	15.75	363.26	77.48	15.00	6.93

Table 1 continued...

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34.	NM 421 × NTP-44	L9 × T2	53.58	106.25	232.42	118.33	15.12	40.81	20.58	16.29	341.41	78.64	16.33	7.98
35.	NM 421 × NTP-51	L9 × T3	53.17	105.25	215.50	115.33	14.90	35.65	18.97	16.06	368.80	76.24	16.75	7.34
36.	NM 421 × NTP-82	L9 × T4	54.58	108.92	236.58	97.75	16.77	43.52	23.48	16.83	381.70	77.98	0.58	10.40
37.	NM 502 × NTP-21	L10 × T1	57.67	114.58	236.25	112.17	16.07	39.01	21.27	16.34	370.75	80.42	8.58	10.34
38.	NM 502 × NTP-44	L10 × T2	56.08	110.92	230.58	114.75	16.69	44.49	23.77	17.64	376.04	80.13	3.67	11.82
39.	NM 502 × NTP-51	L10 × T3	55.33	109.58	209.08	100.08	16.22	38.22	21.78	16.63	374.17	79.39	2.92	10.61
40.	NM 502 × NTP-82	L10 × T4	57.00	112.92	237.25	102.08	17.57	42.33	22.52	16.93	367.07	79.91	4.67	11.31
41.	NM 945 × NTP-21	L11 × T1	55.75	111.17	228.33	111.17	14.12	35.10	18.63	16.32	354.31	78.68	15.75	6.90
42.	NM 945 × NTP-44	L11 × T2	54.67	108.25	214.25	106.67	14.68	38.97	20.89	15.89	331.81	78.78	5.33	7.93
43.	NM 945 × NTP-51	L11 × T3	52.42	105.17	212.67	98.33	16.11	42.76	23.88	16.98	382.08	79.16	2.89	12.68
44.	NM 945 × NTP-82	L11 × T4	55.67	110.58	235.17	103.67	15.84	40.39	21.36	16.90	324.62	78.80	6.67	8.19
45.	NM 141 × NTP-21	L12 × T1	54.25	107.67	222.25	105.00	15.50	40.14	20.55	15.75	391.85	77.97	3.33	10.36
46.	NM 141 × NTP-44	L12 × T2	52.33	103.92	218.25	110.17	16.17	41.67	22.35	16.21	358.72	79.23	2.25	10.48
47.	NM 141 × NTP-51	L12 × T3	51.00	98.92	207.92	104.67	15.91	38.28	21.02	16.04	391.78	80.11	0.00	10.46
48.	NM 141 × NTP-82	L12 × T4	52.42	104.50	226.17	101.75	17.81	46.44	24.22	17.23	375.06	80.43	3.42	12.39
49.	NM 749 × NTP-21	L13 × T1	54.50	108.67	214.75	102.67	13.83	37.47	19.27	15.89	377.48	80.10	5.50	7.62
50.	NM 749 × NTP-44	L13 × T2	54.33	108.25	204.75	101.33	14.34	38.72	21.08	16.17	360.68	78.24	2.33	7.92
51.	NM 749 × NTP-51	L13 × T3	54.00	107.00	196.00	88.08	14.24	36.67	19.49	16.32	378.77	80.47	0.00	7.58
52.	NM 749 × NTP-82	L13 × T4	55.33	109.92	224.17	85.67	15.71	40.57	20.60	16.62	352.44	80.17	0.00	8.79
53.	NM 235 × NTP-21	L14 × T1	57.25	112.92	216.00	102.75	15.98	40.47	24.12	17.42	372.64	81.72	5.50	10.80
54.	NM 235 × NTP-44	L14 × T2	55.33	109.92	212.50	108.17	16.48	42.06	24.02	17.24	368.66	80.93	1.67	10.88
55.	NM 235 × NTP-51	L14 × T3	53.75	106.58	201.08	99.75	15.72	37.45	21.33	16.73	370.74	81.34	2.50	9.92
56.	NM 235 × NTP-82	L14 × T4	56.67	112.58	224.83	97.75	17.98	42.03	23.64	17.46	370.10	79.22	6.47	11.52
57.	NM 818 × NTP-21	L15 × T1	55.42	110.58	224.67	115.08	14.12	35.86	18.96	15.26	378.83	82.93	9.58	7.44
58.	NM 818 × NTP-44	L15 × T2	54.00	106.58	217.67	118.17	14.97	39.72	20.55	15.71	367.70	80.06	14.25	8.40
59.	NM 818 × NTP-51	L15 × T3	53.83	105.00	211.67	113.75	14.48	38.36	19.16	15.56	378.76	81.92	0.33	7.79
60.	NM 818 × NTP-82	L15 × T4	55.00	109.58	231.33	105.33	15.77	41.65	21.25	15.77	372.74	78.48	2.67	8.96
61.	NM 121	L1	54.75	112.58	146.67	71.00	13.27	23.08	12.90	12.30	277.63	78.43	14.92	2.59
62.	NM 161	L2	54.75	112.67	151.75	73.00	13.91	24.56	12.02	12.89	257.45	77.33	5.17	2.96
63.	NM 183	L3	57.83	118.58	145.50	56.92	13.07	21.23	11.15	13.39	264.09	81.23	3.42	2.72
64.	NM 562	L4	55.92	113.58	145.92	63.50	13.79	25.61	13.04	12.22	252.68	82.53	0.00	3.17
65.	NM 617	L5	57.08	116.92	144.92	63.33	14.37	18.73	12.17	13.59	303.46	75.64	0.00	2.33
66.	NM 720	L6	57.33	116.92	178.67	60.83	14.01	26.27	13.53	12.60	243.33	80.93	0.00	2.60
67.	NM 530	L7	51.92	104.50	134.50	57.67	14.63	27.66	14.73	13.49	233.39	79.53	2.17	2.93

Table 1 continued...

Table 1 continued...

68.	NM 414	L8	56.75	115.25	165.42	81.17	12.77	20.51	13.25	11.72	273.92	83.14	11.83	2.30
69.	NM 421	L9	56.75	116.17	181.92	97.08	13.38	24.74	12.46	13.39	277.24	81.63	11.50	2.85
70.	NM 502	L10	61.00	122.92	172.33	75.92	15.03	27.88	14.57	13.83	258.29	82.70	6.92	3.52
71.	NM 945	L11	56.67	115.58	155.50	72.67	13.70	24.21	12.27	13.67	239.43	76.93	2.67	2.58
72.	NM 141	L12	53.33	108.25	139.67	68.50	12.73	20.87	13.23	12.57	292.79	81.49	4.92	2.76
73.	NM 749	L13	56.75	116.67	125.00	55.92	13.27	20.94	13.55	13.57	281.80	80.60	4.00	2.36
74.	NM 235	L14	58.08	118.92	131.25	63.83	13.98	25.04	12.91	13.78	252.14	79.23	1.83	2.84
75.	NM 818	L15	56.75	116.17	151.25	90.25	11.66	19.84	12.47	11.83	294.80	77.34	6.67	2.09
76.	NTP-21	T1	58.00	119.25	178.58	80.42	13.43	22.99	13.47	12.93	266.28	81.90	8.00	2.46
77.	NTP-44	T2	55.75	114.25	169.83	81.75	13.88	26.08	13.45	13.69	238.57	79.50	5.08	2.86
78.	NTP-51	T3	53.42	109.50	158.42	60.67	14.30	22.48	12.98	13.48	286.33	78.50	3.17	2.80
79.	NTP-82	T4	57.00	116.67	178.08	61.67	15.22	28.48	13.80	14.08	229.15	80.47	0.50	3.21
80.	NK-6240	Check-1	55.08	109.92	212.08	94.50	15.18	38.78	21.07	15.94	384.88	77.23	9.08	9.05
81.	30V92	Check-2	56.08	111.92	222.50	84.75	15.30	42.08	22.38	15.40	376.62	81.78	0.17	10.01
82.	900M Gold	Check-3	54.75	108.92	226.33	96.42	15.80	38.03	20.77	15.60	361.37	79.93	3.17	8.91
	Mean		**54.89**	**109.63**	**206.67**	**95.57**	**15.45**	**36.05**	**19.47**	**15.60**	**342.47**	**79.85**	**4.98**	**8.00**
	C.V.		1.32	1.06	2.33	2.96	3.17	4.43	5.01	3.11	2.43	1.11	68.86	11.73
	F ratio		76.16	194.96	489.53	421.38	118.91	254.27	194.92	116.89	370.36	39.29	20.21	146.92
	C.D. 5%		0.58	0.93	3.87	2.27	0.39	1.28	0.78	0.39	6.66	0.71	2.75	0.75
	Range Lowest		49.42	96.92	125.00	55.92	11.66	18.73	11.15	11.72	229.15	75.64	0.00	2.09
	Range Highest		61.00	122.92	241.17	124.83	19.37	48.00	24.70	17.64	391.85	83.14	16.75	12.68

Note: D50%S - Days to 50% silking, DM – Days to maturity, PH – Plant height (cm), EH – Ear height (cm), ROWS/ER – Number of kernel rows per ear, KN/R – Number of kernels per row in an ear, EL – Ear length (cm), EG – Ear girth in circumference (cm), TKW – Thousand kernel weight (g), SH% - Shelling percent, LODG% - Combined root and stalk lodging percent, GY – Grain yield (t/ha).

× T4) to 391.85 grams (L12 × T1) and found that three test crosses had higher test weight over the best check of this trait NK-6240, but 30 crosses were superior to other check 900M Gold for this trait. For SH% trait, no test cross except L15 × L1 had shown significantly higher shelling percent over the best check of this trait 30V92. But 17 crosses had shown significantly higher shelling percent over the next best check 900M Gold. For LODG% trait, test crosses ranged from 0.0% (many crosses) to 16.75% (L9 × T3). The 51 crosses had shown better lodging tolerance with <10% when compared to NK-6240. For GY, test crosses ranged from 6.9 t/ha L11 × T1 to 12.68 t/ha for L11 × T3. The 17 test crosses significantly out yielded best check 30V92 (10.01 t/ha).

ANOVA of Combining ability and L × T

Mean squares of analysis of variance for 12 traits combined over four locations during *kharif*-2015 is presented in table 2. Results showed that there were significant differences among genotypes for all studied traits indicating wide range of variability. Results also showed highly significant differences among four locations for all studied traits, indicating that all four locations differed in the environmental conditions. These findings agreed with those reported by Aly (2013) and Mousa and Aly (2012). Crosses were significantly different for all traits. The source of variation due to crosses was further portioned into lines, testers and their interaction *i.e.*, L × T. The Significance of the means of sum of squares due to lines, testers and line x tester interaction (*SCA* effects) for most of the traits combined over four locations were recorded. Similar results were obtained by Castellanos *et al*. (1998), Shiri *et al*. (2010), Kustano *et al*. (2012) and Mousa & Aly (2012). Significant differences among lines and testers for traits studied contributed for variation among crosses and revealed the presence of additive effects in controlling traits (Dabhokar, 1992). It also indicated substantial variability in lines for all the traits studied due to differences in frequencies of additive favourable alleles. Same results were also reported by Valdemer *et al*. (1981). Testers were also significantly different to each other owing due to their significant mean squares for all traits except for TKW and SH%. Variance due to interaction effects due to line and testers (L × T) were significant for all traits, which suggested the significant contribution of *SCA* effects towards variation among crosses. This also emphasized the presence of non-additive and dominance effects in controlling traits (Shams *et al*., 2010). The significant *GCA* effects of parents and *SCA* effects of crosses indicated that both additive and non-additive gene effects were important in the genetic expression of most of the traits studied (Iqbal *et al*., 2007 and Houqe *et al*., 2016).

Interaction of mean squares with locations: Furthermore, mean squares due to crosses x location interactions are significant and highly significant for PH, KN/R, TKW, SH%, LODG% and GY traits indicating that these crosses differed over four locations for these traits. Line x location interaction was significant or highly significant for all traits, except D50%S and DM, indicating that differences between inbred lines were different over four locations and suggesting the sensitivity of *GCA* effects of lines to environmental fluctuations for GY, yield components, plant height and ear height. Whereas tester × location interaction was significant or highly significant for PH, EH, ROWS/ER, KN/R, LODG% and GY traits, indicating that *GCA* effects of these traits are sensitive to location differences. In common, GCA effects for PH, KN/R, LODG% and GY traits of both lines and testers behaved differently in different locations. This revealed that best *GCA* effects of parents were not the same over all environments especially for GY. Thus, to maximize the hybrid yield potential for each environment the choice must be made with *GCA* effects within each environment. Line × Tester × location *i.e.*, (*SCA* × Loc) interaction mean squares was not significant for all traits except GY. Significant Crosses x Location interactions were due to significant line x location interaction and / or tester x location interaction for agronomic and yield contributing characters. Whereas for GY trait, the third component, line × tester × location was also significantly contributed. These results were in agreement with those obtained by Ibrahim and Mousa (2011), who reported significant interaction for GY, (T × Loc) for EH and (L × T × Loc) for GY. Mousa & Aly (2012), who reported significant interaction of L × Loc for D50%S and GY and (T × Loc) for EH. The significant line × tester × location for grain yield implied that L × T interaction pattern was not consistent across locations and the identification of stable hybrids requires rigorous testing in multi-locations (Xing-Ming Fan *et al*., 2016).

Proportional contribution of lines, testers and interactions : Proportional contribution of lines, testers and interactions to total variance are presented in table 3. Proportional contribution of lines was higher than Testers and L × T interactions for D50%S, DM and ROWS/ER indicating that GCA variances for these traits were due to lines. Testers contributed more for PH and KN/R traits. Contribution of line × tester was greater than that of lines and testers for traits like EL, EG, TKW, SH%, LODG% and GY indicating higher estimate of these traits was due to more of specific combining ability. Whereas, all three components *i.e.*, Lines, Testers and L

× T contributed equally for EH. These results showed that testers, lines and their interaction brought much variation in the expression of studied traits. Similar results were obtained by Aly *et al.* (2011) and Rissi *et al.* (1991)

Table 2 : Mean squares from ANOVA of combining ability for twelve traits combined over four locations during *Kharif*-2015.

Source of variation	DF	D50%S	DM	PH	EH	ROWS/ER	KN/R	EL	EG	TKW	SH%	LODG%	GY
Replications	2	0.56	2.09	20.05	13.39	0.32	2.46	0.21	0.41	5.87	0.78	12.62	0.03
Genotypes	78	77.54**	270.2**	11728.1**	3478.6**	29.6**	667.1**	190.8**	28.62**	26028.7**	30.56**	240.1**	133.2**
Locations (Loc)	3	117.6**	983.4**	31347.0**	7260.8**	40.6**	560.6**	147.2**	68.79**	11454.4**	18.95**	138.9**	211.6**
Parents	18	69.3**	216.5**	3664.6**	1636.1**	8.62**	99.7**	8.93**	6.08**	5856.5**	55.60**	218.7**	1.49**
Parent vs Crosses (Heterosis)	1	2565.7**	8799.8**	769162.9**	193536.6**	917.4**	44474.8**	12106.8**	1868.1**	1775554.5**	2.48*	5.12	8166.7**
Crosses (C)	59	28.9**	142.0**	1350.3**	819.5**	21.06**	97.7**	44.37**	4.32**	2530.0**	23.40**	250.6**	37.31**
C × Loc	177	0.09	0.13	32.4**	1.81	0.20	3.70**	0.63	0.21	82.51*	1.73**	15.36**	1.64**
Lines (L)	14	72.32**	333.1**	1676.1**	1596.5**	58.06**	107.2**	93.90**	11.07**	3940.9*	47.80**	352.3*	98.83**
Testers (T)	3	121.0**	963.1**	14067.8**	6068.**	128.6**	971.9**	248.0**	15.20**	5230.16	0.51	1288.0*	103.8**
L × T	42	6.82**	19.64**	333.3**	185.5**	1.04**	32.15**	13.31**	1.30**	1866.8**	16.9**	142.6*	12.05**
L × Loc	42	0.07	0.12	29.11*	2.54**	0.53**	6.48**	1.70**	0.61**	261.3**	6.96**	19.76*	3.24**
T × Loc	9	0.09	0.17	250.32**	5.02**	0.19*	5.50*	0.14	0.11	28.54	0.04	45.34**	2.30*
L × T x Loc	126	0.02	0.13	18.02	1.34	0.08	2.65	0.31	0.08	26.77	0.10	11.76	1.06**
Error	472	0.62	1.91	22.41	10.93	0.30	2.16	1.14	0.26	84.39	0.65	12.42	0.47

*: Significant at 5% level; **: Significant at 1% level.

Note: D50%S - Days to 50% silking, DM – Days to maturity, PH – Plant height (cm), EH – Ear height (cm), ROWS/ER – Number of kernel rows per ear, KN/R – Number of kernels per row in an ear, EL – Ear length (cm), EG – Ear girth in circumference (cm), TKW – Thousand kernel weight (g), SH% - Shelling percent, LODG% - Combined root and stalk lodging percent, GY – Grain yield (t/ha).

General combining ability (*GCA*) effects

Estimates of *GCA* effects of all traits for the fifteen inbred lines and the four testers pooled over four locations are presented in table 4. The line L7 was identified as the best general combiner which exhibited highest significant positive *GCA* effect of 1.90** for GY. It also exhibited highly significant positive *GCA* effects for yield contributing characters like ROWS/ER, KN/R, EL, EG and SH% and highly significant negative *GCA* effects for D50%S, DM, PH, EH and LODG% indicating its usefulness in breeding for the development of hybrids with highly desirable combination of traits like high grain yield, higher kernel number, high shelling percentage, early maturity, moderate plant height, lower ear placement and lodging tolerance.

The another line L10 was also identified as second best general combiner which exhibited highly significant positive *GCA* effects for GY (1.42**) and its yield contributing characters like ROWS/ER, KN/R, EL, EG, TKW and agronomic characters like D50%S, DM, PH & EH and non-significant negative *GCA* effect for LODG% indicating its usefulness in breeding for the development of hybrids with high grain yield, high kernel number, bolder grains, late maturity, taller plant type and higher ear placement without fear of lodging.

Another five lines *i.e.*, L2, L4, L6, L12 and L14 also showed highly significant positive *GCA* effects for GY with varied directions of effects for other traits indicating their utilization in development of hybrids with unique combination of traits along with high grain yield. Line L6 can be used for the development of taller plants with lower ear placement as it exhibited highly significant positive *GCA* effect for plant height and highly significant negative *GCA* effect for ear height. This opposite direction of *GCA* effects of these traits can be successfully employed in the breeding of dual purpose maize hybrids with higher grain yield

Table 3 : Proportional contribution of lines, testers, and lines x testers to total hybrids variation twelve traits combined over four locations during *kharif*-2015.

	D50%S	D75%M	PH	EH	ROWS/ER	KN/R	EL	EG	TKW	SH%	LODG%	GY
% Contribution of line	47.59	44.72	22.25	34.54	58.40	18.88	34.80	41.35	15.49	13.21	19.75	37.36
% Contribution of testers	35.93	34.61	50.40	35.19	34.60	46.47	24.70	15.24	5.51	0.00	19.76	10.47
% Contribution of L × T	16.48	20.67	27.34	30.27	6.99	34.65	40.50	43.41	79.00	86.79	60.49	52.16

Note: D50%S - Days to 50% silking, DM – Days to maturity, PH – Plant height (cm), EH – Ear height (cm), ROWS/ER – Number of kernel rows per ear, KN/R – Number of kernels per row in an ear, EL – Ear length (cm), EG – Ear girth in circumference (cm), TKW – Thousand kernel weight (g), SH% - Shelling percent, LODG% - Combined root and stalk lodging percent, GY – Grain yield (t/ha).

coupled with higher fodder yield. Similarly, line L2 for tall plants, higher ear placement, high shelling% and bolder kernels, line L4 for high kernel number coupled with longer cob and high shelling%, line L12 for very bolder kernels coupled with more KN/R and line L14 for late maturity, shorter plants, high kernel number and high SH% can be utilized to improve these traits in the breeding programs as they showed highly significant desirable *GCA* effects for the respective traits.

Among the testers, T4 was the best general combiner as it exhibited highly significant positive *GCA* effects for grain yield as well as majority of the yield contributing traits like ROWS/ER, KN/R, EL, EG and significant negative *GCA* effect for LODG%. It also showed highly significantly positive *GCA* effects for flowering, maturity and plant height with highly significant negative *GCA* effects for ear height. This tester possessed higher amount favourable alleles for high grain yield, late maturity, tall plant with lower ear placement. The next best tester for grain yield was T2 which also possessed favourable alleles for earliness.

Out of the fifteen lines studied, seven lines *i.e.*, L7, L10, L2, L4, L6, L12 and L14 and among four testers, two testers *i.e.*, T2 and T4 were proved to be good combiners for grain yield and its components and lodging tolerance. Half of the parental lines (7 out of 15) had desirable additive alleles for various traits and they need to be exploited in future breeding programs. And also, certain parents can be selectively utilized in order to develop a hybrid with desired combination of traits.

Specific combining ability effects

Estimates of *SCA* effects of the 60 crosses for all traits pooled over four locations were presented in the table 5. Out of all traits studied, grain yield is the most important criteria for maize hybrids to access their readiness of commercialization. Total eleven *i.e.*, around 20% of the crosses showed significant and positive *SCA* effects for grain yield indicating good breeding value of the present germplasm under investigation. The crosses exhibiting significant and positive *SCA* effects in the order of merit for grain yield were L11 × T3, L5 × T2, L9 × T4, L8 × T1, L14 × T1, L2 × T1, L6 × T4, L10 × T2, L12 × T4 and L13 × T1. Majority of these crosses had also shown significant positive *SCA* effects for KN/R and TKW except non-significant positive *SCA* effect of KN/R by L2 × T1 and negative *SCA* effect for TKW by L14 × T1. The all crosses showing maximum significant positive *SCA* effects for grain yield, also exhibited favourable *SCA* effects for KN/R and TKW. The cross L11 × T3, which had shown highest desirable *SCA* effect of 4.08**, also performed outstandingly with average grain yield of 12.68 t/ha and yield superiority of 26.6% over the best check 30V92. It also exhibited highly significant positive *SCA* effects for majority of yield contributing traits like ROWS/ER, KN/R, TKW, EL and EG and significant negative (desirable) *SCA* effect for LODG%. Hence It was interpreted that balanced accumulation of favourable *SCA* effects of all yield influencing traits must have been contributed for the outstanding performance in terms of grain yield for this cross. For D50%S, *SCA* affects manifested by these top yielding crosses were noted to less desirable except for L11 × L3 in terms of their importance for earliness.

Relationship between heterosis and *SCA* effects : In table 7, eighteen crosses were presented from 60 crosses based on two criteria *i.e.*, 1). High *SCA* effect for grain yield 2) High standard heterosis. Eleven crosses showing significantly positive *SCA* effect for GY and fourteen crosses exhibiting >10% of standard heterosis over best check 30V92 were listed. There were seven common crosses falling into both the criteria, hence counted them once. Eighteen crosses, thus obtained, were clubbed and sorted according to grain yield rank in the table 6 to study relationship among *SCA* effects of yield, *SCA* effects of other traits, standard heterosis and *GCA* of the parents involved. Out of eleven crosses demonstrating significantly positive *SCA* effects, seven crosses showed >10% standard heterosis, while two crosses showed 4-7% heterosis and remaining two failed to record even satisfactory yield. The above eleven crosses also showed significant *SCA* effects in yield components and other agronomic traits indicating the association between *SCA* of yield and *SCA* of other traits.

Remaining seven crosses from the above eighteen, did not show significant positive *SCA* effect for grain yield, but exhibited >10% standard heterosis. However, four of them showed non-significant positive *SCA* effects for grain yield. These low-*SCA* crosses for GY, still showed desirable *SCA* effects in some yield components especially for thousand kernel weight which might have been indirectly caused for higher yield.

Classification of best specific combinations based on *GCA* of parents : Among the above eighteen crosses, ten crosses involved high × high, five crosses involved high x low and three crosses involved low x low general combining parents. We classified all eighteen crosses into three groups based on *GCA* effects of parental lines. Group 1, both had significantly positive *GCA* effect; Group 2, one parent had positive *GCA* effect and another parent had significantly negative or non-significant *GCA* effect; and Group 3, both parents had significantly negative *GCA* effects. The calculated mean grain yields for the three groups of hybrids were 11.99 t/ha, 11.19 t/ha and 9.41 t/ha, respectively. These findings were in agreement with Fan *et al.* (2008). High × High combinations suggested the importance of additive × additive type of gene action. This indicated that selection could be effective in F2 generation and utilized in transgressive breeding. Similar findings as observed in present study were also reported by Sharma *et al.* (2003), Manivannan *et al.* (2005) and Binodh *et al.* (2008). On the other hand, crosses with high × low *gca* effects indicated the involvement of additive × dominance gene interaction. Peng and Virmani (1990) also reported about the possibility of interaction between positive alleles from good combiners and negative alleles from poor combiners in high x low crosses in sunflower. The cross combinations involved low × low combining parents indicating over dominance and epistatic interactions. Out of these eighteen crosses showing either significant positive *SCA* effects for GY or higher standard heterosis, fifteen had at least one good general combiner. Verma and Srivastava (2004) mentioned that positive SCA effect was usually associated with cross where at least one parent was good general combiner. Hence, it was determined that identification of both general combiners as well as specific combinations are essential part of any breeding program for the successful development of hybrids.

Components of genetic variance (gene action)

By line × tester mating design used, the genetic variance could be translated or portioned into components of genetic variance in terms of additive and non-additive variances. Both of the line variance (σ^2 Line) and tester variance (σ^2 Tester) estimate the *GCA* variance (σ^2 *GCA*) which considered as an indicator of additive (σ^2A) and additive × additive (σ^2AA + σ^2AAA + …) portions of genetic variance (Kansouh, 2011). While, the line x tester variance (σ^2L × T) which estimate the *SCA* variance (σ^2*SCA*) reflected the non-additive genetic portions dominance (σ^2D) and (σ^2DD + …), in addition to the maternal effect. However, Kallo (1988) mentioned that the additive (σ^2A) and dominance (σ^2D) were most important portions. Estimates of components of genetic variance and their interactions with locations were given in table 6. The results showed that the magnitude of (σ^2Line) were larger than the corresponding (σ^2Tester) for all traits except PH and KN/R indicating the importance of choice of parents. σ^2GCA for D50%S, DM, PH, EH, ROWS/ER, KN/R, EL and EG were higher than σ^2*SCA*, while, the TKW, SH%, LODG% and GY gave the reverse. These results indicated the importance of additive gene actions in the inheritance of agronomic characters like D50%S, DM, PH, EH and some yield contributing characters like ROWS/ER, KN/R, EL and EG which could be improved through selfing of elite × elite crosses. Whereas, significance of non-additive gene actions is important in case of TKW, SH% and LODG% which could be improved through heterosis. Even though, the grain yield exhibited slightly higher σ^2*SCA* (0.96), but it was in proximity with that of σ^2GCA (0.88) indicating that both additive and non-additive gene actions are equally important for inheritance of grain yield with prevalence of a non-additive gene action. Soengas *et al.* (2003) found that variance component estimates were appreciably larger for *GCA* than for *SCA* effects for most of the traits. These results were supported by ratio of variance of general and specific combining ability (σ^2*GCA*/σ^2*SCA*) which was greater than unity (>1) for D50%S, DM, PH, EH, ROWS/ER, KN/R, EL and EG and lower than unity (<1) for TKW, SH%, LODG% and GY. The prevalence of these gene actions for various traits was further confirmed by calculated σ^2A/σ^2D ratios which also found more than one for all traits except TKW and SH%. Only two traits *viz*., LODG% and GY conflictingly showed <1 values of σ^2*GCA*/σ^2*SCA* (indicative of non-additive) and >1 (indicative of additive)

Table 4 : Estimates of *GCA* effects of fifteen inbred lines and four testers for twelve traits combined over four locations during *kharif*-2015.

Parents	Code	D50%S	DM	PH	EH	ROWS/ER	KN/R	EL	EG	TKW	SH%	LODG%	GY
Lines													
NM 121	L1	-0.50**	-1.60**	1.01	1.46**	-0.76**	-1.28**	-1.43**	-0.49**	-0.37	0.64**	0.78	-1.29**
NM 161	L2	-0.31**	-0.49*	2.76**	4.94**	0.79**	3.17**	0.63**	0.15*	3.47**	0.69**	0.45	**1.52****
NM 183	L3	1.23**	2.42**	-0.62	-7.11**	-0.78**	-1.38**	-1.86**	-0.12	-14.03**	0.54**	-0.31	-1.56**
NM 562	L4	-0.60**	-1.18**	1.42*	-0.52	1.22**	0.41	1.65**	0.04	2.68*	0.46**	-0.55	**1.17****
NM 617	L5	0.27*	1.01**	-1.74*	-0.38	0.08	-1.47**	-0.55**	0.25**	9.26**	-0.08	0.07	-0.15
NM 720	L6	0.75**	1.86**	8.23**	-6.17**	1.41**	1.42**	1.37**	0.28**	-3.96**	0.67**	-0.20	**1.41****
NM 530	L7	-2.73**	-6.37**	-5.58**	-7.13**	2.08**	0.78**	2.21**	0.56**	0.29	0.58**	-4.78**	**1.90****
NM 414	L8	0.02	0.30	3.98**	-0.15	-1.34**	-1.88**	-1.50**	-0.91**	-13.76**	-1.90**	0.18	-1.73**
NM 421	L9	-0.16	-0.06	9.23**	10.31**	-0.73**	-0.84**	-0.98**	-0.16*	-1.83	-2.24**	7.11**	-1.44**
NM 502	L10	2.11**	4.11**	6.11**	3.52**	0.63**	1.24**	0.93**	0.50**	6.39**	0.13	-0.10	**1.42****
NM 945	L11	0.21	0.90**	0.42	1.21*	-0.82**	-0.47*	-0.22	0.13	-17.41**	-0.98**	2.61**	-0.67**
NM 141	L12	-1.91**	-4.14**	-3.54**	1.64**	0.34**	1.86**	0.62**	-0.09	13.73**	-0.40**	-2.80**	**1.32****
NM 749	L13	0.13	0.57**	-12.27**	-9.31**	-1.47**	-1.42**	-1.30**	-0.14	1.73	-0.09	-3.10**	-1.62**
NM 235	L14	1.34**	2.61**	-8.58**	-1.65**	0.53**	0.73**	1.86**	0.82**	4.92**	0.97**	-1.02*	**1.18****
NM 818	L15	0.15	0.05	-0.85	9.33**	-1.17**	-0.88**	-1.43**	-0.82**	8.89**	1.02**	1.65**	-1.45**
No. of lines with significantly +ve *gca* effects		**5**	**7**	**6**	**7**	**7**	**6**	**7**	**6**	**7**	**8**	**3**	**7**
No. of lines with significantly -ve *gca* effects		**5**	**5**	**5**	**5**	**6**	**7**	**6**	**4**	**4**	**4**	**4**	**6**
Testers													
NTP-21	T1	1.06**	2.49**	5.87**	5.36**	-0.81**	-2.02**	-1.13**	-0.32**	3.22**	0.06	3.60**	-0.82**
NTP-44	T2	-0.46**	-1.04**	-0.77	4.01**	-0.07	1.17**	0.87**	0.05	-6.84**	-0.06	0.44	**0.20****
NTP-51	T3	-1.24**	-2.69**	-12.20**	-2.19**	-0.30**	-1.85**	-0.89**	-0.11**	5.24**	-0.02	-2.30**	-0.33**
NTP-82	T4	0.64**	1.23**	7.10**	-7.18**	1.18**	2.71**	1.15**	0.37**	-1.62*	0.02	-1.74**	**0.95****
No. of tester with significantly +ve *gca* effects		**2**	**2**	**2**	**2**	**1**	**2**	**2**	**1**	**2**	**0**	**1**	**2**
No. of testers with significantly -ve *gca* effects		**2**	**2**	**2**	**2**	**2**	**2**	**2**	**2**	**2**	**0**	**2**	**2**
CD 95% *GCA* (Line)		0.23	0.39	1.34	0.94	0.16	0.42	0.30	0.14	2.61	0.23	1.00	0.19
CD 95% *GCA* (Tester)		0.12	0.20	0.69	0.48	0.08	0.22	0.16	0.07	1.35	0.12	0.52	0.10

*: Significant at 5% level; **: Significant at 1% level.

Note: D50%S - Days to 50% silking, DM – Days to maturity, PH – Plant height (cm), EH – Ear height (cm), ROWS/ER – Number of kernel rows per ear, KN/R – Number of kernels per row in an ear, EL – Ear length (cm), EG – Ear girth in circumference (cm), TKW – Thousand kernel weight (g), SH% - Shelling percent, LODG% - Combined root and stalk lodging percent, GY – Grain yield (t/ha).

Table 5 : Estimation of *SCA* effects of 60 crosses for twelve traits combined over four locations during *kharif*-2015.

S.No	Pedigree	Cross	D50%S	DM	PH	EH	ROWS/ER	KN/R	EL	EG	TKW	SH%	LODG%	GY
1	NM 121 × NTP-21	L1 × T1	-0.06	-0.12	5.61**	-0.73	-0.07	-0.37	0.30	0.02	7.27**	-1.31**	4.90**	0.00
2	NM 121 xNTP-44	L1 × T2	0.21	1.33**	0.42	-0.88	0.20	1.06*	-0.12	-0.15	-5.58*	-0.31	-4.77**	0.11
3	NM 121 × NTP-51	L1 × T3	-0.43	-0.69	0.18	0.23	0.02	0.62	-0.37	0.11	10.27**	0.49*	-2.03*	0.03
4	NM 121 × NTP-82	L1 × T4	0.28	-0.52	-6.21**	1.39	-0.15	-1.31**	0.19	0.02	-11.96**	1.13**	1.90	-0.14
5	NM 161 × NTP-21	L2 × T1	0.00	-0.39	-6.98**	-2.88**	-0.05	0.63	1.53**	0.47**	8.53**	-1.31**	-4.69**	**0.79****
6	NM 161 × NTP-44	L2 × T2	0.02	0.56	-0.75	-4.78**	-0.02	-1.40**	-0.83**	-0.33*	-6.93**	0.30	-0.19	-0.59**
7	NM 161 × NTP-51	L2 × T3	0.13	0.21	4.35**	5.67**	-0.12	-1.58**	-1.06**	-0.12	-14.60**	-0.48*	4.05**	-0.82**
8	NM 161 × NTP-82	L2 × T4	-0.16	-0.38	3.38*	1.99*	0.19	2.35**	0.36	-0.03	13.00**	1.48**	0.83	**0.61****
9	NM 183 × NTP-21	L3 × T1	0.13	0.36	7.31**	0.91	-0.18	0.41	-0.15	-0.02	4.55	-0.98**	2.98**	0.08
10	NM 183 × NTP-44	L3 × T2	-0.02	-0.02	0.88	-1.91*	0.00	-0.29	0.27	-0.09	-6.57*	1.52**	-0.77	0.02
11	NM 183 × NTP-51	L3 × T3	0.42	0.29	-1.52	0.04	0.03	-0.65	-0.08	0.15	7.65**	-1.28**	-1.28	-0.26
12	NM 183 × NTP-82	L3 × T4	-0.53*	-0.63	-6.66**	0.95	0.15	0.52	-0.04	-0.04	-5.62*	0.74**	-0.93	0.16
13	NM 562 × NTP-21	L4 × T1	0.13	1.13**	-1.81	0.99	-0.03	0.48	-0.55	-0.18	-6.68*	0.28	0.15	0.16
14	NM 562 × NTP-44	L4 × T2	-0.35	-0.42	0.08	-1.91*	0.12	-0.38	0.58	0.31*	9.02**	0.83**	-0.35	0.29
15	NM 562 × NTP-51	L4 × T3	0.34	0.98*	-0.40	-2.79**	-0.20	0.52	-0.52	-0.51**	-12.80**	-1.08**	-1.37	-0.42*
16	NM 562 × NTP-82	L4 × T4	-0.12	-1.69**	2.13	3.70**	0.11	-0.61	0.49	0.38**	10.46**	-0.03	1.57	-0.02
17	NM 617 × NTP-21	L5 × T1	0.00	-0.89*	12.11**	-0.90	0.08	-2.03**	-1.03**	-0.12	-3.90	-1.51**	-1.48	-1.20**
18	NM 617 × NTP-44	L5 × T2	0.10	0.39	-1.92	3.45**	0.18	2.86**	2.41**	0.43**	20.96**	0.55*	-0.81	**2.65****
19	NM 617 × NTP-51	L5 × T3	-0.12	0.71	-5.82**	-4.43**	0.10	-0.98*	-0.92**	-0.08	-14.52**	1.29**	1.17	-1.16**
20	NM 617 xNTP-82	L5 × T4	0.01	-0.21	-4.37**	1.89*	-0.36*	0.16	-0.46	-0.22	-2.54	-0.33	1.11	-0.28
21	NM 720 × NTP-21	L6 × T1	-0.47*	-1.33**	1.54	1.56	-0.13	0.49	-0.01	0.12	-10.39**	-0.66**	0.88	-0.26
22	NM 720 × NTP-44	L6 × T2	0.13	0.54	7.69**	-1.18	0.05	-1.27**	-0.46	-0.13	5.38*	-0.31	3.79**	-0.33
23	NM 720 × NTP-51	L6 × T3	0.24	0.86*	-5.46**	2.61**	-0.16	-0.23	-0.03	-0.33*	-9.55**	0.83**	-2.14*	-0.07
24	NM 720 × NTP-82	L6 × T4	0.11	-0.07	-3.77**	-2.99**	0.24	1.01*	0.50	0.35*	14.55**	0.13	-2.53*	**0.65****
25	NM 530 × NTP-21	L7 × T1	0.25	1.57**	-8.31**	1.52	-0.19	-0.83	-0.25	-0.19	-22.31**	1.38**	-3.87**	-0.66**
26	NM 530 × NTP-44	L7 × T2	-0.56*	-2.90**	1.17	-1.88*	-0.02	0.33	-0.15	0.20	17.25**	-1.35**	-0.62	0.30
27	NM 530 × NTP-51	L7 × T3	-1.03**	-1.92**	10.93**	1.15	0.10	1.00*	0.64*	0.48**	-3.27	0.28	2.03**	0.19
28	NM 530 × NTP-82	L7 × T4	1.34**	3.25**	-3.79**	-0.78	0.10	-0.50	-0.25	-0.49**	8.33**	-0.30	2.47*	0.17
29	NM 414 × NTP-21	L8 × T1	-0.33	-0.10	-5.96**	4.70**	0.27	1.90**	0.11	-0.05	12.09**	2.48**	2.84**	**0.88****
30	NM 414 × NTP-44	L8 × T2	-0.31	-1.57**	2.44	0.89	-0.09	-0.54	0.52	-0.04	-10.67**	-0.45	0.67	-0.51*
31	NM 414 × NTP-51	L8 × T3	1.05**	2.50**	4.20**	3.50**	-0.05	-0.40	-0.14	0.18	4.11	-1.57**	-2.18*	-0.24
32	NM 414 × NTP-82	L8 × T4	-0.41	-0.84*	-0.68	-9.09**	-0.12	-0.96*	-0.49	-0.09	-5.53*	-0.46*	-1.33	-0.13
33	NM 421 × NTP-21	L9 × T1	0.36	0.59	3.88**	5.41**	-0.13	-1.14**	-0.60	-0.17	-3.75	-0.17	-0.77	-0.41*
34	NM 421 × NTP-44	L9 × T2	-0.21	-0.54	1.77	0.26	-0.09	0.71	-0.73*	0.01	-15.55**	1.12**	3.73**	-0.38
35	NM 421 × NTP-51	L9 × T3	0.15	0.11	-3.71**	3.46**	-0.08	-1.44**	-0.58	-0.06	-0.23	-1.33**	6.88**	-0.49*

Table 1 continued...

Table 1 continued...

36	NM 421 × NTP-82	L9 × T4	-0.30	-0.15	-1.93	-9.13**	0.31	1.87**	1.90**	0.22	19.53**	0.38	-9.85**	**1.29****
37	NM 502 × NTP-21	L10 × T1	0.09	0.09	2.08	-0.46	0.25	0.01	0.06	-0.23	-4.48	0.39	0.02	0.14
38	NM 502 × NTP-44	L10 × T2	0.02	-0.04	3.06*	3.47**	0.12	2.31**	0.57	0.70**	10.87**	0.23	-1.73	**0.60****
39	NM 502 × NTP-51	L10 × T3	0.05	0.27	-7.00**	-5.00**	-0.13	-0.94*	0.34	-0.14	-3.08	-0.55*	0.26	-0.08
40	NM 502 × NTP-82	L10 × T4	-0.16	-0.32	1.86	1.99*	-0.25	-1.39**	-0.97**	-0.33*	-3.32	-0.07	1.45	-0.66**
41	NM 945 × NTP-21	L11 × T1	0.07	-0.12	-0.14	0.85	-0.25	-2.18**	-1.43**	0.11	2.88	-0.24	4.49**	-1.20**
42	NM 945 × NTP-44	L11 × T2	0.50*	0.50	-7.58**	-2.30*	-0.44**	-1.50**	-1.17**	-0.68**	-9.56**	-0.01	-2.76**	-1.20**
43	NM 945 × NTP-51	L11 × T3	-0.97**	-0.94*	2.27	-4.43**	1.22**	5.31**	3.58**	0.57**	28.64**	0.32	-2.47*	**4.08****
44	NM 945 × NTP-82	L11 × T4	0.41	0.56	5.46**	5.89**	-0.52**	-1.62**	-0.98**	0.00	-21.97**	-0.07	0.74	-1.68**
45	NM 141 × NTP-21	L12 × T1	0.69**	1.42**	-2.27	-5.76**	-0.03	0.53	-0.36	-0.24	9.28**	-1.53**	-2.52*	0.26
46	NM 141 × NTP-44	L12 × T2	0.29	1.21**	0.38	0.76	-0.10	-1.12**	-0.56	-0.15	-13.80**	-0.14	-0.44	-0.65**
47	NM 141 × NTP-51	L12 × T3	-0.26	-2.14**	1.48	1.46	-0.14	-1.51**	-0.12	-0.15	7.19**	0.69**	0.05	-0.13
48	NM 141 × NTP-82	L12 × T4	-0.72**	-0.48	0.42	3.53**	0.28	2.10**	1.04**	0.55**	-2.67	0.98**	2.90**	**0.52****
49	NM 749 × NTP-21	L13 × T1	-1.10**	-2.29**	-1.04	2.87**	0.12	1.14**	0.28	-0.04	6.91**	0.29	-0.06	**0.46***
50	NM 749 × NTP-44	L13 × T2	0.25	0.83*	-4.40**	2.89**	-0.12	-0.81	0.10	-0.13	0.18	-1.44**	-0.06	-0.26
51	NM 749 × NTP-51	L13 × T3	0.69**	1.23**	-1.71	-4.16**	0.01	0.16	0.27	0.18	6.19*	0.75**	0.34	-0.07
52	NM 749 × NTP-82	L13 × T4	0.16	0.22	7.15**	-1.59	0.00	-0.50	-0.66*	-0.01	-13.28**	0.40	-0.22	-0.14
53	NM 235 × NTP-21	L14 × T1	0.44	-0.08	-3.48*	-4.71**	0.25	1.99**	1.97**	0.52**	-1.11	0.86**	-2.14*	**0.84****
54	NM 235 × NTP-44	L14 × T2	0.04	0.46	-0.33	2.05*	0.01	0.39	-0.13	-0.02	4.96	0.19	-2.80**	-0.10
55	NM 235 × NTP-51	L14 × T3	-0.76**	-1.23**	-0.32	-0.16	-0.53**	-1.20**	-1.06**	-0.37*	-5.03	0.55*	0.76	-0.53**
56	NM 235 × NTP-82	L14 × T4	0.28	0.85*	4.13**	2.83**	0.27	-1.18**	-0.78*	-0.13	1.18	-1.60**	4.18**	-0.21
57	NM 818 × NTP-21	L15 × T1	-0.20	0.15	-2.54	-3.36**	0.10	-1.02*	0.11	0.00	1.11	2.02**	-0.73	0.12
58	NM 818 × NTP-44	L15 × T2	-0.10	-0.32	-2.90*	1.07	0.20	-0.34	-0.30	0.08	0.03	-0.73**	7.11**	0.05
59	NM 818 × NTP-51	L15 × T3	0.51*	-0.25	2.54	2.86**	-0.06	1.31**	0.07	0.10	-0.99	1.09**	-4.08**	-0.03
60	NM 818x NTP-82	L15 × T4	-0.20	0.41	2.90*	-0.57	-0.24	0.04	0.13	-0.18	-0.15	-2.38**	-2.30*	-0.14
	CD 95% SCA		0.47	0.78	2.69	1.88	0.31	0.83	0.61	0.29	5.21	0.46	2.00	0.39
No. of crosses with significantly +ve *sca* effects			**6**	**12**	**14**	**19**	**1**	**13**	**7**	**10**	**20**	**19**	**13**	**11**
No. of crosses with significantly -ve *sca* effects			**8**	**11**	**16**	**17**	**4**	**19**	**12**	**7**	**19**	**18**	**15**	**15**

*: Significant at 5% level; **: Significant at 1% level.

Note: D50%S - Days to 50% silking, DM – Days to maturity, PH – Plant height (cm), EH – Ear height (cm), ROWS/ER – Number of kernel rows per ear, KN/R – Number of kernels per row in an ear, EL – Ear length (cm), EG – Ear girth in circumference (cm), TKW – Thousand kernel weight (g), SH% - Shelling percent, LODG% - Combined root and stalk lodging percent, GY – Grain yield (t/ha).

Table 6 : Components of genetic variance (gene action) and their interaction with locations for twelve traits combined over four locations during *kharif*-2015.

Genetic parameter	D50%S	DM	PH	EH	ROWS/ER	KN/R	EL	EG	TKW	SH%	LODG%	GY
σ^2 Line	1.44	6.90	34.45	33.03	1.20	2.19	1.93	0.23	80.34	0.98	7.08	2.05
σ^2 Tester	1.08	5.34	78.03	33.65	0.71	5.39	1.37	0.08	28.59	0.00	7.09	0.57
σ^2 GCA	1.16	5.67	68.86	33.52	0.82	4.71	1.49	0.11	39.48	0.21	7.09	0.88
σ^2 SCA (σ^2 L x T)	0.23	1.48	25.91	14.55	0.06	2.50	1.01	0.09	148.54	1.35	10.85	0.96
σ^2 GCA x Loc	-0.02	-0.06	4.12	-0.25	0.00	0.13	-0.01	0.00	2.12	0.10	0.71	0.08
σ^2 SCA x Loc	-0.21	-0.59	-1.46	-3.20	-0.07	0.16	-0.28	-0.06	-19.21	-0.18	-0.22	0.20
σ^2 GCA /σ^2 SCA	5.07	3.84	2.66	2.30	13.30	1.89	1.47	1.30	0.27	0.15	0.65	0.92
σ^2A	2.32	11.34	137.71	67.05	1.63	9.43	2.98	0.23	78.97	0.41	14.17	1.77
σ^2D	0.23	1.48	25.91	14.55	0.06	2.50	1.01	0.09	148.54	1.35	10.85	0.96
σ^2A / σ^2D	10.14	7.67	5.31	4.61	26.59	3.77	2.94	2.61	0.53	0.30	1.31	1.83
Degree of Dominance	0.31	0.36	0.43	0.47	0.19	0.51	0.58	0.62	1.37	1.81	0.87	0.74
Heritability (h^2_n) %	98.49	92.51	79.94	85.07	98.97	75.20	78.48	80.11	35.96	22.44	52.01	56.47
Genetic Advance 5%	3.11	6.67	21.61	15.56	2.62	5.49	3.15	0.88	10.98	0.63	5.59	2.06
Predictability Ratio	0.91	0.88	0.84	0.82	0.96	0.79	0.75	0.72	0.35	0.23	0.57	0.65

Note: σ^2 Line: Estimate of line variance, σ^2 Tester: Estimate of tester variance, σ^2 GCA: Estimate of GCA variance, σ^2 SCA: Estimate of SCA variance, σ^2A: Additive genetic variance, σ^2D: Dominance genetic variance, Loc: Location, D50%S - Days to 50% silking, DM – Days to maturity, PH – Plant height (cm), EH – Ear height (cm), ROWS/ER – Number of kernel rows per ear, KN/R – Number of kernels per row in an ear, EL – Ear length (cm), EG – Ear girth in circumference (cm), TKW – Thousand kernel weight (g), SH% - Shelling percent, LODG% - Combined root and stalk lodging percent, GY – Grain yield (t/ha)

values of σ^2A/σ^2D, which might be due to complexity of inheritance and involvement of both the effects. Estimated average degree of dominance was less than one (<1), indicating partial dominance for all studied traits with the exception of TKW and SH%, which showed over-dominance since they recorded high values of 1.37 and 1.81, respectively.

Similarly, the magnitude of the interaction for σ^2GCA × Loc was higher than σ^2*SCA* × Loc for all studied traits except grain yield. These results indicated that additive gene actions were more sensitive to location differences than non-additive for these traits but reverse was true for grain yield. These results are in good agreement with those obtained by Lonnquist and Gardner (1961) and Aly *et al*. (2011). Higher estimates (>60%) of narrow sense heritability (H_n) were detected for D50%S, DM, PH, EH, ROWS/ER, KN/R, EL and EG, while moderate H_2 (40-60%) was found for the LODG% and GY. Lower estimates of Hn (<40%) were obtained for TKW and SH%. Traits showing high heritability may be selected in early generations, while traits with low heritability are greatly influenced by the environment and are suggested to be tested over a wide range of environments.

Conclusion and Breeding Strategy

It may be concluded that good combiner lines, L2, L4, L6, L7, L10, L12 and L14 may be used in further breeding programs for utilization in genetic improvement of maize. Higher probability of obtaining significant desirable *SCA* effect coupled with higher standard heterosis for grain yield would be possible, if at least one good general combiner is used in a cross. Also high *SCA* cross combinations with high × high or high × low *GCA* effects may be used for hybrid development as well as pedigree breeding of line development which involves recycling of lines for further accumulation of favourable alleles. Especially, high × high crosses, where additive gene action is easily fixable, selection of traits of interests might be effective in the early generations of line development. The high *SCA* crosses with low × low *GCA* effects could be used for breeding hybrid. The top five yielding crosses were L2 × T4, L11 × T3, L7 × T4, L6 × T4 and L12 × T4 which performed outstandingly over best check 30V92 and these crosses were governed by both additive gene action (because of high *GCA* of lines in it) and non-additive gene actions (due to significant *SCA* effects) except L11 × T3 for which role of over-dominance or epistatic gene action was of predominant. It was found that most of the traits were governed by additive gene action except test weight, shelling percent, lodging percent and grain yield which elucidated the scope of further genetic improvement by derivation of inbred lines from the pedigree crosses consists of good combiners. However, test weight, shelling percent and

Table 7 : Promising hybrids based on *SCA* effects of grain yield and standard heterosis along with other traits exhibiting favorable *SCA*.

S. no.	Genotype	Code	Mean GY across four locations (t/ha)	Rank	SCA of GY (t/ha)	% standard heterosis over best check 30V92	GCA of parents	No. of traits with favourable *sca* effects	Traits with desirable SCA effects
1	**NM 161*NTP-82**	**L2 × T4**	**12.68**	1	0.61**	26.69	**High × High**	4	PH, KN/R, TKW, SH%
2	**NM 945*NTP-51**	**L11 × T3**	**12.68**	2	4.08**	26.64	Low × Low	10	D50%S, DM, EH, ROWS/ER, KN/R, EL, EG, TKW, SH%, LODG%
3	**NM 530*NTP-82**	**L7 × T4**	**12.62**	3	0.17	26.07	**High × High**	1	TKW
4	**NM 720*NTP-82**	**L6 × T4**	**12.61**	4	0.65**	25.97	**High × High**	5	EH, KN/R, EG, TKW, LODG%
5	**NM 141*NTP-82**	**L12 × T4**	**12.39**	5	0.52**	23.78	**High × High**	5	D50%S, KN/R, EL, EG, SH%
6	**NM 617*NTP-44**	**L5 × T2**	**12.30**	6	2.65**	22.88	*Low × High*	5	KN/R, EL, EG, TKW, SH%
7	NM 530*NTP-44	L7 × T2	12.00	7	0.3	19.88	**High × High**	4	D50%S, DM, EH, TKW
8	NM 502*NTP-44	L10 × T2	11.82	8	0.60**	18.08	**High × High**	4	PH, KN/R, EG, TKW
9	NM 562*NTP-82	L4 × T4	11.69	9	-0.02	16.78	**High × High**	3	DM, EG, TKW
10	NM 235*NTP-82	L14 × T4	11.52	10	-0.21	15.08	**High × High**	1	PH
11	NM 530*NTP-51	L7 × T3	11.36	11	0.19	13.49	*HIGH × LOW*	4	PH, KN/R, EL, EG
12	NM 502*NTP-82	L10 × T4	11.31	12	-0.66**	12.99	**High × High**	0	
13	NM 562*NTP-44	L4 × T2	11.26	13	0.29	12.49	**High × High**	4	EH, EG, TKW, SH%
14	NM 161*NTP-21	L2 × T1	11.09	14	0.79**	10.79	*HIGH × LOW*	6	EH, EL, EG, TKW, SH%, LODG%
15	NM 235*NTP-21	L14 × T1	10.80	17	0.84**	7.89	*HIGH × LOW*	6	EH, KN/R, EL, EG, SH%, LODG%
16	NM 421*NTP-82	L9 × T4	10.40	23	1.29**	3.90	*LOW × HIGH*	5	EH, KN/R, EL, TKW, LODG%
17	NM 414*NTP-21	L8 × T1	7.92	46	0.88**	-20.88	Low × Low	3	KN/R, TKW, SH%
18	NM 749*NTP-21	L13 × T1	7.62	49	0.46*	-23.88	Low × Low	4	D50%S, DM, KN/R, TKW

Note: High x High combinations are in bold face, Low x Low are underlines and Low x High are in capital letters. Bolded crosses are high performing hybrids with >20% superiority over best check 30V92.

lodging percent for which role of non-additive is important, can be enhanced by exploitation of heterosis. Hence, grain yield, which is a complex character, can be improved by adopting multiple strategies like exploitation of heterosis, improvement of *GCA* of lines, improvement of *SCA* effects of crosses and evaluation in multi-locations, because this trait was governed by both additive and non-additive gene actions which also showed considerable sensitivity to environment. The tester T4 which was present in maximum number of high yielding crosses (high frequent line), may be used in further crossing programs for quick identification of potential crosses. Also, good number of three way crosses can be predicted based on yield of non-parental single cross data (Jenkins method C by Jenkin, 1934), *SCA* effects of non-parental crosses and *GCA* effects of all three lines. Grain yield of (A × B) × C can be predicted based on mean yield of A × C and B × C single crosses, $\mathrm{SCA}_{\mathrm{AxC}}$ and $\mathrm{SCA}_{\mathrm{BxC}}$ and *GCA* effects of A, B and C parents. Example, (L2 × L6) × T4 may give good yield because average of non-parental single crosses *i.e.*, L2 × T4 and L6 × T4 is very high (12.68 + 12.61)/2 = 12.64 t/ha. And, *SCA* effects of these two single crosses are also significantly high with values of 0.65** and 0.61** respectively. *GCA* of L2, L6 and T4 are also significantly high with values of 1.52**, 1.41** and 0.95**, respectively. In a breeding program of limited resources, predicting three way crosses by ignoring epistatic effects would not be wrong and this concept of predicting will give more favourable genetic balance in three-way. Three-way cross hybrids can be produced at lower cost and advantage of seed production is important at commercial level.

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