Forage Res., **41** (3) : pp. 147-151 (2015) **http://forageresearch.in**

STUDIES ON COMBINING ABILITY FOR YIELD AND YIELD COMPONENTS IN MAIZE (*ZEA MAYS* L.)

B. V. VARAPRASAD AND D. SHIVANI

Professor Jayashankar Telangana State Agricultural University
Agricultural Research Station, Madhira (Telangana), India
(e-mail : rishith_sree@rediffmail.com)

(Received : 22 September 2015; Accepted : 5 December 2015)

SUMMARY

The experiment was carried out involving a set of 60 crosses along with 19 parents and three checks for estimating combining ability variances and effects for yield and its attributing traits at Agricultural Research Station, Madhira, Telangana during **rabi** 2012-13.The differences among the parents, parents vs. hybrids and hybrids were observed to be significant for all the characters studied. sca variances were higher than gca variances indicating the predominance of non-additive gene action. The parents, MRC 1112, MRC 1123, MRC 1176, MRC 1604 and BML 13 recorded positive significant gca effects, while MRC 1176 x BML 7, MRC 1179 x BML 13, MRC 1358 x BML 13, MRC 1556 x BML 13, MRC 1561 x BML 5 and MRC 1604 x BML 7 were good crosses for ear length. The parents MRC 1123, MRC 1271, MRC 1604 and BML 13 exhibited significant positive gca effects indicating that they were good general combiners for 100-seed. For grain yield, MRC 1123, MRC 1604 and BML 13 recorded significant positive gca effects and could be utilized in the development of hybrids, synthetics and composites.

Key words : Maize, combining ability, gca, sca

Maize (*Zea mays* L.) is an important cereal crop belonging to the tribe Maydeae of the family Poaceae. “Zea” (zela) was derived from an old greek name for a food grass. Zea consists of four species of which *Zea mays* L. is economically important. The number of chromosomes in *Zea mays* is 2n = 20. By origin, maize is native to central America and is a tropical crop which has adapted magnificently to temperate environments with much higher productivity. Maize, being a C_4 plant, has the highest potential of per day carbohydrate productivity (Singh *et al.,* 2014).

Combining ability analysis is used in order to realize substantial production and varietal improvement in this allogamous crop, the study on gene effects controlling various characters is essential as high yielding parent or line may or may not combine well when used in hybridization. The knowledge of combining ability effects and the corresponding variances is important in the choice of selecting parents and it can be further used for exploiting heterosis to produce high performing new recombinants. Many biometrical procedures have been developed to obtain information on combining ability and line x tester analysis is one among them which is widely used to study combining ability of the parents to be chosen for heterosis breeding. It also provides a guideline to determine the value of source populations and appropriate procedures to be used in crop improvement programme. The recombination of different desirable traits spread over in different diverse genotypes is important to recombine for the improvement of yield and its related traits in any crop. In the present study, attempts were made to understand combining ability in maize.

Maize is a highly cross pollinated crop and the scope for the exploitation of hybrid vigour will depend on the magnitude of heterosis, biological feasibility and the type of gene action. Though, the science of genetics and plant breeding has greatly contributed to improve the productivity through high yielding synthetics, composites and hybrids viz., single, double, multiple and varietal hybrids, of late, single cross hybrids have become the most popular because single crosses show higher uniformity and heterosis than the double and three-way crosses.

Besides, identification of favourable alleles in the inbreds, the information on combining ability is a pre-requisite for development of superior hybrids, since it helps in the identification of superior parents with better gca and crosses with high sca effects. The main goal of maize breeding is to obtain new hybrids with high genetic potential for yield and positive features that exceed the existing commercial hybrids. The L x T mating design as suggested by Kempthorne (1957) is the appropriate method to identify superior parents and hybrids based on gca and sca, respectively.

MATERIALS AND METHODS

The experiment was carried out at experimental farm of Agricultural Research Station, Madhira during **rabi** 2012-13. Selected 15 inbred lines were crossed with four testers in Line x Tester (L x T) mating design to obtain 60 cross combinations.

During **kharif** 2013, a set of 60 crosses along with 19 parents and three checks viz., DHM 117, 30 V 92 and 900 M Gold were sown in randomized block design replicated thrice. Each entry was sown in a row of 5 m length with a spacing of 75 cm between rows and 20 cm between the plants. The recommended fertilizers of N, P and K were applied in the ratio of 120 : 80 : 60 kg/ha. Necessary plant protection measures were taken to protect the crop from pests and diseases. Observations on 11 different quantitative characteristics were recorded on five random plants except for days to 50 per cent tasselling, days to 50 per cent silking and days to maturity. Estimates of combining ability variances and effects were obtained using line x tester method suggested by Kempthorne (1957) and detailed by Singh and Chaudhary (1985).

RESULTS AND DISCUSSION

The differences among the parents, parents vs. hybrids and hybrids were observed to be significant for all the characters studied. Partitioning of hybrids into females, males and females x males revealed that variance differences were significant for all the traits studied. In the present investigation, sca variances were higher than gca variances indicating the predominance of non-additive gene action which is ideal for exploitation through heterosis breeding (Table 1). The general combining ability (gca) effects of 19 parents and the specific combining ability (sca) effects of 60 hybrids for yield and yield contributing characters were estimated and are presented in Table 2.

Among the parents, MRC 1271, MRC 1544, MRC 1556 and BML 14 recorded significant negative gca effects for days to 50 per cent tasseling. The parents MRC 1176, BML 7 and BML 13 were the poor combiners with significant positive gca effects indicating late in days to 50 per cent tasseling. The parents, MRC 1271, MRC 1544, MRC 1556 and BML 14 which recorded significant negative gca effects were good general combiners for earliness. These results were in agreement with the findings of Hemalatha *et al*. (2013), Aminu *et al*. (2014a) and Lahane *et al*. (2014).

TABLE 1
Estimates of general and specific combining ability variances and proportionate gene action in maize for 11 characters

Character	Source of variation		
	σ^2 gca	σ^2 sca	σ^2 gca/ σ^2 sca
Days to 50% tasselling	0.08	2.17	0.03
Days to 50% silking	0.09	1.57	0.05
Days to maturity	0.07	0.43	0.17
Plant height (cm)	7.94	118.78	0.06
Ear height (cm)	6.73	43.23	0.15
Ear length (cm)	0.06	1.04	0.06
Ear girth (cm)	0.01	0.29	0.03
No. of kernel rows/ear	0.01	0.50	0.02
No. of kernels/row	0.21	5.12	0.04
100-seed weight (g)	0.10	1.80	0.06
Grain yield/plant (g)	2.51	157.54	0.01

Significant negative sca effects for days to 50 per cent tasseling were recorded in seven hybrids out of which MRC 1123 x BML 7, MRC 1179 x BML 13, MRC 1209 x BML 13, MRC 1604 x BML 5 and MRC 1661 x BML 13 were good specific combiners for days to 50 per cent tasseling. MRC 1271, MRC 1544 and BML 14 with significant negative gca effects for days to 50 per cent silking were good general combiners for earliness. For days to maturity, parents MRC 1209, MRC 1271, MRC 1358, MRC 1544 and BML 14 recorded negative significant gca effects and were good general combiners for earliness.

The best specific crosses for days to maturity were MRC 1271 x BML 7, MRC 1556 x BML 5, MRC 1556 x BML 14, MRC 1561 x BML 7, MRC 1564 x BML 7 and MRC 1661 x BML 13 which expressed significant negative effects. The parents MRC 1561, MRC 1604, BML 7 and BML 13 which expressed significant positive gca effects were found as good general combiners, while the parents which recorded negative significant gca effects contributed for dwarfness. The best specific crosses for plant height were MRC 1123 x BML 13, MRC 1176 x BML 7, MRC 1179 x BML 7, MRC 1209 x BML 7, MRC 1358 x BML 13, MRC 1544 x BML 13, MRC 1561 x BML 13, MRC 1564 x BML 7, MRC 1582 x BML 5, MRC 1582 x BML 14 and MRC

TABLE 2
Estimates of general and specific combining ability effects for yield and its attributing traits in maize

Parents	Days to 50% tasselling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	No. of kernel rows/ ear	No. of kernels/ row	100-seed weight (g)	Grain yield/ plant (g)
MRC1112	0.05	-0.03	-0.33	-15.61**	-7.72**	0.18	-0.95**	0.78**	0.52	-1.07**	5.97**
MRC 1123	1.05**	1.06*	-0.17	-2.36	5.53*	2.27**	0.55*	1.87**	0.43	2.43**	19.64**
MRC 1176	1.13**	0.97*	-2***	25.14**	33.94**	0.27	0.63**	-0.13	2.43**	0.10	4.56*
MRC 1179	-0.37	-0.28	0.83	-5.03	-3.89	0.27	-0.03	0.12	0.02	-2.32**	-13.94**
MRC 1209	-0.2	-0.19	-1.00	-9.19**	-9.47**	0.68	-0.87**	-1.13**	-0.57	-0.57	-5.28**
MRC 1271	-0.95*	-1.03*	-1.00	1.64	-5.64**	0.52	0.05	-0.63*	-1.07	1.43**	-6.94**
MRC 1358	-0.2	-0.28	-2.75**	15.89**	-1.89	0.43	-0.20	0.12	-0.32	0.43	7.47**
MRC 1544	-2.53**	-2.11**	1.58**	-16.19**	-6.89**	-0.65	0.63**	0.20	-0.98	0.10	5.39**
MRC 1556	-1.28**	-1.03*	1.17*	8.06*	-4.56*	-0.9 *	-0.03	0.12	1.43*	-1.90**	-7.69**
MRC 1561	0.97*	0.89*	0.58	6.97*	15.94**	-0.73	0.05	-0.55*	2.1**	-0.82*	-3.11
MRC 1564	1.13**	1.64*	0.75	-2.36	-10.81**	-2.32**	-0.37	-0.88**	-1.9**	2.18**	-13.03**
MRC 1582	0.22	-0.19	0.00	-2.19	-8.97**	0.93*	-0.20	-0.55*	-1.32*	0.18	-1.61
MRC 1601	0.72	0.47	1.75**	-20.69**	-8.22**	-1.07**	-0.20	0.53*	-4.57**	-0.82*	-6.94**
MRC 1604	0.88*	1.06*	-0.42	18.06**	11.61**	1.43**	0.88**	-0.38	6.68**	1.35**	18.31**
MRC 1661	-0.62	-0.94*	1.00	-2.11	1.03	-1.32**	0.05	0.53*	-2.90**	-0.73	-2.78
SE (i)	0.3936	0.4111	0.5855	3.3190	2.1216	0.3910	0.2338	0.2473	0.5854	0.3822	1.9909
BML 5	-0.34	-0.46*	0.19	-8.37**	-6.03**	-0.22	0.04	0.14	0.06	-0.17	-5.11**
BML 7	1.59**	1.63**	0.88**	9.03**	8.73**	-0.42*	0.15	0.34**	1.04**	0.50*	1.49
BML 13	0.92**	1.07**	0.7*	12.01**	7.68**	1.76**	0.55**	0.06	0.95**	1.79**	7.67**
BML 14	-2.17**	-2.24**	-1.77**	-12.66**	-10.38**	-1.13**	-0.74**	-0.54**	-2.05**	-2.12**	-4.06**
SE (j)	0.2032	0.2123	0.3024	1.7139	1.0956	0.2019	0.1207	0.1277	0.3023	0.1974	1.0281
Crosses											
MRC1112 × BML5	-1.07	-0.71	-0.36	8.79	2.94	-0.12	0.13	0.11	-1.89	-0.33	-11.39**
MRC1112 × BML7	-0.01	-0.46	1.96	-7.94	-0.81	0.08	-1.65**	-0.09	-0.54	0.33	7.34
MRC1112 × BML13	2.33**	2.09*	-1.20	-8.92	-3.77	0.24	1.62**	0.53	4.22**	0.38	13.16**
MRC1112 × BML14	-1.25	-0.93	-0.40	8.08	1.63	-0.21	-0.09	-0.54	-1.78	-0.38	-9.11*
MRC 1123 × BML5	-0.07	-0.12	0.48	-15.79*	-12.64**	1.13	-1.04*	-0.31	-1.14	-1.50	-12.39**
MRC 1123 × BML7	-1.67*	-1.21	0.46	7.81	15.94**	-2.00*	-0.15	-0.84	0.88	0.50	-3.66
MRC 1123 × BML13	1.33	1.34	-1.37	15.16*	-3.35	-0.84	0.45	0.44	1.97	1.88*	11.16**
MRC 1123 × BML14	0.42	-0.01	0.43	-7.17	0.05	1.71*	0.74	0.71	-1.70	-0.88	4.89
MRC 1176 × BML5	1.51	0.96	-1.02	-19.63**	-8.72*	-1.87*	-0.46	-1.31**	-1.81	-2.50**	-17.31**
MRC 1176 × BML7	-0.76	-0.46	0.29	22.31**	15.19**	2.00*	0.43	1.49**	2.21	2.50**	13.09**
MRC 1176 × BML13	-2.09**	-1.24	1.80	17.66**	3.23	1.82*	0.70	1.44**	1.30	2.54**	21.91**
MRC 1176 × BML14	1.33	0.74	-1.07	-20.34**	-9.70*	-1.96*	-0.68	-1.62**	-1.70	-2.54**	-17.69**
MRC 1179 × BML5	1.34	1.54	0.48	7.54	2.44	0.8	-0.12	-0.56	-0.73	-0.42	-6.14
MRC 1179 × BML7	-1.26	-1.54	0.79	5.81	4.36	-1.00	0.10	-0.09	1.96	0.25	2.92
MRC 1179 × BML13	-1.26	-1.32	-1.7	-20.17**	-8.60*	-0.51	0.37	0.86	3.05*	0.29	11.08**
MRC 1179 × BML14	1.17	1.32	0.43	6.83	1.80	0.71	-0.34	-0.21	-4.28**	-0.13	-7.86
MRC 1209 × BML5	1.51	1.46	-1.02	6.37	9.36*	0.72	-0.29	0.02	-2.81*	1.50	0.19
MRC 1209 × BML7	-1.42	-0.96	0.62	3.64	-4.06	-0.08	1.27**	-0.51	2.54*	-2.17**	-4.41
MRC 1209 × BML13	-1.42	-1.74*	0.80	-15.67*	-13.68**	-2.26**	-0.47	0.78	-0.37	-0.79	5.08

Contd.

Table 2 contd.

MRC 1209 × BML14	1.33	1.24	-0.40	5.66	8.38	1.63*	-0.51	-0.29	0.63	1.46	-0.86
MRC 1271 × BML5	0.93	0.63	1.64	2.87	-5.81	0.88	0.46	0.19	1.02	0.83	-1.81
MRC 1271 × BML7	-0.01	0.21	-5.38**	-3.53	3.11	-1.58*	-0.65	-0.34	-1.29	-1.50	-1.41
MRC 1271 × BML13	-1.67*	-1.24	2.13	-1.51	9.48*	-0.09	-0.05	0.28	-0.20	-0.12	6.08
MRC 1271 × BML14	0.75	0.41	1.60	2.16	-6.78	0.79	0.24	-0.12	0.47	0.79	-2.86
MRC 1358 × BML5	-1.82*	-1.79*	0.39	1.29	0.78	-0.03	-0.29	-0.23	-0.73	-1.50	-6.56
MRC 1358 × BML7	4.91**	4.46**	-0.29	-14.44*	-5.31	-0.83	0.60	-0.43	2.29	0.17	-5.16
MRC 1358 × BML13	-1.09	-0.99	0.22	12.58	4.73	0.99	0.53	1.53**	-0.95	2.88**	18.99**
MRC 1358 × BML14	-2.00*	-1.68*	-0.32	0.58	-0.20	-0.12	-0.84	-0.87	-0.62	-1.54*	-7.27
MRC 1544 × BML5	-0.82	-0.29	-0.61	-6.29	-2.56	-1.28	-0.12	0.02	-0.39	-0.50	-1.48
MRC 1544 × BML7	0.91	0.62	0.04	7.97	10.36*	0.92	0.10	1.16*	-0.71	1.17	11.92**
MRC 1544 × BML13	0.91	0.51	1.22	3.99	-4.60	1.74*	-0.30	-0.89	1.38	-0.12	-7.92*
MRC 1544 × BML14	-1.00	-0.84	-0.65	-5.67	-3.20	-1.37	0.32	-0.29	-0.28	-0.54	-2.52
MRC 1556 × BML5	0.26	0.29	0.14	7.12	3.11	-1.37	0.54	0.11	0.86	2.17**	4.94
MRC 1556 × BML7	-0.34	-0.13	0.46	-11.94	-4.31	0.83	-0.57	-0.09	1.21	-1.83*	7.34
MRC 1556 × BML13	-0.01	-0.24	-0.70	-1.92	-1.27	1.99*	-0.30	-0.47	-2.70*	-2.12**	-16.51**
MRC 1556 × BML14	0.08	0.07	0.10	6.74	2.47	-1.46	0.32	0.46	0.63	1.79*	4.23
MRC 1561 × BML5	-0.32	-0.29	-0.61	-12.46	3.61	1.13	0.46	0.44	3.19**	0.08	14.02**
MRC 1561 × BML7	0.74	0.29	-0.29	-2.19	-13.81**	-1.00	-0.98*	-0.43	-4.12**	-0.58	-21.24**
MRC 1561 × BML13	-1.26	-1.16	1.55	24.49**	7.57	-0.51	0.28	-0.14	-2.37*	0.13	-5.76
MRC 1561 × BML14	0.83	1.16	-0.65	-9.84	2.63	0.38	0.24	0.13	3.30**	0.37	12.98**
MRC 1564 × BML5	0.18	0.63	0.23	-8.13	-3.64	0.72	-0.12	0.44	1.86	0.08	7.94*
MRC 1564 × BML7	-1.09	-0.79	0.21	21.47**	5.61	0.25	0.77	0.24	-2.79*	2.08**	0.01
MRC 1564 × BML13	0.91	-0.24	-0.62	-4.51	2.65	-1.59*	-0.30	-0.81	-1.03	-2.21**	-14.84**
MRC 1564 × BML14	0.00	0.41	0.18	-8.84	-4.62	0.63	-0.34	0.13	1.97	0.04	6.89
MRC 1582 × BML5	0.43	0.13	-0.69	6.04	1.19	-0.87	0.38	0.11	0.27	0.42	3.52
MRC 1582 × BML7	-0.84	-0.29	0.62	-7.36	-3.56	1.67*	-0.07	-0.09	-3.04*	-1.25	-14.08**
MRC 1582 × BML13	0.16	0.26	0.8	-7.34	2.15	0.16	-0.47	0.19	2.38*	0.46	7.74
MRC 1582 × BML14	0.25	-0.09	-0.73	8.66	0.22	-0.96	0.16	-0.21	0.38	0.37	2.81
MRC 1601 × BML5	-1.07	-1.21	0.23	4.54	0.44	-0.20	0.71	0.02	-0.81	0.08	0.19
MRC 1601 × BML7	1.33	1.37	0.54	2.81	-0.98	0.33	-0.07	0.16	1.21	0.42	7.92*
MRC 1601 × BML13	0.99	1.26	-0.95	-7.84	1.40	0.16	-1.13*	-0.56	0.63	-0.54	-7.26
MRC 1601 × BML14	-1.25	-1.43	0.18	0.49	-0.87	-0.29	0.49	0.38	-1.03	0.04	-0.86
MRC 1604 × BML5	-1.91*	-1.79*	0.39	10.79	7.28	0.30	-0.04	0.27	1.61	0.92	20.27**
MRC 1604 × BML7	-0.84	-1.21	0.71	-4.28	-8.48*	0.50	0.52	0.07	2.96*	0.92	6.67
MRC 1604 × BML13	4.16**	4.01**	-2.12	-13.26*	-5.43	-1.34	-1.22*	-2.31**	-6.95**	-2.71**	-39.51**
MRC 1604 × BML14	-1.42	-1.01	1.02	6.74	6.63	0.54	0.74	1.96**	2.38*	0.87	12.56**
MRC 1661 × BML5	0.93	0.54	0.31	6.96	2.19	0.05	-0.21	0.69	1.52	0.67	6.02
MRC 1661 × BML7	0.33	0.12	-0.71	-20.11**	-13.23**	-0.08	0.35	-0.18	-2.79*	-1.00	-7.24
MRC 1661 × BML13	-2.01*	-1.32	0.13	7.24	9.48*	0.07	0.28	-0.89	-0.37	0.04	-3.42
MRC 1661 × BML14	0.75	0.66	0.27	5.91	1.55	-0.04	-0.43	0.38	1.63	0.29	4.64
SE (ij)	0.7871	0.8221	1.1711	6.6380	4.2432	0.7820	0.4675	0.4946	1.1708	0.7644	3.9818

*,**Signifiacnt at P=0.05 and P=0.01 levels, respectively.

1601 x BML 7. These results are comparable with the findings of Bhavana *et al.* (2011) and Aminu *et al.* (2014a) who reported non-additive gene action for plant height.

For ear height, MRC 1556, MRC 1582, MRC 1601, BML 5 and BML 14 were found as poor combiners with highly significant negative gca effects, while MRC 1176, MRC 1561, MRC 1604, BML 7 and BML 13 recorded significant positive gca effects for this trait. The best specific crosses for ear height were MRC 1123 x BML 13, MRC 1176 x BML 7, MRC 1358 x BML 13, MRC 1544 x BML 13, MRC 1561 x BML 5, MRC 1564 x BML 7, MRC 1582 x BML 5, MRC 1582 x BML 14, MRC 1604 x BML 5, MRC 1604 x BML 14 and MRC 1661 x BML 13.

The parents, MRC 1112, MRC 1123, MRC 1176, MRC 1604 and BML 13 recorded positive significant *gca* effects, while MRC 1176 x BML 7, MRC 1179 x BML 13, MRC 1358 x BML 13, MRC 1556 x BML 13, MRC 1561 x BML 5 and MRC 1604 x BML 7 were good crosses for ear length. These results are comparable with findings of Gowda *et al*. (2013) and Leon Muntean *et al.* (2014) who reported the non-additive gene action for ear length.

The parents MRC 1123, MRC 1271, MRC 1604 and BML 13 exhibited significant positive gca effects indicating that they are good general combiners for 100-seed weight, while the best specific crosses were MRC 1176 x BML 7, MRC 1176 x BML 13, MRC 1179 x BML 13, MRC 1209 x BML 5, MRC 1209 x BML 14, MRC 1358 x BML 13, MRC 1556 x BML 5, MRC 1556 x BML 14, MRC 1561 x BML 5, MRC 1561 x BML 14, MRC 1564 x BML 7, MRC 1601 x BML 13, MRC 1604 x BML 5 and MRC 1604 x BML 14. These results are comparable with the findings of Sharma *et al.* (2004), Abrha *et al*. (2013), Lahane *et al*. (2014) and Nanavati (2015) who reported non-additive gene action for 100-seed weight. For grain yield, MRC 1123, MRC 1604 and BML 13 recorded significant positive gca effects and could be utilized in the development of hybrids, synthetics and composites.

Considering the majority of crosses for all the characters investigated, high sca was either due to high x high or low x high or low x low combining parents which further substantiated the operation of non- additive gene action (additive x dominance and dominance x dominance type of epistatic interaction). Hybrids which recorded positively significant sca effects for grain yield and yield contributing characters can be considered as good specific combiners and can be recommended for heterosis breeding.

REFERENCES

Abrha, S. W., H. Z. Zeleke, and D.W. Gissa, 2013 : Line x tester analysis of maize inbred lines for grain yield and yield related traits. *Asian J. Pl. Sci. and Res.,* **3** : 12-19.

Aminu, D., S. G. Mohammed, and B. G. Kabir. 2014a : Estimates of combining ability and heterosis for yield and yield traits in maize population (*Zea mays* L.) under drought conditions in the Northern Guinea and Sudan Savanna Zones of Borno State, Nigeria. *Intl. J. Agric. Inn. and Res.,* **2** : 824-830.

Bhavana, P., R. P. Singh, and R. N. Gadag. 2011 : Gene action and heterosis for yield and yield components in maize (*Zea mays* L.). *Indian J. agric. Sci.,* **81** : 163- 166.

Gowda, R. K., U. Kage, H. C. Lohithaswa, B. G. Shekara, and D. Shobha. 2013 : Combining ability studies in maize (*Zea mays* L.). *Mole. Pl. Br.,* **4** : 116-127.

Hemalatha,V., R. Sai Kumar, V. Swarnalatha, and J. Suresh. 2013 : Combining ability and gene action for morphological parameters in quality protein maize (*Zea mays* L.). *Intl. J. Pl. Ani. and Envl. Sci.* **4** : 230-235.

Kempthorne, O. 1957 : *An Introduction to Genetic Statistics.* John Wiley and Sons, Inc, New York.

Lahane, G. R., R. M. Chauhan, and J. M. Patel. 2014 : Combining ability and heterosis studies for yield and quality traits in quality protein maize. *J. Agric. Res.,* **1** : 135-139.

Leon Muntean, Ioan Has, Voichita Has, Alin Gulea, and Sorin Muntean. 2014 : Combining ability for yield in maize synthetic populations obtained from local populations. *Romanian Agric. Res.,* **1** : 1-8.

Nanavati, J. I. 2015 : Combining ability analysis for quantitative characters in forage maize (*Zea mays* L.). *Forage Res.,* **41** : 30-33.

Sharma, S., M. S. Narwal, R. Kumar, and S. Dass. 2004 : Line x tester analysis in maize (*Zea mays* L.). *Forage Res.,* **30** : 28-30.

Singh, N., S. K. Sharma, R. Kumar, Rajpaul, and S. Singh. 2014 : Effect of sodicity and nitrogen levels on dry matter yield, protein and nutrient uptake in maize. *Forage Res.,* **40** : 237-242.

Singh, R. K., and B. D. Chaudhary. 1985 : *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, Ludhiana.