



## Research Article

# ANALYSIS OF COMBINING ABILITY AND HETEROSIS FOR YIELD AND YIELD CONTRIBUTING TRAITS IN NEWLY DEVELOPED INBRED LINES OF MAIZE (*Zea mays* L.)

ANILKUMAR C.\*, LOHITHASWA H.C., UMA M.S. AND MAHADEVU P.

Department of Genetics and Plant Breeding, University of Agricultural Sciences, Bengaluru, 560065, Karnataka

\*Corresponding Author: Email-anilcgbp@gmail.com

Received: March 16, 2018; Revised: March 19, 2018; Accepted: March 20, 2018; Published: March 30, 2018

**Abstract-** An investigation was carried out to estimate combining ability and heterosis in newly developed inbred lines of maize (*Zea mays* L.) at the College of Agriculture, V. C. Farm, Mandya during 2014. Combining ability analysis using line  $\times$  tester design was conducted in inbred lines by crossing 43 lines with four testers. The variance ratio (ratio of GCA to SCA) revealed that the expressions of traits under this study were predominantly controlled by non-additive gene action. The lines viz., MAI1-48-1, MAI1-41-3, MAI2-9-1-2 and tester CM202 were identified as best general combiners for yield and yield related characters. Among crosses, MAI1-17-11 $\times$ MAI105, MAI1-20-1 $\times$ CM500 and MAI1-8-3 $\times$ MAI105 exhibited highest significant sca effects and high heterosis over checks for grain yield. These hybrids need to be further evaluated across locations and over seasons to select best hybrids for commercial exploitation.

**Key words-** GCA, Heterosis, line  $\times$  tester, maize, SCA

**Citation:** Anilkumar C., et al., (2018) Analysis of Combining Ability and Heterosis for Yield and Yield Contributing Traits in Newly Developed Inbred Lines of Maize (*Zea mays* L.). International Journal of Agriculture Sciences, ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 10, Issue 6, pp.-5460-5464.

**Copyright:** Copyright©2018 Anilkumar C., et al., This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

## Introduction

Maize is unique among the cereals on account of its amenability to diverse uses and it has huge potential in the present era of crop diversification. It has great yield potential and attained the leading position among cereals based on production as well as productivity. India is emerging as one of the potential baby corn producing countries due to low cost of production and high demand within the country. The main purpose of maize breeding is to develop new inbred lines and hybrids that will outperform the existing hybrids with respect to a number of traits. The nature and magnitude of gene action is an important factor in developing an effective breeding programme. Combining ability analysis is useful to assess the potential inbred lines and also helps in identifying the nature of gene action involved in various quantitative characters. Since, Shull (1908) [1] suggested the inbred-hybrid concept, the use of heterosis in maize breeding has been emphasized. The development of superior hybrids depends on the combining ability of lines involved in the production of hybrids. The concepts of general combining ability (*gca*) and specific combining ability (*sca*) proposed by Sprague and Tatum (1942) [2] for the first time. The behavior of a line in hybrid combination is assessed through the estimation of general combining ability (*gca*) and specific combining ability (*sca*) effects. The  $L \times T$  mating design is an appropriate method to identify superior parents and hybrids based on *gca* and *sca* effects, respectively (Kempthorne 1957) [3].

The variance due to general combining ability (GCA) is usually considered to be an indicator of the extent of additive type of gene action, this was advocated by several workers as El – Badawy (2006) [4] and Sedhom et al. (2007)[5], whereas specific combining ability (SCA) is taken as the measure of non-additive type of gene actions in heterosis breeding (Dadheech and Joshi, 2007 [6]; Barakat and Osman, 2008 [7]; Irshad El-Haq et al., 2010[8]). The success of heterosis breeding depends on the amount of genetic diversity present in the material (Moll et al., 1962) [9]. Keeping all these points in view, the present study was

undertaken to estimate the combining ability of parents and heterosis of hybrids.

## Material and Method

The material for the study consisted of forty three inbred lines (used as females) and four testers (used as males) developed at the College of Agriculture (CoA), V C Farm, Mandya. These inbred lines were planted in a single row of 4m length and crossed with four testers (CM500, CM202, MAI105 and NAI137) using line  $\times$  tester mating design (Kempthorne, 1957[3]) during *kharif* 2013. The resulting 172 single cross hybrids, were evaluated along with their parents and six commercial check hybrids during *kharif* 2014 at college of agriculture, V. C. form, Mandya in a simple lattice design. The experimental plot represent southern dry zone (Zone 6) located at latitude of 12°30'N, longitude of 76°50' E and altitude of 694.65 meters above MSL. Each genotype was sown in single row of four meter length with a spacing of 20cm between the plants and 60cm between the rows. The recommended packages of practices for experimental site were followed to raise healthy crop. The data recorded on seven morphological characters viz., plant height (cm), ear height (cm), ear length (cm), ear circumference (cm), number of kernel rows per cob, number of kernels per row, and plot yield (kg). The traits means of the five plants of hybrids and parents were subjected to statistical analysis.

## Statistical analysis

Combining ability of lines and testers was estimated using the following linear model (Arunachalam, 1974[10]).

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + r_k + e_{ijk}$$

Where,  $Y_{ij}$  is trait value of  $ij^{th}$  hybrid,  $\mu$  is population mean,  $g_i$  is *gca* effect of  $i^{th}$  line,  $g_j$  is *gca* effect of  $j^{th}$  tester,  $s_{ij}$  is *sca* effect of  $ij^{th}$  hybrid,  $r_k$  is replication effect and  $e_{ijk}$  is error associated with  $(ijk)^{th}$  observation.

The general combining ability effects of lines and testers were estimated using the

following formulae.

$$\hat{g}_i = \frac{Y_{i..}}{mr} - \frac{Y_{...}}{mfr}$$

Where,  $\hat{g}_i$  is general combining ability effect of  $i^{\text{th}}$  line,  $Y_{i..}$  is total of  $i^{\text{th}}$  line over  $t$  testers and  $r$  replications and  $Y_{...}$  is total of all hybrids over  $r$  replications.

$$\hat{g}_j = \frac{Y_{.j.}}{rf} - \frac{Y_{...}}{mfr}$$

Where,  $\hat{g}_j$  is general combining ability effect of  $j^{\text{th}}$  tester,  $Y_{.j.}$  is total of  $j^{\text{th}}$  tester over  $l$  lines and  $r$  replications and  $Y_{...}$  is total of all hybrids over  $r$  replications.

The specific combining ability effects of crosses were estimated using the following formulae.

$$S_{ij} = \frac{Y_{ij.}}{r} - \frac{Y_{i..}}{rm} - \frac{Y_{.j.}}{rf} + \frac{Y_{...}}{rmf}$$

Where,  $S_{ij}$  is sca effect of  $ij^{\text{th}}$  combination,  $Y_{ij.}$  is  $ij^{\text{th}}$  combinations total over all the replications,  $Y_{i..}$  is total of  $i^{\text{th}}$  line over male parent and  $r$  replications,  $Y_{.j.}$  is Total of  $j^{\text{th}}$  tester over female and  $r$  replications and  $Y_{...}$  is Total of all hybrids over  $r$  replications.

Heterosis expressed as *per cent* increase or decrease of  $F_1$  hybrid over mid-parent (average or relative heterosis), better parent (heterobeltiosis) and the best commercial check (NAH 2049, NAH 1137 and 900MGOLD) were computed as per the method suggested by Tuner (1953)[11] and Hayes *et al.*, (1955)[12].

a) Heterosis over mid-parent (relative heterosis) =  $\frac{\bar{F}_1 - \bar{MP}}{\bar{MP}} \times 100$

b) Heterosis over better parent (Heterobeltiosis) =  $\frac{\bar{F}_1 - \bar{BP}}{\bar{BP}} \times 100$

c) heterosis over check (standard heterosis) =  $\frac{\bar{F}_1 - \bar{CC}}{\bar{CC}} \times 100$

Where,  $\bar{F}_1$  is mean performance of  $F_1$ ,  $\bar{MP}$  is mean mid-parental value =  $(P_1 + P_2)/2$ ,  $P_1$  is mean performance of parent one,  $P_2$  is mean performance of parent two,  $\bar{BP}$  is mean performance of better parent and  $\bar{CC}$  is mean performance of the best commercial check.

Overall status of parents and crosses with respect to *gca* and *sca* and heterosis was determined by following a method suggested by Arunachalam and Bandyopadhyay (1979) [13] that was slightly modified by Mohan Rao *et al.* (2004) [14]. Further the crosses were grouped into different categories viz., High (H) × High (H), High (H) × Low (L) and Low (L) × Low (L) based on overall *gca* status of their parents.

## Results and Discussion

The general analysis of variance for parents (43+4), hybrids (172) and checks (6) for all seven quantitative traits is presented in [Table-1]. Effect of blocks with respect to unadjusted treatment values were significant for all the traits analyzed. The adjusted mean values within replication for the characters in which block effects was found significant were used for further statistical analysis. The analysis of variance for combining ability with respect to seven quantitative traits revealed the significance variance for all the genotypes [Table-2]. The crosses exhibited high level of significance for all the traits. The variance due to crosses was further partitioned into variance due to lines, variance due to testers and variance due to line × testers. Variance due to parents was highly significant for all the traits indicating the presence of sufficient variability among parents. The GCA and SCA variance ratio revealed the preponderance of non-additive gene action in governing the expression of all the characters, which can be exploited through population improvement programmes [Table-3]. This is in accordance with earlier reports by Kambegowda *et al.* (2013)[15], Amiruzzaman *et al.* (2013)[16] and Aminu *et al.* (2014)[17]. While, contrasting results were observed by Legesse *et al.* (2009)[18]. Estimates of *gca* effects revealed that no line was observed to be good combiner for all the traits. Best lines and testers with significant *gca* effects in the desirable direction for each character are presented in [Table-4]. Only 17 out of 43 lines were good general combiners for grain yield. Among them, MAI 1-17-11 was the best with highest *gca* effects in positive direction. Apart from this, it was a good general combiner for plant height, ear height, ear length, ear circumference and number of kernel rows per cob characters in positive direction. MAI 1 -66-1, MAI 1 -17-11 and MAI 1 -37-6 showed highest *gca* effects in positive direction for plant height and ear height traits, hence these lines could be used in breeding for plant height. Among testers, CM 202 recorded significant *gca* effects for most of the traits in desirable direction. It recorded positive *gca* effects for ear height and kernels per row proving to be a best combiner in producing heterotic hybrids. Twenty seven out of forty three lines and two out of four testers were recorded high (H) overall general combining ability status suggesting the ability of these lines to transmit additive genes in the desirable direction [Table-5 and 6]. However, these lines and testers should be evaluated further to confirm their superiority. Best crosses with significant *sca* effects in desirable direction for each characters is presented in [Table-7]. The cross combinations MAI1-1-1 × CM500 and MAI1-5-2 × MAI105 recorded significant positive *sca* effects for plot yield character and among these characters, first cross involving both parents with low *gca* effects and second cross involving both parents having high *gca* effects indicates that yield character is governed by both additive and epistatic gene actions. These results are in agreement with results obtained by Guerrero *et al.* (2014)[19], Kapoor *et al.* (2014)[20] and Kumar *et al.* (2014)[21].

**Table-1 Analysis of variance for hybrids and parents**

Source of variation	Df	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear circumference (cm)	Kernel rows per cob	kernels per row	Plot yield (kg)
Replications	1	251.93	353.78	0.01	0.03	0.44	22.09	0.02
Treatments (unadj.)	224	743.88**	388.05**	7.04**	3.98**	3.85**	64.57**	2.17**
Blocks within reps (adj.)	28	86.36	95.53	0.15	0.03	0.28	13.00	0.01
RCBD Error	224	69.68	85.08	0.12	0.04	0.26	11.95	0.01
Intrablock Error	196	67.30	83.58	0.12	0.04	0.26	11.80	0.01
Total	449	406.44	236.83	3.57	2.01	2.05	38.22	1.09

\* Significant at  $p = 0.05$  and \*\* Significant at  $p = 0.01$

**Table-2 Analysis of variance for combining ability**

Source of variation	Df	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear circumference (cm)	Kernel rows per cob	kernels per row	Plot yield (kg)
Replication	1	114.08	201.685	0.056	0.051	0.405	18.419	0.012
Crosses	171	459.352**	313.768**	5.821**	1.733**	2.799**	20.283**	0.811**
Line Effect	42	752.147**	525.877**	7.549	2.749**	4.662**	23.577	1.130*
Tester Effect	3	695.752	232.23	2.36	5.647**	22.359**	22.581	1.743
Line × Tester Effect	126	356.125 **	245.006 **	5.327 **	1.301 **	1.712 **	19.130 **	0.682**
Error	171	63.322	86.423	0.089	0.042	0.259	12.515	0.008
Total	343	260.907	200.1	2.946	0.885	1.525	16.405	0.409

\* Significant at  $p = 0.05$  and \*\* Significant at  $p = 0.01$

J. Combination MAI1 -37-6 × MAI105 exhibited significant positive sca effect for ear circumference and number of kernels per row. In addition, MAI1-17-11 × CM500 and MAI1-8-3 × MAI105 cross combinations exhibited significant sca effects for ear length and number of kernel rows per cob, respectively. The crosses with significant sca effects and involved parents with low x low or high x low gca effects indicating the presence of non-allelic interactions. Therefore, recurrent selection for specific combining ability could be followed in the segregating generations. The cross combinations, MAI1-58-3 × MAI137 and MAI1-58-3 × NAI137 manifested highest positive heterosis for plant height and ear height over NAH 2049 and these results are in agreement with the results of Geetha (2001)[22] and Chattopadhyay and Dhiman (2005)[23]. MAI1-17-11 × CM500 and MAI1 -20-1 × NAI137 were two best crosses with high significant positive heterosis over checks for ear length and ear circumference, respectively. The crosses, MAI 1 -8-3 × MAI105 and MAI1 -48-1 × CM500 recorded high positive heterosis for number of kernel rows and number of kernels per row over best check 900MGOLD, respectively. Earlier workers including Geetha (2001)[22],

Kumar *et al.* (2013)[24] and Rajesh *et al.* (2014)[25] reported considerable positive heterosis for the trait

**Table-3** Variance due to general and specific combining ability interaction towards variation in the hybrids

Sl. No.	Character	$\sigma^2$ GCA	$\sigma^2$ SCA	$\sigma^2$ GCA/ $\sigma^2$ SCA
1	Plant height (cm)	13.938**	143.620**	0.097
2	Ear height (cm)	6.243**	79.676**	0.078
3	Ear length (cm)	0.103**	2.615**	0.040
4	Ear circumference (cm)	0.089**	0.630**	0.140
5	Kernel rows per cob	0.282**	0.723**	0.390
6	kernels per row	0.231**	3.463**	0.067
7	Plot yield (kg)	0.030**	0.337**	0.090

\* Significant at p = 0.05 and \*\* Significant at p = 0.01

**Table-4** Best lines and testers with significant gca effects in the desirable direction

Sl. No.	Characters	Lines		Testers
1	Plant height (cm)	MAI 1-66-1	MAI 1-17-11	CM202
		15.686 **	14.636 **	4.204 **
2	Ear height (cm)	MAI 1-66-1	MAI 1-37-6	CM202
		19.238 **	10.886 **	2.090 *
3	Ear length (cm)	MAI 1-48-1	MAI 2-16-3-1	MAI105
		2.385 **	1.660 **	0.201 **
4	Ear circumference (cm)	MAI 1-88-2	MAI 1-108-2	MAI105
		1.208 **	1.208 **	0.208 **
5	Kernel rows per cob	MAI 1-66-1	MAI 1-37-6	MAI105
		1.303 **	1.253 **	0.493 **
6	Kernels per row	MAI 1-41-3	MAI 1-8-3	CM202
		2.937 *	2.262	0.362
		3.160 **	2.498 *	0.663 *
7	Plot yield (kg)	MAI 1-17-11	MAI 1-8-3	MAI105
		0.967 **	0.858 **	0.115 **

\* Significant at p = 0.05 \*\* Significant at p = 0.01

**Table-5** Overall general combining ability status of lines

Sl. No.	Lines	Rank	gca status	Sl. No.	Lines	Rank	gca status
1	MAI 1-1-1	295	L	23	MAI 1-97-3	331	L
2	MAI 1-4-1	245	H	24	MAI 1-98-3	398	L
3	MAI 1-5-2	240	H	25	MAI 1-108-2	282	L
4	MAI 1-8-3	202	H	26	MAI 2-4-1-1	246	H
5	MAI 1-11-2	255	H	27	MAI 2-6-4-2	394	L
6	MAI 1-12-1	331	L	28	MAI 2-9-1-2	176	H
7	MAI 1-17-2	320	L	29	MAI 3-2-4-1	256	H
8	MAI 1-17-11	199	H	30	MAI 3-2-5	254	H
9	MAI 1-20-1	206	H	31	MAI 3-3-2	248	H
10	MAI 1-21-4	238	H	32	MAI 3-7-2	231	H
11	MAI 1-22-1	333	L	33	MAI 3-13-6	333	L
12	MAI 1-22-3	232	H	34	MAI 4-5-2	263	H
13	MAI 1-31-2	184	H	35	MAI 4-7-3	264	H
14	MAI 1-37-3	327	L	36	MAI 4-10-3	260	H
15	MAI 1-37-6	219	H	37	MAI 5-12-1-1	351	L
16	MAI 1-41-3	169	H	38	MAI 1-17-13	229	H
17	MAI 1-48-1	146	H	39	MAI 1-43-2	337	L
18	MAI 1-57-3	236	H	40	MAI 1-58-3	261	H
19	MAI 1-59-4	304	L	41	MAI 1-66-1	270	L
20	MAI 1-77-1-1	214	H	42	MAI 1-88-2	257	H
21	MAI 1-85-1	210	H	43	MAI 2-16-3-1	307	L
22	MAI 1-91-3	299	L				

Final norm: 264 H: High L: Low

**Table-6** Overall general combining ability status of tester

Sl.No	Tester	Rank	gca status
1	CM500	36	L
2	CM202	21	H
3	MAI 105	28	H
4	NAI 137	35	L
Final norm: 30 H: High L: Low			

## Conclusion

The present study resulted in the identification of 10 promising hybrids viz., MAI1-17-11 × MAI105, MAI1-20-1 × CM500, MAI1-8-3 × MAI105, MAI1-91-3 × MAI105, MAI1-97-3 × MAI105, MAI1-20-1 × MAI105, MAI1-66-1 × CM202, MAI1-17-11 × CM202, MAI1-41-3 × CM202 and MAI1-8-3 × NAI137 based on mean, sca effects and standard heterosis for grain yield per plot which are superior than the commercial checks NAH-1137 (SH1), NAH-2049 (SH2) and 900MGOLD (SH3) [Table-8]. These hybrids could be evaluated extensively for their utility as new hybrids.

**Table-7** Best crosses with significant sca effects in the desirable direction

Sl. No.	Characters	Crosses		
1	Plant height (cm)	MAI4-10-3 × CM500	MAI1-37-6 × NAI137	MAI5-12-1-1 × CM202
		31.75**	29.33**	28.26**
2	Ear height (cm)	MAI5-12-1-1 × CM202	MAI1-12-1 × CM500	MAI1-97-3 × CM500
		27.26**	24.14**	23.79**
3	Ear length (cm)	MAI1-17-11 × CM500	MAI1-17-2 × NAI137	MAI1-58-3 × MAI105
		3.77**	3.56**	3.55**
4	Ear circumference (cm)	MAI1-20-1 × NAI137	MAI1-22-1 × NAI137	MAI1-37-6 × MAI105
		1.85**	1.72**	1.56**
5	Kernel rows per cob	MAI1-8-3 × MAI105	MAI4-7-3 × CM202	MAI3-3-2 × NAI137
		3.23**	1.97**	1.95**
6	Kernels per row	MAI1-21-4 × CM202	MAI1-48-1 × CM500	MAI1-37-6 × MAI105
		7.11**	5.69*	5.62*
7	Plot yield (kg)	MAI1-1-1 × CM500	MAI1-5-2 × MAI105	MAI3-2-5 × MAI105
		1.123 **	1.005 **	0.981 **

\* Significant at p = 0.05 \*\* Significant at p = 0.01

**Table-8.** Best single cross hybrids based on mean, sca effects, and standard heterosis for grain yield

Hybrid	Mean	sca effect	SH1	SH2	SH3	Type of cross
MAI1-17-11 × MAI105	4.66	0.371 **	59.04 **	32.39 **	22.63 **	H × H
MAI1-20-1 × CM500	4.55	0.974 **	55.29 **	29.26 **	19.74 **	H × L
MAI1-8-3 × MAI105	4.40	0.220 **	50.17 **	25.00 **	15.79 **	H × H
MAI1-91-3 × MAI105	4.40	0.751 **	50.17 **	25.00 **	15.79 **	L × H
MAI1-97-3 × MAI105	4.38	0.585 **	49.32 **	24.29 **	15.13 **	L × H
MAI1-20-1 × MAI105	4.32	0.447 **	47.44 **	22.73 **	13.68 **	H × H
MAI1-66-1 × CM202	4.32	0.905 **	47.27 **	22.59 **	13.55 **	L × H
MAI1-17-11 × CM202	4.30	0.172 **	46.76 **	22.16 **	13.16 **	H × H
MAI1-41-3 × CM202	4.30	0.558 **	46.76 **	22.16 **	13.16 **	H × H
MAI1-8-3 × NAI137	4.25	0.068	44.88 **	20.60 **	11.71 **	H × L

\* Significant at p = 0.05 \*\* Significant at p = 0.01

**Application of research:** This study is helpful in identification of best inbred lines with high specific and general combining ability, and hybrids with high heterosis.

## Abbreviations:

GCA-general combining ability  
SCA-specific combining ability  
MP- mid parent  
CC- commercial check  
BP-better parent  
SH-standard heterosis

**Acknowledgement / Funding:** Author thankful to University of Agricultural Sciences, Bengaluru, 560065, Karnataka

**\*Chairperson of research:** Dr H C Lohithaswa

**University:** University of Agricultural Sciences, Bengaluru, 560065, Karnataka

**Research project name or number:** MSc Thesis

**Author Contributions:** All author equally contributed

**Author statement:** All authors read, reviewed, agree and approved the final manuscript

**Conflict of Interest:** None declared

**Ethical approval:** This article does not contain any studies with human participants or animals performed by any of the authors.

## References

- [1] Shull G.H. (1908) *American Breeders Assoc. Republic*, 4, 296-301.
- [2] Spargue G.F. and Tatum L.A. (1942) *J. American Soc. Agron.*, 34, 923-932.
- [3] Kempthorne O. (1957) John Wiley and Sons, New York.

- [4] El-Badawy M. E. M. (2006) *J. Agric. Sci. Benha Univ.*, 44, 911-922.
- [5] Sedhom A. S., El-Badawy M. E. M., Morsy A. M. and El-Hosary A. A. A. (2007) *J. Agric. Sci. Benha Univ.* 45, 1-20.
- [6] Dadheech A. and JOSHI V. N. (2007) *Indian J. Agric. Res.*, 41, 210-214.
- [7] Barakat A. A., and Osman M. M. A. (2008) *J. Agric. Sci. Mansoura Univ.*, 33, 4667-4679.
- [8] Irshad-El-Haq M., Ajmal S. U., Munir M. and Gulfaraz M. (2010) *Pak. J. Bot.*, 42, 1021:1030.
- [9] Moll R. H., Salhauna, W. S. and Robinson (1962) *Crop Sci.*, 2, 197-198.
- [10] Arunachalam V. (1974) *Indian J. Genet.*, 34, 280-287.
- [11] Turner J. K. (1953) *Agron. J.*, 45, 487-490.
- [12] Hayes H. K., Immer F. R. and Smith D. C. (1955) Mc. Grow Hill Book Co., Inc., New York. pp.165-180.
- [13] Arunachalam V. and Bandopadhyay A. (1979) *Theor. Appl. Genet.*, 54, 203-207.
- [14] Mohan Rao A., Lakshmikanth Reddy G., Kulkarni R. S., Ramesh S. and Lalitha Reddy S. S. (2004) *Helia.*, 27(41), 51-58.
- [15] Kambegowda R., Kage U., Lohithaswa H. C., Shekara B. G., and Shobha D. (2013) *Mol. Pl. Breed.*, 4(14), 116-127.
- [16] Amiruzzaman M., Islam M. A., Hassa L., Kadir M. and Rohman M. M. (2013) *Emir. J. Food Agric.*, 25(2), 132-137.
- [17] Aminu D., Mohammed S. G. and Kabir B. G. (2014) *Int. J. Agric. Innovations and Res.*, 2(5), 824-830.
- [18] Legesse B. W., Pixley K. V. and Botha A. M. (2009) *Maydica*, 54, 1-9.
- [19] Guerrero C. G., Robles M. A. G., Ortega J. G. L., Castillo I. O., Vázquez C. V., Carrillo M. G., Resendez A. M. and Torres A. G. (2014) *American J. Pl. Sci.*, 5, 845-856.
- [20] Kapoor C., Lata S. and Sharma J. K. (2014) *Electronic J. Pl. Breed.*, 5(4), 716-721.
- [21] Kumar G. P., Reddy V. N., Kumar S. S. and Rao P. V. (2014) *Int. J. Plant, Animal and Envir. Sci.*, 4(4), 229-234.
- [22] Geetha K. (2001) *Agric. Sci. Digest.*, 21, 202-203.
- [23] Chattopadhyay K. and Dhiman K. R. (2005) *Indian J. Genet.*, 66(1), 45-46.
- [24] Kuma R., Shahi J. P. and Srivastava K. (2013) *The Boiscan*, 8(4), 1165-1170.
- [25] Rajesh V., Kumar S. S., Reddy V. N. and Sankar A. S. (2014) *Int. J. Plant, Animal and Envir. Sci.*, 4(1), 304-306.