# Combining Ability for Yield and Yield attributes in Maize Inbred-lines (*Zea mays L.*) Using Line x Tester Analysis.

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Abstract: Maize is one of the major crops in the world that plays a major role in meeting the demand for food, livestock ingredients and industrial raw materials. There is need to breed for high-yielding maize genotypes to meet up with the needs of the fast-increasing population in Nigeria and West and Central Africa (WCA) in general. Seven maize genotypes were collected from the Institute of Agricultural Research and Training (IAR&T), Ibadan, Nigeria and crossed in Line x tester mating design at the Teaching and Research Farm of Federal University of Agriculture, Abeokuta, Nigeria (FUNAAB) in 2014. The parental inbred lines used in the crosses and hybrids generated were evaluated at FUNAAB and the Oyan Project site of Ogun Oshun River Basin Development Authority, Nigeria, in 2014. Data collected on grain yield and other yield-related agronomic traits were subjected to analysis of variance (ANOVA) which revealed significant (p < 0.05) entry effects with respect to all the traits except days to anthesis and number of kernel rows per ear. Mean separation was performed for all the characters using Duncan's multiple range test (p ≤ 0.05). Analysis of combining ability effects revealed significant ( $p \le 0.05$ ) general and specific combining ability effects for all the characters. Estimates of dominance variance ( $\sigma$ 2SCA) were larger (-0.002 to 166565.220) than additive variance estimates ( $\sigma$ 2GCA) (-0.10 to 4638.39) for all traits that were considered. 1000-kernel weight was identified as most reliable selection index for yield improvement in maize breeding. Genotypes FAM-98-129 and FOM 128 were found as the best maternal line and best pollen parent, respectively. Hence, they are suggested for use in future breeding programs.

Keywords: gene action, inbred, line x tester, combining ability.

# INTRODUCTION

Maize (Zea mays L.) was introduced to Nigeria before the colonial era (Iken and Amusa, 2004). It has been in the diet of Nigerians for centuries. Though, it started as a subsistence crop, it has risen to a commercial crop status which many agro-based industries depend on as raw materials for the production of finished products such as industrial starch, bio-fuels, livestock feeds etc. (Obi. 1991: USDA/MARKET, 2010). The crop has

been widely studied because of its broad/high genetic diversity and enormous biological influence 1988). (Hallauer and Miranda, Consequently, efforts have been made to increase productivity and enhance genetic stability of the crop, since the role of this crop to the world food database cannot be underrated. Meanwhile, estimation of combining ability and genetic variation are very important especially for hybridization (Fehr, 1993).

Studying the performance of inbred lines in hybrid combinations and comparing their performances for identification of superior parental lines that will produce productive progenies in a wide range of hybrid production is common exercise in crop а improvement programs (Han et al., 1991; Griffing, 1956). Various studies have revealed the use of combining ability principle in solving many agronomic challenges in maize production (Ceyhan, 2003). Vassal et al. (1992) used combining ability studies to develop maize varieties with good ear height and uniform flowering days. According to Iken et al. (2002), it has been established that both general and specific combing ability effects of genetic materials are of practical value in breeding programs they play a strong role in identifying for superior parents hybrid combinations (Duvick. 1999). However, Zehui et al. (2000) observed significant GCA effects for a number of yield-related morphological traits in inbred lines derived from different populations. Kadlubiec et al. (2001) observed higher proportion of GCA effects than SCA effects for yield and various other agronomic traits in flint and dent types of maize inbred lines.

Line x tester of Kempthorne (1957) is one of the mating designs that can be used to study combining ability. The design involves a set of female parents (n) crossed with a genetically different set of male (m) in all possible parents combinations resulting to a total number of 'mn' progenies. It is one of efficient the most methods of evaluating large number of lines as well as providing genetic information on the relative importance of general and specific combining ability effects of pairs of parental genotypes for interpreting the genetic bases of important plant traits (Mather and Jinks, 1982). In addition, it had been found useful in recognizing suitable parents and crosses among parents without necessarily making many (Kumar al.. 2005). crosses et. Therefore, the aims of this study were to examine the combining ability of the inbred lines for yield and other related characters, the roles combining ability plays in determining the yield and to identify superior genotypes that would be useful for further research work.

# MATERIALS AND METHODS.

The experiment involved seven maize genotypes of diverse origin (four

genotypes designated as lines, viz FMS 1-122, FMS-126, FMA-0-1211, FAM-98-129. and three genotypes designated as testers, viz: FEMY-121, FDM-Y-1212 and FOM-128). These were crossed in a line x tester mating design to generate 12 F<sub>1</sub> hybrid progenies. Evaluation of the crosses and parental lines were carried out at two different locations. The parental lines were collected from the Institute of Agricultural Research and Training, Obafemi Awolowo University, Moore Plantation, Ibadan, Oyo State, Nigeria. The lines and the testers were crossed in all possible combination using line x tester mating design technique of Kempthorne (1957) to generate 12  $F_1$ hybrids in FUNAAB in 2013. The parental lines and hybrids were subsequently evaluated in a 4-row plot of 4-meter length with 0.75m spacing between rows and 0.4m within the rows. The experiment was laid out randomized using block design (RCBD) with three replications at each location of Directorate Research Farm, Federal University of Agriculture, Abeokuta. Ogun State, Nigeria (Longititude 3<sup>0</sup>23E, Longititude 3<sup>0</sup>23E and 159masl.) and Project Field, **Ogun-Oshun River Basin Development** Authority Project Site, Ogun State,

3<sup>0</sup>23E. Nigeria (Longititude Longititude  $3^{0}29E$ ). Three seeds were planted per hill, thinned to two plants per stand at three to five leaf stages to attain a final plant density of 66,000 ha<sup>-1</sup> N: P: plants Κ fertilizer application was at the rates of 100:50:90 kg ha<sup>-1</sup> respectively. Other management measures were observed according to standard practices. Data were taken on ten randomly selected competitive plants from each replication at each location for the following characters: days to anthesis (DT), Days to silking (DS), Plant height (PH), Cob weight, 1000-grain Weight (TGW) (kg), number of kernel rows per ear, ear weight with sheath, ear weight without sheath, grain weight and grain yield (kg/plot). Analysis of variance (ANOVA) was conducted for all the parameters measured, using the average of data collected from each environment separately, using SAS 9.3 version (2014) package. Environment was considered random and genotype as fixed effect. Significant means were separated using Duncan's multiple range test (DMRT) at 5% level of probability. Genotypic and phenotypic variances were computed from ANOVA. Line x tester analysis of variance was performed to estimate general combining ability (GCA) and specific combining ability (SCA). The GCA effects for each parent (line/tester) was estimated as the mean of all crosses involving that parent (inbred line/tester) minus the overall mean, and SCA was estimated as mean of a cross minus mean of all inbred line crosses involving that tester and the overall mean.

# **RESULTS AND DISCUSSION.**

Tables 1, 2 and 3 show the mean squares from analysis of variance for and related characters for vield nineteen maize genotypes in Oyan project site, Abeokuta. The seven (7) parents genetically differed (p < 0.01) with respect to days to anthesis, days to silking, plant height, number of kernel rows per ear and 1000-kernel weight. Likewise, the 12 hybrids were not genetically the same with respect to all the traits except days to anthesis and ear weight. Moreover, the parents and hybrids responded to environmental factors differently. Table 4, which presents the combined mean performances of the hybrids across the two locations, further shows that there was existence of variability among and within the entries with

respect to all the traits under study. From the Table 4, FMA-0-1211 recorded highest mean value of 67.84 for days to silking while FOM 128 recorded the lowest value (61.82). Also, parent FMS 1-122 pooled highest value (13.50) while FOM 128 pooled lowest value of 8.66 for number of kernel rows per ear. With respect to 1000-kernel weight, hybrid FMS-126 x FEMY-121 pooled highest mean value (225.52) while FAM-98-129 x FDM-Y-1212 pooled the lowest value of 121.20. For grain yield per plot, FMS-126 x FEMY-121 has highest mean while FAM-98-129 x FDM-Y-1212 recorded the lowest value (590.4). The analyses of variance for combining ability in Table 5 shows significant (p < 0.01) GCA and SCA variances with larger SCA estimates for all traits relative to the GCA estimates. Generally, significant GCA effects were observed for the seven parents for most of the traits that were evaluated. Whereas, the GCA effects were mostly significant but negative for most traits in genotypes FMA-0-1211 and FOM-128. Negative GCA effects were observed for anthesis and silking traits only in FMS-126. Equally, large GCA variances were observed for all traits that were evaluated except days to

anthesis and silking (Tables 6 and 7). This shows that the crosses can be grouped into different heterotic groups based on their performances and the level at which they can successfully combine under different environmental factors. Estimates of genetic variance components of yield and related traits (Table 8) show additive and dominance variances calculated for all but characters with characters. significant mean squares for line x tester were considered. The result shows the presence of both additive and dominance variances. However, dominance variance was larger than additive variance for all traits with the exception of days to earleaf senescence, plant height and number of kernel-rows per ear. The ratio of GCA to SCA variance was less than unity for all characters except for number of kernel rows per ear (10.74) and ranged from 0.001 for days to silking to 10.74 for number of kernel-rows per ear. This shows the predominant role of non-additive gene action in the inheritance of all the characters studied in the maize population. Estimates of dominance variance ( $\sigma^2$ SCA) were larger than additive variance estimates ( $\sigma^2$ GCA) for all characters in the study and the degree of dominance was in

the range of over-dominance for all the characters except days to earleaf senescence, number of kernel rows per ear and cob weight which had partial – dominance (Table 8).

# CONCLUSION

The study has shown the existence of genetic variability, which is the core aim of any breeding program. Days to silking, days to earleaf senescence, plant height and 1000-kernel weight were good indices in selecting for high grain yield. However, FOM 128 responded differently during the study and can serve as a good tester in future research works because of its high general combining ability. Moreover, FMA-0-1211 x FEMY 121 and FAM-98-129 x FDM-Y-1212 showed a very high superiority among all the hybrids. Likewise, FMA-0-1211 x FOM-128 and FMS1-122 x FOM-128 showed that they were good combiners. They can all be subjected to further study before released as hybrid seed to farmers.

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						Mean	square					
Source of variation	Df	Days to anthesis	Days to silking	Days to earleaf senescence	Plant height (cm)	Number of Kernel row/ear.	Ear weight with Sheath (g)	Ear weight without Sheath (g)	Cob weight (g)	Grain weight (g)	1000-kernel weight(g)	Grain Yield/plot (kg).
Entries	18	21.069**	23.250**	298.194**	1316.529**	12.906**	828.770*	671.128*	142.482**	6920.958*	2328.856**	153799.085*
Replication	2	8.184	0.593	33.333	193.892	0.122	392.245	150.520'	2.458	117.257	46903.08	2.265
Parent	6	25.250**	26.530*	291.960**	1473.420**	24.000**	789.440'	383.570'	3.230*	169.320'	2611.411**	67726.710'
Crosses	11	10.750'	20.510**	273.051**	1129.550**	5.110*	824.121	768.451	186.570**	481.440*	2383.011**	192579.222*
Parent vs. crosses	1	8.869	24.589**	119.279**	559.529	2.06	682.916	517.327	136.101**	299.038	3026.853**	119615.474
Lines	3	12.988	6.195*	594.592**	1602.329**	6.148	926.485	578.279	343.733**	46.32	838.593**	18528.138
Testers	2	2.703	8.225*	276.194**	697.121*	13.027*	1336.766	1059.975	6.786	1208.440*	4088.928**	483376.023*
Lines vs. Testers	6	12.322	31.765**	111.231**	1037.308**	1.953	602.056	766.370'	167.928*	456.681	2586.592**	182672.499
Error	36	6.836	3.694	15.314	143.892	1.567	369.915	292.925	30.058	165.690'	12.61	66277.173

Table 1: Mean squares from analysis of variance of yield and yield-related characters for nineteen maize genotypes in location 1-Oyan project site.

\*, \*\* significant at 5% and 1% probability levels, respectively.

						Γ	Mean square					
Source of variation	Df	Days to anthesis	Days to silking	Days to earleaf senescence	Plant height (cm)	Number of Kernel row/ear.	Ear weight with Sheath(g)	Ear weight without Sheath(g)	Cob weight(g)	Grain weight(g)	1000kernel weight(g)	Grain Yield/plot (kg).
Entries	18	2.990*	5.921	171.651**	1034.000 *	3.131	1249.841	1329.241	108.811	796.851	3904.871**	318738.821
Replication	2	0.321	1.061	18.292	162.472	2.222	789.911	491.652	81.753	272.521	4.062	109009.276
Parent	6	2.101	6.371*	95.380**	1608.421	1.881	498.122	460.171	87.472	315.391	4142.900**	126157.644
Crosses	11	2.061	5.041	127.850**	765.831* *	3.881	1770.851	1923.44**	114.411	1111.011**	4129.911**	444405.591**
Parent vs. crosses	1	1.154	5.723	94.372**	718.069	2.278	1240.817	1171.937	68.242	651.624	3507.399**	260649.816
Lines	3	0.822	0.818	142.666**	894.592	3.361	496.972	329.12	109.69	135.438	1894.258**	54175.305
Testers	2	7.571**	20.195* *	101.811**	713.361	6.25	2471.63	3099.584*	93.364	2046.786**	5792.891**	818714.488**
Lines vs. Testers	6	0.850*	2.113	129.121**	718.953	3.361	2174.197	2328.556*	123.786	1286.877**	4693.413**	514751.104**
Error	36	1.222	3.851	6.711**	442.952	3.691	1459.681	860.851	90.961	450.692	7.842	180278.011

Table 2: Mean squares from combined analysis of variance of yield and yield-related characters for nineteen maize genotypes in location 2-FUNAAB.

\*, \*\* significant at 5% and 1% probability levels, respectively.

Source of	df						Mean squ	are.				
variation		Days to	Days to	Days to	Plant	Number	Ear weight	Ear weight	Cob	Grain	1000kernel	Grain
		anthesis	silking	earleaf	height (cm)	of Kernel	with	without	weight(g)	weight(g)	weight(g)	Yield/plot (kg).
				senescence		row/ear.	Sheath(g)	Sheath(g)				
Entries	18	17.878**	21.254**	356.52**	2157.935**	6.653**	1643.85*	1638.18**	149.349**	1042.178**	5838.861**	416871.546**
Location	1	3603.432**	3760.39**	7283.525**	8306.518**	887.053**	67831.517**	44952.713**	3672.009**	22682.392**	24869.431**	9072956.637**
Replication	2	4.55	1.288	18.427	246.899	1.692	1144.653	592.143	51.284	346.713	4.506	138685.114
Genotype x Location	18	6.183	7.915**	113.324**	192.602	9.386**	434.757	362.186	101.944	139.166	394.861**	55666.356
Parent	6	19.22**	24.31**	223.746**	2827.233**	15.555**	779.314	499.461	67.388	332.139	6450.376**	132855.75
Crosses	11	8.862	17.525**	308.053**	1750.15**	1.619	2196.486**	2356.606**	207.529**	1452.079**	6033.755**	580831.866**
Parent vs. crosses	1	109.072	43.946	1686.301	2627.785	8.602	752.07	567.81	1.136	793.507	25.926	317402.8
Parent vs. location	6	8.136*	8.597	163.603**	254.617	10.333*	508.256	344.284	82.528	152.571	303.938**	61028.594
Crosses vs. Location	11	3.957	8.035**	92.847**	145.241	7.377**	398.486	335.292	93.458	140.382	479.175**	56152.949
Lines	3	8.545	4.989	622.683**	2279.567**	0.347	1295.519	858.425	400.566**	150.539	1901.887**	60215.566
Testers	2	8.584	20.612**	121.261**	1384.209**	0.68	3588.792*	3794.073**	24.928	3109.377**	9583.985**	1243750.811**
Lines vs. Testers	6	9.113	22.763**	213.003**	1607.422**	2.569	2182.867*	2626.515**	171.878*	1550.417**	6916.278**	620167.034**
Lines vs. Location	3	5.184	7.748	299.375**	217.034	2.569	127.938	480.923	52.858	31.219	830.964**	12487.877
Testers vs. Location	2	1.691	7.808	256.745**	26.273	18.597**	219.604	365.486	75.223	145.849	297.834**	58339.701
Lines vs.	6	4.059	11.115**	27.35*	148.839	2.745	593.387	468.411	119.836	193.141	363.727**	77256.569
Testers vs.												
Location												
Error	74	4.027	3.683	11.612	288.451	2.576	891.086	562.648	59.764	301.028	9.999	120411.37
*, ** significant	at 5%	and 1% probal	bility levels, re	espectively.								

Table 3: Mean square from combined analysis of variance of yield and yield-related characters for nineteen maize genotypes across two location.

\* significant at 5% and 1% probability levels, respectively. ٠,

ISSN 2229-5518			Days to		Number of	Ear weight	Ear weight				Grain
	Days to		earleaf	Plant height	Kernel	with	without	Cob	Grain	1000kernel	Yield/plot
Entries	anthesis	Days to silking	senescence	(cm)	row/ear.	Sheath(g)	Sheath(g)	weight(g)	weight(g)	weight(g)	(kg).
Lines											
FMA-0-1211	63.895a	67.848a	71.667k	163.022cde	12.333abc	71.73c	58.20cd	17.382cd	39.99cd	162.782g	799.7cd
FMS 126	63.263ab	66.728ab	87.667cde	181.575abcd	12.167abc	86.95bc	71.52cd	22.487bcd	48.67cd	174.107f	973.5cd
FMS 1 -122	63.228ab	67.520a	80.000hi	170.167bcde	13.500a	94.50bc	62.13cd	21.510cd	40.46cd	101.183k	809.2cd
FAM-98-129	62.377abc	66.377ab	76.833ij	133.572fg	12.667abc	83.74bc	68.67cd	27.765abc	40.16cd	197.633c	803.1cd
Tester											
FDM-Y-1212	60.895bcde	66.707ab	89.167cd	179.677abcd	13.167ab	103.45abc	81.16bc	23.457abcd	57.33bc	184.067d	1146.6bc
FEMY-121	60.760bcde	65.712abcd	82.833fgh	173.323bcde	12.667abc	100.62abc	82.88bc	26.243abc	55.84bc	195.850c	1116.7bc
FOM 128	58.887ef	61.828e	83.667efgh	128.383g	8.667d	80.31c	67.87cd	23.308abcd	44.48cd	174.000f	889.7cd
Crosses			U	C							
FMS 1 -122 x FEMY-121	59.843cdef	63.485de	87.000cdef	159.772de	11.333abc	95.19bc	79.49bc	22.852abcd	56.43bc	153.633h	1128.6bc
FMS 1 -122 x FOM 128	62.215abcd	67.845a	91.000c	151.300ef	12.500abc	92.26bc	78.37bc	21.992bcd	56.10bc	196.772c	1121.9bc
FMS-1-122 x FDM-Y-1212	60.595bcde	64.910bcd	75.500jk	162.460de	10.500cd	76.54c	63.21cd	18.947cd	43.84cd	179.812e	876.8cd
FAM-98-129 x FEMY 121	59.238ef	63.582cde	89.167cd	174.033bcde	12.000abc	123.98ab	104.68ab	27.073abc	77.33ab	205.403b	1546.5ab
FAM-98-129 x FOM 128	57.840f	63.130de	82.000gh	169.933bcde	11.167bc	81.18c	69.04cd	23.633abcd	45.38cd	180.183de	907.5cd
FAM-90-129 X FOM 120	57.8401	03.130de	82.000gii	109.9330cde	11.10700	01.100	09.04cu	25.055abcu	45.5800	100.10500	907.5Cu
FAM-98-129 x FDM-Y-1212	61.060bcde	68.215a	88.500cd	181.350abcd	11.500abc	74.83c	44.84d	15.315d	29.52d	121.200j	590.4d
FMS-126 x FEMY-121	59.945cdef	64.728bcd	95.130b	166.915bcde	11.833abc	137.29a	117.00a	32.353ab	84.31a	225.517a	1686.2a
FMS 126 x FOM-128	59.662cdef	63.515de	98.333ab	198.567a	11.333abc	87.10bc	62.20cd	23.707abcd	42.48cd	181.450de	849.7cd
FMS 126 x FDM-Y-1212	59.573def	64.213bcde	100.167a	187.900ab	11.667abc	94.53bc	75.11bcd	33.142a	41.88cd	135.128i	837.7cd
FMA-0-1211 x FEMY 121	59.103ef	64.495bcd	97.000ab	180.650abcd	11.333abc	75.26c	55.25cd	13.582d	41.47cd	131.883i	829.4cd
	57.10501	6.1720 <b>0</b> 0	27.000 <b>u</b> 0	100.00000000	11.555400	. 5.200	23.2304	10.0024		101.0001	027.100
FMA-0-1211 x FOM 128	58.380ef	63.593cde	85.833defg	137.383fg	12.000abc	97.72bc	73.55bcd	22.592bcd	50.88cd	183.733de	1017.7cd
FMA-0-1211 X FDM-Y-1212	61.028bcde	66.078abc	86.333defg	185.833abc	12.000abc	93.13bc	76.93bcd	20.305cd	56 15ha	156.500h	1129.1bc
ГWIA-0-1211 А ГDWI-1-1212	01.0280cde	00.078a00	oo.sssuerg	103.033800	12.000abc	73.13UC	70.950Cu	20.505cu	56.45bc	130.3000	1129.10C

Table 4: Combined mean performances of inneren marze genotype for yolume 7 Jeans April-2016 der sacross two locations.

Means with the same alphabet are not significantly different from one another down the column using Duncan's Multiple Range Tests (p < 0.05).



		Characters										
Source of variation	Df	Days to anthesis	Days to silking	Days to earleaf senescence	Plant height (cm)	Number of Kernel row/ear.	Ear weight with Sheath(g)	Ear weight without Sheath(g)	Cob weight(g)	Grain weight(g)	1000kernel weight(g)	Grain Yield/plot (kg
GCA	6	0.133**	0.002**	11.357**	38.566**	-0.008**	20.928**	9.775**	6.931**	0.966**	386.533**	17.486**
SCA	11	0.565**	2.120**	22.376**	146.552**	-0.001**	143.531**	229.318**	12.457**	138.821**	767.364**	55528.407**
ERROR	74	1.342	1.227	3.87	96.15	0.858	297.028	187.549	19.921	100.342	3.333	40137.123

Table 5: Analysis of variance for combining ability in nineteen maize genotype.

Line	Days to anthesis	Days to silking	Days to earleaf senescence	Plant height (cm)	Number of Kernel row/ear.	Ear weight with Sheath(g)	Ear weight without Sheath(g)	Cob weight(g)	Grain weight(g)	1000kernel weight(g)	Grain Yield/plot (kg).
FMA-0-1211	2.00	1.19**	-10.30**	-26.99**	-0.31**	-12.18**	-2.56**	-3.38**	-0.10**	11.61	-2.02**
FMS 126	-0.29**	-1.33**	16.40'	26.24	0.03**	24.44**	19.59**	13.54	8.10**	19.52	162.13**
FMS 1 -122	-0.73**	-0.18**	0.10**	-6.77**	0.36**	-10.76**	-12.79**	-8.26**	-5.14**	-27.12**	-102.80**
FAM-98-129	-0.98**	0.32**	-6.20**	7.52**	-0.08**	-1.51**	-4.24**	-1.90**	-2.86**	-4.01**	-57.31**
S.E.	0.66	0.63	1.13	5.66	0.53	9.95	7.9	2.57	5.78	1.05	115.66
S.E.(gi - gj) line	0.94	0.9	1.61	8.01	0.75	14.07	11.18	3.64	8.17	1.49	163.57
Tester											
FDM-Y-1212	-0.68**	-1.48**	4.82	-1.99**	0.05**	27.69	28.25	2.02**	25.42	16.34	508.46
FEMY-121	1.37**	2.07**	-4.08**	16.08	-0.36**	-18.65**	-19.89**	-2.06**	-18.49**	-45.54**	-369.95**
FOM 128	-0.69**	-0.59**	-0.74**	-14.09**	0.31**	-9.04**	-8.36**	0.04**	-6.93**	29.2	-138.51**
S.E	0.57	0.55	0.98	4.9	0.46	8.61	6.84	2.23	5	0.91	100.17
S.E.(gi - gj) tester	0.81	0.78	1.39	6.93	0.65	12.18	9.68	3.15	7.08	1.29	141.66
$\delta^2$ gca	0.399	0.009	34.071	115.699	-0.025	62.784	29.327	20.795	2.899	52.459	1159.599

# Table 6: General combining ability (GCA) effects of parents.

\*, \*\* significant at 5% and 1% probability levels, respectively.

### Table 7: Specific combining ability (SCA) effects for characters in maize.

Line x Tester	Days to anthesis	Days to silking	Days to earleaf senescence	Plant height (cm)	Number of Kernel row/ear.	Ear weight with Sheath(g)	Ear weight without Sheath(g)	Cob weight(g)	Grain weight(g)	1000kernel weight(g)	Grain Yield/plot (kg).
FMS1-122 × FEMY-121	-1.40**	-2.37**	0.17**	5.85**	-0.27**	-13.31**	-16.67**	1.16**	-16.81**	-62.56**	-336.13**
FMS1-122 × FDM-Y-1212	-1.96**	-3.08**	-13.92**	-6.85**	-1.52**	-4.25**	-1.06**	-2.57**	1.93**	51.69	38.62**
FMS1-122 × FOM-128	3.35	5.45	13.74	1.00**	1.81**	17.56**	17.73**	1.41**	14.87**	10.86	297.51**
FMS-126 × FEMY-121	1.12**	2.64	-10.31**	-33.09**	0.38**	34.27**	36.19	3.22**	30.74**	73.28	614.97
FMS-126 × FDM-Y-1212	-1.68**	-1.95**	8.65	-9.21**	0.47**	-4.91**	0.58**	8.87**	-10.18**	-45.59**	-203.73**
FMS-126 × FOM-128	0.56**	-0.68**	1.65**	42.3	-0.86**	-29.37**	-36.77**	-12.10**	-20.56**	-27.69**	-411.18**
FMA-0-1211 × FEMY-121	-0.12**	1.03**	9.73	27.38	-0.94**	-54.57**	-54.92**	-12.50**	-41.68**	-67.33**	-833.75**
FMA-0-1211 × FDM-Y-1212	1.66**	0.63**	-2.70**	19.67**	0.81**	27.51**	36.6	5.01**	32.2	43.81	644.00'
FMA-0-1211 × FOM-128	-1.55**	-1.67**	-7.03**	-47.05**	0.14**	27.06**	18.31**	7.48**	9.48**	23.52	189.75**
FAM-98-129 × FEMY-121	0.40**	-1.30**	0.40**	-0.14**	0.83**	33.61**	35.39	8.12**	27.75	56.59	554.96
FAM-98-129 × FDM-Y-1212	1.98**	4.4	7.96	-3.60**	0.25**	-18.35**	-36.12**	-11.32**	-23.94**	-49.91**	-478.88**
FAM-98-129 × FOM-128	-2.38**	-3.10**	-8.36**	3.74**	-1.08**	-15.25**	0.73**	3.21**	-3.80**	-6.69**	-76.07**
S.E. (SCA)	1.15	1.11	1.96	9.81	0.93	17.23	13.69	4.46	10.01	1.82	200.34
S.E.(sij - skl)	1.63	1.56	2.78	13.86	1.31	24.37	19.36	6.31	14.16	2.58	283.32
$\delta^2$ sca	1.69	6.36	67.13	439.66	-0.00	430.59	687.95	37.37	416.46	2302.09	166585.22

Table 8:   Estimates	of genetic comp	onents of val	nance for eleve	en characters ii							
Source of variation	Days to anthesis	Days to silking	Days to earleaf senescence	Plant height (cm)	Number of Kernel row/ear.	Ear weight with Sheath(g)	Ear weight without Sheath(g)	Cob weight(g)	Grain weight(g)	1000kernel weight(g)	Grain Yield/plot (kg).
$\delta^2 A$	1.596	0.036	136.284	462.796	-0.1	251.136	117.308	8.32	11.596	209.836	4638.396
$\delta^2 D$	1.695	6.36	67.13	439.657	-0.0023	430.593	687.95	37.371	416.463	2302.093	166585.22
$S.E.\delta^2 A$	0.099	0.002	8.517	28.924	-0.8006	15.696	7.331	5.198	0.724	289.899	13.114
$S.E.\delta^2 D$	0.565	2.12	22.376	146.552	-0.0008	143.531	229.318	12.457	138.821	767.364	55528.407
$\delta^2$ gca	0.399	0.009	34.071	115.699	-0.025	62.784	29.327	20.795	2.899	52.459	1159.599
$\delta^2$ sca	1.695	6.36	67.13	439.657	-0.0023	430.593	687.955	37.371	416.463	2302.093	166585.22
Predictability ratio( $\delta^2$ gca/ $\delta^2$ sca) Degree of	0.235	0.001	0.507	0.263	10.714	0.145	0.042	0.556	0.006	0.022	0.006
dominance $(2\delta^2 D/\delta^2 A)^{\frac{1}{2}}$	1.457	18.797	0.992	1.378	0.216	1.851	3.424	0.947	8.475	4.684	8.475

 Table 8:
 Estimates of genetic components of variance for eleven characters in maize.