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COMBINING ABILITY ANALYSIS AND DETERMINATION OF CONTROLLING GENE ACTION FOR YIELD AND OTHER KEY TRAITS OF OPEN POLLINATED MAIZE (*ZEA MAYS* L.) VARIETIES AND THEIR TOPCROSSES WITH INBRED LINE TESTERS IN UGANDA

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ABSTRACT: *The study was carried out with 38 top crosses which were evaluated with parents and checks. The objective of the study was to determine combining ability and the type of controlling gen action for yield and yield related traits of 19 OPVs using their top crosses in terms of grain yield, days to anthesis, plant height and grain texture. Line x tester analysis result of mean squares of ANOVA revealed statistically significant interaction of genotypes (female, male and crosses) with environment variations for selected traits under study. Baker's ratio of 1.00 for grain yield, suggests that additive genes were highly most important than non-additive for the control of yield. The higher value of broad sense coefficient of genetic determination (H) was high for yield, days to anthesis, plant height and grain texture. Female parent KC2014 and male parent inbred line TA (CML536) had significantly positive GCA effect for grain yield. These parents were the best general combiners for grain yield across sites. Similarly, female parent OPVs (MM3, Longe 5, Longe 5D, SITUKA MI and VP MAX) and male parent inbred line TB (CML202) had highly significant negative GCA for days to anthesis, indicated that these parents can breed for earliness. Therefore, the exhibited variations between OPVs in terms of the GCA and SCA effects can be exploited to produce topcrosses which will help in selection of parents for hybrid development and variety improvement.*

KEY WORDS*:* broad and narrow sense coefficient of genetic determination, combining abilities, open pollinated varieties, topcrosses

INTRODUCTION

The performance of a hybrid is related to the general (GCA) and specific (SCA) combining abilities of the parent lines involved in the cross [11]. The concept of combining ability was first introduced by [11]. It is categorized into GCA, that measures the average performance of a line in all its crosses, expressed as a deviation from the overall mean of all the crosses, and SCA, the deviation of the line's performance from the expected value. One of the mating designs used to generate crosses to study combing ability is line x tester crossing method. It is used to breed both self and cross-pollinated plants and to estimate favourable parents and crosses, and their combining abilities [7]. [9] Defined general combining ability as the ability of parents or cultivars to combine amongst each other during the process of hybridization so that favorable genes/characters are transmitted to their progeny. [1]noted that GCA results from the additive effects of many alleles at different loci that cumulatively enhance performance in different agro-ecologies. [8] reported that significant values for GCA and SCA may be interpreted as indicating the performance, respectively, of additive or non-additive (i.e. dominant or epistatic) effects.

The performance of parent may not necessarily reveal it to be a good or poor combiner. Therefore, gathering information on nature of gene effects and their expression in terms of combining ability is necessary. General combining ability (GCA) is attributed to additive gene effects and additive x additive epistasis and is theoretically fixable. On the other hand, specific combining ability attributable to non-additive gene action may be due to dominance or epistasis or both and is non-fixable. The presence of non-additive genetic variance is the primary justification for initiating the hybrid programme [2,10]. Narrow sense coefficient of genetic determination (NS-CGD) is the proportion of total phenotypic variation that is due to the additive effects of genes whereas Broad sense coefficient of genetic determination (H) is a value that expresses the degree of this correspondence. Specifically, BS-CGD (H) is the percentage of the phenotypic variance that is attributable to differences among individuals in genotypic value [5]. Therefore, this study was intended mainly to determine the general and specific combining abilities and additionally to calculated narrow and broad sense heritability of 19 local and introduced open pollinated maize varieties in Uganda.

MATERIALS AND METHODS

The research was conducted at four sites: i) The National Crops Resources Research Institute (NaCRRI) Namulonge (Central Uganda) ii), National Semi-Arid Resources Research Institute (NaSARRI) Serere (Eastern Uganda) iii) Bulindi Zonal Agricultural and Development Research Institute (Western Uganda) and iv) Ngetta Zonal Agricultural and Development Research Institute, Ngetta (Northern Uganda). The description of the study sites for this study was conducted in 3 optimum sites and one site that expected random drought.

Genetic materials

Nineteen open pollinated maize varieties and two inbred line testers sourced from East African Countries (Uganda, Tanzania, Kenya and Ethiopia) and CIMMYT, respectively, were used in this study with their identities. The heterotic groups of the 19 OPVs were not known while the two inbred lines namely CML536 and CML202 were from the heterotic groups A and B, respectively. OPVs are random mating populations and hence heterosis may be expressed when testcrossed with the inbred lines. Therefore, the 19 OPVs were test crosses with these two inbredline to produce 38 topcrosses (MM3/CML536, MM3/CML202, Longe4/CML536, Longe4/CML202, Longe5/CML536, Longe5/CML202, Longe5D/CML536, Longe5D/CML202, Longe5RS/CML536, Longe5RS/CML202, SITUKA/CML536, SITUKA/CML202, STAHA/CML536, STAHA/CML202, TMV1/CML536, TMV1/CML202, ECAVL1/CML536, ECAVL1/CML202, ECAVL2/CML536, ECAVL2/CML202, ECAVL17/CML536, ECAVL17/CML202, ECAVL18/CML536, ECAVL18/CML202, KakSyn-II/CML536, KakSyn-II/CML202, Ambsyn2/CML536, Ambsyn2/CML202, Ambsyn5/CML536, Ambsyn5/CML202, KC2014/CML536, KC2014/CML202, SUWAN/CML536, SUWAN/CML202, VP MAX/CML536, VP MAX/CML202, OUI-1/CML536 and OUI-1/CML202)

Experimental design and data collection

The 38 topcross hybrids, their 19 OPV parents and 8 checks (including single, double, 3-way and varietal cross hybrids) were evaluated in four different agro-ecologies of Uganda. The experimental design used was 5 x 13 α-Lattice design with two replications. Two row plots of 5 m long were used with an inter-row spacing of 0.75 m and intra-row spacing of 0.25 m.

Statistical analysis

The statistical analysis for within location of selected traits was carried out using REML in GENSTAT 12th edition to get the predicted means of the topcrosses and $MS_{LEE.}$ The means of 38 topcrosses and MS_{LEE} for 4 locations were retrieved. The retrieved means were subjected to GENSTAT 12th edition for further ANOVA for combining ability to determine the effects of location, females, males, hybrid performance and their interactions. The following North Carolina (NDC) II linear model was used:

$$Y_{ijk} = \mu + Loc_k + GCA_f + GCA_m + SCA_{fxm} + \mathcal{E} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots [5.1]$$

Where: Y_{ijk} is the observed value of i^{th} and j^{th} parent crosses in k^{th} Location, μ is over all mean crosses, Loc_k is location effects, GCA_f is the General combing ability of female parent, and GCA_m is the general combining ability of male parent, SCA_{ij} is specific combining ability of the interaction effect between the i^{th} female and the j^{th} male and Ɛ is pooled error.

The Mean Square (MS) of pooled error for combined ANOVA was obtained by the following formula: First the mean squares $MS_{LEE}/Rep = M_1, M_2, M_3$ and M_4 and the crossponding degree of freedom (df_1, df2, df_3 and df_4) for each of the four locations were determined and then the MS of pooled error = (M_1 x df_1 + M_2 x df_2 + M_3 x df_3 + M_4 x df_4)/ total degree of freedom (df_1 + df_2 + df_3 + df_4). In the analysis, location was considered as random effects, and the male, female parents and their crosses were considered as a fixed effect. The 19 female OPV parents as lines and the two male inbred lines as testers were used. The mean squares were determined for location, female and male and the effects of their interaction. The female, male, crosses and their partitions were tested against their respective interaction with location, and interactions with location term together with random effect tested against pooled error by using F-test. General combining ability of females and males (GCAf, GCAm) and specific combining ability of female x male (SCA) effects were calculated by using the following formula:

$$GCA_f = \mu_f - \mu,\ GCA_m = \mu_m - \mu, SCA_{ij} = Y_{ij} - [\mu + GCA_f + GCA_m] \quad \ldots\ldots\ldots\ldots\ldots [5.2]$$

Where: μ_f is the mean of female parent, μ_m is the mean of male parent, $[\mu + (GCA)_f + (GCA)_m]$ is the predicted or expected value of the cross based on 2 GCA of its parents (GCA_f, GCA_m).

The significance of GCA_f and GCA_m effects were obtained by computing standard error (SE) for female and male parents separately and tested against t-test to check whether it was different from zero or not using the pooled error and degrees of freedom. The SE of female and male were calculated as:

$$SE\ female = \sqrt{\frac{pooled\ error}{number\ of\ males\ x\ number\ locations}} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots [5.3]$$

$$SE\ male = \sqrt{\frac{pooled\ error}{number\ of\ females\ x\ number\ locations}} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots [5.4]$$

And also the SE of specific combining ability of the crosses were determined by:

$$SE\ of\ SCA_f = \sqrt{\frac{pooled\ error}{number\ of\ location}} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots [5.5]$$

Genetic variances and components across sites were determined as follows: The relative importance of GCA and SCA was determined using Baker's ratio $(2GCA/(2GCA+SCA))$. The broad-sense and narrow-sense coefficient of genetic determination were calculated using the formulas:

$$\mathrm{BS.CGD} = \frac{(\sigma^2_{\mathrm{GCA_f}}+\sigma^2_{\mathrm{GCA_m}}+\sigma^2_{\mathrm{SCA_{fxm}}})}{(\sigma^2_{\mathrm{GCA_f}}+\sigma^2_{\mathrm{GCA_m}}+\sigma^2_{\mathrm{SCA_{fxm}}}+((\sigma^2_{\mathrm{GCA.Loc_{(f)}}})/4)+((\sigma^2_{\mathrm{SCA.Loc_{(fxm)}}})/4)+((\sigma^2_{\mathrm{MSpooled\ error}})/4)} \ldots.\ [5.6]$$

$$\mathrm{NS.CGD} = \frac{(\sigma^2_{\mathrm{GCA_f}}+\sigma^2_{\mathrm{GCA_m}})}{(\sigma^2_{\mathrm{GCA_f}}+\sigma^2_{\mathrm{GCA_m}}+\sigma^2_{\mathrm{SCA_{fxm}}}+((\sigma^2_{\mathrm{GCA.Loc_{(f)}}})/4)+((\sigma^2_{\mathrm{SCA.Loc_{(fxm)}}})/4)+((\sigma^2_{\mathrm{MSpooled\ error}})/4)} \ldots.\ [5.7]$$

In all the calculations above, variance component with negative values are replaced with zero since variances are never negative.

RESULTS

The mean squares for genotypes, estimates of genetic variance and components across four sites for days to anthesis, grain yield, plant height and grain texture in season 2015B are presented in Table 1. The mean square and the variance component due to male parent (tester) was larger than the female parent (OPVs) for all selected traits except for gran texture. The effect of location was significant for all traits. The contribution of male parents (testers) to the total variation was significant for days to anthesis and plant height. The interaction between female parents and male parents (SCA) exhibited a significant contribution to the variation only for grain texture. There were no significant ($P > 0.05$) differences observed in $\mathrm{SCA}_{\mathrm{f\ x\ m}}$ for days to anthesis, grain yield and plant height. Baker's ratio for grain yield was highest.

Specific combining ability ($\mathrm{SCA}_{\mathrm{f\ x\ m}}$) of topcrosses for four selected traits across sites are presented in (Table 2) and General combining ability (GCA) of female and male are presented in (Table 3) below. The highest and lowest significant positive effect of specific combining ability in terms of days to anthesis was observed for Ambasyn2 x Tester A (1.06) and SITUKA MI x Tester B (0.54) respectively. Similarly, in terms of grain texture the highest negative value was obtained when ECAVL 17 test crossed by tester A. The highest positive GCA of female and male parents in terms of grain yield observed was 0.78 and 0.36 respectively. And also both significant positive and negative was seen for all four selected traits.

DISCUSSION

The observed analysis result of mean squares of ANOVA revealed statistically significant interaction of genotypes (female, male and crosses) with environment variations for days to anthesis, grain yield, plant height and grain texture, indicating that the performance of genotypes are inconsistent across the different locations/environments. However, grain yield for crosses across location was not significantly affected by the effects of $\mathrm{SCA}_{\mathrm{f\ x\ m}}$ * location interaction indicating that properly selected parents can be used successfully to improve this trait. The type of gene action involved in the variations observed among different traits was determined using estimates of genetic variance components. The observed Baker's ratio of 1.00 for grain yield, suggests that additive genes are more important for controlling yield compared to non-additive gene actions. The higher value of broad sense coefficient of genetic determination (H) for yield, days to anthesis, plant height and grain texture, suggests that environmental effects had small role in the variation observed for the trait. This result points to less need for using many locations and replications in this type of trials. The high magnitude of the narrow-sense coefficient of genetic determination for all presented traits suggests smaller environmental effects. Therefore, higher value for both coefficients of genetic determination is an indication that crop improvement is possible through selection.

The results of this experiment indicated the presence of poor (non-significant SCA) for grain yield thus there were no significant differences among crosses. This non-significant differences among the crosses could be an indication that the parents used to produce these crosses are related. Therefore, the possibility of selection of parents which can be involved in making topcross hybrids that are adapted to the different agro ecologies of Uganda is low. Even though the expressed additive (GCA) and non-additive gene effects (SCA) seem to be small on the average, they may be very important for specific cross combinations [5]. For example, the GCA of crosses from parent KC2014 was significant positive for grain yield indicating the increased concentration of favorable alleles. [4] suggested that the performance of a single-cross progeny could be adequately predicted on the basis of GCA, if SCA is not significant. On the other hand, [6], reported that, on average, hybrids produced by crossing inter-population lines have more positive SCA effects than those produced by crossing intra-population lines which tend to have more negative SCA effects. Highly significant differences due to specific combining ability were observed for days to anthesis and grain texture, implying the importance of non-additive gene effects in addition to additive gene effect for the control of these traits.

Open pollinated female parent KC2014 and male inbred line TA (CML536) had significantly positive GCA effect for grain yield. These parents were the best general combiners for grain yield across sites, suggesting that they can be used as parents to improve yield. The remaining parents exhibited either non-significant positive or negative GCA effects for grain yield, meaning that their contribution to yield was average or below average. The line KC2014 exhibited a highly significant positive GCA for yield and therefore a contribution to improved yield, but also showed consistently stronger undesirable GCA effects for plant height and grain texture, implying contribution risk of lodging and adding undesirable GCA effect among progeny. Female parent OPVs (MM3, Longe 5, Longe 5D, SITUKA MI and VP MAX) and male parent inbred line TB (CMLA202) had highly significant negative GCA for days to anthesis is an indication that these parent can breed for earliness. This finding was in line with [3] who reported the combining abilities of OPVs for different agronomic traits using their topcrosses.

CONCLUSION AND RECOMMENDATIONS

The exhibited variations between OPVs in terms of the GCA effects can be exploited to produce topcrosses which will help in selection of parents for hybrid development and variety improvement. In this study, for most of the traits, additive variances were found to be important and with predominant role than non-additive. Therefore, improvement of these traits could be achieved through selection. The OPVs KCL2014, MM3, Longe 5, Longe 5D, SITUKA MI and VP MAX are recommended for use in a breeding programme for the development of inbred line and hybrid development. However, further work is necessary to validate the suitability of these OPVs under study and other OPVs through crossing them with other inbred lines from different sources then re identifying their combing abilities.

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Illustrations

Table 1: Mean squares of genotype, estimates of genetic variance and components across sites for selected traits in Uganda, 2015B

	AD (Days)			GY (t ha^{-1})			PH (cm)			Tex (Score 1-5)		
SOV	d.f.	MS	σ^2	d.f.	MS	σ^2	d.f.	MS	σ^2	d.f.	MS	σ^2
Loc	3	554.43 ***	-	3	264.21 ***	-	3	36539.67 ***	-	3	2.97 ***	-
GCAf	18	17.85 ***	1.99	18	1.20 ns	0.05	18	530.81 ***	54.23	18	1.41 ***	0.16
GCAm	1	219.65 **	2.86	1	19.60 ns	0.20	1	10693.89 **	136.31	1	0.12 ns	-0.003
SCAf x m	18	2.41 ns	0.2	18	0.58 ns	-0.01	18	164.27 ns	15.16	18	0.30 **	0.04
Loc * GCAf	54	1.89 ***	0.81	54	0.82 **	0.17	54	97.01 ns	-10.28	54	0.11 ***	0.02
Loc * GCAm	3	2.04 ***	0.09	3	4.10 ***	0.19	3	334.27 *	11.40	3	0.38 ***	0.02
Loc * SCAf x m	54	1.61 ***	1.33	54	0.62 ns	0.15	54	103.63 ns	-13.95	54	0.13 ***	0.07
Pooled Error	140	0.27	0.27	150	0.47	0.47	173	117.58	117.58	173	0.06	0.06
BR			0.96			1.00			0.93			0.79
NS-CGD			0.85			0.51			0.80			0.66
BS-CGD			0.89			0.51			0.86			0.83

*, **, ***Statistically significant at $\alpha = 0.05, 0.01$ and 0.001 respectively, ns- non significant, AD-Days to anthesis, GY-grain yield, PH-Plant height, Tex- Grain texture, SOV- Source of variation, d.f.- degree of freedom, GCAf- General combining ability of female, GCAm- General combining ability of male, Loc- Location, SCAfxm- Specific combining ability of crosses, BR-Baker's ratio, NS-CGD narrow sense coefficient of genetic determination, BS- Broad sense coefficient of genetic determination, σ^2- Variance component

Table 2: Specific combining ability (SCA $_{f\ x\ m}$) of topcrosses for four selected traits across sites in Uganda, 2015B

X	SCA f x m (Topcrosses)							
	Male (inbred line testers)							
Female	AD (Days)		GY (t ha-1)		PH (cm)		Tex (Score 1-5)	
(OPVs)	TA	TB	TA	TB	TA	TB	TA	TB
MM3	0.51	-0.51	0.04	-0.04	-7.09	7.09	0.00	0.00
Longe 4	-0.35	0.35	-0.46	0.46	-4.53	4.53	0.04	-0.04
Longe 5	-0.84 ***	0.84 **	0.01	-0.01	-4.87	4.87	0.09	-0.09
SITUKA MI	-0.54 *	0.54 *	0.47	-0.47	7.72	-7.72	-0.22	0.22
STAHA	-1.02	1.02 ***	-0.07	0.07	-1.30	1.30	0.26 *	-0.26 *
ECAVL1	-0.57 *	0.57 *	-0.11	0.11	0.83	-0.83	0.17	-0.17
ECAVL17	0.12	-0.12	-0.07	0.07	-1.94	1.94	-0.42 ***	0.42 ***
Ambsyn2	1.06 ***	-1.06 ***	-0.29	0.29	-2.12	2.12	-0.01	0.01
Ambsyn5	-0.10	0.10	0.53	-0.53	7.52	-7.52	0.36 **	-0.36 ***
KC2014	0.25	-0.25	0.00	0.00	-5.69	5.69	0.11	-0.11
SUWAN	0.16	-0.16	-0.41	0.41	-5.13	5.13	-0.29 *	0.29 *
VP MAX	1.05 ***	-1.05 ***	0.11	-0.11	3.23	-3.23	0.12	-0.12
SE	0.26	0.26	0.34	0.34	5.42	5.42	0.12	0.12

*, **, *** Statistically significant at $\alpha = 0.05, 0.01$ and 0.001 respectively AD-Days to anthesis, GY-grain yield, PH-Plant height, SOV- Source of variation, SCA_{fxm}- Specific combining ability of crosses, SE-standard error of the mean, TA- Tester A, TB- Tester B, Tex- Grain texture,.

Table 3: General combining ability effects of male and female parents for selected traits across sites in Uganda, 2005B

	GCA_f			
Female Parents (OPVs)	AD (days)	GY (t ha^{-1})	PH (cm)	Tex (Score 1-5)
MM3	-2.41 ***	-0.55 *	6.48	-0.06
Longe 5	-1.16 ***	0.15	1.26	0.18 *
Longe 5D	-1.75 ***	-0.40	6.67	0.09
SITUKA MI	-1.92 ***	0.03	0.14	0.04
STAHA	1.21 ***	0.29	11.98 **	0.65 ***
TMV1	0.81 ***	0.14	6.08	-0.92 ***
ECAVL1	-0.57 ***	0.44	0.12	0.38 ***
ECAVL2	1.57 ***	0.31	6.99	-0.06
ECAVL17	1.25 ***	0.10	4.45	0.69 ***
ECAVL18	1.68 ***	0.16	0.67	-0.70 ***
Ambsyn2	3.38 ***	-0.78 ***	8.35 *	-0.31 ***
Ambsyn5	0.33	-0.60 *	-9.02 *	0.17 *
KC2014	0.24	0.73 ***	19.90 ***	0.57 ***
SUWAN	-0.84 ***	-0.05	-1.66	-0.44 ***
VP MAX	-1.32 ***	-0.07	-14.15 ***	0.17 *
SE	0.19	0.24	3.83	0.08
	GCA_m			
Male Parents	AD (days)	GY (t ha-1)	PH (cm)	Tex (Score 1-5)
TA	1.20 ***	0.36 ***	8.39 ***	0.03
TB	-1.20 ***	-0.36 ***	-8.39 ***	-0.03
S.E.	0.06	0.08	1.24	0.03

*, **, ***Statistically significant $\propto = 0.05, 0.01$ and 0.001 respectively, ns-statistically non-significant, AD-Days to anthesis, GY-grain yield, PH-Plant height, TA- Tester A, TB- Tester B, Tex- Grain texture, GCA_f- General combining ability of female, GCA_m- General combining ability of mal, SE-standard error of the mean.