GENETIC STUDIES OF AGRONOMIC AND KERNEL QUALITY TRAITS IN WHITE MAIZE (*Zea mays* L.) INBRED LINES

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ABSTRACT
Field experiments were conducted at National Horticultural Research Institute, Bagauda (11°33´N; 8°23´E) in the Sudan Savannah and Institute for Agricultural Research, Samaru (11⁰11´N; 07⁰38'E) in the Northern Guinea Savanna ecological zones of Nigeria. The experiments were conducted between July-October, 2014 rainy season to estimates mean squares for general combining ability (GCA), specific combining ability(SCA) and interaction between general combining ability and location (GCA x location) and specific combining ability and location Interactions (SCA x location) for agronomic traits and kernel quality traits. The study comprised of 15 hybrid lines, 6 parental lines along with 4 checks which were laid out in partially balanced lattice design with three replications. Analysis of variance revealed significant (P≤ 0.01) GCA for days to maturity (27.74), ear length (8.85cm) , ear diameter (22.25cm), plant height (1501.60cm), field weight (1.70kg), moisture content at harvest (16.48%) and yield (10947553.16 kgha⁻¹) indicating the additive gene action contributing the expression of these traits. The mean squares due to SCA were highly significant (P≤ 0.01) for days to maturity (7.49), ear length (10.06cm), ear diameter (26.96cm) and moisture content at harvest (6.78%) indicating the preponderance of non-additive gene action in the expression of these traits. The mean squares for GCA× location and SCA× location were not significant for all traits except percent whole kernel which shows highly significant GCA × location interaction (2077.97%) and this indicated that, different parental genotypes behaved differently with respect to this trait under different location.
KEYWORDS: Agronomic traits, Genetic, General Combining Ability, Inbred lines, Kernel Quality and Specific Combining Ability

INTRODUCTION

Maize or corn (*Zea mays* L.), belongs to the grass family Poaceae and tribe Maydeae, originated 5000 to 10,000 years ago (Hallauer, 1997; Paliwal and Smith, 2002). The origin of maize is controversial; however, it is believed to have originated in the mid-altitude regions of Mexico and Guatemala or Mesoamerica (Paliwal and Smith, 2002). It is one of the three most important cereal crops in the world together with wheat and rice. In industrialized countries, it is largely used as livestock feed and as a raw material for industrial products, while in developing countries, it is mainly used for human consumption. Africans consume maize as a starchy base in a wide variety of porridges, pastes, grits, and beer. In sub-Saharan Africa, it is a staple food for an estimated 50% of the population. It is an important source of carbohydrate, protein, iron, vitamin B, and minerals (Dilip *et al.,*2013). It is fast becoming a very important commodity in animal feed, food and beverage industries (USAID, 2010). Worldwide maize is cultivated in an area of 159 million hectares with a production of 796.46 million metric tons (USDA, 2010). Accordingto FAOSTAT (2014). The area in West African countries planted to maize increased from 3.2 million hectares in 1961 to 8.9 million hectares in 2005. The United States is the world's largest producer and exporter of maize with a corn production volume amounting to about 385 million metric tons with total of 96,000,000 acres of land in 2017-2018 (USDA 2018). Other top producing countries include China, Brazil, Mexico, Argentina, India and France. Nigeria is the 10th largest producer of maize in the world, and the main producing country in tropical Africa (USAID, 2010).

It is cultivated both as rain fed and under irrigation on more than 5 million hectares, spread through the six agro-ecological zones and maize production is put at about 26 million tons from 3,845,000 hectares (FAO, 2009). In Africa, maize is grown by small- and medium-scale farmers who cultivate 10 hectares or less (DeVries and Toenniessen, 2001) under extremely low-input systems where average yield is 1.3 tons ha^{-1} (Bänziger and Diallo, 2004). It is essential to have knowledge of the nature and magnitude of genetic variability created through hybridization for various traits, since the nature and magnitude of variability are pre-requisite for any crop improvement which would assist breeders in planning successful breeding program. Estimation for General and Specific Combining Ability mean squares are useful for detecting the degree of variability among genotypes. The objectives of the present study were (i) to estimate the variability and type of gene action in the white maize inbred lines for General Combining Ability (GCA), Specific Combining Ability (SCA), General Ability by location (GCA x location) and Specific Combining Ability by location Interactions (SCA x location) for agronomic and kernel quality traits and (ii) to evaluate suitable selection criteria for further breeding.

MATERIALS AND METHODS
The experiment consists of 6 white maize inbred lines which were crossed using half diallel mating design. The

15 hybrids, 6 parents and 4 checks were evaluated at National Horticultural Research Institute, Bagauda Research Farm (11°33´N; 8°23´E) in the Sudan Savannah and Institute for Agricultural Research Farm, Samaru (11^{0}11´N; 07^{0}38′E) in the Northern Guinea Savanna ecological zones of Nigeria in a 5 × 5 partially balanced lattice design with three replications between July to October, 2014. Each plot consists of two rows 4 m long, with inter and intra row spacing of 0.75 m x 0.25 m and 1m alleys respectively. All agronomic practices were kept uniform in all plots. Data were taken on five centered plants for observations and measurements leaving the plants on either end of the plot to avoid the border effect. Data were recorded for agronomic traits (days to 50% tasselling (pollen shed) , days to 50% silking, anthesis silking interval, plant height, days to maturity, ear height, % whole kernel, % kernel without pericarp damage, density, milling test, moisture content at harvest and grain yield. Analysis of variance was computed using computer statistical software (SAS Institute, 2004) at both 5% and 1% probability level of significant.

Combining Ability estimation
Plot-mean values were used in the Diallel analysis of fixed effects method 2 model 1 (Griffing's. 1956).The model below was used for combining ability analysis across the location:

$$y_{ijkt} = \mu + g_i + g_j + S_{ij} + l_t + (gl)_{it} + (sl)_{ijt} + r_{kt} + e_{ijkt}$$

Where:

y_{ijk} = The yield of a cross between i^{th} and j^{th} parent in the kth replication in the tth location.

μ= Overall mean

g_i = Effect common to all progeny of the ith parent

g_j = Effect common to all progeny of the jth parent

S_{ij} = Effect specific to the progeny of mating i^{th} and j^{th} parents

l_t = The average effect of the tth location

$(gl)_{it}$ =Genotype x location interaction effect in the ith parent in that location

$(gl)_{jt}$ =Genotype x location interaction effect in the jth parent in that location

$(sl)_{ijt}$ =Specific effect of mating i^{th} parent and j^{th} parent in that location.

r_{kt} =Effect of the k replication in t location

e_{ijt} =Experimental error

$i =$ 1-6 parents
j = 1-6 parents
k = 1-3 replications
l =1-2 locations

RESULTS AND DISCUSSION
The mean squares due to GCA were highly significant (P≤ 0.01) for days to maturity (27.74), ear length (8.84cm) and ear diameter (22.25cm) and significant (p≤ 0.05) for plant height (1501.60cm), field weight (1.70kg), moisture content at harvest (16.48%) and yield (10947553.16kgha^{-1}) indicating that the additive gene action contributed more to the expression of these traits . The finding of the present study corroborate with the work of Shushay *et al.* (2013) who reported significant mean squares due to GCA of lines for grain yield, plant height, ear height and days to anthesis in maize genotypes. The mean squares for SCA were highly significant (P≤ 0.01) for days to maturity (7.49), ear length (10.06cm), ear diameter (26.96cm) and moisture content at harvest (6.78%) in maize indicating the preponderance of non-additive gene action in the expression of these traits. Hossein *et al.* (2014) reported significant mean squares due to GCA and SCA for days to silking, plant height, ear height, 1000-kernel weight, ear length, number of rows per ear, number of leaf and kernel yield maize. Melkamu *et al.*(2013) reported maize lines shows significant both GCA and SCA for Grain yield, Number of ears per plant, Days to anthesis, days to silking, anthesis silking interval, ear height, plant height, ear position, plant aspect and ear aspect. In quality protein maize diallel analysis, Demissew (2014) reported GCA mean squares were significantly different (P≤ 0.01) for grain yield , Number of ears per plant, Days to anthesis, days to silking, anthesis silking interval, ear height, plant height, ear position, plant aspect and ear aspect while mean squares for SCA were significantly different for Grain yield, number of ears per plant, days to anthesis, days to silking, ear height, plant height, Ear position, Plant aspect and Ear aspect. The mean squares for GCA× location and SCA× location were not significant for all traits except percent whole kernel which showed highly significant GCA × location interaction. Similar result was reported by Bitew *et al.* (2017) for grain yield, number of ears per plant, days to anthesis, days to anthesis,

days to silking, ear height, plant height, ear position, plant aspect and ear aspect in maize. The GCA values where less than the SCA values for most of kernel quality and agronomic traits in maize lines depicting the importance of non-additive gene action over additive. This agrees with the work of Naazar *et al.*, (2001). The significant (P≤ 0.05) GCA x location interaction for percent whole kernel suggests that different parental genotypes behaved differently with respect to this trait under different location. This demonstrated the need to select different inbred for hybrid production for specific locations for the affected trait. The non-significant SCA x location interaction for all traits indicated good hybrid performance for the traits repeated over different locations, revealing that these hybrids should be produced over wide range of environment. The GCA to SCA mean square ratio were less than unity for some studied traits. This suggested that non-additive gene action could be more important than additive gene action. The importance of additive gene action for different traits has been reported in several investigators in different times in maize (Dagne *et al.*,2008; Legesse *et al.*,2009; Nzuve *et al.*,2013; Hossein *et al.*,2014; Mwai *et al.*, 2015).

CONCLUSION
Significant mean squares due to GCA for all traits and SCA for the most of the traits studied were detected, indicated that both additive and non-additive gene actions contribute to the expression of the traits. The significant GCA x location interaction for percent whole kernel suggesting that different parental genotypes behaved differently with respect to this trait under different locations. This demonstrated the need to select different inbred lines for hybrid production for specific locations for the affected trait. The non-significant SCA x location interaction for all traits indicated a good hybrid performance for the traits repeated over different locations which revealed that these hybrids should be produced over wide range of environment.

Table 1: Origin and Descriptions of the Genotypes

Genotype	Pedigree	Colour	Source, Description
P1	P43SRC9FS100-1-1-8-#1-B1-13-B1-B-B-B-B-B-B-B-B	White	IITA, Dent
P2	1368× HI ×4269-1368-7-2-B-B-B-B-B	White	IITA, Dent
P3	9071-B-B-B	White	IITA, Dent
P4	(TZMI501×KU1414×501)-1-4-3-1-B-B-B-B-B-B-B-B	White	IITA, Dent
P5	1368×ICAL224-1×1368-3-1-B-B-B-B-B-B-B-B-B-B-B	White	IITA, Dent
P6	TZL-COMP3-C2-S2-34-4-1-2-B-B-B-B-B-B-B-B	White	IITA, Dent

Table 2: Format of analysis of variance (ANOVA) for combining ability of maize inbred lines across locations in 2014 rainy season.

Source of variation	Df	MS	EMS
Crosses	$n[(n-1)/2]-1$	m_c	$\sigma_e^2 + r\sigma_{cl}^2 + rl\sigma_c^2$
GCA	$(n-1)$	m_g	$\sigma_e^2 + r\sigma_{cl}^2 + rl\sigma_s^2 + r(n+2)\sigma_g^2$
SCA	$n(n-3)/2$	m_s	$\sigma_e^2 + r\sigma_{cl}^2 + rl\sigma_s^2$
Crosses $\times$ *Location*	$(l-1)(n[n-1)/2]-1)$	m_{cl}	$\sigma_e^2 + r\sigma_{cl}^2$
GCA $\times$ *Location*	$(n-1)(l-1)$	m_{gl}	$\sigma_e^2 + r\sigma_{sl}^2 + r(n+2)\sigma_{gl}^2$
SCA $\times$ *Location*	$(n(n-3)/2)(l-1)$	m_{sl}	$\sigma_e^2 + r\,\sigma_{sl}^2$
Error	$l(r-1)(n[(n+1)/2]-1)$	m_e	σ_e^2

Key: n=parent, c=crosses, g=gca, s=sca, l=location, and e=error.

Table 3: Mean squares analysis for combining ability for fourteen traits of maize combined across locations (Samaru and Bagauda) in 2014

Source of variation	Df	Days to Maturity	Plant Height (cm)	Ear Height (cm)	Ear Length (cm)	Ear Diameter(cm)	Field Weight (kg)	% whole kernel	% kernel with out Pericarp damage	Milling test	%Moisture content at harvest	100- grain Weight (g)	Volume (m³)	Density (kgm⁻³)	Grain Yield (kgha⁻¹)
Location	1	0.02	85.18	36.91	1.83	176.44	26.48	58652.72**	2061.13**	5.75	16.32*	8406167	100.05**	530392.70*	3603389
Replication (loc)	4	26.26*	1468.47**	397.95*	6.4	131.4	20.3**	3406.72**	205.21	0.66	23.32**	5555291.00**	37.51*	183942.3	20276536.30**
Parent	5	58.11**	3604.91**	839.97*	51.10**	712.05	69.76	251.36	1040.56	55.04**	4.59	11812663	46.1	383970.2	49182618.40**
Parent × Location	5	4.24	93.87	115.99	0.47	534.4**	62.78**	837.76	494.84	2.99	7.53	5338917	47.56**	419103.7	3676300
Crosses	14	14.73**	784.02*	241.92	9.63**	25.28**	1.19*	375	319.47	5.93	10.25**	595657.60*	13.21	16853.09	7674936.08*
GCA	5	27.74**	1501.60*	282.4	8.85**	22.25**	1.70*	566.02	310.98	3.01	16.48*	554271.7	7.21	10872.15	10947553.16*
SCA	9	7.49**	385.36	219.43	10.06**	26.96**	0.91	268.88	324.19	7.55*	6.78**	618649.8	16.53	20175.83	5856815
Crosses × Location	14	0.33	320.57	172.84	0.21	0.01	0.4	1156.5**	141.03	2.49	1.32	398421.1	15.75	21807.16	2572765
Parent × Cross × Location	1	3.78	701.42	170.87	2.78	432.02	60.55	150.52	1020.51*	0.02	3.37	871371.6	59.76*	459600.63*	4409629
GCA × Location	5	0.38	229.83	188.49	0.17	0.01	0.35	2077.97**	80.04	3.38	0.48	309116.1	13.99	14039.34	2238177
SCA × Location	9	0.3	370.98	164.15	0.23	0.03	0.43	644.57	174.92	2	0.26	448035	16.72	26122.61	2758646
Error	80	3.27	83.8	49.2	1.19	55.97	6.69	128.85	84.99	1.22	1.3	1030289	4.96	39426.3	724272

*, ** significant at 5% and 1% levels of probability respectively

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