Analyzing combining abilities and heterotic groups among Ghanaian maize landraces for yield and resistance/ tolerance to Maize Streak Virus Disease

Oppong Allen[1],*, Appiah-Kubi David[1], Ifie E. Beatrice [2], Abrokwah A. Linda[1], Ofori Kwadwo[2], Offei K. Samuel[2], Adu-Dappah Hans[1], Mochiah B. Moses[1], Warburton L. Marilyn[3]

[1] CSIR—Crops Research Institute, P.O. Box 3785 Kumasi, Ghana.
[2] West Africa Centre for Crop Improvement (WACCI), PMB 30, University of Ghana, Legon. Ghana
[3] USDA-ARS Corn Host Plant Resistance Research Unit (CHPRRU), PO Box 9555, Mississippi State, 39762, USA
* Corresponding Author : E-mail: alnopp@yahoo.co.uk

KeyWords: *Landraces, hybrid, yield, combining abilities, MSVD.*

Abstract

Maize is an important cereal crop in Ghana. Yields in farmer fields have always been low because of over reliance on unimproved local landraces for cultivation. This study was conducted to determine if the productivity of these landraces can be improved by developing hybrid varieties that combine high yield and resistance to the Maize Streak Virus Disease (MSVD). Seventeen local landrace populations were assembled and then crossed with 5 exotic inbred lines (CML202, CML442, CML444, TZEI 23 and TZEI17). A crossing block using the North Carolina Design II was used to generate F^1 top-cross hybrids which were evaluated in multi-locational trials for two years. GCA, SCA and heterosis were estimated and heterotic groups assigned to the landraces. This study was able to identify high heterosis among some of the top-cross hybrids and assigned some of the landraces into heterotic groups. Highly significant GCA and SCA effects were identified which implies MSVD incidence/resistance as well as yield related traits can be improved. CML442, CML444 and TZEI17 contributed positively to yield increases as well as improved tolerance/resistance to MSVD. Landraces LA3, LA80, LA76, and LA457 displayed highly significant SCA effects for yield, which suggests dominance and epistatic gene action. The high yielding hybrids identified show that some inbred lines and landraces combinations can contribute to significantly raise farmers' yields and improve resistance/tolerance to MSVD in Ghanaian environments.

Introduction

Maize (*Zea mays* L) is a major cereal crop and an important component of human and animal diets as well as raw material for industry (http://www.iita.org/maize, USAID/EAT, 2012). In Ghana, maize production is estimated at around 1.79 MT per annum (USAID/EAT, 2012) from an area of approximately 992,000 ha with yield estimates of about 1.8 ton/ha in farmer fields (MOFA, 2011). This is generally low compared to global average of 4-5 ton/ha and over 8 tons/ha in the United States of America (USA) (FAOSTAT, 2013). This low productivity may be partly attributed to frequent biotic and abiotic stresses including disease outbreaks, drought and poor farming practices (Morris *et al.*, 1999). Other factors include continuous use of unimproved landraces, poor soils and erratic rainfall patterns (Akande and Lamidi, 2006, Bua and Chelimo, 2010, USAID/EAT, 2012).

Research efforts have been intensified by Maize breeders in Ghana to develop varieties for improved productivity and with adequate resistance or tolerance to the Maize streak virus disease (MSVD) (Wiredu, 2010; Ragasa et al., 2013). The Maize streak virus (MSV) causes this major foliar disease (Storey, 1925) that affects maize throughout the Sub-Saharan Africa (Pingali and Pandey, 2001). Its prevalence in farmers' fields has been reported in several regions of Ghana (Oppong et al., 2015). An economic loss of between US $120 – US $480 million based on a conservative yield reduction of about 6% - 10% yearly in Africa has been reported (Martin and Shepherd, 2009).

To improve productivity of the crop and management of the disease, the incorporation of landraces and exotic germplasm into breeding programs have been suggested (Carena, 2005, Hallauer and Miranda, 1981, Michelini and Hallauer, 1993, Soengas et al., 2003). Landraces and wild relatives represent an extraordinary genetic resource of maize, with significant allelic diversity, much of which have not been incorporated into improved varieties (Sharma et al., 2010b,

Warburton *et al.*, 2008). These constitute a possible source of diversity that can be exploited to widen the improved gene pool from which breeders can harness useful genes and alleles for breeding to meet biotic and abiotic challenges. For instance, Bertoia (2006) and Balestre *et al.* (2009) have all reported that landraces with no history of breeding for grain production generated crosses with good yield potential which can be exploited in breeding programs.

Information on combining abilities, heterosis, and heterotic grouping is an important component for the successful development of new high yielding hybrids in any breeding program (Legesse *et al.*, 2009, Mohammed, 2009, Romanus et al., 2007). Such information can show the type of gene action involved in controlling quantitative traits, thereby assisting breeders in selecting suitable parent materials and guide crossing and selection methods for highest gain from selection (Hallauer and Miranda, 1988). Heterosis and increased uniformity of parents are the basis of the modern hybrid maize seed industry (Gerdes and Tracy, 1993). Early hybrid maize breeders observed that heterosis was greater in crosses between genetically diverse inbreds than in crosses between related inbreds. By relating levels of heterosis with pedigrees, the concept of heterotic groups was established (Anderson, 1944, Hallauer and Miranda, 1981). Maize breeders have relied on maintenance and exploitation of two or more heterotic breeding groups in the development of inbreds and hybrids. The recognition and use of heterotic groups has contributed to the efficiency and success of hybrid maize breeding programs (Barata and Carena, 2006).

Significant values of general combining ability (GCA) and specific combining ability (SCA) may be interpreted as indicating the performance of additive and non-additive gene action, respectively (Sprague and Tatum, 1942). GCA helps breeders to exploit existing variability in breeding materials to identity genotypes conferring desirable attributes and to distinguish relatedness among genotypes (Melania and Carena, 2005, Vacaro et al., 2002). SCA helps breeders to determine heterotic patterns among populations or inbred lines to identify promising single crosses and assign them into heterotic groups (Hede *et al.*, 1999, Parentoni et al., 2001, Vasal *et al.*, 1992). The estimation of additive and non-additive gene action through this technique could be useful in determining the possibility of commercial exploitation of heterosis from landraces for hybrid development (Stuber, 1994).

In Ghana, hybrid maize cultivation has not received much patronage by Ghanaian farmers (Ragasa *et al.*, 2013, USAID/EAT, 2012). Most of the cultivated maize is dominated by open pollinated varieties (OPVs) compared to developed countries (Troyer, 2004). This may be due to lack of information or availability of preferred hybrid varieties which farmers can readily adopt. It has become imperative that maize productivity in Ghana be raised to meet the high demand of ever increasing population, and hybrids are one key to increased yield. Development of hybrids from local germplasm may aid in wider hybrid adoption, as has been achieved in Costa Rica and Honduras, where Almekinders *et al.* (1994) found that hybridization between local and improved maize was highly valued by farmers. It is anticipated that such hybrids developed from or with contribution from local germplasm which are also resistant or tolerant to the MSVD will facilitate easy adoption by farmers. Thus, the main objective of this study was to exploit local landraces and exotic germplasm to identify suitable parents that can be used to produce new high yielding, MSV disease resistant/ tolerant hybrids. The specific objectives of this study were to determine general and specific combining ability of crosses involving selected Ghanaian maize landraces and inbred line testers with respect to yield and resistance/tolerance to MSVD; and to determine heterosis and assign heterotic groups with respect to yield ability of crosses.

Materials and Methods

Location of Experiments

Crossing blocks were established at the experimental fields of the CSIR-CRI at Fumesua. Evaluation trials were conducted in three locations namely; Fumesua (6.712N; 1.523W) and Akomadan (7.396 N; 1.973W) in the Ashanti region and Wenchi (7.7333N; 2.1W) in the Brong Ahafo region. Wenchi lies at the heart of the transition zone of Ghana. Fumesua and Akomadan both lie in the semi-deciduous rain forest of Ghana. All the locations have two seasons of rainfall with the major season starting from March and ending in July. The minor season starts from September and ends in December. Wenchi has been identified as a good MSV hotspot for disease evaluation under natural conditions (personal communications, MB. Ewool).

Source of Germplasm

Inbred lines with resistance to the MSVD were supplied by CIMMYT, Zimbabwe and IITA, Ibadan, Nigeria. However, both the IITA and CIMMYT inbred lines belonged to different heterotic groups from each other. Local maize landraces or farmer varieties were collected from farmers in various locations across Ghana by the CSIR-CRI. The collections were made in

Table 1- Characteristics of genotypes selected for genetic studies

Genotype	Pedigree	Colour	Maturity	Source	Heterotic group
CML202	B	White	Intermediate/late	CIMMYT	B
CML444	CML202-B	White	Intermediate/late	CIMMYT	B
CML442	CML202-B	White	Intermediate/late	CIMMYT	A
TZEI17	TZEComp5-YC6 inbred 35	Yellow	Early	IITA	A
TZEI23	TZE-Y Pop STR Co S6 inbred 62-2-3	Yellow	Early	IITA	B
LA03		White	Intermediate	Wenchi B/A	-
LA30		White	Intermediate	Bekwai, A/R	-
LA76		White	Intermediate	Juapong E/R	-
LA80		White	Intermediate	Ejura, A/R	-
LA97		White	Intermediate	Golokwati VR	-
LA99		Yellow	Intermediate	Anum E/R	-
LA246		Yellow	Intermediate	Akrofu-Agove,V/R	-
LA276		White	Intermediate	Kpeve, V/R	-
LA400		White	Intermediate	Ejura, A/R	-
LA424		Yellow	Intermediate	Ejura, A/R	-
LA457		White	Intermediate	Golokwati, V/R	-
LA463		White	Intermediate	Kpong, E/R	-
LA467		White	Intermediate	Golokwati, V/R	-
LA518		Yellow	Intermediate	Kpana, N/R	-
LA537		Mixed	Intermediate	Elubu, W/R	-
LA558		White	Intermediate	Nabogu, N/R	-
LA580		White	Intermediate	Wenchi, B/A	-

December 2007 and have undergone two cycles of sibbing for phenotypic characterization in the main seasons of 2008 and 2009. Four CSIR-CRI released varieties namely; Obatanpa, Mamaba, Etubi and Enibi in addition to F_1 hybrids of the crosses TZEI17 x TZEI23 and CML202 x CML442 were used as checks in this study (Table 1).

Establishment of Crossing blocks

Two crossing blocks were established at Fumesua; one in the major season of 2012 and another in the minor season of 2012. In the major season crossing block, 17 local landraces were crossed with 5 inbred line testers (CML202, CML444, CML442, TZEI17 and TZEI23), however seeds of CML442 did not germinate. The landraces were used as female parents while the inbred lines that germinated were used as the male parents. The North Carolina Design II (line by tester) was used with the four inbred lines used as males. Planting was done on 5m row plots at a spacing of 75cm x 40 cm, two hills per stand 2 rows per genotype for the females and 15 rows for male parents. The landraces were not selfed but were sibbed and open pollinating before they were used in the crossing block. Planting date of the landrace parents and the inbred lines were staggered to ensure synchronization of flowering. All cultural practices, including fertilizer application and weeding were done to ensure good growth and yield.

Artificial pollination was done by collecting bulked pollen from each of the male parents (inbred lines) and then crossed with 5 plants each of the female parents (landraces). The same process was repeated in the minor season of 2012 where another crossing block was established again at Fumesua. This time all five inbred lines (CML202, CML444, CML442, TZEI17 and TZEI23) germinated and were crossed with the 17 local landraces as described above. F_1 hybrids involving crosses of CML202 x CML442 and TZEI17 x TZEI23 were also made and used as controls.

Evaluation of F1 top-cross hybrids and parents

Two evaluation trials were established; one in the minor season of 2012 and the other in the major season of 2013 in three locations namely; Fumesua and Akomadan in Ashanti and Wenchi in the Brong Ahafo region. The different locations were selected to provide diversified environments to assess the performance of the F_1 hybrids generated above. Seeds were planted in two rows per plot in two replications at planting density of approximately 66,667 plants per hectare. A spacing of 75 cm between rows and 20 cm between plants was used with one plant per hill. Each row was 5 m long. In the minor season of 2012, the trial was set up using a 9 by 10 alpha-lattice design with two replications. The evaluation trial involved 68 F1 top-cross, 17 landrace parents, one F1 hybrid (TZEI17/TZEI23) and four CSIR-CRI released varieties (Obatanpa, Mamaba, Etubi and Enibi).

The 2013 major season trials were also conducted in Fumesua, Akomadan and Wenchi. Planting was done as in the previous year using the same planting distance and population density per hectare (66,667 per hectare). A 9 by 12 rectangular lattice design with two replications was used. In this trial there were six

controls including two F1 hybrids; TZEI17 x TZEI23 and CML202 x CML442 and the four CSIR-CRI released varieties (Obatanpa, Mamaba, Etubi and Enibi).

In both trials all agronomic practices followed prescribed recommendations by maize breeders at the CSIR-CRI. A basal NPK application rate of 120 kg/ha and a top dressing of 60Kg/ha sulphate of ammonia were applied. Guard rows were planted around all trials to avoid biases. Data were collected were on MSV disease incidence (Vi) measured by counting number of infected plants per plot and then expressed as a percentage, Virus severity (Vs) scored for each plot based on a scale of 1 to 5, where, 1=no disease, 2=mild infection, 3=moderate infection, 4=severe infection and 5=very severe infection, plant height (PH in centimeters, cm) measured from base of the plant to tassel/flag leaf, total leaf count (LC) mean of the number of leaves per plot at 65 days after planting, Anthesis silking interval (ASI), ear diameter (Ed, in cm), was measured as the diameter of the cob with grains per plot, thousand grain weight (1000Gwt in grammes) weight of 1000 grains per plot, cob width (CW in cm) was measured as the diameter of cob after shelling per plot and Yield per hectare (Yld/ha in kg). Yield per plant was calculated by dividing the shelled grain weight at 15% moisture content (MC) by the number of plants per plot. Yield per hectare was estimated by multiplying the yield per plant per plot by plant density per hectare as described by Tollenaar and Lee (2006).

Statistical analyses

All analyses were carried out with PROC GLM in SAS (SAS Institute, 2009) using the mixed model with test option and environment and year considered as random. Analysis of variance (ANOVA) was computed for the genotypes for separate locations (data not shown) and then across locations/environments for 2012, 2013 and combined 2012 and 2013 seasons also across locations to generate entry means adjusted for block effects according to the lattice design (Cochran and Cox, 1960; Menkir et al., 2003; Vasal et al., 1992). The pooled error mean square was calculated for each trait. Line by tester analysis was done to partition the genotype source of variation into that due to parental line and tester general combining ability (GCA) effects as well as due to specific combining ability (SCA) effects from the adjusted means using the method of Kempthorne (1957). In these analyses the checks and the parents were not included. The mean squares for GCA effects for the line and testers were tested for significance using the interactions with site x line and site x tester as error term respectively. The SCA for line x tester was tested with the interaction of mean squares due to site x Line x Tester as an error term. Interaction of site x GCA and site x SCA effects were tested with error mean square of the error term. In the combined 2012 and 2013 GCA and SCA analysis year was considered as environment for the traits to obtain 6 environments. The model below by Fan et al. (2009) was used for data analysis:

$$Yijkl = \mu + al + bkl + vij + (av)ijl + eijkl$$

$$vij = gi + gj + sij$$

where $Yijkl$ = observed value from each experimental unit;

μ =population mean;

al = location effect;

bkl = block or replication effect within each location;

vij = F_1 hybrid effect = $gi + gj + sij$

[where gi = general combining ability (GCA) for the ith parental line;

gj = GCA effect of jth tester;

and sij = specific combining ability for the $ijth$ F_1 hybrid];

$(av)ijl$ = interaction effect between ith F_1 hybrid and lth location; and $eijkl$ = residual effect.

Percentage heterosis was calculated for the combined 2012 and 2013 yield data based on the formula of (Flint-Garcia et al., 2009b) as follows:

High Parent Heterosis = (F_1-HPV)/HPV x 100

Where HPV is the High parent value and

F1 is the mean of the F_1 hybrid

Lines were assigned to heterotic groups by using SCA effects for yield where positive SCA between lines and tester generally indicates that lines are in opposite heterotic groups while lines in the same heterotic group with tester exhibit negative SCA effects as described by (Vasal *et al.*, 1992). Based on the combined 2012 and 2013 GCA and SCA results, testers CML202 CML442 was used to assign opposite heterotic groups to the lines.

Results and discussion

General Analysis of variance

The general analysis of variance showed that genotype was significant for most traits except Vs, Vi and ASI, genotype x year interaction was significant for all traits except Yld/ha and ASI, genotype x location interaction was not significant for all traits but the genotype x location x year interaction was significant for Vi, Vs, ED and ASI (Supplemental Tables 3 and 4). These findings show that traits varied depending on environment, and

thus testing the genotypes in multiple environments is necessary to measure the degree to which these traits varied (Falconer and Mackay, 1996).

Yield

The highest yield across locations was 8902.34 kg/ha for the cross CML442/LA80. In general, crosses involving CML444 gave higher yields while those involving TZEI23 gave the lowest yields. The highest yield for the controls was CML202/CML442 with a yield per hectare of 7059.26 kg/ha, and for local checks, Obatanpa performed best with a mean yield of 5612.43 kg/ha. The highest yielding landrace parent was LA276 with a yield of 5986.54 kg/ha (Table 4; Supplemental Table 1). The high yields obtained from some of the crosses indicate the potential to raise yield substantially in some Ghanaian maize landraces when crossed with suitable materials. Similar findings have been reported in other studies as reported by Almekinders et al., (1994), Dhillon et al., (2002), Prasanna, (2012), Vasal et al., (1987).

Virus disease incidence and severity

Virus disease incidence was highest for the landrace parents compared with the hybrids. Across years the landrace parents with the highest mean virus incidence was LA537 (35.8%) followed by LA580 (32.5%), and LA99 (27.9%) (Table 5). Crosses involving the inbred lines used as testers had a reduced disease severity and incidence (such as crosses with CML444, CML442 and CML202) (Table 5; Supplemental Table 2). This result demonstrates that the maize streak virus disease severity and incidence can be managed if farmers adopt hybrid varieties that have at least one resistant parent. The correlation of incidence and disease severity observed in the landrace parents and that of the corresponding top-cross hybrids was significant, especially in the 2012 trial where disease pressure was also high ($r=-0.2$, $p<0.05$) (data not shown). The landrace parents were more susceptible to MSVD compared with the top-cross hybrids (which reflected in the yield/ha). This observation supports the report that MSV disease is mostly controlled by a single dominant gene (Storey and Howland, 1967; Efron *et al.*, 1989, Kim *et al.*, 1989, Pernet *et al.*, 1999a, Rose, 1978; Kyetere *et al.*, 1995). However, it appears the resistance or tolerance improves with certain tester/parent crosses suggesting the existence of minor genes contributing to resistance within some of the genotypes agreeing with what Kim *et al.*, (1989).

Combining ability analysis

The GCAline mean squares were significant at $p<0.05$ for ASI, Vi, and Yld/ha, and at $p<0.001$ for 1000Gwt, PH, LC, Vs and CW (Tables 2 and 3). GCATester was significant at $p<0.05$ for ASI, at $p<0.01$ for 1000Gwt, and Vs, and at $p<0.001$ for Ed PH, LC and CW. The GCAline by environment interaction (GCAline*Env) mean square was significant at $p<0.05$ for ASI, and at $p<0.001$ for Ed, 1000Gwt, Vi and CW. The GCATester by environment interaction (GCATester*Env) mean squares were highly significant at $p<0.001$ for ASI, Ed, 1000Gwt, Vs, Vi, CW and Yld/ha, and significant at $p<0.05$ for Ed. The SCALine*tester effects were significant for Ed and CW at $p<0.001$, at $p<0.01$ for Vi and at $p<0.05$ for Vs. SCA by environment interaction (SCA*Env) was significant at $p<0.01$ for ASI, Ed and 1000Gwt while Vi and CW were highly significant at $p<0.001$. Significant GCA effects for both tester and line (which is seen for traits such as ASI, 1000Gwt, PH, LC, Vs and CW) indicates additive gene action in the inheritance of these traits; this is good for hybrid development and in particular, for the development of the inbred parents of new hybrids. Additive variation is a component of narrow sense heritability which affects gain from selection. This information can be used by breeders during selection of new parental lines from a population (such as the

Table 4 - Mean grain yield (kg/ha) across locations for combined 2012 and 2013 seasons for top tenand bottom ten genotypes

Top 10 performing genotypes		Bottom 10 performing genotypes	
Genotype	Yld/ha (kg)	Genotype	Yld/ha (kg)
CML442/LA80	8902.34	TZEI17/LA537	4885.48
CML444/LA30	7818.14	LA99	4728.72
CML444/LA580	7586.02	LA76	4588.91
CML444/LA76	7554.09	LA246	4562.17
CML442/LA3	7455.18	LA518	4412.72
CML442/LA400	7327.73	LA580	4222.05
CML442/LA558	7307.97	LA80	4209.55
TZEI17/LA80	7247.36	LA457	4205.1
CML202/LA30	7240.65	LA97	4095.94
CML442/CML202	7059.26	LA537	3491.44
SE	930.92		
LSD	2585.43		

Table 5 - Mean virus incidence (%) and severity scores for the combined 2012 and 2013 seasons for top 10 and bottom 10 genotype

	Top 10 performing genotypes			Bottom 10 performing genotype	
Genotypes	Vs	Vi	Genotypes	Vs	Vi
CML202/LA3	1	0	LA537	2.33	35.8
CML202/LA30	1	0	LA580	1.95	32.5
CML442/CML202	1	0	LA97	2.33	28.0
CML442/LA276	1	0	LA99	2.13	27.9
CML442/LA30	1	0	LA424	1.96	26.5
CML442/LA400	1	0	LA518	2.25	25.0
CML442/LA457	1	0	LA400	2.21	23.0
CML442/LA463	1	0	LA80	2.14	22.1
CML442/LA467	1	0	LA76	3.71	19.8
CML442/LA537	1	0	LA3	1.71	19.6
CML442/LA558	1	0	TZEI23/LA537	1.83	17.8
CML442/LA76	1	0	Enibi	2.08	17.3
CML442/LA80	1	0	Mamaba	1.88	17.2
CML442/LA99	1	0	TZEI23/LA97	1.83	17.2
CML444/LA580	1	0	CML444/LA97	1.92	16.7
CML444/LA76	1	0	TZEI23/LA80	1.79	16.7
SE	0.53	5.1			
LSD	1.48	14.17			

landraces in this study) and it is an indicator for the potential of these lines for hybrid variety development. SCA is an indication of non-additive gene action, which is more difficult for breeders to take advantage of in selection of fixed lines, and was significant only in a few traits including Ed, Vi, Vs, and CW. Similar findings have been reported by other researchers (Fato *et al.*, 2012, Legesse *et al.*, 2009, Soengas *et al.*, 2003, Vasal *et al.*, 1992). Significant variation partitioned between environments for most traits also suggests that new hybrids to be developed from the landraces will have to be tested in more than one environment. This is generally found to be true for important quantitative traits in maize. Although line x tester effects were not significant for yield, significant differences were found for some of the yield related traits including cob width and ear diameter, and for the disease resistance traits such virus incidence and severity. This should still allow the development of higher yielding hybrids from this material.

General combining ability effects for lines and testers

General combining ability effects for ASI for the lines in the combined 2012 and 2013 analysis ranged from -0.73 (LA518) to 0.49 (LA424) (Supplemental Table 5). ASI was negative for eight of the lines, with line LA518 being significant at $p<0.01$ with the rest having positive GCA with LA424 being significant at ($p<0.01$). For the testers CML444 and TZEI17, GCA effects for ASI was negative while GCA effects for rest of the testers was positive with CML442 being significant at ($p<0.05$). Seven of the lines had negative GCA for CW, and the rest had positive GCA effects, for which line LA246 and LA99 were significant at ($p<0.01$) and ($p<0.05$) respectively. All tester GCAs were negative for this trait except CML444, which had positive and significant GCA at ($p<0.01$). ED GCA effects for lines ranged from -0.004 to 0.13. Tester GCA effects was negative and significant at ($p<0.01$) for CML202 and TZEI17 but not

Table 2 - Mean squares from the analysis of variance for anthesis silking interval (ASI), ear diameter (Ed), 1000 grain weight (1000Gwt) and plant height (PH) for the combined 2012 and 2013 seasons

Source	DF	ASI	Ed	1000Gwt	PH
Replication	1	3.494	0.124	11.478	1025.61
Environment (Env)	5	352.266***	6.859***	210227.652***	92665.309***
GCALINE	16	3.933*	0.13	2857.918***	1617.668***
GCATESTER	4	14.832*	3.081***	26671.858**	17845.403***
GCA LINE *Env	80	1.841*	0.074***	866.694***	338.932
GCATESTER*Env	17	4.746***	0.2067***	4064.155***	465.071
SCALINE*Tester	63	1.853	0.0886***	770.1913	406.928
SCA*Env	244	1.73**	0.0467**	604.24**	338.308
Error	417	1.287	0.033	451.047	299.724

*, **, *** Significant at the 0.05, 0.01, and 0.001 probability level, respectively

Table 3 - Mean squares from the analysis of variance for leaf count (LC), MSV incidence and severity score (Vs), yield per hectare (yld/ha) and cob width (CW) for the combined 2012 and 2013 seasons

Source	DF	LC	Vi	Vs	Yld/ha	CW
Replication	1	0.528	373.211**	0.005	2128025	0.017
Environment (Env)	5	143.985***	9631.047***	15.587***	300300978***	0.574***
GCALINE	16	5.165***	244.358*	0.355***	3432008*	0.118***
GCATESTER	4	63.089***	869.428	2.424**	1.5E+07	1.674***
GCA LINE *Env	80	0.715	111.98***	0.123	1746484	0.036***
GCATESTER*Env	17	1.302*	528.295***	0.418***	5181562***	0.068***
SCALINE*TESTER	63	0.808	140.957**	0.176*	2213277	0.054***
SCA*Env	244	0.729	81.292***	0.116	1938623	0.019***
Error	417	0.676	37.857	0.113	1871528	0.014

*, **, *** Significant at the 0.05, 0.01, and 0.001 probability level, respectively

for TZEI23 which was significant at ($p<0.05$). For 1000 Gwt GCA effects ranged from -14.07 to 11.54. Testers CML202, TZEI17 and TZEI23 had negative and significant GCA effects and the rest were positive and significant (CML442 at $p<0.01$ and CML 444 at $p<0.05$). GCA for the rest of the traits for the lines and testers can be found in supplemental Table 6. Significant GCA effects for yield is a requirement for the development of inbred lines for hybrid production (Pswarayi and Vivek, 2008; Vasal et al., 1992b). Significant and positive GCA effects imply additive gene action, which indicate that inbred lines with superior performance for these traits can be developed from the landraces. Three of the testers CML442 CML444 and TZEI17 had negative GCA effects for MSV incidence. This implies that the testers contributed in reducing the incidence of MSV disease and therefore can be relied on to improve productivity thus, confirming the importance of using a resistant parent for hybrid maize production to manage the incidence and severity of the MSVD

Specific combining ability

Specific combining ability effects yield, virus incidence and severity for each line crossed to each tester can be found in Table 6; Supplemental Table 6. Significant SCA effects imply dominance and epistasis (Sprague and Tatum 1942; Legesse et al., 2009). For hybrid development, positive SCA for yield is required (Sprague and Tatum 1942; Fan et al., 2003 Legesse et al., 2009). This suggests the possibility of selecting inbred lines from some of the landraces which can be utilized for hybrid maize production as has been reported by several authors (Beck et al., 1990, Fan et al., 2003, Hallauer and Miranda, 1988, Vasal et al., 1987, Vasal et al., 1992, Vasal et al., 1992b) Soengas et al., 2003; Almekinders et al., 1994; Dhillon et al., 2002). The best specific combinations for Yld/ha are crosses between (CML444 x LA76, CML444 x LA580, CML444 x LA30, CML442 x LA558, CML442 x LA80, TZEI17 x LA457 and TZEI23 x LA3 (Table 6)

For resistance/tolerance to MSV disease genotypes that contribute least SCA effects are required (Fato et al., 2012, Legesse et al., 2009). The following crosses had significantly negative SCA for virus severity; CML202 x LA3, CML202 x LA30, CML442 x LA80, CML442 x LA97, CML444 x LA580 and CML444 x LA76 (Supplemental Table 6) while the following had significantly negative SCA for virus incidence; CML442 x LA80, CML442 x LA97, CML444 x LA580, TZEI17 x LA80 and TZEI23 x LA276 making them potential hybrids for the management of MSV disease.

Heterosis and heterotic groups

Heterosis for yield ranged from -2.40% for TZEI17/LA276 to 111.48% for CML442/LA80 (Table 7). Highest heterosis was found with crosses involving tester CML444 and CML442 and a few of the crosses with TZEI17, while TZEI23 gave the lowest heterosis. High heterosis suggests the possibility of using these genotypes for hybrid maize production as have been reported by Alvarez et al. (1993) and Gissa et al. (2007). The testers CML202 and CML442 were used to group the lines into opposing heterotic groups; these groups are presented in Table 6. CML444 was not used for the heterotic grouping because it belongs to the same group as CML202. Crosses with the two IITA testers (TZEI17 and TZEI23) created GCA that were negative for both with respect to grain yield, which is considered the most important trait for heterotic grouping (Legesse et al., 2009, Soengas et al., 2003, Vasal et al., 1992). Thus, the lines tested here do not belong to either IITA heterotic group. Lines LA276, LA30, LA424, LA467, LA537, LA580 and LA99 were classified into CIMMYT group A, since they demonstrated negative SCA when crossed to tester CML442, which also belongs to CIMMYT group A. Lines LA400, LA558 and LA80 were classified into CIMMYT group B, based negative SCA effects when crossed to tester CML202. Lines LA246 and LA3 had positive SCA with both testers; this means they belong to neither group A or B suggesting they belong to a completely separate heterotic group and

thus have an equally good chance of forming good hybrids with lines from both CIMMYT A and B groups (Table 6). Lines LA457, LA463, LA518 and LA76 were assigned to both groups because they had negative SCA effects with both testers. Two other lines, LA97 and LA99, could not be assigned because of missing data from their crosses with the tester CML202. Two of the lines were temporarily assigned to both groups because their SCAs were positive with both testers which is similar to groupings made by Legesse et al. (2009); Parentoni et al. (2001); Vasal et al. (1992), although it can be argued that they may belong to heterotic groups other than the above.

Conclusions

This work has shown the potential for improving the yield of Ghanaian maize landraces and at the same time manage MSV disease by crossing them with known, adapted and disease resistant maize testers (CML442, CML444 and TZEI17). In the future, inbred lines can be developed out of the promising landraces; LA3, LA80 LA76, and LA457 identified in this work for high yielding MSV resistant/tolerant hybrids. In the meantime, these lines identified should be tested in multiple environments and the most stable top crosses hybrids registered for cultivation and use by consumers.

References

Akande, SR, & Lamidi, GO, 2006. Performance of quality protein maize varieties and disease reaction in the derived-savanna agro-ecology of south-west nigeria. Afr. J. Biotechn. 5: 1744-1748.

Almekinders, CJM, N.P., L. & G.H., D. B. 1994. Local seed systems and their importance for an improved seed supply in developing countries. Euphytica 78 207–216.

Alvarez, AG, Garay, J., Gominez, JI, & Galarreta, RD, 1993. Heterosis entre dos sintoticus de maiz expresada sobre caracteres morfologicos y reproductivos. Invest Agr Prod Prot Veg 8: 334-340.

Anderson, E. 1944. Sources of effective germplasm in hybrid maize. Ann. Mo. Bot. Gard. 31: 355-361.

Balestre, M., Souza, JC, Von Pinho, RG, Lunezzo De Oliveira, R. & Valente Paes, JM, 2009. Yield stability and adaptability of maize hybrids based on gge biplot analysis characteristics. Crop Breeding and App Biotechn. 9: 219-228.

Barata, C. & Carena, MJ, 2006. Classification of north dakota maize inbred lines into heterotic groups based on molecular and testcross data. Euphytica, 151: 339-349.

Beck, DL, Vasal, SK, & Crossa, J. 1990. Heterosis and combining ability of cimmyt's tropical early

Table 6 - Estimates of specific combining ability effects for grain yield across locations for combined 2012 and 2013 seasons and heterotic groups of lines

	SCA Yld (kg/ha)					
LINE	CML202	CML442	CML444	TZEI17	TZEI23	CIMMYT Heterotic Group
LA246	493.63	58.23	-514.47	-37.46	2.28	-
LA276	597.82	-166.3	-191.46	- 445.26	168.32	A
LA3	167.26	344.17	- 864.56*	- 150.11	722.66*	-
LA30	474.16	- 631.61	691.84*	- 245.88	- 403.53	A
LA400	-178.46	477.94	- 428.94	472.59	- 131.07	B
LA424	405.76	- 655.94	284.47	- 309.61	- 79.55	A
LA457	- 705.86*	- 114.35	-118.73	800.78*	-66.69	A, B
LA463	- 262.96	- 87.99	401.84	- 51.59	- 211.07	A, B
LA467	334.34	- 65.5	144.44	174.42	- 647.34	A
LA518	- 675.26	- 361.12	576.13	- 24.04	259.37	A, B
LA537	296.39	- 164.62	238.59	- 748.84*	246.13	A
LA558	- 116.08	823.52*	- 227.42	- 145.32	136.97	B
LA580	119.55	- 368.98	754.59*	- 208.5	9.91	A
LA76	- 398.27	- 358.19	1022.36**	169.24	40.56	A, B
LA80	- 435.86	1730.23***	- 896.55*	633.68	- 193.29	B
LA97	N/A.	85.23	- 177.68	451.21	- 280.17	-
LA99	N/A.	- 449.56	71.71	- 332.75	440.13	-
SE	348.768					
LSD.05	685.5625					
LSD .01	902.4967					

NB: N/A shows that data could not be taken for the respective cross

and intermediate maturity maize (zea mays l) germplasm. Maydica, 35: 279-185.

Bertoia, L., López, C. & Burak, R. 2006. Biplot analysis of forage combining ability in maize landraces this research was supported by the dep. Of agronomy, facultad de ciencias agrarias, universidad nacional de lomas de zamora. Crop Sci., 46, 1346-1353

Bua, B. & Chelimo, B. 2010. The reaction of maize genotypes to maize streak virus disease in central uganda. Second RUFORUM Biennial Meeting held from 20-24 September, 2010. Entebbe, Uganda.

Carena, M. J. 2005. Maize commercial hybrids compared to improved population hybrids for grain yield and agronomic performance. Euphytica, 141: 201-208.

Dhillon, B. S., Vasal, SK, & Prasanna, BM, 2002. Maize. In: Chopra, V. L. & Prakash, S. (eds.) Evolution and adaptation of cereal crops. New Delhi:: Oxford & IBH.

Efron, J. M., Kim, SK,, Fajemisin, JM, Mareck, JH, Tang, CY, Dabrowski, ZT, Rossel, HW, Thottappilly, G. & Buddenhaggen, IW, 1989. Breeding for resistance to maize streak virus: A multidisciplinary team approach. Plant Breed. , 103:1-36.

Fan, XM, Tan, J., Chen, HM, & Yang, J. Y. 2003. Heterotic grouping for tropical and temperate maize inbreds by analyzing combining ability and SSR markers. Maydica 48: 251-257.

Fan, XM, Zhang, YM, Yao, WH, Chen, HM, Tan, J., Xu, CX, Han, XL, Luo, LM, & Kang, MS, 2009. Classifying maize inbred lines into heterotic groups using a factorial mating design. Agron. J. 101: 106–112.

FAOSTAT. 2008. Statistical databases and data-sets of the food and agriculture organization of the united nations http://faostat.fao.org/default.aspx [Online].

FAOSTAT. 2013. Statistical databases and data-sets of the food and agriculture organization of the united nations http://faostat.fao.org/default.aspx [Online].

Fato, P., Derera, J., Tongoona, P., Makanda, I. & Sibiya, J. 2012. Heterotic orientation of tropical maize inbred lines towards populations zm523 and suwan-1 under downy mildew infestation. Euphytica 1007/s10681-012-0716.

Flint-Garcia, S., Buckler, E., Tiffin, P., Ersoz, E. & Springer, N. 2009. Heterosis is prevalent for multiple traits in diverse maize germplasm. PLoS ONE, 4, e7433.

Gerdes, JT, & Tracy, WF, 1993. Pedigree diversity withing the lancaster surecrop heterotic group of maize. Crop Sci. 33: 334-337

Gissa, DW, Zelleke, H., Labuschagne, MT, Hussien, T. & Singh, H. 2007. Heterosis and combining ability for grain yield and its components in selected maize inbred lines. South African Jnl of Plt and Soil, 24: 133-137.

Hallauer, AR, & Miranda, FJB. 1981. Quantitative genetics in maize breeding. Ames: Iowa State University, 1981. 468p.

Hallauer, AR, & Miranda, JB, 1988. Quantitative genetics in maize. Iowa State Univ. Press, Ames.

Hede, A. R., Srinivasan, G., Stolen, O. & Vasal, SK, 1999. Identification of heterotic pattern in tropical inbred maize lines using broad synthetic testers. Maydica, 44: 325-331.

Http://Hdl.Handle.Net/10568/24696.

Http://Www.Iita.Org/Maize.

Kim, SK, Efron, Y., Fajemisin, JM, & Buddenhagen, I. W. 1989. Mode of gene action for resistance in maize to maize streak virus. Crop Sci. , 29: 890–894.

Kyetere, D., Ming, R., Mcmullen, M., Pratt, R., Brewbaker, J., Musket, T., Pixley, K. & Moon, H. 1995. Monogenic tolerance to maize streak virus maps to the short arm of chromosome 1. Maize Genet. Coop. News Lett. 69, 136–137.

Legesse, BW, Pixley, K. & Botha, A. M. 2009. Combining ability and heterotic grouping of highland transition maize inbred lines. Maydica, 54: 1-9.

Melania, MD, & Carena, M. J. 2005. Alternative maize heterotic patterns for the northern corn belt. Crop Sci. 45: 2186-2194.

Michelini, LA, & Hallauer, AR, 1993. Evaluation of exotic and adapted maize (zea mays l.) germplasm crosses. Maydica.

MOFA 2011. Facts and figures. Statistics, Research and Information Directorate (SRID).

Mohammed, MI. 2009. Line x tester analysis across locations and years in sudanese x exotic lines of forage sorghum. Jnl of Plt Breed. and Crop Sci. 1: 311-319.

Parentoni, SN., Magalhaes, JV, Pacheco, CA, Santos, MX, Abadie, T., Gama, EEG, Guimaraes, PEO, Meirelles, WF, Lopes, MA, Vasconcelos, MJV& EP 2001. Heterotic groups based on yield-specific combining ability data and phylogenetic relationship determined by rapd markers for 28 tropical maize open pollinated varieties. Euphytica, 121:197-208.

Prasanna, BM, 2012. Diversity in global maize germplasm: Characterization and utilization. Jnl of Biosciences 37: 843-855.

Pernet, A., Hoisington, D., Franco, J., Isnard, M., Jewell, D., Jiang, C., Marchand, J.-L., Beynaud, B., Glaszmann, J.-C. & Gonzalez De Leon, D. 1999a. Genetic mapping of maize streak virus resistance from the mascarene source. I resistance in line d211 and stability against different virus clone. Theoretical and Applied Genetics, 99: 540-553.

Pswarayi, A. & Vivek, B. S. 2008. Combining ability amongst cimmyt's early maturing maize (zea mays l.) germplasm under stress and non-stress conditions and identification of testers. Euphytica, 162: 353-362.

Ragasa, C., Dankyi, A., Acheampong, P., Wiredu, A. N., Chapo-To, A., Asamoah, M. & Tripp, R. 2013. Patterns of adoption of improved maize technologies in ghana. Ghana strategy support program. International Food Policy Research Institute.

Romanus, KG, Hussein, S. & Mashela, WP, 2007. Combining ability analysis and association of yield and yield components among selected cowpea lines. Euphytica, 162: 205–210.

Rose, DJW, 1978. Epidemiology ofmaize streak disease. Annual Review of Eniomotogy 23, 259 82.

Sharma, L., Prasanna, BM, & Ramesh, B. 2010. Analysis of phenotypic and microsatellite-based diversity of maize landraces in india, especially from the north east himalayan region. Genetica, 138, 619-631.

Soengas, P., Ordas, B., Malvar, RA, Revilla, P. & Ordas, A. 2003. Performance of flint maize in crosses with testers from different heterotic groups. Maydica, 48: 85-91.

Sprague, G F. & Tatum, LA, 1942. General vs. Specific combining ability in single crosses of corn. J. Am. Soc. Agron. 34: 923-932.

Storey, HH, & Howland, A. K. 1967. Inheritance of resistance in maize to the virus of steak disease in east africa. Ann. appl. Biol. 59: 429-436.

Stuber, CW (ed.) 1994. Heterosis in plant breeding: Wiley.

Tollenaar, M. & Lee, E. A. 2006. Dissection of physiological processes underlying grain yield in maize by examining genetic improvement and heterosis. Maydica, 51: 399-408.

Troyer, AF, 2004. Review & interpretation background of u.S. Hybrid corn ii: Breeding, climate, and food. Crop Sci. 44: 370–380.

USAID/EAT 2012. The market for maize, rice, soy, and warehousing in northern ghana. In: Gage, D., Bangnikon, J., Abeka-Afari, H., Hanif, C., Addaquay, J., Antwi, V. & Hale, A. (eds.) United States Agency for International Development: Enabling Agricultural Trade. Fintrac Inc.

Vacaro, E., Barbosa-Neto, JF, Pegoraro, DG, Nuss, CN, & Conceicao, LDH, 2002. Combining ability of twelve maize populations. Pesquisa-agropecuaria-Brasileira 37: 67-72.

Vasal, SK, Beck, DL, & Crossa, J. 1987. Studies on the combining abilities of CIMMYT maize germplasm. CIMMYT Research Highlights, CIMMYT Mexico, El Batan.

Vasal, SK, Srinivasan, G., Crossa, J. & Beck, DL, 1992. Heterosis and combining ability of cimmyt's subtropical and temperate early-maturity maize germplasm. Crop Sci. 32: 884-890.

Vasal, SK, Srinivasan, G. & Gonzales , C. 1992b. Lodging resistant tropical maize inbred lines from tuxpeno. Maize Gen. Coop Newsletter Vol 66: 73-74.

Warburton, ML, Reif, JC, Frisch, M., Bohn, M., Bedoya, C. & Xia, XC, 2008. Genetic diversity in CIMMYT nontemperate maize germplasm: Landraces, open pollinated varieties, and inbred lines. Crop Sci. 48: 617 - 624.