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Full Length Research Paper

Estimation of heterosis and combining ability in maize (*Zea mays* L.) for maize lethal necrosis (MLN) disease

Kiyyo J. G.[1]* and Kusolwa P. M.[2]

[1]Ilonga Agricultural Research Institute, P. O. Box 33 Kilosa, Tanzania.
[2]Department of Crop Science and Horticulture, Sokoine University of Agriculture, P. O. Box 3005, Morogoro, Tanzania.

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Nature of gene action and genetic parameters for disease resistance are important attributes in developing resistant cultivars. This provides the sustainable, economically justifiable and environmentally friendly means of controlling plant diseases. In this study, 6 x 6 full diallel cross involving genetically divergent maize inbred lines was performed with the aim of developing resistant cultivars against Maize Lethal Necrosis (MLN) disease under MLN disease hot spot areas in Mlangarini, Ngaramtoni and Kiru six in the Northern Zone of Tanzania during 2015 cropping season. The experimental materials consisted of thirty single cross hybrids, six parents and two local checks. The experiment was laid down in a randomized complete block design (RCBD) with three replications per location. The general combing ability (GCA) and specific combining ability (SCA) effects were significantly different for MLND response among genotypes across all locations. The combined analysis revealed that GCA was highly significant at P≤0.001 than SCA in all locations with mean squares of (5.551*), (1.61***) and (4.527***) for Mlangarini, Kiru six and Ngaramtoni respectively. The GCA: SCA ratios were 1.894, 1.726 and 1.403 for Mlangarini, Kiru six and Ngaramtoni respectively. The implication of GCA/SCA ratio of more than a unity proves that GCA is significant in all locations where this study was conducted. The results also revealed the presence of both additive and non-additive genetic effects, with the former more pronounced than the later. This implies that developing composite variety will be the better option in combating the disease. However the best cross was observed between CML 144 X CML444 with mean square -0.10, -0.45* and -0.18* for Mlangarini, Kiru six and Ngaramtoni respectively.**

Key words: Diallel cross, general combing ability (GCA), heritability, Maize Lethal Necrosis disease (MLND), specific combining ability (SCA), *Zea mays.*

INTRODUCTION

The popularity of maize in Africa has been increasing to the extent of replacing traditional crops like sorghum and millet (DeVries and Toenniessen, 2001). An estimate of 90% of the maize produced in Africa is consumed as food (Katinila et al., 1998). Despite the importance of maize as the main staple crop, average yields in farmers' fields are relatively low averaging 1.2 metric tons per hectare compared to the estimated potential yields of 4 to 5 metric tons per hectare (WEMA, 2010). While farmers are keen on increasing maize productivity, their efforts are

*Corresponding author. E-mail: jkiyyo@gmail.com.

hampered by a wide range of constraints such as pest and diseases, low soil fertility and unpredictable weather. Currently the outbreak (MLN) disease has been a serious threat for maize production in Tanzania and other East African countries (Wangai et al., 2012). According to the survey conducted by CIMMYT in 2012, potential yield loss of more than 60% was reported in the affected areas. Infection rate and damage can be very high seriously affecting yields and sometimes causing complete crop loss (Wangai et al., 2012). The disease is caused by the co-infection of Maize Chlorotic Mottle Virus (MCMV) and any *potyvirus* group such as Sugar Cane Mosaic Virus (SCMV).

Biologically maize is the natural host for more than 50 viruses and an experimental host for about 30 more (Lapierre and Signoret, 2004), but only some cause diseases that seriously affect yield (Ali and Yan, 2012; Redinbaugh and Pratt, 2009). Among the most aggressive are the members of the *Potyviridae* and *Maize Chlorotic mottle virus* (MCMV), which form the devastating complex known as maize lethal necrosis virus (Uyemoto et al., 1980; Wangai et al., 2012). Although plants have evolved passive and active defense mechanisms that are responsible for the suppression of virus multiplication and spread, such mechanisms require interaction of plant and viral factors to confer plant resistance or susceptibility (Gomez et al., 2009). Identifying the loci conferring resistance to virus diseases, offers an approach to develop genetically resistant lines that are able to reduce the yield losses caused by diseases. Estimation of genetic effects and variances in a population is of great importance to plant breeders in making decision concerning the type of breeding programme to be used and in selecting breeding materials that will show the greatest success against various stresses.

Therefore, in this study full diallel cross was used in order to gather important genetic information of the parental materials to combat maize lethal necrosis virus. This technique has been extensively used and hailed by plant breeders as a long over-due methodology for rationalizing the genetic study of continuous variation (Jawahar, 2006). The strength of diallel technique is that, additional information such as reciprocal effects, maternal and paternal effects and allelic distribution can be obtained quite in early generation such as F_1, thus useful to define breeding strategy without losing much time. Moreover, diallel design is a useful tool of obtaining combining ability of the parents used in the cross. Combining ability has a prime importance in plant breeding since it provides information for the selection of parents and also provides information regarding the nature and magnitude of involved gene action (Griffing, 1956). The knowledge of genetic structure and mode of inheritance of different characters help breeders to employ suitable breeding methodology for their improvement (Kiani et al*.*, 2007). However little is known about MLN disease and there are limited information about the viruses causing the disease. Although Sugar Cane Mosaic virus was common in East Africa and well known in sugar cane crops, Maize Chlorotic Mottle Virus is new virus in most part of the region.

MATERIALS AND METHODS

The experimental materials used in this study were thirty single cross developed from six maize inbred lines (CKH 10767, CKH 114272, CML312, CML444, CML503 and CML144) and 2 local checks (SeedCo527 and Selian H308). The six inbred lines were selected based on their genetic diversity of the disease response. While CML144 was known to be resistant, CML503 was the highly susceptible material. The rest lines are moderately resistant to the disease.

The breeding nursery was established at Kiru six secondary school gardens under irrigation system during 2014 off season for developing single cross hybrids. Crossings were performed in 6 x 6 full diallel fashion according to Griffings (1956) Design 1 model 1 using six heterotically divergent parents. In order to increase genetic variation, resistant, moderately resistant and susceptible inbreds were used in the ratio of 3:2:1. Both ear and tassel bagging were done prior to flowering in order to avoid unintended cross and self-pollination. In the breeding nursery sowing dates were adjusted to facilitate nicking in flowering so that sufficient crosses can be made.

Evaluation trials were laid down in a randomized complete block design (RCBD) with three replications. Each entry was planted in one row plot of 5 m long; inter and intra row spacing was kept to 0.75 m by 0.30 m respectively. Three spreader rows of maize inbred line CML 503 were planted as border rows as the highly susceptible check. Pesticides were not applied to allow movement of insect vectors in the field**.** The F_1's hybrids were evaluated for general and specific combining ability for disease resistance in Mlangarini, Kirusix and Ngaramtoni in the Northern zone of Tanzania. These are the locations currently having high MLN disease occurrences. Parental lines were concurrently evaluated together with the developed hybrids in order to study their genetic information on disease scores, days to 50% flowering and grain weight from ten plants randomly selected in each row. These plants were tagged three weeks after emergence. Disease severity scores were rated on scale of 1-5 according to Shekhar and Kumar (2012) as follows: 1= Resistant (No Symptoms), 2=Moderately Resistant, 3= Moderately Susceptible, 4= Susceptible, 5= Highly Susceptible (plant dead completely). The disease scores were recorded three weeks after emergence (3WAE), six weeks after emergence (6WAE), nine weeks after emergence (9WAE) and twelve weeks after emergence (12WAE). Data collected were normalized using square root transformation and subjected to analysis of variance (ANOVA) using Window stat version 9.2 software developed by international crops research institute for the semi-arid tropics (ICRISAT), Hyderabad, India. The main focus in the analysis was given only to data relating MLN disease response. The statistical model used was;

$$Yij = \mu + gi + gj + sij + \varepsilon ij,$$

where: Yij is the mean value of the combination ($i \neq j$) or parental ($i = j$); μ is the general mean; *gi, gj* are the effects of the general combining ability of i^{th} and j^{th} parent respectively; *Sij* is the specific combining ability effect for the crosses. For this model to be adequate the following assumption must be considered. Firstly, it is assumed that the trait to be studied is not under the influence of the multiple allelism. Secondly there should be no maternal effects, while the genotypes studied should be a regular diploid in nature.

Table 1. Means squares for disease response among thirty maize hybrids (direct and reciprocals cross) and their parents across three locations in the Northern zone of Tanzania.

Source of variation \ Location	df	Mlangarini	Kiru Six	Ngaramtoni
		Probability level		
Replicates	2	0.6340	0.3964	0.5444
Treatments	35	5.678***	2.911***	0.072***
Parents	5	0.002***	0.018***	0.1613
Hybrids	29	5.648***	5.375***	0.00042***
Parent Vs. Hybrids	1	0.011*	0.1904	0.8021
F1's	14	7.030***	0.005**	0.00063***
Reciprocals	14	3.898***	6.541***	0.010*
Error	70			
Total	107			

Level of significance: *≤ 0.05, **≤0.01, ***≤0.001.

Table 2. Means squares for GCA, SCA and Reciprocal crosses for parents and hybrids across three locations based on disease response in the Northern zone of Tanzania.

Source of variation \ Location	df	Mlangarini	Kirusix	Ngaramtoni
		Probability		
GCA	5	5.551***	1.61***	4.527***
SCA	15	0.011*	0.0472*	0.1227
Reciprocal	15	0.4127	0.0775*	0.4919
Error	70			

Probability levels: *≤0.05, ***≤0.001

Another assumption is that there is no epistasis and each gene assorts independent of the other.

The Griffings fixed model was used since the parental materials were chosen from the population based on their known traits in order to study both GCA and SCA focusing on MLN disease response. While the GCA effects can aid breeders to exploit existing variability in breeding materials to choose genotypes having desirable attributes and to distinguish relatedness among the breeding materials (Ai-Zhi et al., 2012; Matta and Viana, 2003; Sprague and Tatum, 1942); the SCA is the manifestation of non-additive component of genetic variance and associated with interaction effects, which may be due to dominance and epistatic component of genetic variation that are non-fixable in nature. Such non-fixable components are potential parameters for heterosis breeding which is very much useful in maize and other crops where commercial exploitation of heterosis is required.

The heterotic effects of F_1 are normally estimated as percentages over mid-parent and better parent using the following formula:

Mid Parent heterosis$= \frac{\text{F1}-\text{mid parent}}{\text{Mid parent}} \text{X } 100$

Better parent heterosis $= \frac{\text{F1}-\text{Better parent}}{\text{Better parent}} \text{ X } 100$, whereby the mid parent is obtained as $\frac{\text{P1}-\text{P2}}{2}$

RESULTS

Analysis of variance showed highly significant differences among genotypes for MLN response indicating the presence of sufficient genetic variation among treatments (Table 1). On the other hand there are highly significant differences for disease resistance among parents (P≤0.001) at Mlangarini and Kiru six but not significant in Ngaramtoni.

Reciprocal effects were significant in Mlangarini and Kiru six at (P≤0.001) indicating the presence of maternal effects in controlling the disease reaction among the studied genotypes (Table 1).

Both GCA and SCA were determined in respect to disease response against maize lethal necrosis virus in the study areas. However, GCA was found to be significant at P≤0.001 than SCA (Table 2).

The parents respond differently to MLN based on their genetic background. Generally CML 144, CML 503 and CML 444 were the best combiners. However only CML 144 showed highly negative GCA which imply that it is the best combiner for disease resistance whereas CML 503 and CML 444 were found to be susceptible lines with positive and highly significant GCA effects (Table 3). Moreover, only one cross (CML 144 x CML444) showed the promising results with SCA effects of (-0.45*) in Kirusix. Other cross with significant positive SCA effect were CML312 x CML444 (0.48*) and (0.73**) in Mlangarini and Ngaramtoni respectively. For the selection purposes therefore only the crosses with significant

Table 3. GCA effects for parents and the estimate of heritabilities for disease reaction based on three locations in Northern zone of Tanzania.

Parent	Mlangarini	Kirusix	Ngaramtoni
CKH10767	0.046	-0.130	0.046
CKH114272	-0.176*	-0.130	0.046
CML144	-0.593***	-0.546***	-0.565***
CML312	-0.343***	-0.046	-0.231*
CML444	0.463***	0.231**	0.296**
CML503	0.602***	0.620***	0.407**
h^2	0.675	0.569	0.491
H^2	0.854	0.734	0.666
GCA/SCA ratio	1.894	1.726	1.403
Predictability ratio	0.791	0.775	0.737

Probability levels: *≤0.05, **≤0.01 and ***≤0.001 respectively; H^2 = Broad sense heritability; h^2 = Narrow sense heritability.

Table 4. SCA effects of 15 single cross hybrids for disease response for Mlangarini, Kirusix and Ngaramtoni in Northern zone of Tanzania.

Cross	Mlangarini	Kirusix	Ngaramtoni
CKH10767 x CKH114272	-0.10	0.16	0.04
CKH10767 x CML144	0.15	-0.09	-0.35
CKH10767 x CML312	-0.27	-0.26	-0.35
CKH10767 x CML444	0.26	-0.04	0.29
CKH10767 x CML503	0.12	0.41	0.34
CKH114272 x CML144	-0.13	0.24	-0.02
CKH114272 x CML312	-0.05	-0.09	-0.02
CKH114272 x CML444	0.48*	-0.04	0.12
CKH114272 x CML503	-0.16	-0.09	0.18
CML144 x CML312	-0.13	0.32	-0.24
CML144 x CML444	-0.10	-0.45*	-0.10
CML144 x CML503	0.43*	-0.01	0.12
CML312 x CML444	0.48*	0.38	0.73**
CML312 x CML503	0.01	0.32	-0.05
CML444 x CML503	-0.13	-0.29	0.57*

Probability levels: *≤0.05, **≤0.01 and ***0.001.

negative values are desirable for disease resistance, while the significant positive values indicate the susceptibility. In this case CML312 x CML444 will not be a useful cross (Table 4).

The estimate of narrow sense heritability (h^2) was moderate, ranging from 0.491 to 0.675 than the broad sense heritability (H^2) which ranged from 0.666 to 0.854 for the MLN. This result was in agreement with that reported by Mahmoud et al. (1990), that the low narrow sense heritability indicates that environmental factors had pronounced effects for the disease response.

On the other hand the predictability ratio ranged from 0.737 to 0.791. According to Patel et al. (2014) the predictability ratio approaching unity indicates the preponderance of additive genetic effects (Table 3).

Estimates of heterosis among mid (MP) and better (BP) parents

Heterosis is the deviation in performance among homozygous parents and their resulting off-springs. Significant differences were observed among 30 F_1 hybrids for disease response. The heterosis for the yield would have been very important information in this study. However it was not possible to obtain adequate data due to excessive missing variables on yield since most of the genotypes dead before maturity thus only heterosis for disease reaction is reported. Since disease is undesirable

Table 5. Estimation of heterosis relative to Mid-parent (MP) and better parent (BP) for disease response in three Locations in Northern zone of Tanzania.

F_1	Mlangarini			Kiru six			Ngaramtoni		
	Mean	MP	BP	Mean	MP	BP	Mean	MP	BP
CKH10767 x CKH114272	3.67	-4.35	-8.33	4.67	27.27	27.27	4.33	4.00	0.00
CKH10767 x CML144	3.67	10.00	-8.33	3.67	10.00	0.00	3.33	-16.67	**-23.08**
CKH10767 x CML312	3.67	0.00	-8.33	4.00	14.29	9.09	3.67	-8.33	-15.38
CKH10767 x CML444	4.67	16.67	16.67	4.33	0.00	-13.33	5.00	15.38	15.38
CKH10767 x CML503	4.67	3.70	-6.67	5.00	15.38	0.00	5.00	7.14	0.00
CKH114272 x CKH10767	4.00	4.35	0.00	3.33	-9.09	-9.09	4.33	4.00	0.00
CKH114272 x CML144	3.33	5.26	-9.09	4.00	20.00	9.09	3.67	-4.35	-8.33
CKH114272 x CML312	3.67	4.76	0.00	4.00	14.29	9.09	4.33	13.04	8.33
CKH114272 x CML444	5.00	**30.43****	**25.00***	4.67	7.69	-6.67	4.33	4.00	0.00
CKH114272 x CML503	4.00	-7.69	**-20.00***	4.67	7.69	-6.67	5.00	11.11	0.00
CML144 x CKH10767	3.67	10.00	-8.33	3.00	10.00	-18.18	3.33	-16.67	**-23.08**
CML144x CKH114272	3.00	-5.26	-18.18	3.33	0.00	-9.09	3.67	-4.35	-8.33
CML144 x CML312	3.00	0.00	-10.00	3.67	15.79	10.00	3.00	-18.18	-18.18
CML144 x CML444	4.00	20.00	0.00	3.33	16.67	**-33.33**	3.33	-16.67	**-23.08**
CML144 x CML503	4.00	4.35	**-20.00***	4.00	0.00	**-20.00**	4.00	-7.69	**-20.00**
CML312 x CKH10767	3.33	-9.09	-16.67	3.33	-4.76	-9.09	3.67	-8.33	-15.38
CML312 x CKH114272	3.33	-4.76	-9.09	3.67	4.76	0.00	3.67	-4.35	-8.33
CML312 x CML144	3.00	0.00	-10.00	4.00	26.32	20.00	3.33	-9.09	-9.09
CML312 x CML444	5.00	**36.36****	**25.00***	4.33	4.00	-13.33	5.00	25.00	15.38
CML312 x CML503	4.33	4.00	-13.33	5.00	20.00	0.00	5.00	15.38	0.00
CML444 x CKH10767	5.00	**25.00****	**25.00***	4.00	-7.69	-20.00	4.67	7.69	7.69
CML444 x CKH114272	4.67	**21.74***	16.67	3.67	15.38	-26.67	5.00	20.00	15.38
CML444 x CML144	3.67	10.00	-8.33	3.33	16.67	**-33.33**	4.33	8.33	0.00
CML444 x CML312	4.33	18.18	8.33	5.00	20.00	0.00	5.00	25.00	15.38
CML444 x CML503	5.00	11.11	0.00	4.67	-6.67	-6.67	4.67	0.00	-6.67
CML503 x CKH10767	5.00	11.11	0.00	5.00	15.38	0.00	5.00	7.14	0.00
CML503 x CKH114272	4.67	7.69	-6.67	4.33	0.00	-13.33	4.67	3.70	-6.67
CML503 x CML144	5.00	**30.43****	0.00	4.33	8.33	-13.33	4.33	0.00	-13.33
CML503 x CML312	4.33	4.00	-13.33	5.00	20.00	0.00	3.67	-15.38	**-26.67***
CML503 x CML444	5.00	11.11	0.00	4.67	-6.67	-6.67	4.00	-14.29	-20.00

Probability levels *≤0.05 and **≤ 0.01.

phenomenon therefore heterosis in the negative direction will be favoured in the selection of the best crosses. The exceptional crosses both positive and negative are indicated in bold (Table 5). The best cross combinations are therefore those showed significant negative values. These includes CKH 114272 X CML 503 (-20*), CML 144 X CML 503 (-20*) in Mlangarini and CML 503 x CML 312 (-26.67) in Ngaramtoni. The poor crosses are the ones showed highly significant positive values. For example CML312 x CML444 (36.36**) and CML503 x CML144 (30.43**) are among the poor crosses for disease resistance.

DISCUSSION

In respect to the experimental findings it is evident that both additive and non-additive gene effects were important with predominance of additive gene effects in inheritance of resistance trait. On the basis of general combining ability the most promising parents identified were CML144, CML312 and CKH114272. For SCA effects for disease resistance, the promising cross was CML 144 x CML444. The highly significant GCA principally imply the preponderance of additive genetic effects, therefore breeding strategy for controlling the disease is mainly to focus on developing composite or synthetic cultivars. As indicated in (Table 1), there is no significant difference among parents in Ngaramtoni location, implying that no parents showed significant resistance to MLN virus. This revealed that, there is a favourable environment for the disease progression than other locations where the study was also conducted (Figure 1). Derera et al. (2007) also found that disease

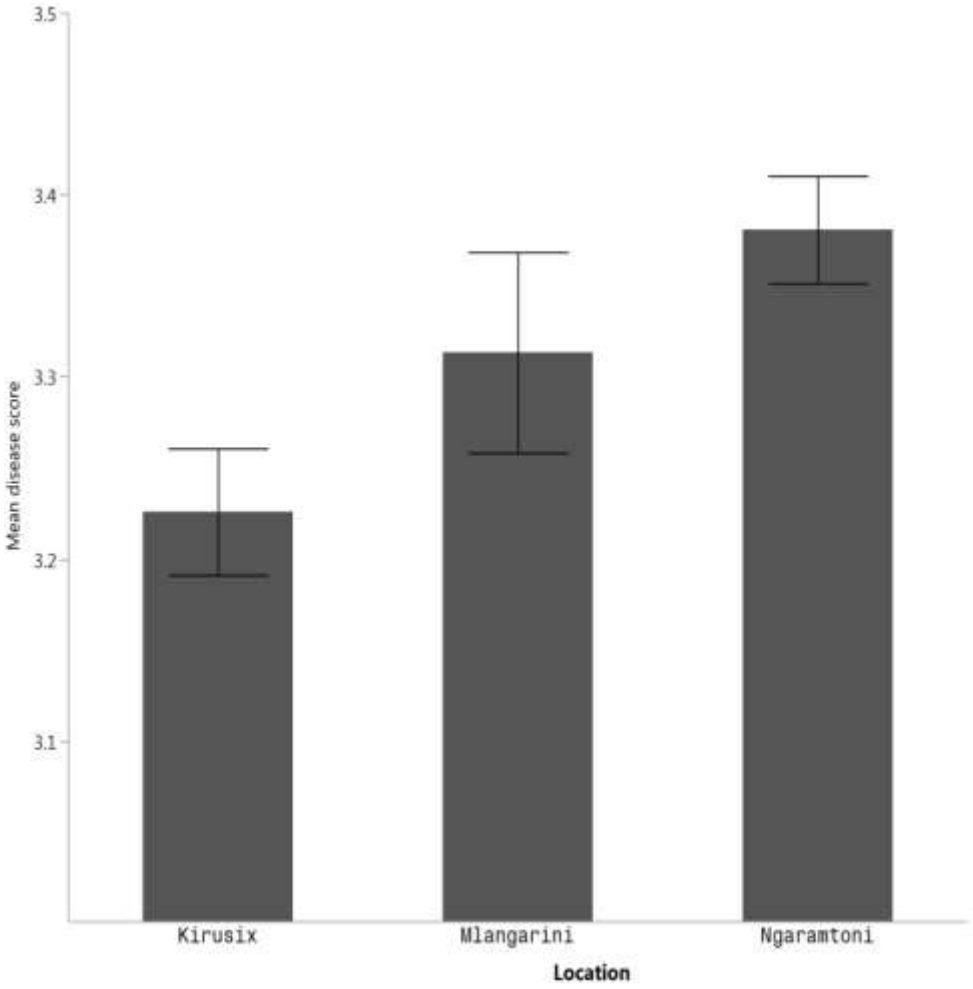

Figure 1. Multi-location evaluation trials for MLN disease response among single cross hybrids and their parents (statistics given in Table 2).

development was highly affected by the environment indicating that incidence and severity may differ between locations and seasons, and between seasons within location.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Evaluation of seventy six sugarcane families at early selection stages

Eid M. Mehareb[1], Yang kun[2], Zhao Jun[2], Fouz F Aboelenen[1], Qin Wei[2], Zan Fenggang[2], Liu Jiayong[2], Xia Hongming[2], Yao Li[2], Zhao Peifang[2], Zhao Yong[2] and Wu Caiwen[2*]

[1]Sugar Crops Research Institute, Agriculture Research Center, Egypt.
[2]Sugarcane Research Institute, Yunnan Academy of Agriculture Science, China.

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An experiment was conducted on sugarcane families belonging to the early selection stage of the Sugarcane Research Institute, Kaiyuan, Yunnan Academy, China, to evaluate them for the selection of superior families for the later stages of the breeding program. Seventy-six full-sib families and check variety were evaluated. The experiment was conducted during two growing seasons, corresponding to the plant cane and first ratoon, 2015/2016 and 2016/2017, respectively. The traits of cane yield (TCH) and juice quality were measured. Results indicate the use of the traits with high heritability as selection criteria together with sugar yield (TSH) could lead to genetic improvement in TSH. The study indicated that high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for TCH (22.85 and 27.74) and TSH (22.66 and 28.08). The results also revealed that seven families *viz.*, LC03-1137×YZ89-7, LC03-1137×PS45, YT93-159×YR11-95, YR05-346×YZ05-51, FN38×GT96-211, YR10-509×FR96-405 and YT03-373×YR08-1276 were the best families across all other bi-parental families for most studied traits at early selection stages suggesting the possibility of evaluation of a large number of clones of these families, followed by selection of superior clones within these families during the next selection stages.

Key words: Sugarcane, family selection, heritability, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), plant cane, first ratoon.

INTRODUCTION

Sugarcane (*Saccharum* spp., L) is one of the major cash and industrial crops in the world. It is a source of raw material to sugar industry and various agro-based industries. New sugarcane varieties are developed through the selection of vegetatively propagated clones obtained from true seeds that are derived from the hybridization of superior parents. Individual selection during the initial stage is of low efficiency given the low broad sense heritability for the majority of traits (Skinner, 1982). Several research projects demonstrated that family selection, when followed by individual clone selection, was superior in terms of genetic gain and more cost effective than either family or individual clone selection alone (Kimbeng and Cox, 2003). Evaluation of a large number of clones for families, then the possibility of selection of superior clones within these families during

*Corresponding author. E-mail: gksky_wcw@163.com.

the next selection stages have also been reported (Skinner et al., 1987; Cox and Hogarth, 1993; Shanthi et al., 2008; Stringer et al., 2010; Mahmoud et al., 2012).

Heritability values are categorized as low (0 to 30%), moderate (30 to 60%) and high (60% and above) as stated by Robinson et al. (1949). Also PCV and GCV values are ranked as low, medium and high with 0 to 10, 10 to 20 and >20%, respectively (Shivasubramanian and Menon, 1973). Silva et al. (2002) estimated the variability among 18 families of sugarcane for stalk height, stalk diameter, average brix, stalk number and stalk weight. Their results showed highly significant differences among families for most traits. Oliveira et al. (2009) evaluated 80 full-sib sugarcane families for yield of canes per hectare. They observed significant differences among evaluated crosses. Heritability of traits on individual basis was of medium magnitude (0.22), while heritability on family mean basis was 0.73, indicating the effectiveness of family selection at early stages. Mehareb and Abazied (2017) estimated genetic variability, and found high genetic variance (σ^2g) relative to environmental variance for all traits under study across seasons. The highest values of PCV and GCV were observed for reducing sugar (54.31 and 47.22%, respectively) followed by TSH (19.85 and 19.24%, respectively), respectively. Heritability estimates exceeded 80% for all studied traits, except for purity and reducing sugar. The objective of this study was to evaluate 76 sugarcane families of the Sugarcane Research Institute, Kaiyuan, Yunnan Academy, China and make selection intensity under 10% based on TSH at early selection stages.

MATERIALS AND METHODS

Plant material and experimental conditions

The study was carried out at breeding nursery of Sugarcane Research Institute, Yunnan Academy, China. Materials of sugarcane (*Saccharum* spp.) consisted of seventy six bi-parental crosses (families) that could be considered representative of the sort of breeding materials processed in the sugarcane breeding program in China. The seventy six bi-parental (7752 seedlings) hybrid combinations which correspond to the 2014 series were crossed in three crossing locations; Hainan, Kaiyuan and Ruili (Table 1).

Seeds (fuzz) were germinated in the greenhouse in March 2015. A total of 7752 and discussions seedlings from 76 families were transplanted in field in June, 2015. Check variety (ROC22) buds were planted in the greenhouse in May, 2015. After buds germination, they were transplanted with families' seedling in field during the first week June, 2015. After harvested plant cane in January 2016, the first ratoon was harvested in January, 2017. The field was irrigated right after planting and all other agronomic practices were carried out as recommended as at when due.

Experimental design and data collection

The experiment was arranged in a randomized complete block design. Each family had three replicates and 34 seedlings per replicate, each replicate had two rows per plot (17 seedlings per row), length 6 m and space 1 m per row with three replications. Each family was represented in the experiment by a random selection of 34 seedlings. The following traits were measured for each family:

1. Traits of cane yield and its contributing traits:

a. Stalks number per stool.
b. Stalk length (cm) was measured from soil surface to the visible dewlap.
c. Stalk diameter (cm) was measured at mid stalk with no reference to the bud groove.
d. Stalk weight (kg) was calculated by dividing cane yield per stool by number of stalks per stool.
e. Ton cane per hectare (TCH) was calculated on a plot basis.
f. Stool weight (kg) was calculated by dividing cane yield per stools by number of stools per plot.

2. Juice quality traits and TSH:

a. Brix (percent soluble solids) was determined with a hydrometer.
b. Ton sugar hectare (TSH) was calculated according to the formula (Wu et al., 2009):

$$\text{Sugar yield (TSH)} = \frac{\text{Cane yield} \times \text{Sugar content}}{100}$$

3. Disease and other characters:

a. $$\text{Mosaic \%} = \frac{\text{Number of mosaic plants}}{\text{Number of plants per family}} \times 100$$

b. Smut: From 0 to 9 (0, 1, 2 resistant, 3, 4 tolerant 5 intermediate and 6, 7, 8, 9 susceptible)
c. Pithiness: From 0 to 4 (0 not pithiness).

Statistical analysis

Analyses of variance were performed for the collected data according to Gomez and Gomez (1984) using MSTAT-C computer package by Freed et al. (1989). The comparison among means was done using the least significant difference (LSD) test at 5% level of probability. Variance components were calculated by equating appropriate mean squares for the differences among genotypes to their expectations and solving for the components. Broad-sense heritability (H%) was estimated using variance components following the formula (Allard, 1960):

$H\% = (\sigma^2g / \sigma^2ph) \times 100$

Where, σ^2g and σ^2ph are genotypic and phenotypic variances respectively.

Estimation of variance components

Genotypic and phenotypic components of variance were estimated according the following formulae:

Genotypic variance (σ^2g) = $g_{MS} - E_{MS}$
Phenotypic variance (σ^2p) = $\sigma^2g + E_{MS}$

Where, g_{MS} refers to genotypic mean squares and E_{MS} refers to error mean squares.

Coefficient of variability

Both genotypic and phenotypic coefficients of variability were

Table 1. Bi-parental hybrid families of experimental sugarcane pedigree and origin.

Family code	Female	Male	Site of crossing	Family code	Female	Male	Site of crossing
1	LC03-1137	YZ89-7	Hainan	39	YR11-256	RB85-5156	RuiLi
2	YZ89-7	CP89-2143	Hainan	40	LC03-182	YR11-101	RuiLi
3	YT01-127	ROC10	Hainan	41	ZZ92-126	YR06-2885	RuiLi
4	LC05-136	ROC25	Hainan	42	YR05-326	CP86-1664	RuiLi
5	NJ97-128	YT00-236	Hainan	43	YR11-98	FR93-1054	RuiLi
6	ROC10	FN95-1702	Hainan	44	YZ08-1606	YR05-157	RuiLi
7	YT93-159	NJ97-128	Hainan	45	YZ03-194	YR11-103	RuiLi
8	YT00-236	LC03-1137	Hainan	46	DZ07-36	YR06-4806	RuiLi
9	GT94-119	ROC10	Hainan	47	YR11-256	FN39	RuiLi
10	CT88-898	YZ08-2060	Kaiyuan	48	FR96-405	DZ93-88	RuiLi
11	FN38	GT96-211	Kaiyuan	49	YZ07-2007	YR05-770	RuiLi
12	YZ07-2800	YZ05-51	Kaiyuan	50	YT82-882	YR11-103	RuiLi
13	YZ04-241	VMC92-228	Kaiyuan	51	LC05-136	YR05-770	RuiLi
14	YZ05-51	Q96	Kaiyuan	52	YZ08-2138	YR05-784	RuiLi
15	SP80-3280	RB85-5156	Kaiyuan	53	YR11-101	FN39	RuiLi
16	RB85-5156	SP80-3280	Kaiyuan	54	YR11-95	LZ2	RuiLi
17	YZ04-241	YY07-70	Kaiyuan	55	LC05-136	YR05-157	RuiLi
18	CT88-87	YZ07-2384	Kaiyuan	56	YR05-285	RB85-5156	RuiLi
19	YY07-70	YZ04-241	Kaiyuan	57	ROC22	YR11-103	RuiLi
20	YL7	F128	Kaiyuan	58	YR11-256	YZ08-1606	RuiLi
21	SP80-3280	YY11-32	Kaiyuan	59	SP80-3280	LC03-1137	RuiLi
22	SP80-3280	YY07-65	Kaiyuan	60	YZ05-51	YR05-157	RuiLi
23	RB85-5156	YY07-124	Kaiyuan	61	YT03-373	YR08-1276	RuiLi
24	YZ07-2138	YY03-188	Kaiyuan	62	LC03-182	FR96-405	RuiLi
25	YZ08-2060	CT88-898	Kaiyuan	63	YR11-256	DZ93-88	RuiLi
26	CT99-8602	YZ08-1609	Kaiyuan	64	YR09-928	LC05-136	RuiLi
27	RB85-5156	YT93-159	Kaiyuan	65	QZ06-156	YR11-95	RuiLi
28	CP94-1100	YR11-103	RuiLi	66	YR10-509	FR96-405	RuiLi
29	YR11-98	CP94-1100	RuiLi	67	Q166	YR07-928	RuiLi
30	YZ03-194	YR11-95	RuiLi	68	CT89-103	YR10-550	RuiLi
31	YR11-256	YG35	RuiLi	69	YR05-346	YZ05-51	RuiLi
32	YT93-159	YR11-95	RuiLi	70	LC03-182	PS45	RuiLi
33	RB85-5156	YR99-151	RuiLi	71	Q171	YR05-326	RuiLi
34	LC03-1137	PS45	RuiLi	72	ZZ99-213	YR05-282	RuiLi
35	YR11-256	DZ03-68	RuiLi	73	LC03-182	YZ05-51	RuiLi
36	YZ06-267	YR11-103	RuiLi	74	FN91-21	YZ05-51	RuiLi
37	YT00-236	YR05-189	RuiLi	75	YZ06-407	DZ93-94	RuiLi
38	DZ93-94	YR11-101	RuiLi	76	FN1110	YZ05-51	RuiLi
77	ROC22 (check variety)						

computed for each character according to Burton and De Vane (1953):

1. Genotypic coefficient of variation (GCV) was estimated as: (GCV)% = (σg/general mean) × 100%.
2. Phenotypic coefficient of variation (PCV) % was estimated as: (PCV) % = (σp/general mean) × 100%. Where, σg = genotypic standard deviation and σp = phenotypic standard deviation.

RESULTS AND DISCUSSION

Data presented in Table 2 show that the analysis of variance for all the studied characters revealed highly significant differences ($p < 0.01$) among all evaluated treatments (families and check). This indicates the existence of sizable variability and that considerable improvement can be achieved in these characters by selection; however, there was no significance for blocks. The mean squares due to families differed significantly for all studied characters, indicating sufficient genetic variation in genotypes for all the studied characters. Similar results were outlined by Silva et al. (2002) and Oliveira et al. (2009).

Table 2. Mean squares of studied traits.

SV	DF	Stalk number/stool	Stalk length	Stalk Diameter	Stalk weight	Stool weight
Blocks	2	1.30	577.23	0.01	0.02	1.54
Treatments	76	1.71**	1375.50**	0.11**	0.15**	3.84**
Families	75	1.71**	1336.80**	0.11**	0.14**	3.86**
F vs. check	1	1.36	4278.05**	0.19*	0.61**	1.69
Error	152	0.91	322.12	0.04	0.04	1.70
SV		**TCH**	**Brix**	**TSH**	**Pithiness**	**Mosaic**
Blocks	2	329.95	4.98	28.10	1.38	0.40
Treatments	76	1946.68**	3.01**	68.03**	0.72**	0.51**
Families	75	1933.32**	3.05**	67.55**	0.73**	0.50**
F vs. check	1	2948.52*	0.03*	103.56*	0.08	1.08*
Error	152	632.96	1.30	23.94	0.22	0.21

Highly significant ($p < 0.01$) variance estimates of families versus checks were found for stalk height and stalk weight, while significant differences ($p < 0.05$) were found for stalk diameter, TCH, brix, TSH and mosaic, whereas none significant differences were found for Stalk number/stool and weight/ stool.

For pithiness character, there was no significant between families and check variety. This may indicate that the evaluated new families do not have pith value as check variety. Similar results were reported by Tahir et al. (2014) who observed significant differences for the contrast of the checks versus new genotypes for the parameters.

Performance of families (bi-parental crosses)

Table 3 reveals that stalks length, stalk diameter and stalk weight varied significantly among evaluated crosses. Stalk length varied from 177.67 cm for the cross 8 (YT00-236×LC03-1137) to 291.00 cm for the check cultivar ROC22. Stalk diameter differed significantly among the evaluated families, stalk diameter varied from 2.01 cm for the cross 63 (YR11-256×DZ93-88) to 305 cm for cross 7 (YT93-159×NJ97-128), two families; 7 (YT93-159×NJ97-128), 5 (NJ97-128×YT00-236) (2.96 cm), recorded significantly greater stalk diameter values than the check variety ROC22 (2.65 cm). Stalk weight differed among the evaluated families, stalk weight varied from 0.59 kg for the cross8 (YT00-236 xLC03-1137) to 1.85 kg for cross 7 (YT93-159×NJ97-128), the family 8 (YT00-236×LC03-1137) which produced the lowest stalk weight (0.59 kg) was found to be inferior for both stalk length (177.67 cm) and stalk diameter (2.04 cm). This was in agreement with previous results (Mehareb et al., 2015) in which the family which produced the lowest stalk weight was found to be inferior for both stalk diameter and stalk length. The cross 7 (YT93-159×NJ97-128) recorded the highest mean stalk weight 1.85 cm, which was 114.9% of the mean of the check cultivar (1.61 kg). Stool weight varied significantly among the evaluated families, and ranged from 7.87 kg for the cross 7(YT93-159×NJ97-128), which recorded significantly greater stool weight values than the check variety ROC22 (5.41 kg) and 1.53 kg for cross 8 (YT00-236×LC03-1137).

Most of the crosses had higher number of stalks/stool than Roc22 (58 crosses), but ten families: 31(YR11-256×YG35), 63(YR11-256×DZ93-88), 25(YZ08-2060×CT88-898), 50(YT82-882×YR11-103), 15(SP80-3280×RB85-5156), 61(YT03-373×YR08-1276), 32(YT93-159×YR11-95), 45(YZ03-194×YR11-103), 37(YT00-236×YR05-189) and 29 (YR11-98×CP94-1100), recorded significantly greater number of stalks/stool (6, 5.58, 5.50, 5.50, 5.18, 5.17, 5.04, 5.01, 4.97 and 4.95), respectively. Seven families; 1 (LC03-1137×YZ89-7), 34 (LC03-1137×PS45), 32 (YT93-159×YR11-95), 61 (YT03-373×YR08-1276), 69 (YR05-346×YZ05-51), 66(YR10-509×FR96-405) and 11 (FN38×GT96-211) had the highest means of TCH (158.24 , 148.69 ,142.34, 137.61, 136.07, 125.09 and 122.82 t/ha, respectively), which were 129 , 121.21, 116.04, 112.18, 110.93, 101.97 and 100.13%, respectively of the mean of TCH for the check cultivar ROC22 (122.67 t/ha), respectively.

Data in Table 3 revealed that brix percentage, TCH and TSH varied significantly among evaluated crosses. Majority (about 36) of the families had higher brix percentage values than the check variety ROC22 (22.74%).

Selected 10% selection intensity based on TSH

Figure 1 presents 10% selection intensity based on TSH. Results reveals that seven bi-parental crosses *viz.*, LC03-1137×YZ89-7, LC03-1137 × PS45, YT93-159 × YR11-95, YR05-346 × YZ05-51, FN38× GT96-211, YR10-509×FR96-405 and YT03-373×YR08-1276 were higher than check variety ROC22, recorded greater TSH, gave

Table 3. Means value of some traits of the studied sugarcane families.

Family code	Stalks number/stool	Stalk length (cm)	Stalk diameter (cm)	Stalk weight (kg)	Stool weight (kg)	TCH (tones)	Brix (%)	TSH (tones)	Pithiness (%)
1	4.38	283.00	2.65	1.56	6.81	158.24	18.59	29.43	1.93
2	4.14	216.70	2.20	0.82	3.43	58.19	15.03	8.65	1.73
3	4.00	210.30	2.42	0.97	3.72	58.91	18.25	10.80	1.27
4	2.92	245.70	2.39	1.09	3.23	68.70	18.97	13.10	1.20
5	3.17	253.70	2.96	1.74	5.73	94.76	18.31	17.19	2.27
6	3.25	191.60	2.40	0.87	2.74	43.74	18.06	7.88	1.33
7	4.15	252.90	3.05	1.85	7.87	115.87	16.20	19.26	2.50
8	2.49	177.70	2.04	0.59	1.53	31.34	18.25	5.68	1.33
9	3.71	248.00	2.60	1.33	4.89	109.01	19.44	21.19	2.07
10	3.14	218.20	2.06	0.73	2.32	40.15	17.65	7.07	1.60
11	4.26	243.30	2.55	1.24	5.29	122.82	19.24	23.58	1.80
12	3.50	277.50	2.40	1.26	4.53	95.54	18.78	17.99	1.00
13	3.12	259.30	2.28	1.06	3.30	78.80	18.83	14.81	1.80
14	2.88	225.70	2.37	0.99	2.93	61.14	19.31	12.06	1.07
15	5.18	260.00	2.46	1.23	6.37	101.58	18.68	19.00	1.47
16	4.18	267.00	2.28	1.09	4.55	92.38	19.04	17.62	1.67
17	3.27	245.00	2.36	1.07	3.52	76.19	17.26	13.13	1.40
18	4.72	259.70	2.31	1.09	5.23	110.79	18.43	20.56	1.73
19	3.36	226.80	2.43	1.05	3.56	68.19	17.84	12.28	1.60
20	4.09	252.30	2.25	1.00	4.20	92.82	17.93	16.60	2.73
21	3.98	230.50	2.45	1.09	4.32	83.54	18.99	15.89	1.33
22	3.58	234.10	2.20	0.90	3.28	61.47	17.32	11.07	1.60
23	4.11	258.30	2.21	0.98	4.17	53.44	18.89	10.19	1.73
24	3.81	231.30	2.62	1.26	4.80	76.31	18.75	14.41	1.33
25	5.50	228.50	2.38	1.02	5.59	102.55	17.98	18.50	1.50
26	3.06	240.30	2.33	1.03	3.15	53.68	20.85	11.15	1.40
27	4.63	268.70	2.29	1.11	5.25	87.36	18.32	15.94	1.67
28	4.41	255.00	2.17	0.94	4.25	103.79	19.45	20.28	1.47
29	4.95	279.00	2.31	1.16	5.76	112.92	19.49	21.91	1.67
30	4.43	256.70	2.34	1.10	4.88	93.62	19.33	18.03	1.47
31	6.00	245.70	2.17	0.91	5.42	121.26	17.88	21.61	2.20
32	5.04	263.00	2.51	1.30	6.53	142.34	18.37	26.17	1.33
33	4.03	261.00	2.42	1.20	4.91	89.63	19.41	17.30	1.27
34	4.56	278.60	2.51	1.37	6.29	148.69	19.66	29.25	2.47
35	3.63	250.00	2.39	1.12	4.07	92.86	18.05	16.61	1.73
36	4.43	253.70	2.23	1.00	4.39	98.50	17.40	17.36	1.13
37	4.97	230.70	2.55	1.20	5.72	94.20	17.21	16.23	1.80
38	3.31	259.70	2.10	0.90	2.97	49.62	18.16	9.05	1.73
39	4.35	244.50	2.36	1.07	4.67	94.26	18.00	17.03	2.10
40	4.24	286.30	2.21	1.13	4.98	101.69	19.84	20.03	1.67
41	3.72	260.00	2.58	1.34	4.97	115.08	18.52	21.47	2.07
42	4.27	266.00	2.48	1.28	5.47	107.47	19.52	21.02	3.27
43	3.31	243.70	2.43	1.15	3.53	65.59	16.77	11.00	1.73
44	3.37	251.80	2.53	1.26	4.24	77.03	18.69	14.54	2.13
45	5.01	259.70	2.20	0.99	4.86	79.61	16.47	13.39	1.53
46	3.12	263.00	2.41	1.20	3.74	58.71	18.48	10.79	1.67
47	4.81	248.70	2.51	1.23	5.93	102.57	19.15	19.68	1.60
48	3.34	251.00	2.41	1.13	3.77	87.61	20.01	17.61	2.13
49	3.69	237.00	2.32	1.01	3.65	66.50	18.65	12.45	2.27

Table 3. Contd.

50	5.50	252.30	2.20	0.96	5.29	119.23	18.35	21.89	1.93
51	4.19	237.10	2.41	1.10	4.49	77.96	18.47	14.49	1.33
52	4.08	238.00	2.65	1.32	5.32	97.40	18.11	17.63	1.27
53	4.22	249.30	2.24	0.98	4.07	90.95	18.64	17.06	1.80
54	4.86	276.70	2.44	1.29	6.29	122.23	16.99	20.78	2.07
55	3.21	236.30	2.51	1.20	3.91	77.43	19.08	15.01	1.53
56	2.37	267.30	2.86	1.72	4.13	87.70	20.16	17.91	2.67
57	4.79	261.70	2.17	0.97	4.68	108.72	18.09	19.66	1.47
58	3.94	246.00	2.56	1.26	4.94	90.32	16.66	15.12	2.13
59	4.77	276.30	2.61	1.48	7.16	96.13	18.12	17.45	2.13
60	3.61	271.30	2.43	1.26	4.57	91.37	18.97	17.35	1.93
61	5.17	233.00	2.68	1.32	6.35	137.61	16.49	22.86	1.33
62	4.28	268.80	2.10	0.93	3.97	81.85	19.35	15.87	1.53
63	5.58	289.00	2.01	0.93	5.09	109.20	19.92	21.77	3.67
64	3.13	243.50	2.50	1.19	3.84	49.17	18.80	9.10	2.20
65	4.49	261.30	2.23	1.02	4.60	84.38	17.85	15.00	1.67
66	4.48	283.30	2.31	1.19	5.33	125.09	18.68	23.36	2.27
67	3.80	289.50	2.52	1.45	5.45	104.37	18.96	19.80	1.30
68	3.85	271.50	2.37	1.19	4.59	91.29	18.22	16.63	1.60
69	4.66	269.30	2.45	1.27	5.72	136.07	17.35	23.62	1.00
70	2.98	269.70	2.41	1.24	3.68	72.30	19.08	13.72	1.67
71	4.53	279.70	2.40	1.28	5.66	94.87	18.38	17.42	1.40
72	3.72	276.30	2.63	1.50	5.58	117.14	17.59	20.57	2.93
73	3.59	268.80	2.45	1.27	4.47	89.22	19.87	17.60	1.47
74	3.34	267.30	2.54	1.35	4.50	97.51	17.03	16.51	1.73
75	3.75	255.00	2.31	1.08	3.99	84.88	19.01	16.06	1.67
76	3.66	238.00	2.55	1.22	4.54	88.95	18.70	16.46	1.50
77	3.35	291.00	2.65	1.61	5.41	122.67	18.53	22.74	1.60
LSD	1.54	28.95	0.31	0.30	2.10	29.60	1.84	5.64	0.76

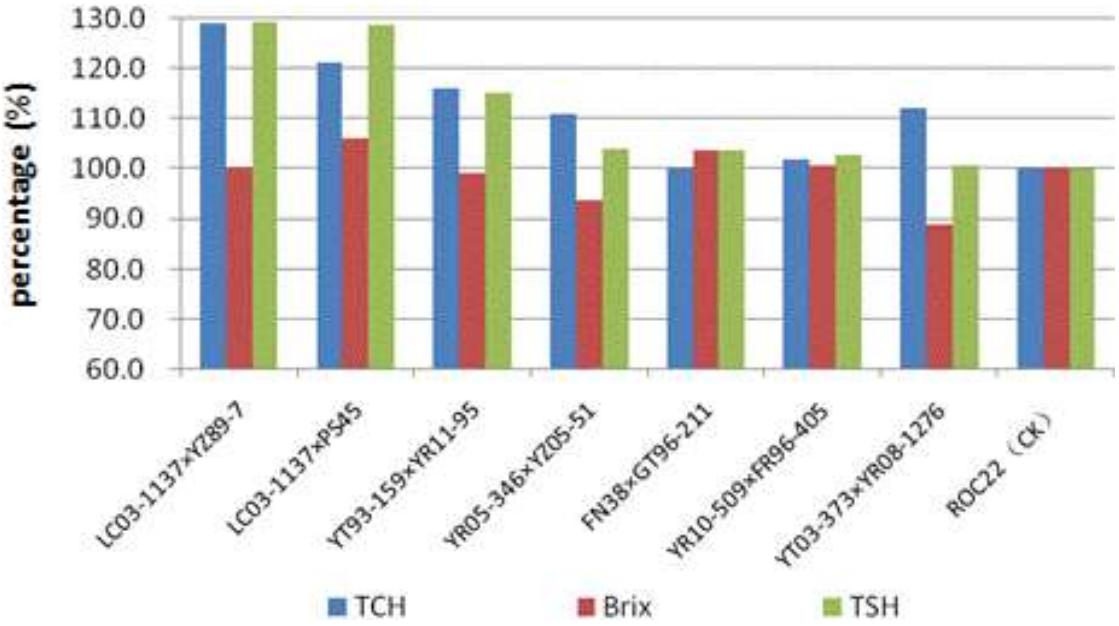

Figure 1. 10% selection intensity based on TSH.

Figure 2. Disease (mosaic) resistance for 10% selection intensity based on TSH.

the highest means of TSH (29.43, 29.25, 26.17, 23.62, 23.58, 23.36 and 22.86 t/ha, respectively, TSH in Table 3), which were 129.44, 128.63, 115.11, 103.88, 103.69, 102.74 and 100.53% of the mean of the check cultivar ROC22 (22.74 ton/hectare), respectively. These were the best crosses across all other bi-parental crosses for most studied traits either in plant cane or in first ratoon crops, suggesting the possibility of evaluation of a large number of clones of these bi-parental crosses, followed by selection of superior clones within these crosses during the next selection stages (Skinner et al., 1987; Cox and Hogarth, 1993; Shanthi et al., 2008; Stringer et al., 2010; Mahmoud et al., 2012). Data in Figure 2 showed that the highest infection with mosaic showed by the check cultivar ROC22 so, all families were more resistance than the check variety and all families do not show any infection by smut.

Genetic components

Genetic variance is important as it describes the amount of genetic variation present for the trait. Table 4 shows high genetic variance (σ^2g) relative to environmental variance for all traits under study expect for Stalk number/stool. The results also indicate that high estimates of genotypic and phenotypic coefficients of variation GCV and PCV were recorded for TCH (22.85 and 27.74), TSH (22.66 and 28.08) and Pithiness (23.27 and 27.88). High genotypic and phenotypic coefficients of variation for TCH were reported earlier by Singh and Sangwan (1980). Traits exhibiting relatively high GCV estimates may respond favorably to selection. However medium estimates of GCV and PCV were recorded for stool/row (10.67 and 13.93), stalk number/stool (12.86 and 18.79), weight/ stalk (16.08 and 19.21) and Mosaic (14.71 and 19.28) for as much medium estimates of GCV and high estimates of PCV were recorded for weight/stool (18.27 and 24.36), while, height (7.27 and 8.33), diameter (6.49 and 8.31) and brix (4.12 and 5.48) resulted in low estimates of GCV and PCV.

In present study, high heritability (broad sense) estimates were recorded for height (75.90%), stalk weight (75.04%), pithiness (69.18%), TCH (67.26%), stalk diameter (66.19%) and TSH (64.57%). This suggests that a large proportion of the total variance is heritable and selection of these traits would be effective. High values of GCV and PCV were coupled with high heritability and high genetic advance for TCH, TSH and pithiness. Knowledge of variability and heritability of characters is essential for identifying those amenable to genetic improvement through selection (Vidya et al., 2002).

Results of the current study indicate that use of the traits with high heritability as selection criteria together with TSH could lead to genetic improvement in TSH. The effectiveness of selection depends not only on heritability but also on genetic advance (Butterfield and Nuss, 2002). In this respect, Gupta and Chatterjee (2002), Agrawal (2003), Delvadia and Patel (2006) and Patel et al. (2006) reported that high heritability with high genetic advance

Table 4. Genetic parameters of evaluated traits of the studied sugarcane families.

Parameter	Stalk number/stool	Stalk length	Stalk diameter	Stalk weight	Stool weight
σ^2 ph	0.57	445.60	0.04	0.05	1.29
σ^2 e	0.30	107.37	0.01	0.01	0.57
σ^2g	0.27	338.23	0.02	0.03	0.72
H %	47.02	75.90	66.19	75.04	56.08
GCV%	12.86	7.27	6.49	16.08	18.27
PCV%	18.79	8.33	8.31	19.21	24.36
GA 20%	12.37	8.85	7.70	20.18	19.13
	TCH	**Brix**	**TSH**	**Pithiness**	**Mosaic**
σ^2 ph	644.44	1.02	22.52	0.24	0.17
σ^2 e	210.99	0.43	7.98	0.07	0.07
σ^2g	433.45	0.58	14.54	0.17	0.10
H %	67.26	57.30	64.57	69.18	58.59
GCV%	22.85	4.12	22.66	23.27	14.71
PCV%	27.74	5.48	28.08	27.88	19.28
GA 20%	26.12	4.40	25.38	27.00	15.82

were observed for TSH, indicating the presence of additive gene action and that the direct selection for the trait was effective.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Performances of selected tropical white maize single-cross hybrids for yield and yield attributing traits

Yazachew Genet Ejigu[1,2*], Pangirayi Bernard Tongoona[2] and Beatrice Elohor Ifie[2]

[1]Ethiopian institute of Agricultural Research, Ethiopia.
[2]West Africa Centre for Crop Improvement, University of Ghana, PMB 30, Legon, Accra, Ghana.

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In Ghana, the production of hybrid maize is at its infant stage, occupying only about 3% of the area devoted for maize production. Therefore, the yields of this crop are low, 1.7 t ha^{-1} due to the use of open pollinated varieties (OPVs), shortage of high yielding varieties, biotic and abiotic stresses. Thus, the present study was designed to identify superior crosses based on their agronomic performance. Thirty-two hybrids and three checks were evaluated using a 5 x 7 alpha lattice design replicated twice at the University of Ghana, WACCI research farm during 2015/-16 offseason using drip irrigation. Analysis of variance revealed that genotype mean squares were highly significant (P ≤ 0.001) for days to 50% anthesis and silking, plant and ear height, plant aspect, ear length, number of kernel rows ear^{-1}, number of kernels row^{-1} and yield. Similarly, mean squares of genotypes were significant (p ≤ 0.05) for ear rots, anthesis-silking interval, and husk cover. Based on the mean grain yield performance, six promising single crosses, L8 x T2, L1 x T2, L16 x T1, L16 x T2 L4 x T2, L9 x T1 having grain yield of 6377, 6011, 5848, 5222, 5150 and 5135 kg ha^{-1}, respectively were identified as possible candidates for release after establishing the stability of their performance in multi-locational trials and should be promoted for adoption and commercialization in the country.

Key words: Grain yield, hybrids, maize, single crosses.

INTRODUCTION

In Ghana, maize is the major crop in terms of area coverage and 2nd staple food after rice where it is mainly, consumed among households (MoFA., 2011). However, low yields of 1.7 t ha^{-1} has been reported in Ghana as compared to 6.0 (China) and 9.9 t ha^{-1} (U.S.A) (FAOSTAT, 2013). This prominent difference in grain yields has been attributed partially to the use of open pollinated varieties (OPVs), shortage of high yielding varieties, biotic and abiotic stresses (Fening et al., 2011; Ragasa et al., 2013). MoFA (2011) reported that attainable grain yields of about 6 t ha^{-1} have been recorded in maize yield variety trials. This report therefore shows that the average maize yield of 1.7 t ha^{-1} currently found in Ghana, is about 70% less than that obtained in maize yield varietal trials by researchers. Efforts are being made to bridge the gap between the present low

*Corresponding author. E-mail: yazachewgenet@gmail.com.

grain yield and the attainable grain yield by promoting the use of superior hybrid maize varieties. At present, there is a growing demand for use of hybrid seeds and this has an effect in the driving of the emergence of seed companies in Ghana (Ragasa et al., 2014). Studies have shown that single cross hybrids have uniform production, are higher yielding and more stable in performance as well as in other plant characteristics. Divan et al. (2013) reported that single cross hybrid seed was higher yielding in many parts of the world, due to the expression of heterosis (hybrid vigor).

So far, in Ghana, the production of hybrid maize is at its infant stage, occupying only about 3% of the area devoted for maize production in Ghana (Ragasa et al., 2013). This may be due to lack of superior hybrids as compared to open pollinated varieties, which farmers can readily adopt. Ragasa et al. (2014) showed that there is a demand to develop superior white maize varieties because of the increasing population, urbanization, poultry and fish sectors in Ghana.

Therefore, the objective of this study was to identify superior single crosses based on their agronomic performances.

MATERIALS AND METHODS

Description of experimental area

The experiment was conducted during 2015/16 offseason using drip irrigation at research field of West Africa Centre for Crop Improvement, University of Ghana. The University is located at 5.6508° N, latitude and 0.1869°W longitude and an altitude of 97 m above sea level (m.a.s.l).

Genetic materials used for the study

Eighteen white tropical maize inbred lines with diverse genetic backgrounds were selected from the pool of inbred lines at the West Africa Centre for Crop Improvement (WACCI). This comprises of ten lines from the International Institute for Tropical Agriculture (IITA), six from International Maize and Wheat improvement Center (CIMMYT) and the two testers 1368 from IITA and CML 444 from CIMMYT maize breeding programmes. The 16 inbred lines were crossed to the two testers using the line by tester mating method and it generated 32 (16 × 2) cross combinations.

Development of single cross hybrids

Emerging ears of each female parent were covered with shoot bags before silk emergence to prevent contamination with unwanted pollen. The tassels of the male parents (testers) were covered with tassel bag when one-fourth of the tassel had dehisced. Self-pollination from three to five plants per plot was done for all parental lines to bulk seeds of parental lines for future breeding. Pollination was done when a uniform growth of the silk was visible on the covered ears. The tassel bag containing freshly shed pollen was transferred over the silks after removing the shoot bags from the ears. Before putting tassel bags on the tassel, all details like date of pollination and labels were clearly written on the bags by waterproof pencil. In order to avoid contamination and to get enough fresh pollen, the tassel bags were put on tassel one day earlier than the intended pollination date. The tassel bags were held in position with the help of paper clips.

Data analysis and procedures

Analysis of variance for all agronomic parameters studied was calculated using the PROC GLM procedure and test for significant differences among the genotypes was performed using SAS software (SAS, 2002).

RESULTS AND DISCUSSION

The mean performances of genotypes included in the study were computed for traits, which showed significant mean squares difference. Days to 50% anthesis ranged from 52 (L8 × T1 and L8 × T2) to 59 days (L3 × T1) with the overall mean of 56 days (Table 1). Testcrosses, L5 × T1, L5 × T2, L6 × T1, L6 × T2, L9 × T1, L11 × T1, L11 × T2 and L15 × T1 demonstrated significant fewer days than the hybrid between the two testers check (1368 x CML 444). L8 × T1 and L8 × T2 showed significant fewer days to 50% anthesis than the checks Obatanpa and Mamaba. On the other hand, 13 crosses revealed statistically the same days to 50% anthesis with checks Obatanpa and Mamaba. Days to 50% silking showed a similar pattern to days to anthesis and varied from 53 to 60 for L8 × T1 and L3 × T1, respectively. L5 × T1, L5 × T2, L8 × T1, L8 × T2, L9 × T1, L11 × T2 and L15 × T1 had significant fewer days to 50% silking than the three checks. Five testcrosses had the same days to 50% silking as the hybrid check 1368 × CML 444. Mean performance for anthesis-silking interval manifested that most of crosses had shorter anthesis-silking intervals than checks Obatanpa and Mamaba which indicate that there was better synchronization of anthesis and silking for crosses. Similar findings to this result were reported by pervious investigators (Abrha et al., 2013; Hosana et al., 2015)

Mean performance of maize streak disease scored demonstrated that there were crosses, which had less disease scored than cheeks. It indicated that some testcrosses had better gene resistance to maize streak virus. From the results, except for L15 × T2, all testcrosses showed significant better performances than the commercial hybrid check (Mamaba). Similarly, L8 × T2, L7 × T1 and L11 × T2 performed better than the check Obatanpa. This finding is in agreement with previous work by Gichuru et al., (2011) who reported the genetic variation of germplasm in their reaction to maize streak virus disease.

Plant height among the studied testcrosses ranged from 124 (L10 × T1) to 207 cm (Obatanpa), respectively with over all mean of 154.9 cm. All genotypes were significantly shorter than Obatanpa with L10 × T1 (123 cm) and L6 × T2 (135 cm) being the shortest crosses among the 32 crosses. On the other hand, L16 × T1 (157

Table 1. Mean performance of single crosses for yield and yield-contributed traits of selected tropical white maize.

Crosses	AD	SD	ASI	MSD	PH	EH	PlAsp	HC (%)	Rot (%)	EL	RE	NKR	Yld
1 × T1	57	59	3	3.3	169.9	81.2	3.5	48.7	25.9	17	13	38	4516
L1 x T2	58	59	1	3.4	143.5	84	2.5	15.0	18.2	18	15	35	6011
L2 x T1	57	58	2	2.9	163.1	81	3	3.3	3.3	16	16	35	4871
L2 x T2	57	58	1	3.2	148.5	76.1	2	1.4	3.1	17	16	36	5056
L3 x T1	59	60	1	3.2	137.2	51.9	4	23.3	14.3	14	15	27	3196
L3 x T2	58	58	0	3.1	152.1	81.1	2.5	3.3	11.1	15	15	32	4950
L4 x T1	56	57	2	2.9	165.1	80.1	2.5	3.3	9.3	13	13	27	4209
L4 x T2	57	58	2	3.5	158.8	73.5	2.5	9.9	3.1	18	15	40	5150
L5 x T1	54	56	2	3	168.2	68.9	3.5	4.9	3.1	16	16	37	4702
L5 x T2	55	56	1	2.6	166.8	77.8	3	6.7	1.9	17	14	38	4997
L6 x T1	55	57	3	3.3	150.9	68.7	3.5	0.0	0.0	16	11	34	4313
L6 x T2	55	58	3	3.3	135.3	59.1	3	4.3	11.5	16	13	32	3977
L7 x T1	56	57	2	2.3	146.5	70.1	3	3.3	1.7	16	14	34	4959
L7 x T2	58	59	1	2.9	138.3	64.2	3	5.0	0.0	16	14	36	4587
L8 x T1	52	54	2	2.9	150.5	65.9	3	0.0	2.0	14	12	34	4059
L8 x T2	52	53	1	2.3	161.2	83	1	1.5	0.0	17	14	38	6377
L9 x T1	54	55	1	2.8	150.7	68.1	3	9.7	3.1	15	15	34	5135
L9 x T2	56	57	1	2.6	156.2	78.8	2.5	1.7	2.2	16	15	26	4694
L10 x T1	57	58	1	3.4	123.7	52.6	4	16.7	16.4	15	12	33	3589
L10 x T2	57	58	1	3.4	144.0	69.8	4	0.0	5.5	11	14	24	3754
L11 x T1	55	57	2	2.9	166.5	63.5	3.5	4.5	1.4	15	16	33	4073
L11 x T2	55	56	1	2.4	163.7	76.7	2	4.9	6.4	10	14	23	4860
L12 x T1	57	58	1	3.4	145.4	69.3	2.5	0.0	5.1	19	11	40	4319
L12 x T2	57	58	1	2.8	159.2	78.8	2	8.3	12.6	19	14	37	4479
L13 x T1	57	58	1	2.6	168.2	83.4	3.5	16.7	14.3	14	15	30	4906
L13 x T2	57	58	1	2.8	151.8	73.9	3	38.3	56.7	18	14	36	4952
L14 x T1	57	59	2	3.3	141.5	56.8	3.5	18.3	9.8	14	13	28	2872
L14 x T2	56	57	2	3.4	163.0	72.8	3.5	15.0	7.7	16	16	33	4829
L15 x T1	54	55	1	3	170.7	72.4	3.5	3.3	6.9	13	15	30	5022
L15 x T2	58	58	1	4.1	140.6	66.4	4	6.7	11.1	17	12	38	4890
L16 x T1	57	59	2	3.5	156.5	77.9	3	1.5	0.0	16	15	36	5848
L16 x T2	56	58	2	3.4	154.2	84.2	3	3.3	5.4	16	18	35	5222
check1	57	59	2	3.1	143.9	62	3	28.3	43.6	15	16	33	3831
check2	55	58	3	3.4	207.3	99.1	4	8.1	1.6	15	13	33	4288
check3	55	58	4	4.4	157.3	69.8	4.5	15.0	15.6	16	15	34	3824
G. mean	56	57	1.4	3.1	154.9	72.65	3	9.5	9.5	16	14	33	4668
CV	1	1	29	13	10	8	15	31	24.8	5.9	7.2	5.6	10
SE(d)	0.7	0.6	0.7	0.4	5.8	5.5	0.5	7.3	7.7	0.8	1	1.9	465.6
R^2 (%)	94	95	81	89	96	92	90	88.0	90	94	89	95	90

G.mean = mean, CV = coefficient of variation, SE (d) = standard error difference, R^2 = the model explain the variability of the response data around its mean, AD= days to 50% anthesis, SD = days to 50% silking, ASI = anthesis - silking interval, MSD = maize streak virus disease, PH = plant height, EH = ear height, PLASP = plant aspect, HC% = husk cover in percentrot % = ear rot in percent, EL = ear length, RE = number of kernel rows ear^{-1}, NKR = number of kernels row^{-1} and Yld = grain yield kg ha^{-1}, Check1 = 1368 x CML 444, Check 2 = Obatanpa, Check3 = Mamaba

cm), L4 × T2 (159 cm), L12 × T2 (159 cm) and L8 × T2 (161 cm) were significantly taller than the hybrid between the two testers (144 cm). The remainder of the testcrosses' plant height, which ranged from 163 to 170 cm, was not significantly different from the check Obatanpa. However, L1 × T1 was significantly taller than Mamaba (Table 1). Hybrids with shorter plant height indicate less stem and root lodging.

Ear height varied from 52 (L3 × T1) to 99 cm (Obatanpa). L3 × T1 (59 cm), L6 × T2 (59 cm), L10 × T1 (53 cm), L14 × T1 (57 cm) recorded significantly shorter ear heights from the check Mamaba and none of the

crosses showed significantly different ear height than check 1368 × CML 444. Similarly, all genotypes had shorter ear heights than the check Obatanpa. The overall mean of ear height was 72.65 cm, whereas check 1368 × CML 444, Obatanpa and Mamaba had 62, 99 and 70 cm, respectively. Testcrosses that have short plant height and ear length indicate less stem and root lodging. Mean performance of plant aspect of genotypes included under study, four crosses, L8 x T2, L2 x T2 , L11 x T2 , L12 x T2 (2) exhibited good and significant plant aspect. It indicates that these testcrosses had better uniformity of plant height and ear height, less disease occurrence and good grain filling. Mean performance of genotypes for husk cover percentage ranged from zero to 50%, indicating that there were genetic variations among genotypes included under study for this trait. Most of crosses tested revealed good and significant husk cover percentages. Mean performance of genotypes for ear rots manifested considerable significant differences and varied from 0 to 57%. The testcrosses L13 x T2 (57%) and L1 x T1 (26%) had significantly high number of ears with ear rot, while the remaining testcrosses were not damaged significantly by ear rots. Thus, selecting these crosses with good husk cover may reduce yield losses caused by ear rots and weevils before harvesting. The current investigation is in agreement with the pervious researchers report (Hosana et al., 2015)

Mean performance of ear length varied from 10 (L11 x T2) to 19 cm (L12 x T1 and L12 x T2) with overall mean of 15.5 cm. Of 32 genotypes tested, eight testcrosses showed significant higher ear length than the overall mean. Thus, testcross L1 x T2, L12 x T1, L12 x T2, L4 x T2 and L13 x T2 had the longest ear length. Among 32 genotypes included in the study, L1 x T2, L12 x T1 L12 x T2, L4 x T2, L13 x T2, L2 xT2, L5 x T2 and L15 x T2 showed significantly longer ear length than the three checks included in the study. Testcrosses, L4 x T1, L10 x T2, L11 x T2, 15 x T1 showed significantly shorter ear length than the checks. The means of checks for ear length were 15, 15 and 16 cm for 1368 x CML 444, Obatanpa and Mamaba, respectively.

Genotype mean performance of the number of kernel rows ear^{-1} was significant among tested materials in the study. Mean performance of this trait varied from 11 to 18, kernel rows ear^{-1} with the grand mean of 14 kernel rows. Of the 35 genotypes tested, the maximum number of kernel rows ear^{-1} was recorded from a cross L16 x T2 with 18 kernel rows ear^{-1}, while L6 x T1 and L12 x T1 had the least number of kernel rows ear^{-1}.

Mean of number of kernels row^{-1} varied from 23 (L11 x T2) to 40 (L4 x T2 and L12 x T1) with over all mean of 33 kernels row^{-1}. Among the genotypes tested, L4 x T2 and L12 x T1, L1 x T1 , L5 x T2, L8 x T2, L15 x T2 with 40, 40, 38, 38, 38 and 38 kernels row^{-1}, respectively, had higher and significant number of kernels row^{-1} as compared to the three checks used in the experiment. Similarly, L5 x T1 and L12 x T2 with 37 kernels row^{-1} each showed significant and higher number of kernels than check 1368 x CML 444 and Obatanpa. On the other hand, L11 x T2, L10 x T2, L9 x T2, L3 x T1, L4 x T1 with 23, 24, 26, 27 and 27 kernels per row, respectively showed significant and lower number of kernels as compared to the three checks. Thus, it is possible that crosses with higher ear length, higher number of kernel rows ear^{-1} and higher number of kernels row^{-1} can increase grain yield of maize.

The mean grain yield of genotypes tested in this study ranged from 2872 (L14 x T1) to 6377kg ha^{-1} (L8 x T2) with overall mean of 4668 kg ha^{-1}. Among 32 crosses evaluated, 17 testcrosses manifested significant higher grain yield than the best commercial hybrid check Mamaba. In general, L8 x T2, L1 x T2, L16 x T2, L16 x T1, L4 x T2 and L9 x T1 revealed significantly higher grain yield as compared to all the three checks included in the study and are identified as the potential hybrids for production after further testing to confirm stability. The means of three checks were not significantly different. These indicate that there were genetic variations among genotypes for this trait in agreement with several authors report (Hosana et al., 2015; Miranda et al., 2012; Vah, 2013).

CONCLUSION AND RECOMMENDATIONS

This study was conducted to identify superior single-cross hybrids (SCH) developed from line x tester mating design. The experiment had two phases. In the first phase of the experiment, thirty-two (16 x 2) cross combinations were generated through line x tester mating design. In the second phase, the 32 F_1 crosses including the hybrid between the two testers, one popular open pollinated variety and a standard hybrid checks were evaluated for their agronomical performance using a 5 x 7 alpha lattice design at WACCI research field in 2015.

The results obtained in the present investigation were encouraging and tremendous increase in grain yield was obtained in most of the hybrids. Six promising testcrosses (L8 x T2, L1 x T2, L16 x T1, L16 x T2, L4 x T2 and L9 x T2) which had higher yield as compared to the checks were identified based on their mean performance which can improve the production and productivity of maize yield in the country.

Therefore, promising testcrosses (L8 x T2, L1 x T2, L16 x T1, L16 x T2, L4 x T2, and L9 x T1) identified in this study should be used in maize research programme as possible candidates for release after confirming the stability of their performance in multi-locations and one more season.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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