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Combining abilities for grain filling traits in early maturity maize

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ABSTRACT

Early maturity in maize (*Zea mays*) carries a yield less of 20-30 % compared for late maturity varieties. Thus, deployment and use of grain filling traits is vital. Fifty-five (55) FI crosses were generated using North Carolina mating Design II using (6) tropical medium-late and (16) exotic early maturing maize inbred lines as female and male parents, respectively. Fewer than antipicated (96) crosses were obtained with very limited seed amounts of exotic inbred lines and abiotic and biotic stresses susceptibility. Subsequently, sixty (60) hybrids (including early maturing checks-SC 301 and SC 403 and three fillers) were planted in a (10x6) α-lattice design with two replications in three trial sites in Uganda. Combining ability analyses indicated significant differences ($P<0.001$ to 0.05) among genotypes for grain filling traits, flowering, and grain yield. The differences between means of the top eleven (11) hybrids: (F5xP13, F1xP13, F3xP1, F5xP1, F5XP9, F3XP3, F5xP2, F3xP2, F5XP12, F3xP10 and F3xP14) and bottom eleven (11) hybrids:, F1xP8, F2xP1, SC 403, F3xP11, F2xP14, F2xP9, F1xP9, F2xP12, F2xP2, SC 301and F2xP8) for grain filing rate and single plant grain yield were 36% and 31%, respectively. Broad and narrow sense coefficients of genetic determination were high for majority of traits. Bakers Ratio was high for majority of grain filling and flowering traits implying that additive gene action was more important than non-additive gene action. Early maturing and high yielding hybrids were identified and these could serve as baseline germplasm for developing early maturity and high yielding maize varieties.

Key words: Combining ability, grain filling traits, Inbred lines, North Carolina Design II, *Zea mays*

RÉSUMÉ

La précocité du maïs (Zea mays) entraîne généralement une baisse de rendement de l’ordre de 20 à 30 % par rapport aux variétés tardives, d’où l’importance de traits liés au remplissage du grain. Cinquante-cinq (55) croisements F1 ont été produits suivant la méthodologie du North Carolina Design II, à partir de six lignées tropicales à maturité moyenne-tardive (femelles) et de seize lignées précoces exotiques (mâles). Le nombre total de croisements initialement visé (96) n’a pas pu être atteint, en raison d’une production limitée de semences pour certaines lignées exotiques et d’une sensibilité aux stress

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production limitée de semences pour certaines lignées exotiques et d'une sensibilité aux stress abiotiques et biotiques. Au total, soixante (60) hybrides (incluant les témoins précoces SC 301 et SC 403, ainsi que trois croisements « de remplissage ») ont été évalués en champ dans un dispositif α-lattice 10 × 6 avec deux répétitions, sur trois sites d'essai en Ouganda. Les analyses de capacité de combinaison mettent en évidence des différences significatives ($p < 0{,}001$ à 0,05) entre les génotypes pour les traits de remplissage du grain, les dates de floraison et le rendement. Parmi les onze meilleurs hybrides (F5×P13, F1×P13, F3×P1, F5×P1, F5×P9, F3×P3, F5×P2, F3×P2, F5×P12, F3×P10, F3×P14) et les onze moins performants (F1×P8, F2×P1, SC 403, F3×P11, F2×P14, F2×P9, F1×P9, F2×P12, F2×P2, SC 301, F2×P8), l'écart moyen pour le taux de remplissage du grain et le rendement grainier par plante atteint respectivement 36 % et 31 %. Les coefficients de détermination génétique, à la fois au sens large et au sens strict, se révèlent élevés pour la plupart des caractères. Le ratio de Baker suggère une plus forte contribution des effets additifs comparativement aux effets non additifs pour la majorité des paramètres de floraison et de remplissage. Plusieurs hybrides précoces et à haut rendement ont ainsi été mis en évidence ; ils pourraient servir de base à la constitution de variétés à la fois précoces et productives pour les régions où la saison de croissance est courte.

Mots-clés : capacité de combinaison, traits de remplissage du grain, lignées pures, North Carolina Design II, Zea mays

INTRODUCTION

Among cereals, maize, rice and wheat account for half of global production (FAO, 2022). In Uganda, there has been an increase in maize area under production from (0.6 to 1) million hectares in 2000 to 2013 with the total maize production statistics of 3.4 million tonnes in 2018 (UBOS, 2018).This shows that maize is an important food security and income generation crop in Uganda (WFP and IFAD, 2019). In a survey of 500 households carried out in drought prone areas of Uganda and some of their neighbors, it was found that earliness was the second most important trait after grain yield in maize varieties selection and more important than drought tolerance (Setimela *et al.*, 2017). Farmers' preference for early maturity was based on the ability of the preferred maize varieties to escape drought. They are ideal for intercropping as they compete less for moisture, nutrients and light when compared to late maturing ones; they also have variable planting dates which enable multiple plantings thereby spreading risks of crop failure. Moreover they provide early and reliable harvest before the full season crop which strengthens food security situation of smallholder farmers (Langyintuo and Setimela, 2007; Pswarayi and Vivek, 2008). While breeding programs continue to improve grain yields of early maturing maize varieties, maturity earliness continues to carry a yield redaction of around (20-30) % compared to late maturity varieties (Magorokosho *et al.*, 2009).

Genetic diversity exists in the length of the linear phase which accounts for 90% of grain yield in cereals (Pswarayi and Vivek, 2008) but this diversity has not been fully exploited (Setimela *et al.*, 2014). There is limited information on the inheritance of grain filling rate and duration in early maturity maize. Fortunately, early maturing and high yielding exotic maize inbred lines are available at National Crops Resources Research Institute (NaCRRI) in Uganda. These can be used as good sources of earliness trait for introgression into the well-adapted tropical inbred lines in crosses to produce high yielding early maturing hybrids. However, there is no information on combining ability for grain filling traits, earliness and grain yield between exotic and well adapted tropical inbred lines. Therefore, in this study we aimed to determine combining abilities for grain filling traits in early maturity maize. The findings we hope will inform decision making in breeding programs for combining earliness with high yields in early maturity maize.

MATERIALS AND METHODS

Plant materials and experimental Design. Six (6) tropical and sixteen (16) exotic inbred lines sourced from NaCRRI and Iowa, USA respectively, as shown in Table 1 were crossed in a North Carolina mating design 11 using tropical and exotics as females and males, respectively. Fifty-five (55) FI hybrids were generated. Fewer FI hybrids than expected were obtained owing to the high number of missing crosses hence forcing planting fewer hybrids. This was as result of very limited seed amounts of exotic inbred lines and stress (abiotic and biotic) susceptibility at multiplication. A total of 60 hybrids including two early checks (SC301,SC 401 and three fillers were grown in a (6x10) α-lattice design with two replications at three trial sites i.e. National Crops Resources Research Institute (NaCRRI) in Central Uganda, is located at longitude; 32^{o} 35˙E at an elevation of 1,150 (m) above sea level; National Semi-Arid Resources Research Institute (NASARRI) in Eastern Uganda is located at longitude 33^{o}27˙E at an elevation of 1,140 (m) above sea level ; while Bulindi Zonal Agricultural Research and Development Institute (BulindiZARDI) in Western Uganda is located at longitude 31^{O}26˙E at an elevation of 1,060 (m) above sea level. NaCRRI receives mean annual rainfall of 1,270 mm, NASARRI 975mm, and BUlindiZARDI 1,036 mm.

Trial establishment and management. Six FI hybrids (female) and 5 exotic male parents were used in the study (Table 1). A plot consisted of two rows of 4 m long spaced at 0.75 m and 0.25 m between rows and within rows respectively. Necessary agronomic management practices were done.

Data collection. To evaluate grain filling traits (grain filling rate and effective gain filling duration), a destructive sampling method as described by Gasura *et al.* (2013) was used. In this case, fresh cobs were removed weekly, beginning at 10 days after silking and visually assessing blister stage of development designated as the beginning of the linear phase. Destructive sampling was repeated until the kernels developed a black layer at the point of their attachment to the cob. Plants from which cobs were harvested were left standing to maintain the initial plant density. Since effective grain filling is highly correlated with days to physiological maturity (DPM), effective grain filling duration (EGFD) was determined by subtracting days at blister stage from DPM (Gasura *et al*., 2013). Likewise, DPM was determined as days after planting until the kernels developed a black layer at the point of their attachment to the cob. Grain filling rate (GFR) was determined as grain yield on plant basis divided by Effective grain filling duration (EGFD). Data on other agronomic traits, grain yield, and selected yield components were recorded for each plot after thinning (Pswarayi and Vivek, 2008) as indicated in Table 2. Data on flowering and other grain yield and its related traits were collected basingon using field book guide (Trevor, 2014**).**

Table 1. Maturity status and origin of maize inbred lines used in this study

Code	Line Name	Maturity	Code	Line Name	Maturity	Origin
F1	CKLO5022	Intermediate	P6	PHPR5	Early	NaCRRI
F2	NML97	Intermediate	P7	PHT55	Early	NaCRRI
F3	CML543	Intermediate	P8	PHR03	Early	NaCRRI
F4	CML547	Early	P9	PHJ70	Early	NaCRRI
F5	CML444	Intermediate	P10	PHM49	Early	NaCRRI
F6	CML536	Intermediate	P11	PHBB3	Early	NaCRRI
	Exotics (Males)					
P1	LH190	Early	P12	LH211	Early	Iowa, USA
P2	LH213	Early	P13	PHWG5	Early	Iowa, USA
P3	PHEG9	Early	P14	PHW52	Early	Iowa, USA
P4	LP215D	Early	P15	PHR63	Early	Iowa, USA
P5	LH210	Early	P16	PHP85	Early	Iowa, USA

Data analysis. Data collected were subjected to analysis of variance using Genstat 18th Edition. Combining ability for grain filling and selected agronomic traits was portioned into general and specific combining abilities (Grifing, 1956). A single site analysis was performed as well as a combined location analysis with genotypes/lines considered as fixed and locations as random. The parents were considered fixed because they were purposely selected. As a result of missing crosses, the formulas for calculating genetic variance were adjusted accordingly. The analyses were based on the statistical linear models as shown below;

Within location analysis model

$$Yijk = \mu + GCAFj + GCAMk + SCA\ jk + \varepsilon ij$$

Across location analysis model

$$\begin{aligned} Yijkl = \mu + Ei + GCA(F)j + GCA(M)k + SCA\ jk \\ + GCA(F) * E\ i\ j + GCA(M) * E\ i\ k \\ + SCA * E\ i\ j\ k + el \end{aligned}$$

Where: GCA (F)j: Female parent effect; GCA(M)k: male effect; SCAjk: Cross effect; Yijkl: observation of parents k and j in environment i; GCA(F)j: Genotype effect for the female parent j; GCA(M)k: Genotype effect for the male parent k, GCA (F)*E ij: Interaction GCA effect of parent j in environment i; GCA (M)*E ik: Interaction GCA effect of parent k in environment i; SCA jk: Cross effect between parents j and k; SCA*E ijk; Interaction of cross effects with environment i; el: error term l. (Grifing, 1956)

Expected Mean Squares (EMS). The values for each of the terms from sources of variance were calculated. The EMS were used to calculate estimates of variance component for crosses. Variance components of GCA males (GCAM) and GCA females (GCAF) as well as SCA were calculated according to Comstock and Robinson (1948). Accordingly the GCA and SCA values were used to calculate Narrow Coefficient of Genetic Determination (NS-CGD) and Baker's Ratio (B.R) on across mean basis. The importance of additive and non-additive gene actions was estimated from GCA and SCA mean squares, respectively. The NS-CGD, BS-CGD, and B.R were determined for individual location according to the formulas below

Table 2. Agronomic, yield and yield component traits used in the study

Trait	Units	Trait description
Days to 50% Anthesis (DA)	Days	Number of days after planting when 50% of the plants have shed pollen
Days to 50% silking (DS)	Days	Number of days after planting when 50% of the plants have extruded silk
Anthesis Silking Interval	Days	DS-DA
Days to physiological maturity	Days	Days after planting until the kernels develop a black layer at the point of their attachment to the cob
Plant height	cm	Height between the base of a plant to the insertion of the first tassel branch of the same plant
Ear height	cm	Height between the base of a plant to the insertion of the top ear of the same plant
Moisture Content	%	Percentage moisture as determined by the moisture meter
Kernel row per ear	Number	Number of kernel rows on the cob
Kernel Per Ear	Number	Number of kernels per cob
Thousand Kernel weight	g	Weight of one thousand kernels
Grain Yield	Tons/ha	Shelled grain weight adjusted to 12.5% moisture and converted to tons per hectare

Source: (Pswarayi and Vivek, 2008)

$$BS - CGD = \frac{\sigma^2 GCA_F + \sigma^2 GCA_M + \sigma^2 SCA}{\sigma^2 GCA_F + \sigma^2 GCA_M + \frac{\sigma^2 e}{2}}$$

$$NS - CGD = \frac{\sigma^2 GCA_F + \sigma^2 GCA_M}{\sigma^2 GCA_F + \sigma^2 GCA_M + \frac{\sigma^2 e}{2}}$$

$$B.R = \frac{\sigma^2 GCA_F + \sigma^2 GCA_M}{\sigma^2 GCA_F + \sigma^2 GCA_M + \sigma^2 SCA}$$

Where;
$\sigma^2 GCA_F, \sigma^2 GCA_M$ are the variance components of GCA effects for the females and males, respectively

$\sigma^2 SCA, \frac{\sigma^2 e}{2}$ are variance components due to SCA effects and one due to experimental error respectively

RESULTS

Variability of grain filling, grain yield and maturity traits in the maize genotypes used in this study Results indicated significant GCA effects with different significance levels ($P < 0.001$, 0.01 and 0.05) for both female and male parents for grain filling, grain yield, and flowering traits (GFR, GY, ASI and AD) except for DPM for both parents, and EGFD for the female parent (Table 3). Significant differences ($P < 0.05$) for female x environment interaction were only observed for GY. The values for GCA effects of the male parents were generally larger than those for GCA effects of female parents for EGFD and AD, whereas for the other studied traits (GFR, DPM, GY, and ASI) GCA effects of females were generally larger than those GCA effects of the males (Table 3). Broad and narrow sense coefficients of genetic determination ranged from 0.08 to 0.86, and 0.04 to 0.86, respectively. Bakers Ratio values ranged from 0.07 to 1 (Table 3)

The average grain yield of hybrids ranged from 41 to 72 g per plant, an equivalent of 5 to 10.3 t/ha (Table 4). The highest grain yielding hybrid was F5xP9, with a grain yield of 72 g per plant (equivalent to 10.3 t/ha) and was among the hybrids with the highest grain filling rate of 2.14 g per day per plant. The lowest yielding hybrid was F2xP8, with a grain yield of 41 g per plant (equivalent to 4.5 t/ha). There was a difference of 36% and 31.05% between the means of top eleven (F5xP13, F1xP13, F3xP1, F5XP1, F5x P9, F3xP3, F5xP2, F3xP2, F5xP12 and F3xP10 and F3xP14) and bottom eleven , F1xP8, F2xP1, SC 403, F3xP11, F2xP14, F2xP9, F1xP9, F2xP12, F2xP2, SC 301 and F2xP8) eleven hybrids for grain filling rate and grain yield, respectively (Table 4). The GFR means of top and bottom eleven hybrids were 2.10 g d^{-1} and 1.54 g d^{-1}, respectively, while for single plant grain yield, the means of the top and bottom eleven plants were 65.17 g and 49.73 g, respectively. However, the top eleven hybrids had a 1.09 days' shorter effective grain filling duration when compared to the bottom eleven hybrids**.**

The highest yielding hybrids exhibited anthesis 2.11 days later than the lowest yielding hybrids. It was evident that the highest yielding hybrids were associated with short and negative ASI values compared to the lowest yielding hybrids as shown in Table 4. When the hybrids and early maturity commercial checks (SC403 and SC301) were compared, the top eleven hybrids outperformed the commercial checks by 44% and 25% for both GFR and GY respectively. The mean grain yield of the top eleven hybrids was also 25% higher than that of the early maturity commercial checks. The commercial checks had long ASI values when compared with the top eleven hybrids. In terms of anthesis, commercial checks flowered one day earlier on average compared to the top two earliest flowering hybrids.

Table 3. A combined ANOVA showing mean square and combining ability values for grain filling, grain yield and maturity traits across three locations

SOV	DF	GFR	EGFD	DPM	GY	AD	ASI
Loc	2	2.17^{ns}	215.25^{ns}	289.57**	4633.92^{ns}	36.31^{ns}	24.08**
GCAf	4	0.60**	0.71^{ns}	9.58^{ns}	645.54*	11.20*	15.08***
GCAm	13	0.22**	15.7**	7.80^{ns}	191.85**	12.68***	3.02***
SCA	21	0.05^{ns}	5.76^{ns}	6.20^{ns}	35.180^{ns}	1.57^{ns}	0.72^{ns}
GCAf. Loc	8	0.10^{ns}	3.24^{ns}	8.96^{ns}	130.31*	2.05^{ns}	0.87^{ns}
GCAm x Loc	26	0.06^{ns}	5.78^{ns}	6.1^{ns}	60.73^{ns}	1.36^{ns}	0.59^{ns}
SCA x Loc	42	0.04^{ns}	4.78^{ns}	4.72^{ns}	27.47^{ns}	1.76^{ns}	0.53^{ns}
Pooled error	125-137	0.07	5.20	4.70	62.14	2.18	0.83
BS-CGD		0.66	0.20	0.08	0.61	0.69	0.86
NS-CGD		0.64	0.20	0.04	0.60	0.69	0.85
B. R		0.85	0.64	0.07	0.74	1.00	0.98

*SOV: Source of variation, DF: Degrees of freedom, GFR: Grain filling rate (g/day/plant), EGFD: Effective grain filling duration, DPM; Days to physiological maturity, GY: Grain yield/plant, AD: Anthesis date, ASI: Anthesis silking interval; *, **, ***: significance at 0.05, 0.01, 0.001 levels of probability, respectively, BS and NS-CGD: Broad and narrow coefficient of genetic determination, respectively, and B.R; Baker's Ratio.*

Table 4. Means of grain filling rate, grain yield and maturity traits for the top 11 and bottom 11 F1 maize hybrids

F1 Hybrids	GFR (g/plant/day)	GY (g/plant)	EGFD (days)	AD (days)	ASI (days)	DPM (days)
Top 11						
F5xP13	2.36	70.68	29.67	66.16	-1	108.8
F1xP13	2.25	65.24	29.17	64.83	0	108
F3xP1	2.21	62.77	28.5	64.67	0.67	107.8
F5xP1	2.16	65.76	30.5	65.66	-1	109.2
F5xP9	2.14	71.95	33.84	65.33	-2.5	110.7
F3xP3	2.12	66.78	31.17	66.66	-0.5	111.3
F5xP2	2.11	66.69	31.34	65.33	-1.83	108.8
F3xP2	2.07	61.97	29.67	63.33	0.67	107.7
F5xP12	2.06	68.68	33.5	63.66	-2	109.2
F3xP10	2.02	63.73	31.17	66.33	0.17	111.7
F3xP14	1.64	52.61	33.34	66	0.67	113.5
Mean	**2.10**	**65.17**	**31.08**	**65.27**	**-0.61**	**109.7**
SD	**0.18**	**5.19**	**1.82**	**1.07**	**1.15**	**1.86**
Bottom 11						
F1xP8	1.63	47.82	29.5	64	-1	106.5
F2xP1	1.63	48.72	30	65.66	0	109.7
SC 403	1.62	58.25	36.02	60.86	1.82	112.7
F3xP11	1.62	50.91	31.17	64.33	1.83	111.3
F2xP14	1.6	51.04	31.5	65.33	0	110.8
F2xP9	1.59	49.91	31.5	61.17	0.17	106.8
F1xP9	1.56	54.17	34.67	62	-1.33	109.3
F2xP12	1.53	49.43	32.19	63.56	-0.04	109.7
F2xP2	1.48	49.81	33.84	63.16	-1.17	109.8
SC 301	1.36	45.99	33.64	60.2	1.15	109
F2xP8	1.36	40.95	29.84	64.5	0.33	108.7
Mean	**1.54**	**49.73**	**32.17**	**63.16**	**0.16**	**109.48**

SD	**0.10**	**4.37**	**2.13**	**1.85**	**1.10**	**1.8**
Min	**1.36**	**40.95**	**28.50**	**60.2**	**-2.5**	**106.5**
Max	**2.36**	**71.95**	**36.02**	**66.66**	**1.83**	**113.5**
Diff	**0.56**	**15.44**	**-1.09**	**2.11**	**-0.77**	**0.22**
% Diff	**36.33**	**31.05**	**-3.39**	**3.34**	**-478.7**	**0.2**
CV (%)	**15**	**14**	**8**	**2**	**-2.26**	**2**
LSD	**0.3**	**9**	**2.6**	**1.69**	**1.04**	**2.47**

F: Female parent, P: Pollen parent, SD: Standard deviation, GFR: Grain filling rate (g/plant/day), GY: Grain yield (g) /plant, EGFD: Effective grain filling duration, AD: Anthesis date, ASI: Anthesis silking interval, DPM; Days to Physiological Maturity; % Diff: Percentage difference, CV; Coefficient of Variation, LSD; Least significant difference

DISCUSSION

Variability of grain filling, grain yield and maturity traits in combined maize genotypes. Based on mean square values, there were significant differences observed for grain filling, grain yield and maturity traits (Table 3). This implies that parental lines used for the hybridization study were genetically diverse. This is in line with Wang *et al*. (1999) who found a lot of genetic diversity most especially for grain filling traits in exotic maize germplasm. This presents a potential for production of high yielding and early maturing maize hybrids.

Significant differences for GCA across environments implied that parents were contributing differently to the progeny. This is because they were genetically variable in terms of the measured traits. Desirable parents would be those with significant and non-significant GCA in the right direction. For instance, the right direction for earliness is negative GCA whereas that for yield is positive GCA. Superiority of GCAm to GCAf mean squares for EGFD and AD implied that male parents were playing a greater role in contributing favorable genes for those traits, meaning the traits were determined paternally. This is in agreement with observation by Derera *et al*. (2008) who reported similar findings.

There were moderately high broad and narrow sense coefficients of genetic determination (60-86%) for majority of the studied traits. This is in line with the report of Gasura *et al*. (2013) who found high values of broad sense coefficient of genetic determination for grain filling traits. This calls for repeatability of the experiment in a wide range of environments except for EGFD and DPM, where there was a high genetic contribution to the observed phenotypic variation. The environmental contribution to the phenotypic variation was, on average, 30%.

Baker's ratio was high for both EGFD and GFR. The results of this study are similar to the findings of Pswarayi and Vivek (2008). This implies that GCA effects were more important than the SCA for these traits. Therefore, it can be concluded that additive gene action controls grain filling rate and duration, which is in agreement with the findings of Wang *et al*. (1999) who reported that additive gene action was more important than non-additive gene action for the same traits. Similarly, the high Baker's ratio in this study suggests that hybrid performance can be fairly predicted based on the parent's general combining ability effects (Fasahat, 2016).

Variability of grain filling rate, grain yield and maturity traits in hybrids. The highest yielding hybrid was F5xP9 with a GY of 72 g per plant (equivalent to 10.3 t/ha) (Table 4). The hybrid originated from a cross between F5 and P9 that had positive GCA effects for GY and GFR. Generally, the highest yielding hybrids had the highest GFR and shortest EFGD. This is consistent with the findings of Brdar *et al*. (2008) who reported that high yielding genotypes had high GFR and short grain filling durations. Similarly, Wang *et al.* (1999) found exceptional hybrids that had high GFR and shorter EGFD that resulted into high yields. The association of high GY and high GFR is a manifestation that GFR influences GY in most cereal crops. This corroborates the findings of

Chen *et al*. (2019) that GFR influences GY to a larger extent in most of the genotypes. Short ASI and negative GCA values for ASI could have contributed to higher grain yields since short ASI increases the number of grains per plant (Cárcova and Otegui, 2007). Short and negative ASI are associated with high yielding modern short season maize hybrids which increases chances of pollination and allocation of 50% dry matter during flowering period (Lee and Tollenaar, 2007). Similarly, the short and negative ASI showed that the females flowered earlier than the males in a short interval. This increased the chances of complete pollination thus increasing grain yield. This partly explains the differences between grain yields in hybrids reported in study.

High Bakers ratios for grain filling traits (Table 3), implied that additive gene action was more important than non-additive gene action for majority of the traits and the predictability of progeny performance from the average performance of the parents was more reliable. This is in agreement with Gasura *et al*. (2013) who reported similar findings. Lastly, additive gene action was more important than non-additive action which is in line with the observations of Wang *et al.* (1999) that grain filling traits, kernel weight and silking were controlled majorly by additive gene actions.

CONCLUSIONS

In this study, parental lines that are good combiners for grain filling rate and duration have been identified and they include F5xP13, F5xP9, F3xP3, F5xP2 and F5xP12. Some of these lines are early maturing as depicted by significant negative GCA effects for anthesis date and significant GCAs for grain filling rate. Grain filling traits in maize are controlled majorly by additive gene action. Therefore, these high performing inbred lines and hybrids could be used as a baseline germplasm for developing early maturing and high yielding maize varieties.

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DECLARATION OF CONFLICT OF INTEREST

The authors declare that they have no conflict of interest in the paper.

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