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# Potential of Temperate, Tropical, and Sub-Tropical Exotic Maize Germplasm for Increased Gains in Yield Performance in Sub-Tropical Breeding Programs

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Abstract: Exotic germplasm (i.e., germplasm beyond the breeder's target area) has traditionally been used to broaden the genetic base of local (germplasm within the breeder's target area) populations, but little has been done to assess gains that could be induced by this breeding practice in the sub-tropical regions of Africa. Here, eight maize (Zea mays L.) inbred lines developed from pedigree crosses of exotic and local (i.e., sub-tropically adapted lines; STALs) were inter-mated together with six elite STALs, in a partial diallel mating scheme, in order to depict yield gains that can be made when exotic genes are integrated within the sub-tropical maize germplasm pool. The crossing scheme yielded a total of 91 F<sub>1</sub>s which were evaluated together with nine commercial checks in multi-environmental trials (METs) at eight locations representing agro-ecologies in which maize is predominantly grown in Zimbabwe. Across site Analysis of Variance (ANOVA) showed differences in grain yield (GY) performance of the F1s. Significant genotype x environment effects was also detected for GY (i.e., GEI; p < 0.05). F<sub>1</sub>s of parents with a temperate background [i.e., P7 (S) x P2 (T)] showed the highest GY potential (e.g., G44; GY = 10.52 tha<sup>-1</sup>). Apart from showing high GY potential, G44 also demonstrated to be stable across diverse agro-ecologies and to mature earlier than the best commercial check hybrid. In conclusion, incorporation of exotic genes, especially those from temperate regions, may improve the yielding ability and stability and can introduce earliness in the maturity of maize populations in sub-tropical regions.

Keywords: adaptability; exotic germplasm; inbred line; variability

# 1. Introduction

Maize (*Zea mays* L.) is a very important crop worldwide and has diverse applications. For instance, 66% of the globally produced maize is used as livestock feed, 20% as direct food for humans, 8% for industrial purposes, and 6% is recycled as seed or wasted [1,2]. In sub-Saharan Africa (SSA), maize is the primary source of calories, contributing about 19% of the calorie intake [3,4]. Regardless of its importance in SSA, maize productivity is limited by multiple factors, including the abiotic (especially drought and heat stress) and the biotic (e.g., pests and diseases), which are known to be exacerbated by climate change [5–8]. In addition, lack of access to farming inputs (e.g., fertilizers, pesticides, and irrigation), common under small-holder farming set-ups in SSA, worsens the situation with yields per household averaging <1.5 tha<sup>-1</sup>, a phenomenon threatening food and nutrition security [9]. As the global population is estimated to double by the year 2050, coupled with the continued decline in land suitable for agriculture [10], there is a need to develop sustainable solutions that can lead to increased maize productivity under these predicted climatic and socio-economic scenarios.



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**Copyright:** © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). Plant breeding is traditionally regarded as the most cost-effective way to improve the adaptation of crops to the changing environment. In this regard, it is important to note that, regardless of the current challenges constraining maize productivity, the crop harbours enormous genetic diversity that offers incredible opportunities for genetic enhancement for adaptation to stress conditions [11,12]. Therefore, this available variation should be harnessed in order to protect and increase maize yields under the predicted climate change-induced and social scenarios. In a study completed by Cairns et al. [13], it was mentioned that only a fraction of the available maize genetic diversity has been utilised to date. Broadening the genetic base of maize and breeding climate-resilient, high-yielding cultivars that are adapted to the diverse agro-ecologies will greatly depend on the efficient and swift discovery and incorporation of a novel or favourable alleles and haplotypes [14].

In order to improve genetic variation in maize for increased adaptation to the changing environment, exploitation of exotic materials in maize breeding programs is suggested to be very key [15]. On the global scale, exotic maize germplasm can be classified into two main categories (i.e., temperate and tropical) based on the environmental conditions (especially day length characteristics) in which they are adapted [16]. Exotic germplasm can be a source of novel alleles that can be introduced, introgressed, or integrated into locally adapted material to confer resistance against biotic and abiotic stresses [17–19]. For instance, in a study by Meseka et al. [18], a line x tester mating design was used to determine the combining ability of 12 yellow and 13 white exotic maize inbreds and classify them into heterotic groups. The exotic inbred lines were crossed to two adapted testers representing two African heterotic groups, and the resulting testcrosses, along with hybrid checks, were evaluated in separate trials at two locations for 2 years in Nigeria. The study identified 15 exotic inbred lines having negative general combining ability (GCA) effects for aflatoxin and 13 with positive GCA effects for grain yield, whereas six combined the two desired traits. In addition, five white and six yellow endosperm test crosses were found to be good specific combiners for the two desired traits. The conclusion from this study was that the exotic lines with negative GCA effects for aflatoxin accumulation can be used as donor parents to develop backcross populations for generating new inbred lines with much higher levels of resistance to aflatoxin accumulation. In a separate study conducted by Whitehead et al. [15] on maize, crosses, backcrosses, and test crosses were evaluated to identify superior progenies that were intermated to form germplasm sources that include 75% temperate germplasm and either 25% subtropical or 25% tropical germplasm. The backcrosses (25%) and test crosses (12.5%) with 25% exotic germplasm had maturities and agronomic traits similar to the elite temperate germplasm sources. The conclusion from this study was that the populations formed by intermating superior backcross progenies, based on backcross and test cross data, provides additional germplasm resources for future use in temperate maize breeding programs.

Regardless of this overwhelming evidence on the potential harboured in exotic germplasm in increasing genetic variation and to promote adaptation of maize to stress, very little is understood in SSA, on how exotic germplasm can effectively be exploited in maize breeding programs. Here, we aim to depict yield gains that can be made when exotic genes from temperate, tropical, and sub-tropical gene pools are integrated within the sub-tropical maize germplasm pool. The information will be useful in guiding maize breeders in the sub-tropical regions on exotic materials to target for beneficial integrations.

#### 2. Methodology

## 2.1. Germplasm and Methodology

A total of eight maize inbred lines derived from pedigree crosses of exotic and local inbred lines (i.e., sub-tropically adapted inbred lines; STALs) were inter-mated together with six elite STALs (Table 1) in a partial diallel mating scheme [20]. The crossing scheme yielded a total of 91  $F_{1s}$  which were evaluated together with nine commercial checks in multi-environmental trials (METs) at eight locations representing agro-ecologies in which maize is predominantly grown in Zimbabwe (Table 2).

Parental Number	Name	Genetic Background	Genetic Background [Coded]
P1	CL115324	Pedigree start = STAL $\times$ Temperate	Temperate (T)
P2	CL1210884	Pedigree start = STAL $\times$ Temperate	Temperate (T)
P3	DJ-154	Pedigree start = STAL $\times$ Temperate	Temperate (T)
P4	CL1210969	Pedigree start = STAL $\times$ Temperate	Temperate (T)
P5	C1008-1	Pedigree start = STAL $\times$ Tropical	Tropical (E)
P6	CL1211291	Pedigree start = STAL $\times$ Sub-tropical	Sub-tropical (S)
P7	CL1211293	Pedigree start = STAL $\times$ Sub-tropical	Sub-tropical (S)
P8	CL1212428	Pedigree start = STAL $\times$ Tropical	Sub-tropical (S)
P9	CL1214868	Pedigree start = STAL $\times$ STAL	Local (L)
P10	CL1210571	Pedigree start = STAL $\times$ STAL	Local (L)
P11	CL1310262	Pedigree start = STAL $\times$ STAL	Local (L)
P12	DJ9-5	Pedigree start = STAL $\times$ STAL	Local (L)
P13	DJ9-1	Pedigree start = STAL $\times$ STAL	Local (L)
P14	CML444	Pedigree start = STAL $\times$ STAL	Local (L)

**Table 1.** Local and exotic lines mated using the partial diallel mating design during the 2016 winter season in Zimbabwe.

**Table 2.** Geographic and climatic conditions of the test fields representing agro-ecologies where maize is predominantly grown in Zimbabwe.

Site	Chiredzi	CIMMYT-Harare	Chibhero	Kadoma	Ratray Anold
Latitude	21°1′10′′ S	17°49′ S	17°26′ S	18°20′ S	15°49′ S
Longitude	31°34′23′′ E	31°01′ E	31°05′ E	30°97′ E	20°01′ E
Soil type	Paragneiss clay	Red clay soil	Sandy loam soil	Red Clay	Red Clay
Type of Irrigation	Overhead sprinkler	Overhead sprinkler	Overheard sprinkler	Overheard sprinkler	Overheard sprinkler
Rainfall received	<450 mm	750–1000 mm	750–1000 mm	650–800 mm	550–800 mm
Altitude (mas)	445	1480	1480	1149	
Mega Environment	Е	А	С	С	В
Natural region	IV	IIa	IIa	III	IIb

## 2.2. Trial Establishment, Experimental Design, and Site Management

A total of 100 hybrids (i.e., 91  $F_{1s}$  + 9 checks) were laid-out at each of the eight locations using an alpha (0.1) lattice design with two replications. Each replication consisted of 20 incomplete blocks, which harboured five hybrid plots, each. Each of the plots was 3 m long, with in-row spaces of 0.25 m and inter-row spaces of 0.75 m, in order to achieve a plant population of about 53,000 plants/hectare. Basal fertiliser (N7%, P6%, K6%) was applied at a rate of 400 kg ha<sup>-1</sup> at planting, followed by a split application of top dressing at a rate of 200 kg ha<sup>-1</sup> at 4 and 8 weeks, respectively.

Briefly, the managed drought stress (MDS) was imposed by withdrawing irrigation on the maize crop three weeks before flowering. Delayed planting was completed to coincide with high temperatures with the flowering stage in October for the managed heat stress (MHS) trial, but for this experiment, irrigation was supplied as normal until physiological maturity. The random drought stress (RDS) trial was established at a location where, according to history, there are high chances of mid-season or terminal droughts during the maize growing season. Both the MDS and the MHS trials were established during the 2017 winter period.

## 2.3. Data Collection

Agronomic traits were recorded as follows: grain yield (GY, measured as grain weight per plot, and the moisture was adjusted to 12.5% then estimated to yield per hectare); grain moisture content (MOI, measured using a moisture meter at the harvesting stage); days to 50% anthesis and silking (AD and SD, recorded as days to the shedding of pollen and visible development of silk on half of the plants in a plot); anthesis silking interval (ASI, calculated as the difference between anthesis and silking days); root lodging (RL, obtained by recording the number of plants lodged from the roots per plot); stem lodging (SL, obtained by recording the number of plants lodged or bent from the first node above ground); leaf senescence (LS, measured on a scale of 1–10 under low nitrogen conditions); and, plant and ear height (PH and EH, measured from ground to the node below the ear and from the ground to the last node before the tassel). Gray leaf spot (GLS), Northern leaf blight (NLB), and Maize streak virus (MSV) scores were taken using a scale of 1–5 [21].

## 2.4. Data Analysis

Multi Environmental Trials (METs) data were subjected to analysis of variance (ANOVA) following the residual maximum likelihood (REML) procedures in the CIMMYT Fieldbook [22] for each site. An across site analysis of variance (ANOVA) was carried out on traits that showed to be significant in at least two locations (see Table S1) using the GenStat Software 17th Edition [23]. Across site ANOVA was completed according to the linear model by Barreto et al. [24] as follows:

$$Y_{ijkl} = \mu + r_j B_k + L_i + El + [EL]_{il} + \varepsilon_{ijkl})$$

where  $Y_{ijkl}$  is the response variable,  $\mu$  is the grand mean,  $r_j B_K$  is the effect of the  $k_{th}$  block nested in the jth replication, k represents blocks, j represents replications,  $L_i$  is the effect of  $i_{th}$  location, i represents locations,  $E_l$  is the effect of the lth entry and l represents entries,  $EL_{il}$  is the interaction effect of the  $l_{th}$  entry and the ith location, and  $\varepsilon_{ijkl}$  is the experimental error.

The relationship between grain yield and anthesis date of the best 10 selected crosses in terms of grain yield performance within the different genetic backgrounds were visualized using a scatter plot, and the graph was plotted using 'ggplot' function in the ggplot2 R package [25]. To visualize how the best 10 selected performed across the different agro-ecologies for grain yield, a 3-dimensional pie-chart was created using the '*pie3D*' function in the plotrix v3.7–2 R package [26]. The general and the specific GCA effects of the parental inbred lines were predicted using the Analysis of Genetic Designs in R (ADG-R) Software v5.0 [27]. In order to identify among the best 10 selected crosses, crosses that were both high yielding and stable across the different agro-ecologies where maize was evaluated in this study, the 'ranking' GGE biplot was plotted. For the definition of an ideal genotype, see Yan and Kang [28] (p. 88). In brief, genotypes positioned furthest away from the average environment coordinate (AEC) were judged to be 'least stable', whereas those closest to the AEC were regarded as 'most stable'.

## 3. Results

#### 3.1. Agronomic Performance of the F1s within and across Locations

Differences due to genotype effects were significant for GY (p < 0.05) at five locations which are: Kadoma, Ratray Anold, CIMMYT-Harare (diseases), CIMMYT-Harare (LN), and Chibhero. The other agronomic traits (i.e., AD, ASI, EPO, HC, ER, NLB, and GLS) also showed to be significant in at least one location (Table S1). In addition, across site analysis of variance (ANOVA) also revealed significant genotype effects on GY, AD, ASI, HC, EPO, and GLS. Significant genotype x environment interaction (GEI) effects were also detected for these traits. Broad sense heritability (H<sup>2</sup>) for GY was 51.33 %, which was relatively lower than that of the other agronomic traits (Table 3).

	G١	$(Tha^{-1})$	Α	D (Days)	A	SI (Days)		EPO (cm)	i	HC (%)		ER (%)	ET	(Score 1-5)	GLS	5 (Score 1–5)
Source of Variation	Df	Mean Sq	Df	Mean Sq	Df	Mean Sq	Df	Mean Sq	DF	Mean Sq	Df	Mean Sq	DF	Mean Sq	Df	Mean Sq
Location	4	802.9 ***	4	14,242.7 ***	3	214.968 ***	6	5,252,421 ***	4	5156.8 ***	3	0	3	0	3	28.4028 ***
Genotype	99	16.76 ***	99	42.8 ***	99	28.003 ***	99	519,550 ***	99	729.9 ***	99	227.501 ***	99	0.69171 ***	99	1.8292 ***
Replication (Location)	5	9.65 *	5	26.5 ****	4	87.008 ***	7	585,832 ***	5	458.3 ***	4	26.091	4	0.06564	4	0.5879 ***
Genotype × Location	396	8.16 ***	391	10.2 ****	297	17.975 ***	594	135,493 ***	396	175.9 ***	297	0.061	297	0.00063	292	0.2338 ***
Block (Replica- tion × Location)	190	4.48	190	5.9	152	11.243	266	101,578 *	190	100.2	152	65.085	152	0.13882	152	0.0962
Residuals	305	3.93	283	5.9	244	10.636	427	79891	305	100.5	244	63.541	240	0.13078	221	0.1178
Grand mean		7.4821		75.6232		1.6028		0.5339		7.0942		7.1903		2.2072		2.0842
Broad sense heritability		0.5133		0.7699		0.2823		0.744		0.7594		0		0.1559		0.8774
LSD (5 %)		3.9872		4.5967		3.4582		0.0822		19.5947		15.7009		0.524		0.6507
CV		27.1885		3.1013		110.0849		7.8539		140.9215		111.4093		12.1133		15.929

**Table 3.** An across site analysis of variance for major traits that showed at least two or more sites significant for an agronomic trait under observation.

\*, \*\*\* Significant at 0.05, 0.01, and 0.001 probability levels, respectively. GY = grain yield; AD = anthesis date; ASI= anthesis silking interval; EPO = ear position; HC= husk cover; ER = ear rots; ET = northern leaf blight disease; GLS = grey leaf spot disease; Df = Degrees of freedoms.

The best performing  $F_1$  was genotype 44 (GY = 10.52 tha<sup>-1</sup>), a cross between an inbred of sub-tropical origin (i.e., P7) and an inbred line of temperate background (i.e., P2). In the second position, there was genotype 2 [9.921 tha<sup>-1</sup>; Cross = P10 (L) × P1 (T)]. In the third position, there was genotype 74 [9.74 tha<sup>-1</sup>; Cross = P5 (E) × P2 (T)]. However, G2 and G74 were surpassed in performance by the best local check hybrid (G100; SC727; 9.975 tha<sup>-1</sup>), although their means were not significantly different from each other (LSD = 3.9872 tha<sup>-1</sup>; Table 4). Amongst the top 10 F<sub>1</sub> selections, a cross between inbred lines with a tropical genetic background [i.e., G72; P5 (E) × P8 (E)] showed the lowest GY (i.e., 5.858 tha<sup>-1</sup>) performance compared to the other groups (Table 4; Figure 1). In terms of days required to flower, G44 (cross = SxT; AD = 76.425 days) required fewer days to mature compared to the best-performing hybrid check (SC727; AD = 80.468 days) (Table 4; Figure 2).

**Table 4.** Mean grain yield, general- and specific combining ability effects for the best 10 selections completed within each unique crossing group sharing the same genetic background, developed using the partial diallel mating scheme.

Genotype	Cross	HybridCode_ and Genetic Background	Genetic Background	GCA_Parent 1 (tha-1)	GCA_Parent 2 (tha-1)	SCA (tha-1)	Grain Yield (tha-1)	Anthesis Date (Days)
G2	$\text{P10}\times\text{P6}$	2{LXS}	LXS	0.446 **	0.643 ***	0.765	9.26	75.169
G4	$\text{P10}\times\text{P1}$	4{LXT}	LXT	0.446 **	0.390 **	1.606 **	9.921	79.885
G18	$\text{P13}\times\text{P12}$	18{LXL}	LXL	-0.577 ***	-0.293 *	1.87 **	8.43	72.608
G26	P6xP7	26{SXS}	SXS	0.643 ***	0.468 ***	-0.48	8.092	77.088
G40	P7xP5	40{SXE}	EXS	0.468 ***	-0.066	-0.018	7.83	79.443
G44	P7xP2	44{TXS}	TXS	0.468 ***	0.789 ***	1.814 **	10.52	76.425
G53	P1xP2	53{TXT}	TXT	0.390 **	0.789 ***	-0.13	8.454	74.931
G72	P5xP8	72{EXE}	EXE	-0.066	-0.505 **	-1.046	5.858	72.953
G74	P5xP2	74{TXE}	TXE	-0.066	0.789 ***	1.546 *	9.74	78.813
G85	P8xP14	85{LXE}	LXE	-0.505 **	-0.288 *	2.559 ***	9.278	76.862
G100	Check	100{CHECK}	CHECK				9.975	80.468

\*, \*\*, \*\*\* Significant at 0.05, 0.01, and 0.001 probability levels, respectively. GCA—stands for General combining ability; SCA—represents Specific combining ability; L—represents the sub-tropically adapted lines developed within the CIMMYT-Zimbabwe breeding program; S—denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and sub-tropically adapted; E—denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and tropically adapted; and, T—denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and tropically adapted; and, T—denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and tropically adapted; and, T—denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and tropically adapted to temperate conditions.



**Figure 1.** Pie chart showing grain yield performance of the best 10 selections completed within each unique crossing group sharing the same genetic background. L-represents the sub-tropically adapted lines developed within the CIMMYT-Zimbabwe breeding program; S-denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and sub-tropically adapted; E-denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and tropically adapted; and T-denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and adapted to temperate conditions.



**Figure 2.** Interaction plot showing the relationship between grain yield performance and anthesis dates of best the 10 selections completed within each unique crossing group sharing the same genetic background. L—represents the sub-tropically adapted lines developed within the CIMMYT-Zimbabwe breeding program; S—denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and sub-tropically adapted; E—denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and tropically adapted; and, T—denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and tropically adapted; and, T—denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and adapted to temperate conditions.

# 3.2. Identification of Ideal Exotic Germplasm for Use in Sub-Tropical Breeding Programs

Two inbred lines of temperate [i.e., P2 (GCA =  $0.789 \text{ tha}^{-1}$ )] and sub-tropical [i.e., P6 (GCA =  $0.643 \text{ tha}^{-1}$ )] background showed the highest GCA effects for GY (Table 1). Interestingly, P2 was involved in the cross that showed the highest GY (i.e., G44) among all the best-selected F<sub>1</sub>s. (Table 4; Table S2; Figure 1).

Apart from showing high GY potential within their respective hybrid groups, some of the selected high-yielding genotypes also proved to be stable under diverse environments. These were for example, genotypes 44 (TxS) and 85 (LxE) which were stable across the five sites where GY was significant. Genotype 100 (the best commercial check hybrid) also showed reasonable stability across the locations (Figure 3).



Ranking biplot (Total - 71.69%)

**Figure 3.** AGGE comparison biplot of the best 10 selections completed within each unique crossing group sharing the same genetic background, developed using the partial diallel mating scheme. Only sites where GY was significant (p < 0.05; Table S1) were included in the biplot. L-represents the sub-tropically adapted lines developed within the CIMMYT-Zimbabwe breeding program; S-denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and sub-tropically adapted; E-denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and tropically adapted; and, T-denotes inbred lines developed from a pedigree start cross with one of the parents being exotic and adapted to temperate conditions.

## 4. Discussion

Exotic germplasm integration and introgression (i.e., germplasm beyond the breeder's target area) have traditionally been used to broaden the genetic base of the local (germplasm within the breeder's target area) populations, a phenomenon key in crop improvement programs [29]. This strategy is usually under-utilized in sub-Saharan Africa (SSA), regardless of the overwhelming evidence pointing to its potential benefits in promoting crop adaptation to the changing environment [17–19]. Here, eight maize (*Zea mays* L.) inbred lines developed from pedigree crosses of exotic and local inbred lines (i.e., sub-tropically adapted lines;

STALs) were inter-mated together with six elite STALs, in a partial diallel mating scheme, in order to depict yield gains that can be made when exotic genes are integrated within the sub-tropical maize germplasm pool. Data generated in the multi-environmental trials conducted across eight locations representing the different agro-ecologies where maize is predominantly grown in Zimbabwe demonstrated the potential of exotic germplasm, especially germplasm with a temperate background, to increase grain yield potential and stability in the local (sub-tropical) populations. Furthermore, temperate germplasm also showed the ability to introduce earliness in flowering (i.e., positively correlated with maturity) but maintaining high-yielding abilities in the sub-tropical germplasm.

In more detail, the genetic variation observed among the hybrids (Table 3) was expected because the crosses were developed using material from different backgrounds. Grain yield variation in maize genotypes is a factor of the genetic variability in genotypes [30]. In a study by Xavier et al. [31], in which they incorporated different exotic genes from different sources, genetic variation was also shown to be high.

As expected, higher yields coupled with earliness in flowering were observed on crosses between the inbred lines of sub-tropical origin and inbreds of temperate origin (for example, G44). Similar findings were previously reported by Nastasic et al. [32]. This result corresponds to the fact that the crosses from two distant sources result in higher levels of heterosis. The results contradict Abadassi [33], who discouraged the use of temperate germplasm in tropical breeding programs, citing that the temperate material will introduce undesirable traits, especially diseases in the tropical maize populations. However, in the same study, it was indicated that temperate germplasm introduces earliness in the tropical population. Of interest, tropical and subtropical germplasm was reported to introduce a degree of lateness in the temperate germplasm [34].

The study also identified inbred lines, specifically those from the temperate background (e.g., P2), which showed positive GCA effects for grain yield. These are important in future breeding programs, as they can be used to develop new inbred parents that can contribute to gains in yield performance in sub-tropical maize populations. In addition, the lines with positive GCA effects for grain yield can also be important as pollen donors or female parents in the development of high-yielding single-cross, three-way-cross, or double-cross hybrids that can potentially replace or complement commercial maize varieties currently in the seed market SSA. Furthermore, inbred lines with positive GCA effects for grain yield performance can effectively be used to develop synthetic and/or open-pollinated varieties (OPVs), known to be more adapted to stress conditions compared to hybrids [35]. Crosses with high specific combining abilities may be better alternatives to the currently used single-cross testers in the sub-tropical maize breeding programs.

Lastly, the wide adaptation (stability) observed in some of the  $F_1s$ , particularly genotype 44, which was also shown to be high-yielding is important. Genotypes of this nature can potentially compete commercially with the best single-cross commercial hybrids. Most single-cross hybrid cultivars are very productive under optimal management conditions but shows to be poorly adapted under stress conditions [36]. Therefore, high-yielding and stable genotypes, such as genotype 44, can potentially complement or replace the 3-waycross hybrids currently dominating the seed market in SSA.

In the USA, it was noted that tropical and subtropical germplasm introduced a degree of lateness in the temperate germplasm [34], in regard to that, in this study there was a notable difference in the flowering dates that was brought about by the temperate germplasm. Wen et al. [37] reported that introduction of temperate maize inbred lines with unique alleles into tropically adapted lines could be beneficial for enhancing heterosis in grain yields. In this study, F<sub>1</sub>s with parents of temperate background flowered earlier than the local late maturing check SC727. Temperate germplasm can be used to introduce earliness and reduce plant heights [33]. However, it was noted that, in general, GY increased as the time frame to maturity increased (Figure 2).

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In conclusion, data demonstrated that incorporation of exotic genes, especially those with a temperate background, may improve the yielding ability and stability, and can introduce earliness in maturity in the sub-tropical maize populations.

**Supplementary Materials:** The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/agronomy13061605/s1, Table S1: An individual site summary of mean squares and their significant levels for agronomic traits under observation at eight sites for the single cross hybrids evaluated during the 2017–2019. Table S2. Local and exotic lines mated using the partial diallel mating design during the 2016 winter season in Zimbabwe.

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