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Genetic Trends in Seven Years of Maize Breeding at Mozambique's Institute of Agricultural Research

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Abstract: Assessing genetic gains from historical data provides insights to improve breeding programs. This study evaluated the Mozambique National Maize Program's (MNMP's) genetic gains using data from advanced germplasm trials conducted at 21 locations between 2014 and 2020. Genetic gains were calculated by regressing the genotypic best linear unbiased estimates of grain yield and complementary agronomic traits against the initial year of genotype evaluation (n = 592). The annual genetic gain was expressed as a percentage of the trait mean. While grain yield, the primary breeding focus, showed no significant improvement, significant gains were observed for the plant height (0.67%), ear height (1.74%), ears per plant (1.31%), ear position coefficient (1.22%), and husk cover (4.7%). Negative genetic gains were detected for the days to anthesis (−0.5%), the anthesis–silking interval or ASI (−9.31%), and stalk lodging (−5.01%). These results indicate that while MNMP did not achieve the desired positive genetic gain for grain yield, progress was made for traits related to plant resilience, particularly the ASI and stalk lodging. MNMP should seek to incorporate new breeding technologies and human resources to enhance genetic gains for grain yield and other key traits in the maize breeding program, while developing and deploying high-yielding, climate-resilient maize varieties to address emerging food security challenges in Mozambique.

Keywords: maize; genetic gain; grain yield; complementary agronomic traits; Mozambique

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1. Introduction

Mozambique is a developing country in sub-Saharan Africa, where agriculture is one of the most important activities and is mainly dominated by small-scale farming communities [1]. Maize is the most important cereal and the second main food crop after cassava [2], providing an annual food supply of nearly 56 kg per capita. It serves as a primary source of calories for a vast majority of the population, supplying 489 Kcal per capita per day and 10 g of protein per capita per day [3]. The crop is annually cultivated on an estimated area of 1.8 million ha, with a total annual production of 2.0 million metric tons (MMT) and productivity of 1.1 tons per hectare. Most maize (~90%) is produced by small-scale growers who own, on average, 1.3 ha of land parcels and practice mixed cropping on

over ninety-five per cent of the arable land. Small-scale farming mainly depends on rainfall, and most growers neither use improved seed varieties nor apply fertilizers or pesticides; therefore, the grain yields are quite low (0.2 to 1.2 t/ha) [1].

Over the last 60 years, maize production in Mozambique increased more than five-fold, from 0.37 MMT to 2.0 MMT between 1961 and 2022. During the same period, the maize area expanded from 0.425 million ha (M ha) to 1.82 M ha, representing a more than four-fold increase. On the other hand, no significant productivity growth was observed as the grain yield increased only from 0.87 t/ha in 1961 to 1.07 t/ha in 2022 [3]. This increased production is mainly attributed to an expansion in the area under maize production [4], as opposed to other regions of the world where an increase in maize production is largely associated with increased yields [5]. Recent reports showed that the production gains in many countries in sub-Saharan Africa (SSA) over the last 50 years are largely associated with an increased area under maize cultivation, rather than the production rate per unit piece of land [6]. Crop area expansion for increased production is not sustainable and is a major driver of biodiversity loss [7]. Various studies have indicated the potential for increasing maize productivity in African countries beyond the current levels by adopting improved genetics and agronomic practices [6,8,9].

Maize cultivation and productivity in Mozambique declined due to civil war (1982–1997), flooding, and drought (1999–2000) [10,11]. Thereafter, maize production improved by about 29% [12]. These unexpected events also paralyzed the operations of the national research and extension systems in Mozambique [11]. Despite the past challenges, Mozambique's Institute of Agricultural Research (IIAM) has worked with international partners, particularly the Consultative Group for International Agricultural Research (CGIAR), to enhance agricultural productivity through research for development in the past four decades [13].

Maize breeding in Mozambique started around 1977, right after the nation's independence, and focused primarily on introducing new germplasm, selecting for drought tolerance and resistance to downy mildew and the maize streak virus [14]. During this period, the program also started developing inbred lines. Still, the priority was to develop and release open-pollinated varieties (OPVs); the first famous OPV, called Matuba, was released in 1986, with Obrigon Flint following in 1988. From 2002/2003, the focus was on hybrid development adapted to the low-land areas, tolerant to drought, resistant to downy mildew, and with highly enhanced nutritional value (quality protein maize (QPM)) [15]. The first two hybrids were released in 2008; one was developed by Mozambican plant breeders using locally selected material from populations sourced from the International Institute of Tropical Agriculture (IITA), and the other QPM was developed by a South African breeder based on a South African inbred line and two inbred lines from Ghana [1]. From there, the release of hybrids started growing in 2011. The Mozambique maize program has released eleven open-pollinated varieties and nine hybrids so far.

In all regions of Mozambique, maize is mainly produced by smallholder farmers (more than 90%) under rainfed conditions, where the risk of crop failure is high, especially under semi-arid conditions in southern Mozambique [2,16]. Over eighty per cent of Mozambique's cultivated maize is consumed as food, with a remaining small percentage used for feed, seed, or industrial materials [2]. The Southern region often produces less than the volume consumed; as a result, it must rely on supplies from other areas of the country or imports from South Africa. Low maize productivity is attributed to a lack of modern cultural practices, reliance on rainfed agriculture, limited access to inputs, and continued use of low-yielding varieties [2]. The supply of quality seeds in Mozambique is very limited due to several constraints encountered throughout the seed value chain. These include a limited supply of early-generation seeds, breeding programs targeting only a few main

crops, a reduced number of private companies specialized in seed production, limited coverage of agro-dealers and extension services, and the limited capacity of institutions to regulate and control the seed sector, allied with issues of fake seeds, free distribution of seeds, IIAM's weak capacity to forecast seed demand at the beginning of the cropping season, and unaffordable prices of improved seeds [17].

The National Directorate of Rural Extension and Sasakawa Global 2000 program and non-governmental agencies such as the International Fertilizer Development Center have made efforts to provide improved maize varieties (open-pollinated varieties and hybrids) and inorganic fertilizers (NPK and urea) to farmers [18]. Furthermore, CGIAR, through the International Maize and Wheat Improvement Center (CIMMYT) and IITA, has continuously supported maize breeding in Mozambique, shared improved maize germplasm, and, more recently, enabled the integration of novel breeding tools and technologies to increase genetic gains in the breeding program. The annual economic impact of adopting CGIAR maize germplasm in Mozambique was estimated to range between USD 18.45 million and USD 26.56 million [19].

The Mozambique maize breeding program has been mainly focused on developing varieties for high grain yield. Besides unpredictable climatic conditions, which are likely to cause flooding and drought stress, maize production is also affected by other abiotic and biotic stresses. The fall armyworm (FAW) has recently become a major pest in Mozambique, and it was reported to have caused a loss of 49,000 tons of maize after it was reported in 2017 [20]. The focus of the breeding efforts at IIAM has been to develop high-yielding maize varieties that are tolerant to major stresses, particularly drought, downy mildew, maize streak virus (MSV), and the FAW [21,22]. The contribution of the breeding efforts has not been analyzed for the key traits in the IIAM maize breeding program. Assessing the progress made in genetic improvements for higher grain yield can enable the breeding program to establish the bases for optimization for better genetic gains in the future, particularly with the emerging need for rapid varietal release and replacement to enhance resilience against the adverse effects of climate change [23,24]. Through its partnership with CGIAR, particularly CIMMYT and IITA, the maize breeding program of IIAM has taken significant steps in recent years to modernize operations to achieve higher genetic gains. The CGIAR-supported efforts to modernize breeding pipelines in Africa can design program-specific optimization packages based on needs assessments and analyses of the genetic trends using Mozambique's historical germplasm evaluation data [25]. This paper reports the trends of improvements in maize yield and other important traits in the IIAM breeding program from 2014 to 2020.

2. Materials and Methods

2.1. Maize Germplasm

The panel (n = 592) consisted of three-way crosses and local checks, which were evaluated for multiple traits in main advanced varietal (AVT) and value for cultivation and use (VCU) trials between 2014 and 2020. The datasets for the AVT and VCU trials were combined because MNMP conducts these two trials simultaneously, and the germplasm development stage is run by the same institution. The three-way crosses were selected based on their superior performance in preliminary yield trials prior to being evaluated in the AVT and VCU trials. The most promising candidates from the AVT trials were then evaluated over multiple locations across the target environments at the VCU stage (Table 1). The mean number of crosses evaluated per year was 85, with the lowest number of crosses (n = 14) being evaluated in 2020 and the highest number (n = 179) in 2018 (Table 2). Across the trials, popular commercial varieties (Molocue, Pan53, and SP-1) were used as checks.

Table 1. Description of the locations for the advanced maize trials conducted between 2014 and 2020 in Mozambique.

Location	District	Province	Latitude	Longitude	Altitude (masl)
Mazeminhama Agronomic Post	Namaacha	Maputo	26°27′ S	32°15′ E	61
Umbeluzi Agricultural Research Station	Boane		26°03′ S	32°15′ E	12
Ricatla Agronomic Post	Marracuene		25°46′ S	32°38′ E	43
Maniquenique Agronomic Post	Chibuto	Gaza	24°44′ S	33°32′ E	13
Chókwè Agricultural Research Station	Chókwè		24°32′ S	33°00′ E	33
Nhacoongo Agronomic Post	Jangamo	Inhambane	24°18′ S	35°11′ E	30
Sussundenga Agricultural Research Station	Sussundenga	Manica	19°20′ S	33°13′ E	635
Messambuzi Agronomic Post	Rotanda		19º 30′ S	32º 55′ E	966
Chemba Agronomic Post	Chemba	Sofala	17°14′ S	34°49′ E	100
Lamego Agronomic Post			19°21′ S	34°19′ E	644
M'tengomodzi Agronomic Post	Angónia	Tete	14°22′ S	33º 46′ E	1200
Tete Agricultural Training Center			16°9′ S	33°35′ E	140
Mocuba Agricultural Research Station	Mocuba	Zambézia	16°50′ S	36°59′ E	134
Nametil Agronomic Post	Mogovolas	Nampula	15°43′ S	39°21′ E	171
Nampula Agronomic Post	Rapale		15°09′ S	39°20′ E	432
Namialo Agronomic Post	Meconta		14°58′ S	39°51′ E	230
Ribáuè Agricultural Research Station	Ribáuè		14°59′ S	38°16′ E	535
Mutuáli Agronomic Post	Malema		14°53′ S	37°03′ E	570
Namapa Agronomic Post	Namapa		13°43′ S	39°50′ E	200
Lichinga Agricultural Research Station	Lichinga	Niassa	13°18′ S	35°14′ E	1356
Mapupulo Agronomic Post	Montepuez	Cabo-Delgado	13°12′ S	38°53′ E	476

Table 2. Summary of the number of experiments and entries per year and the number of hybrids at each first-year level tested.

Year	Experiments (*n*)	All Genotypes (*n*)	Genotypes Tested for the First Time (*n*)
2014	8	63	63
2015	19	86	58
2016	19	54	31
2017	15	86	77
2018	21	200	179
2019	13	184	170
2020	6	16	14
Total	101	689	592

2.2. Description of the Locations and Trials

The trials were conducted in twenty-one locations spanning ten Mozambique provinces at altitudes ranging from 12 to 1356 masl. The locations were the target environments for the varieties developed in the breeding program and offered opportunities to identify the best candidate varieties under relevant stress conditions (Table 1). An experiment was defined as a unique combination of trial, year, season, and location. One hundred and one experiments were conducted over seven years (Table 2). The genotypes were assessed for major agronomic traits across the locations (Tables 1 and 3).

Table 3. Summary of entry broad-sense heritability (*H*) within each experiment from an analysis of multiple maize traits in Mozambique and the genetic-to-error variance ratio.

Trait	Experiments (*n*)	*H*	Experiments with H < 0.20	$\sigma^2_{genotype}/\sigma^2_{error}$
Grain yield (all, kg ha^{-1})	96	0.509	24.0	0.67
Exps. with average yield > 3000, kg ha^{-1}	57	0.570	19.3	0.70
Exps. with average yield < 3000, kg ha^{-1}	39	0.418	30.7	0.51
Days to anthesis	93	0.606	19.4	3.61
Anthesis–silking interval (days)	93	0.370	34.4	2.62
Plant height (cm)	89	0.564	18.0	0.94
Ear height (cm)	89	0.566	22.5	1.07
Ear position coefficient	89	0.577	14.6	0.74
Ears per plant (*n*)	98	0.328	37.8	0.27
Poor husk cover (%)	80	0.563	18.8	0.84
Root lodging (%)	75	0.269	45.3	0.19
Stalk lodging (%)	65	0.283	55.4	0.22

2.3. Measurement of the Agronomic Traits

The traits measured were the days to anthesis, days to silking, plant height, ear height, ears per plant, root lodging, stalk lodging, poor husk cover, and grain yield. The days to anthesis (AD) and days to silking (SD) were recorded when 50% of the plants had shed pollen and 50% had silk, respectively. The anthesis–silking interval (ASI) was calculated as the difference between the days to silking and days to anthesis. The plant height was measured in cm from the base of the plant to the first tassel branch. The ear height was measured as the distance (cm) from the base of the plant to the node with the uppermost ear. The ratio of ear height to plant height formed the ear position coefficient. The ears per plant (EPP) was calculated as the number of ears harvested per plot divided by the number of plants per plot. The number of plants per plot with root and stalk lodging was counted and expressed as a percentage of the total number of plants in a plot. Poor husk cover was computed as the percentage of plants whose primary ears had short husks, which led to the exposure of the kernels. The grain texture was visually estimated per plot using a 1-to-5 scale where 1 represents flint, round-crown kernels and 5 represents dent kernels with a floury endosperm. Ear rot was visually estimated per plot using a visual scale of 1–5, where 1 represents no ear rot, and 5 represents very heavy infection. At harvest, two plants from either end were eliminated, the rest were hand-harvested, and the grain yield and moisture content were measured. The grain yield was adjusted to a 12.5% moisture content and expressed in kg ha^{-1}. Not all traits were assessed in each experiment, with a larger number of traits assessed in the AVT trials than in the IVT trials.

2.4. Statistical Analysis

The genetic gain was determined based on a regression of the trait genetic values against the year when the genotype was first evaluated in the advanced variety testing stage in a model reported earlier [25]. The data within each experiment were analyzed using the following model:

$$y_{ij} = \mu + g_i + r_j + e_{ij} \quad (1)$$

where y_{ij} is the mean phenotypic value of the trait within an experiment; g_i is the random effect of the *i*th genotype, with $g_i \sim N\left(0, \sigma^2_{g_i}\right)$; r_j is the random effect of the *j*th replication, with $r_j \sim N\left(0, \sigma^2_{r_j}\right)$; and e_{ij} is the residual error, with $e_{ij} \sim N\left(0, \sigma^2_{e_{ij}}\right)$. Observations with

a standardized residual greater than 1.75 were removed from all further analyses. The entry-mean heritability was then calculated within each experiment as follows:

$$H = \frac{\sigma_g^2}{\sigma_g^2 + \left\langle \frac{\sigma_e^2}{r} \right\rangle} \quad (2)$$

where σ_g^2 and σ_e^2 are the genetic and error variances, and r is the number of replications.

An analysis of variance was also conducted over experiments within a year using the following model:

$$y_{ijk} = \mu + g_i + x_k + r(x)_{jk} + gx_{ik} + e_{ijk} \quad (3)$$

where y_{ijk} is the mean phenotypic value of the trait within an experiment within a year; x_k is the random effect of the kth experiment, with $x_k \sim N(0, \sigma_x^2)$; $r(x)_{jk}$ is the random effect of the jth replication nested in the kth experiment, with $r(x)_{jk} \sim N\left(0, \sigma_{r(x)}^2\right)$; and e_{ijk} is the residual error, with $e_{ijk} \sim N(0, \sigma_e^2)$. The entry-mean heritability (H) for individual traits across experiments within a year was computed using the following model:

$$H = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{gx}^2}{x} + \frac{\sigma_e^2}{xr}} \quad (4)$$

where σ_{gx}^2 is the genotype-by-experiment variance, and x is the number of experiments used in that trial.

The genotypic best linear unbiased estimates (BLUEs) for each trait were then computed in a mixed model analysis using the following model:

$$y_{ijkl} = \mu + g_i + c_j + y_k + x(y)_{kl} + r(x)_{lm} + gy_{ik} + gx(y)_{ikl} + \varepsilon_{ijkl} \quad (5)$$

where y_{ijklm} is the phenotypic value for genotype i tested in control group j, year k, experiment l, and replicate m; μ is the overall mean; g_i is the fixed effect of the ith genotype; c_j is the fixed effect of the jth control, where j = 1 for the control population consisting of the checks and j = 2 for the hybrid group; y_k is a random effect for the kth year, with $y_k \sim N\left(0, \sigma_{y_k}^2\right)$; $x(y)_{kl}$ is a random effect for the lth experiment nested in the kth year, with $x(y)_{kl} \sim N\left(0, \sigma_{x(y)_{kl}}^2\right)$; gy_{ik} is the random effect of the interaction of the ith genotype and kth year, with $gy_{ik} \sim N\left(0, \sigma_{gy_{ik}}^2\right)$; $gx(y)_{ikl}$ is the random effect of the interaction of the ith genotype and lth experiment nested in the kth year, with $gx(y)_{ikl} \sim N\left(0, \sigma_{gx(y)_{ikl}}^2\right)$; $r(x)_{lm}$ is a random effect of the mth replication nested in the lth experiment, with $r(x)_{lm} \sim N\left(0, \sigma_{r(x)_{lm}}^2\right)$; and ε_{ijklm} is the residual error, with $\varepsilon_{ijklm} \sim N\left(0, \sigma_{\varepsilon_{ijklm}}^2\right)$. Data from experiments with an entry-mean heritability (hereinafter referred to as broad-sense heritability and denoted by H) of <0.20 were excluded from the analysis. The analysis provided the BLUE for each genotype. The first year of testing (FYT) for each genotype was assigned as the first year for which the genotype was tested in the AYT or VCU trials. The genetic gain was estimated by regressing the BLUE of each line onto its FYT value. This approach has been reported before [26–29].

The variance components from model 5 (above) were used to calculate H over all the years and experiments using a slight modification of Equation (4) (above), where y is the number of years:

$$H = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{gy}^2}{y} + \frac{\sigma_{gx(y)}^2}{yx} + \frac{\sigma_e^2}{yxr}}$$

3. Results

The dataset consisted of one hundred and one experiments conducted across twenty-one locations in Mozambique between 2014 and 2020, evaluating five hundred and eighty-nine maize test hybrid genotypes and three local commercial checks. The number of evaluated genotypes ranged from 16 (2020) to 200 (2018) (Table 2). Most (87.6%) of the test hybrids were evaluated for one year.

3.1. Heritability

The primary trait of interest for the IIAM maize breeding program is grain yield. This study analyzed the genetic trends for grain yield and other traits considered complementary to this primary trait (Table 3). The average *H* value varied across the traits, ranging from 0.269 for root lodging to 0.606 for days to anthesis (Table 3). On average, the error variance was more than 30% greater than the genetic variance for the grain yield, ears per plant, and shoot and root lodging (Table 3). Generally, the heritability of the traits was considered low when $H < 0.2$, moderate for heritability between 0.2 and 0.4, and high for $H \geq 0.4$. As part of the quality check, the experiments with $H < 0.2$ were excluded prior to the determination of genetic trends for individual traits. The most heritable traits were the grain yield, plant height, ear height, ears per plant, husk cover, and days to anthesis (Table 3). The traits with moderate heritability were stalk lodging, root lodging, the ear position coefficient, and the ASI (Table 3).

An analysis of variance components and heritability over the years and experiments was conducted (Table 4). The error variance was greater than 30% of the total for all traits, and the genotype x environment variance ranged from 6.99% (ear position) to 64.8% (anthesis day) of the total variance. Only the grain yield in experiments with a mean yield greater than 3000 kg ha^{-1} had an H value greater than 0.40 for any year. Nearly all other traits had *H* values less than 0.20, with the ears per plant, the ASI, and stalk lodging having H values less than 0.10.

Table 4. Variance components for genotype, genotype x location, genotype x year, genotype x location x year, and error expressed as percentage of total variance, as well as heritability (H) of multiple maize traits in Mozambique.

Trait	Percentage of Total Variance ($\sigma^2_{ge}+\sigma^2_{ge}+\sigma^2_{error}$)						H
	σ^2_g	σ^2_{gl}	σ^2_{gy}	σ^2_{gly}	σ^2_{ge}	σ^2_{error}	
Grain yield (GY) all exp.	3.87	7.01	1.41	29.87	38.28	57.84	0.232
GY AYT trial	6.47	21.91	0.35	9.71	31.97	61.56	0.313
GY VCU trial	6.24	3.11	5.99	11.89	20.98	72.78	0.341
Exp. with avg GY > 3000 kg ha^{-1}	8.53	11.90	0.37	17.51	29.77	61.69	0.411
Exp. with avg GY < 3000 kg ha^{-1}	2.10	4.99	7.71	11.09	23.79	74.11	0.134
Days to anthesis	1.67	0.00	0.00	64.78	64.78	33.55	0.110
Anthesis–silking interval	0.29	8.52	0.00	30.10	38.62	61.09	0.022
Plant height	8.56	15.30	2.29	19.01	36.60	54.83	0.380
Ear height	13.53	9.27	1.46	26.51	37.25	49.22	0.523
Ear position coefficient	16.88	1.06	0.94	4.99	6.99	76.13	0.678
Ears per plant	0.10	0.00	0.00	7.25	7.25	92.65	0.011
Poor husk cover	5.03	26.34	6.01	2.09	34.44	60.53	0.226
Root lodging	1.54	0.00	0.00	18.30	18.30	80.16	0.136
Stalk lodging	0.00	0.05	0.00	13.00	13.05	86.95	0.000

3.2. Genetic Gain Analysis for Grain Yield and Complementary Traits

The regression of the genotypic BLUEs against the first year of testing for individual genotypes revealed significant ($p < 0.05$) changes over a period of seven years for days to anthesis, plant height, ear height, ear position, ears per plant, poor husk cover, stalk lodging, and ASI (Table 5). None of the regression models explained more than 11% of the variation for these traits, and the significant regression modelled an average of just 2.6%.

Table 5. Genetic gains for different maize traits based on trials conducted by Mozambique national maize breeding program between 2014 and 2020.

Trait	Experiments (*n*)	Genotypes (*n*)	Model				Genetic Gain (Slope) as % Mean
			r^2	$\bar{x}$	Slope	*p*-Value	
Grain yield (kg ha^{-1}) all experiments and trials	73	590	0.000	3060	−1.001	0.960	−0.03
Grain yield (kg ha^{-1}) AYT trial	33	511	0.021	2947	−75.31	<0.001	−2.56
Grain yield (kg ha^{-1}) VCU trial	61	120	0.005	3168	−77.42	0.005	−2.34
Experiments with yield > 3000 kg ha^{-1}	46	521	0.006	4344	−42.93	0.081	−0.99
Experiments with yield < 3000 kg ha^{-1}	27	508	0.026	1626	125.01	<0.001	7.69
Days to anthesis	75	590	0.012	65.5	−0.612	0.041	−0.93
Anthesis–silking interval	61	590	0.015	3.53	−0.174	<0.001	−4.93
Plant height (cm)	73	590	0.017	169.1	1.146	0.002	0.68
Ear height (cm)	69	590	0.032	83.9	1.463	<0.001	1.74
Ear position	76	589	0.045	0.51	0.006	<0.001	1.18
Ears per plant	61	442	0.051	0.88	0.012	<0.001	1.36
Poor husk cover	65	539	0.023	16.97	1.053	<0.001	6.21
Root lodging	41	590	0.005	7.43	−0.181	0.082	−2.44
Stalk lodging	29	501	0.017	5.44	−0.381	0.004	−7.00

We conducted several analyses of grain yield. The initial regression analysis used data from all experiments and trials and showed no significant (p = 0.960) change in the grain yield over the 7 years (Table 5 and Figure 1). Significant negative changes were found when the data from the AYT (−75.31 kg ha^{-1} yr^{-1}) and VCU (−74.11 kg ha^{-1} yr^{-1}) trials were analyzed separately (Table 5). Because GY is the primary trait in the IIAM maize breeding program, a further statistical exploration was conducted in which the experiments were put into two categories: high grain yield potential (GY > 3000 kg ha^{-1} = GYH) and low grain yield potential (GY < 3000 kg ha^{-1} = GYL). The average heritability of experiments was higher in the high-grain-yield-potential experiments (0.57) than in the lower-grain-yield-potential experiments (0.418). The grain yield showed no significant genetic gain in the high-grain-yield-potential experiments but increased significantly in the lower-grain-yield-potential experiments at a rate of 125 kg ha^{-1} year^{-1}, representing a gain of 7.69% per year compared to the mean of 1626 kg ha^{-1} for the 27 low-grain-yield-potential experiments (Table 5). Non-significant gains for grain yield overall and in the high-grain-yield-potential experiments occurred despite its relatively high heritability. Despite their relatively low heritability, significant gains were noted for the ASI, ears per plant, and shoot lodging.

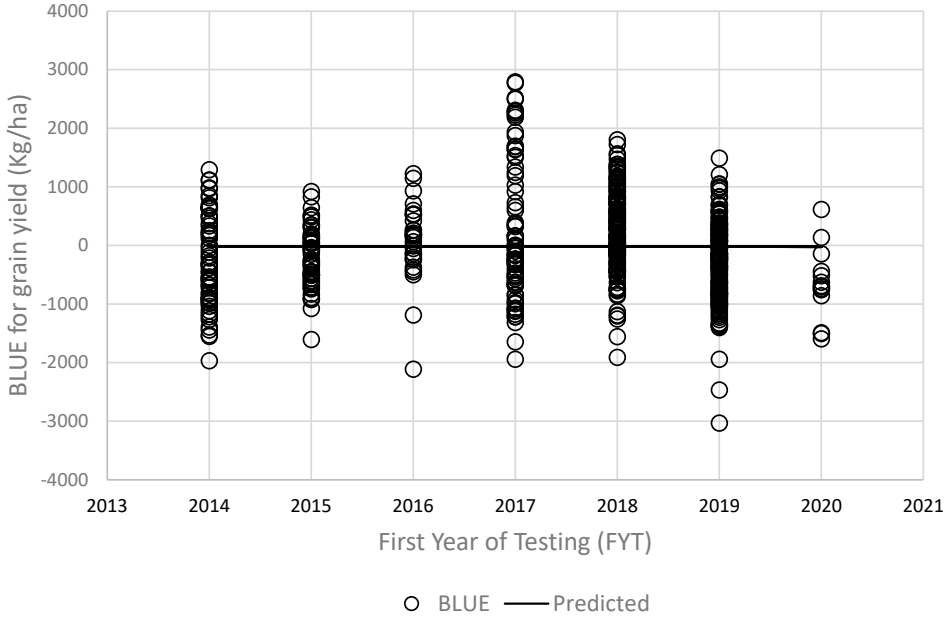

Figure 1. Genetic gain for grain yield (kg ha^{-1}) in maize genotypes evaluated in advanced trials conducted by the Mozambique maize breeding program between 2014 and 2020. Best linear unbiased estimates (BLUEs) are expressed relative to the mean of 3060 kg ha^{-1}.

The flowering time was measured based on the days to anthesis, days to silking and anthesis–silking interval (ASI). The days to anthesis varied from 27 to 101 days, with a mean of 65.5 days, and it decreased significantly ($p = 0.041$) at a rate of −0.15% per year (Table 5 and Figure 2). Additionally, the ASI ranged from −8 days to 32 days, with a mean of 3.5 days, and it decreased significantly ($p < 0.003$) by −4.93% per year (Table 4 and Figure 3).

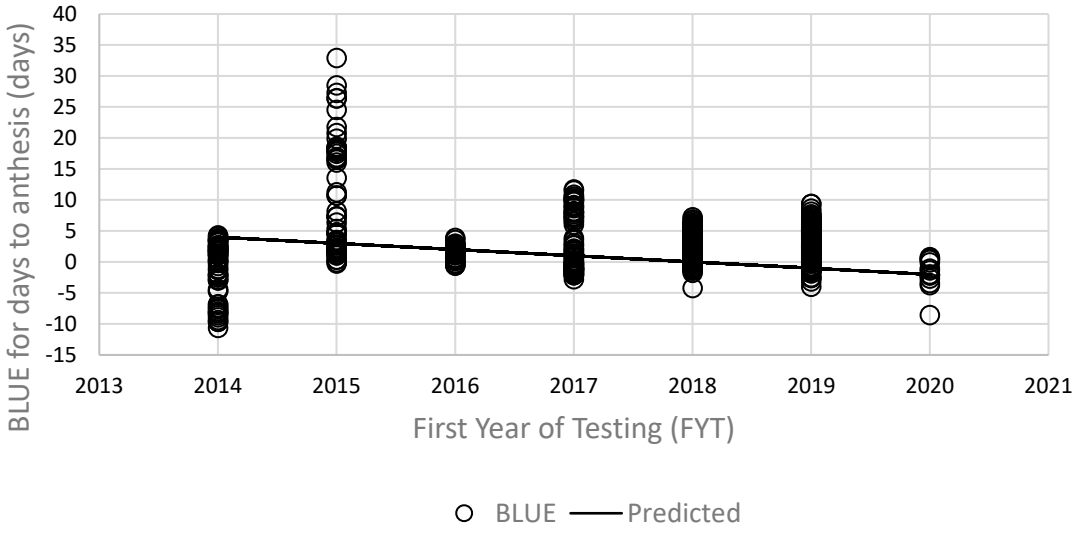

Figure 2. Genetic gain for the days to anthesis in maize genotypes evaluated in advanced trials by the Mozambique maize breeding program between 2014 and 2020. Best linear unbiased estimates (BLUEs) are expressed relative to the mean of 65.5 days.

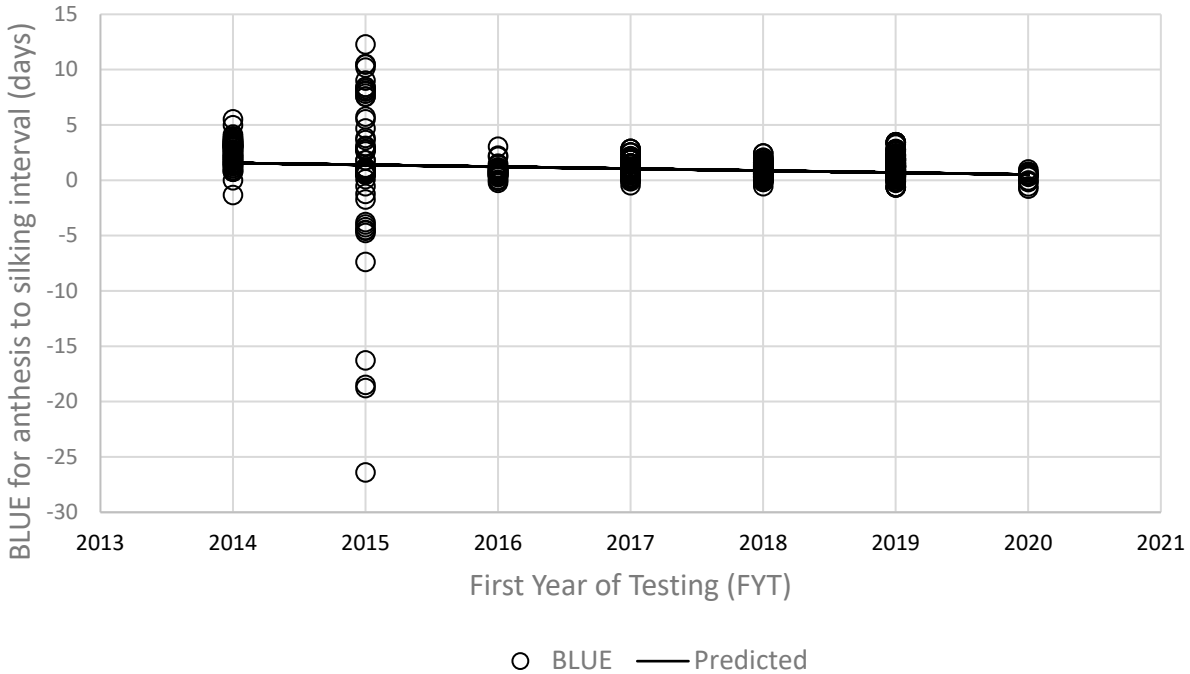

Figure 3. Genetic gain for the anthesis–silking interval in maize genotypes evaluated in advanced trials conducted by the Mozambique maize breeding program between 2014 and 2020. Best linear unbiased estimates (BLUEs) are expressed relative to the mean of 3.53 days.

The plant height varied from 41.5 cm to 287 cm, with a mean of 169.1 cm, and the plants continued to become significantly ($p = 0.002$) taller at a rate of 0.68% per year over

the seven years (Table 5 and Figure 4). The ear height ranged from 14 cm to 180 cm, with a mean of 83.9 cm and a significant gain ($p < 0.001$) of 1.74% per year (Table 5 and Figure 5).

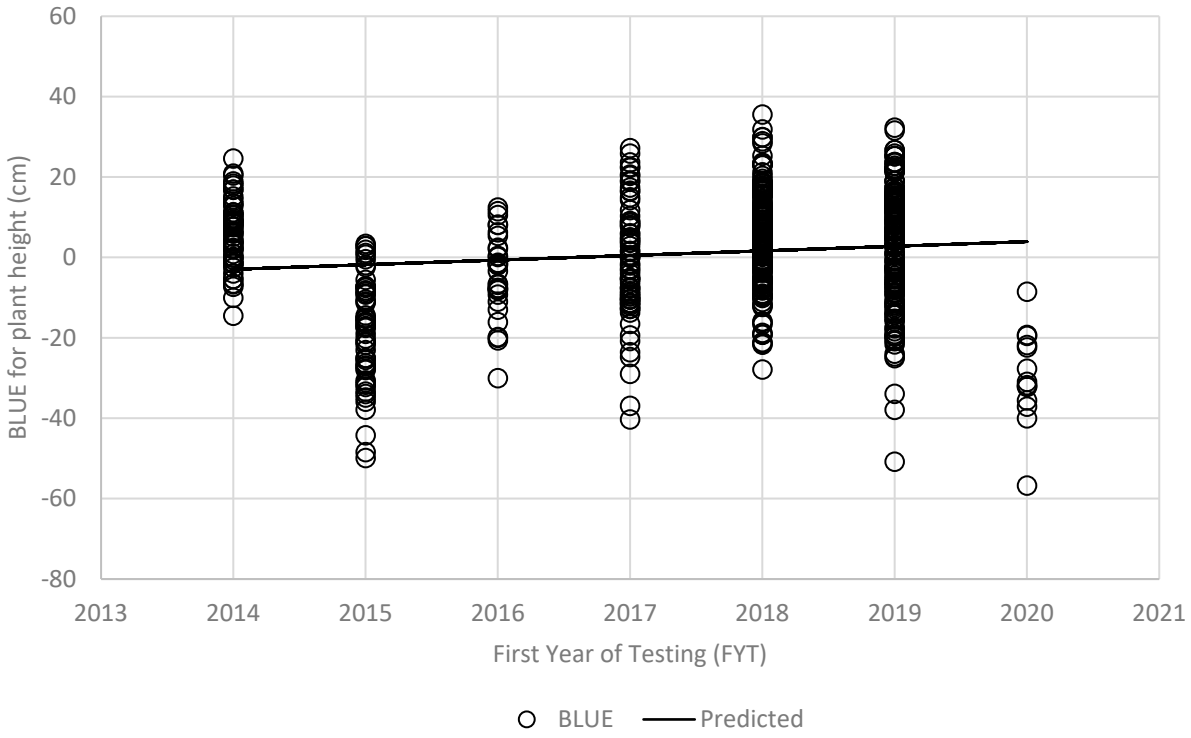

Figure 4. Genetic gain for plant height in maize genotypes evaluated in advanced trials conducted by the Mozambique maize breeding program between 2014 and 2020. Best linear unbiased estimates (BLUEs) are expressed relative to the mean of 169.1 cm.

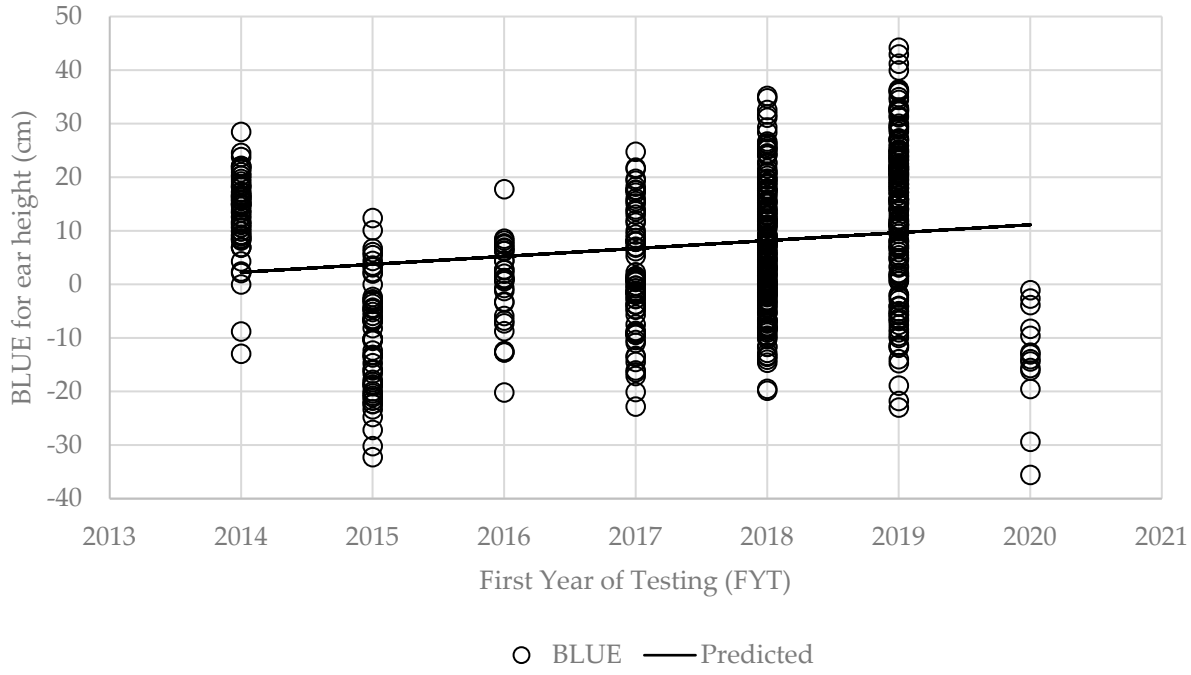

Figure 5. Genetic gain for ear height in maize genotypes evaluated in advanced trials by the Mozambique maize breeding program between 2014 and 2020. Best linear unbiased estimates (BLUEs) are expressed relative to the mean of 83.9 cm.

The ear position coefficient ranged from 0.1 to 0.89, with a mean of 0.51, and it increased significantly ($p < 0.001$) at a rate of 1.18% per year (Table 5 and Figure 6). The number of ears per plant ranged from 0 to 1, with a mean of 0.88 and a significant gain ($p < 0.001$) at a rate of 1.36% per year (Table 4 and Figure 7).

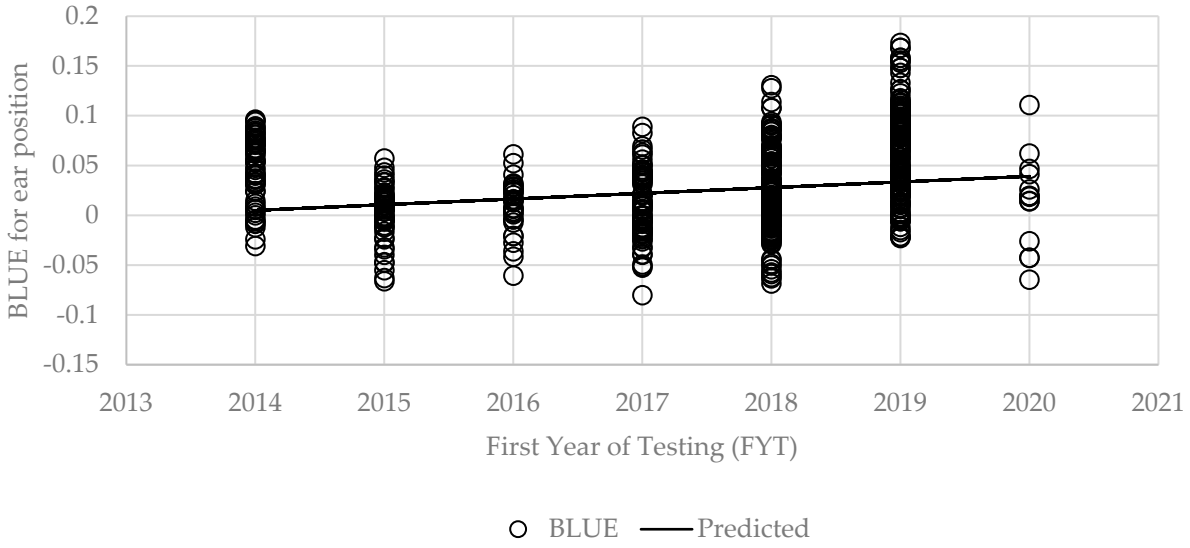

Figure 6. Genetic gain for the ear position coefficient in maize genotypes evaluated in advanced trials conducted by the Mozambique maize breeding program between 2014 and 2020. Best linear unbiased estimates (BLUEs) are expressed relative to the mean of 0.51.

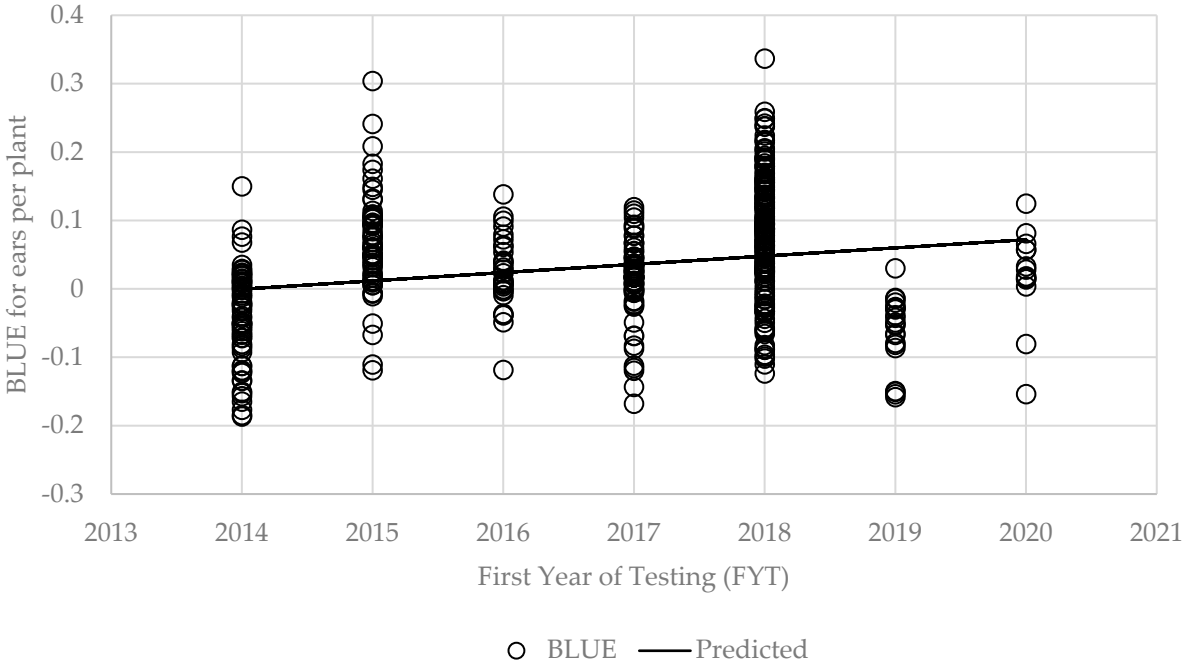

Figure 7. Genetic gain for ears per plant in maize genotypes evaluated in advanced trials conducted by the Mozambique maize breeding program between 2014 and 2020. Best linear unbiased estimates (BLUEs) are expressed relative to the mean of 0.88 ears per plant.

The incidence of poor husk cover ranged from 0 to 100%, with a mean of 16.9.0%, and it increased significantly ($p < 0.001$) by 6.2% per year (Table 5 and Figure 8).

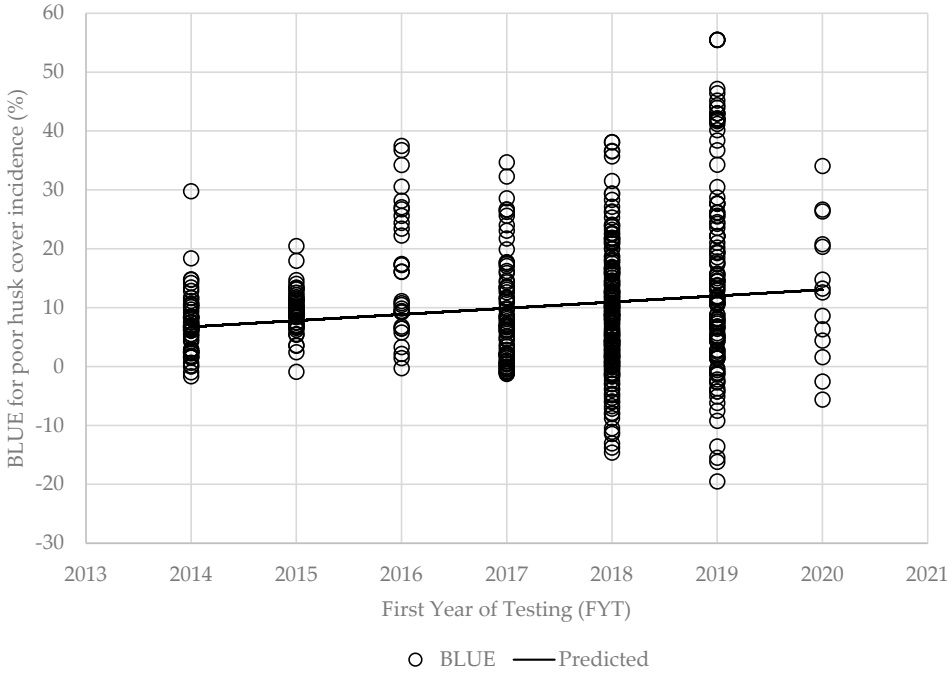

Figure 8. Genetic gain for husk cover in maize breeding genotypes evaluated in advanced trials by the Mozambique maize breeding program between 2014 and 2020. Best linear unbiased estimates (BLUEs) are expressed relative to the mean of 16.9%.

The incidence of shoot lodging ranged from 0% to 100%, with 47% of plots having lodged at a rate of less than 25% and a marginal 2% of the plots having an incidence of 50%. The shoot lodging mean incidence was 5.4% and presented a significant negative (p = 0.004) gain of −7.0% per year (Table 5 and Figure 9). Furthermore, the incidence of root lodging ranged from 0 to 100, with 63% of plots having an incidence of less than 25% and a marginal 3% having an incidence of greater than 50%. Although root lodging decreased, the change was insignificant (Table 4).

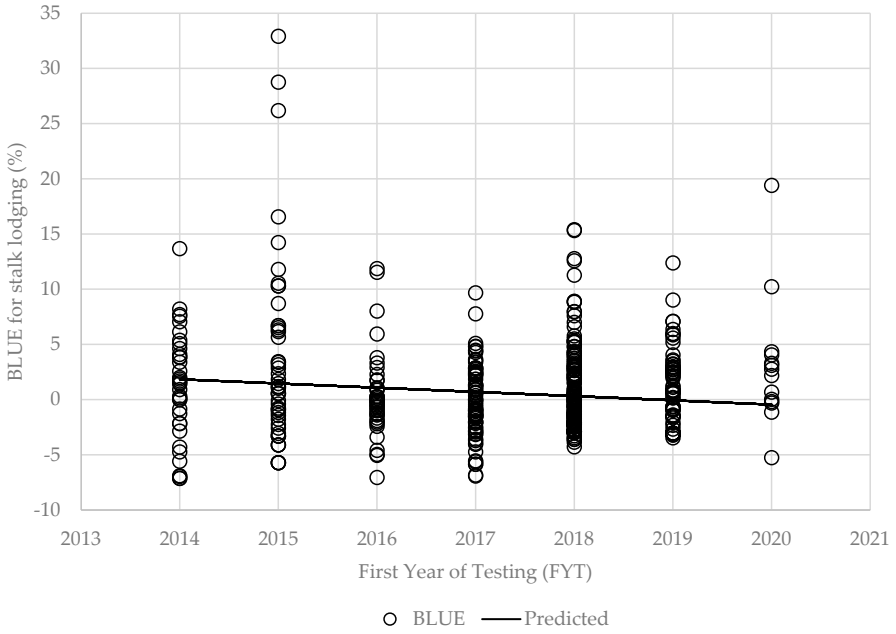

Figure 9. Genetic gain for stalk lodging in maize genotypes evaluated in advanced trials by the Mozambique maize breeding program between 2014 and 2020. The best linear unbiased estimates (BLUEs) are expressed relative to the mean of 5.44%.

The mean grain yield of all experiments and for those with H > 0.20 was 3041 kg ha^{-1}. The mean yield ranged from 309 to 7241 kg ha^{-1}. The average range of genotype means within an experiment was 3275 kg ha^{-1}. This difference ranged from 477 to 7193 kg ha^{-1}. Supplementary Tables S1 and S2 provide additional information on the mean yield and heritability values per location and a statistical summary of genotypes for each experiment, respectively.

4. Discussion

The current study provides insights into the efforts made by the Mozambique national maize breeding program to improve grain yield and other related traits between 2014 and 2020. The findings show that the program met with challenges in achieving significant genetic gains for grain yield but significantly improved other important agronomic traits. The observed high heritability for most traits indicates a strong genetic basis that would allow for further improvements of key traits such as the grain yield, plant height, ear height, and days to anthesis [30]. The observed marginal relationship between the genotypic values (BLUEs) of individual traits and the year of first testing indicates that other experimental factors, particularly the environment, affected the genotypic data used in the regression model [31]. The current study provides an opportunity for the programs to learn about their progress in breeding and an opportunity for them to improve how they collect and store historical data for similar studies. The findings show the importance of improving experimental approaches to better manage environmental variability, which is particularly critical in resource-limited breeding programs [31].

The inconsistency in improving GY was a major barrier to achieving the goal of developing high-yielding varieties that would enhance food security in Mozambique. A lack of genetic gain in all the experiments within the two trials and among the high-yield experiments was recorded even though the broad-sense heritability within most of the AYT and VCU experiments and over the years was acceptable. Genotype-by-environment interactions for grain yield were a major source of variance, accounting for an average of 29%, while errors accounted for 66% of the variance. Gains could be low when such interactions are large. Many maize growers in Mozambique experience low yields. It is encouraging that the program is increasing GY in low-yield environments at a rate of 125 kg ha^{-1} year^{-1}. Recent studies showed significant genetic gains for GY in the national maize breeding programs of other sub-Saharan African countries such as Kenya, Uganda, and Zimbabwe [26–28].

The breeder's equation explains the factors that affect a selection response, including heritability, selection intensity, and the duration of a breeding cycle [32]. The genetic gains reported in this study resulted from selections made in earlier breeding stages and the heritability and selection intensity at that stage. Early-stage trials tend to have low heritability due to limited replications and the number of trial locations. Low heritability in the early stages of trialing may also explain the observed lack of a significant change in trait values over the breeding period. Some non-significant trends may be due to a lack of selection pressure in the earlier stages. Furthermore, limited resources could have hindered the design and execution of appropriate breeding trials [31]. It is also possible that testing was conducted under resource constraints, hindering the program from selecting from an optimally large population of plants, resulting in ineffectiveness over the years. It is also possible that the parental lines used in the program do not have superior alleles for developing superior hybrids with grain yield beyond the current plateau. There is a need for the program to critically assess the various reasons for the lack of genetic gains for grain yield across all the environments and mobilize appropriate resources for the optimization of the breeding pipelines.

The maturity-associated traits (i.e., the days to anthesis and ASI) showed significant negative gains over the study period. The observed trends for these two traits indicate selection for earlier maturity and an improved synchronization in the time to maturity of the male and female flowers. Improved synchrony in flowering ensures pollination and grain-filling efficiency and can result in enhanced grain yield [33]. Furthermore, having early maize genotypes with a short ASI enables the crop to escape drought stress and related grain quality problems, such as the accumulation of mycotoxins [34–36]. The Mozambique national maize breeding program implemented Drought-Tolerant Maize for Africa, a multinational breeding project that CIMMYT spearheaded between 2012 and 2015 [37]. The current study shows that the project enabled significant progress in enhancing earliness, a trait positively correlated with drought tolerance in maize [35]. Until recently, most sub-Saharan African national programs have focused on trait-based breeding approaches while responding to regional or global goals that drive resource availability [38]. However, the data for the days to anthesis of different genotypes in 2015 varied greatly because of El Nino-induced adverse stress response, thus reflecting sensitivity to borderline 2015–2016 El Nino conditions (extensive rainfall deficits).

Positive genetic gains were observed in the plant height, ear height, and position coefficient. The average height of the plants increased at a rate of 0.68% per year, while the ear height increased by 1.74% annually. These findings indicate that the program has simultaneously selected taller plants and those with ears much higher above ground. Taller plants utilize more water and soil nutrients to grow and accumulate more biomass. Within the highlands of Kenya, taller maize varieties have been reported to produce a higher grain yield because the nutrients accrued over the long growing days are used in the development of larger ears and more kernels, as compared to the medium or shorter genotypes that are cultivated in the lower zones [28,39]. The Mozambique production environments range from low to mid-altitudes (Table 1). Tall maize plants could also be more suitable for livestock feed [40]. Unfortunately, an increase in plant height has a direct and quantifiable impact on crop lodging [41,42].

The number of ears per plant and the ear position coefficient showed a positive gain over the 7-year breeding period. These two traits are negatively correlated with resistance to lodging [43,44]. The observed increase in the number of ears per plant was a direct intervention to reduce the number of barren plants, as the mean number of ears became close to one ear per plant over time (0.88). Increasing the number of ears per plant can enhance yield potential, particularly in drought-prone environments where water availability may limit kernel setting [45]. However, having more than one ear per plant may create an architecture that may induce stress in the plant under limited light and soil nutrients [46]. The observed gain in the ear position coefficient is most likely associated with the increased plant height. Owing to the potential risk of lodging, the breeding program must focus on balancing the plant height, ears per plant, and ear placement to ensure crop resilience under stress conditions [44,47].

The stalk and root lodging incidence decreased over time, but only the former showed a significant negative change during the breeding period. The observed reduction in stalk lodging indicates that the IIAM maize breeding program was successful in selecting for an improvement of this trait. Interestingly, the reduction worked even as the plants became taller and the distance of the ears from the ground increased. Improving lodging resistance, particularly in high-yielding environments, is crucial for maintaining plant stability and optimizing yield. A selection for maize genotypes with high stalk bending strength might have favored a decrease in the incidence of stalk lodging [48]. However, the lack of significant gains in root lodging highlights the need for further efforts to address both types of lodging, as abiotic stresses such as wind and heavy rains and biotic stresses

such as stalk borers and stalk rot diseases are likely to affect farming systems due to climate change [47,49–51]. Besides selecting for correlated aboveground traits, studies have shown that root resistance could be enhanced by selecting maize genotypes with extensive fibrous roots [52].

The incidence of poor husk cover showed a significant positive genetic gain over the 7-year breeding period. Poor husk cover makes the ear more vulnerable to damage because it eases the penetration of water, insects, and microbial species through the silk channel [53]. Consequently, genotypes with open husks are vulnerable to damage by weevils, ear rot, and the accumulation of mycotoxins, compromising grain quality and risking the health of maize consumers [54,55]. While the breeding team may not have selected for increased open husks, it is possible that there was no selection applied against this trait. Addressing this issue will require targeted selection to improve post-harvest quality traits alongside yield improvements [55,56].

A critical factor that may have affected the outcomes of this study is the quality of data used for the analysis. The data quality concern is particularly relevant because of the high percentages of experiments with relatively low heritability estimates for some traits (e.g., root and shoot lodging). Within the experiments, the error variance tended to be relatively large compared to the genetic variance for several key traits, including grain yield. This could be due to excess micro-environmental variations within a field and/or data quality and experimental management issues. Heritability reflects the proportion of phenotypic variance attributable to genetic factors, and low heritability often indicates high genotype-by-environment interaction variance or poor experimental conditions [31]. In the case of the IIAM maize trials, the observed low heritability may be partly due to inconsistent trial management, a lack of replication, and suboptimal experimental setups, all of which are common issues in resource-limited breeding programs [31,57]. This study provides insights into the need to optimize the breeding process to minimize experimental variance and increase the data quality and the heritability of trials. Among the promising strategies are the use of experimental designs and analyses that account for within-trial spatial variation, accurate data collection, filtering, and curation within the available resources, along with the utilization of the publicly available Enterprise Breeding System data management platform for crop breeding programs within the CGIAR partnership network (https://ebs.excellenceinbreeding.org/get-ready/, accessed on 24 December 2024).

As a precaution, the genetic gain reported here is not derived from a recurrent selection breeding program, as used in the breeder's equation [32,58]. The analyzed data were from trials conducted using test maize hybrids. The hybrids were developed at different times and may not have shared genetic lineages but were tested in specific years after their selection from earlier breeding stages. Furthermore, the individual years here did not represent consecutive cycles of breeding. The data we analyzed also came from a small subset and can only be interpreted as a change in trait values over seven years.

5. Conclusions and Recommendations

The civil war in Mozambique (1977–1992) severely disrupted the country's agricultural research infrastructure, including human resources and the facilities for breeding programs. The long-term effects of this conflict are still evident today as IIAM continues to recover from damage to research stations, a loss of technical expertise, and insufficient financial investment [10]. Although the government has made efforts to rebuild agricultural research infrastructure, these efforts have not been sufficient to fully utilize modern breeding methods, such as marker-assisted selection, genomic selection, and high-throughput phenotyping, which are critical for achieving meaningful genetic gains [59,60]. Like other breeding programs in resource-constrained countries, the IIAM maize program is also faced

with a lack of qualified human resources due to a lack of competitiveness and, hence, an inability to retain the best breeders. The maize breeding program has therefore been operating on minimal funding for equipment, skilled personnel, and breeding technologies and may not have been able to fully exploit the genetic variation available in the maize germplasm, leading to slower progress compared to other African breeding programs [26–28].

The results of this study underscore the critical need for Mozambique's maize breeding program to focus on improving grain yield and enhancing resilience traits. Despite the limited progress in grain yield, the program has improved on other important agronomic traits relevant to developing more resilient maize varieties [61]. These improvements are important in the context of climate change because Mozambique's maize-growing regions are increasingly affected by climate change aspects such as drought, erratic rainfall, and other climatic stresses. Integrating the traits enhances rapid genetic gains and the development of resilient varieties to beat the emerging threats to maize production in Mozambique [62].

It is anticipated that a lack of resources could hinder the application of modern breeding methods that would fast-track genetic gain. Therefore, there is a need for the program to work closely with international organizations such as CIMMYT and IITA in partnerships that would mobilize resources to access critical resources and expertise. Through these partnerships, the program can adopt advocated breeding strategies, such as the product profile breeding approach, which focuses on developing maize varieties that meet specific markets and environmental needs [63]. This approach enables breeders to prioritize the traits most critical for the target environment and market, thus increasing the likelihood of developing varieties that perform well under the specific conditions farmers face in Mozambique. Besides bilateral partnerships, the government of Mozambique must prioritize increased funding for research infrastructure and capacity building. In addition to strengthening strategic alliances with international organizations, African governments must allocate adequate resources to establish research facilities that can propel their countries towards achieving self-sufficiency in food production, as this is a basic need for their citizens.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/agronomy15020449/s1, Table S1: Entry-mean heritability (EMH) and per-plot heritability (H) for all traits and experiments. "NA" indicates that the trait was not assessed in that experiment; Table S2: Summary of genotype means within each experiment. The means of all genotypes, minimum and maximum genotype means, and range of genotype means are presented.

Author Contributions: Conceptualization, P.F., P.C., C.S. (Constantino Senete), E.N., C.S. (Clay Sneller), L.M., D.W. and B.D.; methodology, software, validation, and formal analysis, P.F., P.C., C.S. (Constantino Senete), E.N., C.S. (Clay Sneller), L.M. and B.D.; investigation, P.F., P.C., C.S. (Constantino Senete) and E.N.; resources, P.F., P.C., C.S. (Constantino Senete), E.N. and B.D.; data curation, S.M., E.N., L.M. and C.S. (Clay Sneller); writing—original draft preparation, C.S. (Clay Sneller), S.M., P.F., E.N., L.M. and B.M.P.; writing—review and editing, P.F., P.C., C.S. (Constantino Senete), E.N., C.S. (Clay Sneller), L.M., D.W., B.D. and B.M.P.; visualization, C.S. (Clay Sneller), S.M. and E.N.; supervision, B.D, L.M. and P.F.; project administration, B.D. and P.F.; funding acquisition, B.D. and P.F. All authors have read and agreed to the published version of the manuscript.

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Data Availability Statement: Except for the data available within this manuscript, no other data are provided in any other form. The lead breeders may be contacted to provide any other relevant information.

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