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Research Article

Genetic Variability for the Yield and Yield-Related Traits in Some Maize (*Zea mays* L.) Inbred Lines in the Central Highland of Ethiopia

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After rice and wheat, maize (*Zea mays* L.) is the third most significant and valuable crop in terms of industrial production in the world. The experiment was conducted to determine the nature and magnitude of genetic variability for various traits of maize inbred lines at the Ambo Plant Protection Research Center experimental field during 2013/2014, the major cropping season. The experiment's design was described in 5×5 triple lattice designs. The results of the analysis of variance revealed that genotypic mean squares were significant for all traits, indicating that the inbred lines under study had a higher level of genetic diversity. In terms of genotypic and phenotypic variation, the largest coefficient was found in grain yield per hectare (28.49 and 35.43) followed by the number of tassel branches (23.14 and 24.92), respectively. Both days to 50% silking (91.57) and days to 50% tasseling (86.56) showed a high magnitude of broad-sense heritability. The results of the phenotypic and genotypic correlation analyses showed that grain yield per plant significantly correlated positively with five traits at both the phenotypic and genotypic levels. The number of kernels per row, aboveground biomass production per plant, harvest index, and grain yield per hectare might all be employed as selection criteria to increase the maize grain yield, according to path coefficient analysis at the phenotypic and genotypic levels. The grain yield and other significant yield components were found to be superior with inbred lines AMH169-55 and AMH169-86. Therefore, it is advised that these lines be used to further enhance the maize crop.

1. Introduction

Maize (*Zea mays* L.) is one of the most essential cereal crops grown worldwide, leading to the overall crop yield production (Gebre et al. [1]). According to Shaka et al. [2], maize comes in second place in terms of land area to wheat while taking the first place in terms of output and productivity. After rice and wheat, it is the third most widely utilized cereal crop for human consumption (Mbuvi et al. [3]). According to [4], maize originated from South America and belongs to the grass family called Poaceae. With chromosomal number $2n = 20$, it is the only species in the genus *Zea*.

Maize is a broadly cultivated crop throughout the world. According to the USDA [5], the annual production of maize for the top six countries of the world from 2019 to 2020 in terms of million metric tons were as follows: United States: 346.0, China: 260.8, Brazil: 102, Argentina: 51, Ukraine: 35.9, and India: 26, and account for 75.18% of the world's maize production. Ethiopia ranked 13th in the world and 4th in Africa by annual maize production.

According to Smale et al. [6], the most valuable cereal crop grown in Africa is maize. About 50% of the population relies on it as a staple food. It is a significant source of minerals, protein, carbohydrates, and vitamin B. African

populations utilize maize in various forms such as porridge, beer, and pastes. Fresh green corn is consumed in the form of boiled and roasted. The grain, tassel, stalk, cob, and leaves of the maize plant are all economically valuable and can be used to make a wide range of food and nonfood goods.

Based on the altitude and annual rainfall, Ethiopia's maize-growing regions are essentially divided into four ecological zones (Abera et al. [7]). These are the midaltitude subhumid zone (1000–1800 masl, with annual rainfall of 800–1500 mm), the highland subhumid zone (1800–2600 masl, with annual rainfall of 1000–2000 mm), the low moisture zone, which is between 500 and 1800 masl and receives less than 800 mm of rainfall, and the low altitude subhumid zone, which is below 1000 masl.

Maize is one of the most important cereal crops grown in Ethiopia. Among all the cereals crops, maize ranks first in terms of overall production and second next to teff in terms of area coverage [8]. It makes up roughly 24%–31% of the country's cereal consumption and is primarily supplied by Ethiopian local production. It is eaten as a staple in a variety of dishes, including as bread, injera (separately or combined with teff), porridge, "nefro.," and grits. Moreover, it is eaten roasted or boiled (particularly when it is still green). Furthermore, it is brewed to create the native spirits "tella," "araki," and others [9].

According to Larik et al. [10], any breeding program must start with germplasm, which is a vital source of information since it allows for the development of genetic variability. The true potential value of the genotype can be determined by investigating the genetic diversity, heritability, and genetic advance in the germplasm. In addition, understanding the relationships between the traits is crucial to the effectiveness of selection in any breeding program.

According to Hallauer et al. [11], the goal of maize breeding programs is always to increase genetic diversity in traits that are economically significant while maintaining a suitable level of genetic variability. It is crucial to understand the level of genetic variability already present in the germplasm for enhancing the genetic diversity of local germplasm. According to Ahmad et al. [12], an efficient long-term plant breeding program needs genetic diversity at a detectable level within a population to enable and support it.

According to Malik et al. [13], the most crucial agronomic characteristics of maize include grain yield, 1000 kernel weight, tassel branches, days to silking, plant height, days to tasseling, ear weight, ear height, leaf width, leaf length, leaf area, kernel rows, and kernel moisture. The yield of grains is significantly influenced by genotypes with desired characteristics. The kernel set of maize, which is susceptible to environmental factors during the tasseling and silking stages, is closely associated with the grain production [14].

The majority of local maize cultivars growing in the highland parts of Ethiopia are low-yielding variants. Our nation's maize breeding program struggles to produce high-yielding hybrids and synthetic varieties for highlands because it lacks genetically varied source materials (Legesse et al. [15]).

However, not enough research has been done to fully understand and describe the extent and nature of genetic variability, phenotypic coefficient of variation, genotypic coefficient of variation, genetic advance, broad-sense heritability, and the relationship between the yield and traits that are related to the yield of maize inbred lines developed for central highland of Ethiopia.

Therefore, the purpose of the current study is to find out the nature and magnitude of the genetic variability of various traits of maize inbred lines. The specific objectives were to estimate the genetic variability, genetic advance, heritability, and phenotypic and genotypic coefficients of variation and assess the extent of association between the yield and yield-related traits of maize inbred lines.

2. Materials and Methods

2.1. Description of the Research Site. The experiment was carried out on the experimental field of the Ambo Plant Protection Research Center (APPRC) from June 3 to December 30, 2013/14, during the major cropping season of Ethiopia in the West Shewa zone of Oromia Regional State. The Ambo Plant Protection Research Center is situated 115 kilometers from Addis Ababa at an altitude of 2185 meters above the sea level, with coordinates of 8057′ N and 38007′ E. The agroecology of APPRC is intermediate highland having the major soil type vertisols consisting of 1.5% organic matter, 18% silt, and 67% clay. The pH of the soil is 6.12. Temperatures range from 10.13°C to 27.63°C, with an average annual rainfall of 1242.90 mm.

2.2. Experimental Materials. Twenty-five maize inbred lines, which have been maintained at the Ambo Plant Protection Research Center, were used for the study as indicated in Table 1. All the inbred lines were selected based on suitability to high land and picked based on the available amount of seeds.

2.3. Experimental Design and Trial Management. The study was conducted in a 5×5 triple lattice design with three replications. The plot size was 3 m long and 1.5 m wide and consisted of two rows with 12 plants per row which comprised a total of 24 plants per plot. The distances between the rows and the plants were 75 cm and 25 cm, respectively. An alley of 1.5 m was left between the plots. The two rows were utilized to collect data. One row was sown around the experimental field as a border to protect it from damage by unwanted animals or pests. DAP and urea were applied to the plots at rates of 150 and 200 kg ha^{-1}, respectively. Three equal portions of nitrogen were applied. The initial application was made during sowing together with the phosphorus dose. The second and third nitrogen applications for maize were made at the knee-high stage and the third at the tasseling stage, respectively, during the growth stage. Two seeds were sown per hill and then seedlings were thinned to one plant at the 4-5 leaf stage to maintain 53, 333 plants/ha. Weeding was carried out in accordance with local

TABLE 1: Maize inbred line samples used for the study.

S/N	Inbred lines	Origin
1	AMH169-1	AMB11N37-LD-2
2	AMH169-5	AMB11N37-LD-10
3	AMH169-8	AMB11N37-LD-29
4	AMH169-12	AMB11N37-LD-37
5	AMH169-16	AMB11N37-LD-48
6	AMH169-22	AMB11N37-LD-75
7	AMH169-28	AMB11N37-LD-111
8	AMH169-33	AMB11N37-LD-124
9	AMH169-100	AMB11N37-LD-292
10	AMH169-51	AMB11N37-LD-188
11	AMH169-55	AMB11N37-LD-208
12	AMH169-56	AMB11N37-LD-212
13	AMH169-57	AMB11N37-LD-216
14	AMH169-75	AMB11N37-LD-248
15	AMH169-81	AMB11N37-LD-262
16	AMH169-86	AMB11N37-LD-273
17	AMH169-87	AMB11N37-LD-274
18	AMH169-92	AMB11N37-LD-284
19	AMH169-98	AMB11N37-LD-290
20	AMH169-113	AMB11N37-LD-323
21	AMH169-114	AMB11N37-LD-325
22	AMH169-115	AMB11N37-LD-326
23	AMH169-116	AMB11N37-LD-327
24	AMH169-117	AMB11N37-LD-328
25	AMH169-50	AMB11N37-LD-184

recommendations. The experimental plants were protected from being damaged by pests using chemicals.

2.4. Data Collection. With the exception of days to 50% tasseling and silking, five plants were randomly selected to record observations of all the quantitative traits. For statistical analysis, the mean of five plants for each entry in each replication was calculated. The data recording for each quantitative trait were carried out at the different growth stages of the maize inbred lines as indicated in Supplementary Figures 1–5.

2.5. Quantitative Traits. Quantitative traits were collected from days to 50 percent tasseling, a number of kernel rows per ear, days to 50 percent silking, the number of kernels per row, plant height (cm), the number of ears per plant thousand kernels weight (g), ear height (cm), grain yield per plant (g), number of leaves per plant, grain yield per hectare (kg), leaf length (cm), aboveground biomass yield per plant (g), leaf width (cm), harvest index (%), ear length (cm), a number of tassel branches, and ear diameter (cm).

2.6. Analysis of Variance. All of the traits were subjected to analysis of variance using the procedure developed by [16] which is indicated in Table 2 by using the SAS GLM procedure, 2004, V.9.0 [17] and SPSS software. Differences for mean separations of various traits were computed using least significance differences (LSD) at 0.05 and 0.01 of probability.

TABLE 2: Analysis of variance.

Sources of variation	Degree of freedom	Mean square
Replication	$r-1$	M_{sr}
Genotypes	$g-1$	M_{sg}
Error	$(r-1)(g-1)$	M_{se}
Total	$gr-1$	

Note. e = error, g = number of genotypes, Ms = mean square, and r = number of replication.

2.7. Estimation of Genetic Parameters

2.7.1. Genotypic and Phenotypic Coefficients of Variation. The genotypic and phenotypic components and coefficients of genotypic and phenotypic variation were computed using the formula developed by the authors in [18].

$$\text{Genotypic variance}\left(\sigma^2 g\right) = \frac{\text{Msg} - \text{Mse}}{r},$$

$$\text{Phenotypic variance}\left(\sigma^2 p\right) = \sigma^2 g + \sigma 2e. \tag{1}$$

$$\text{Environmental variance}\ (\sigma 2e) = \text{mean error square},$$

where Mse = environmental variance, Msg = mean square due to the genotype, and r = the number of replication.

$$\text{Phenotypic coefficient of variation}\,(\text{PCV}) = \frac{\sqrt{\sigma^2 p}}{\overline{X}} \times 100,$$

$$\text{Genotypic coefficient of variation}\,(\text{GCV}) = \frac{\sqrt{\sigma^2 p}}{\overline{X}} \times 100. \tag{2}$$

The values of GCV and PCV were classified as low, moderate, and high [19] as follows.
Low: 0–10%, moderate: 10–20%, and high: >20%.

2.7.2. Heritability (H^2). According to Hanson et al. [20], the ratio of genotypic variance to phenotypic variance, presented as a percentage, was used to measure heritability in a broad sense.

$$\text{Heritability}\left(H^2\right) = \left(\frac{\text{Vg}}{\text{Vp}}\right) \times 100, \tag{3}$$

where Vg = genotypic variance and Vp = phenotypic variance.

The heritability percentage was grouped as low, moderate, and high as described by Robinson et al. [21] as follows: low: 0–30%, moderate: 30–60%, and high: >60%.

2.7.3. Genetic Advance. According to Robinson et al. [21], the following formula was used to determine the amount of genetic advance that may be predicted by choosing 5% of the superior offspring.

$$\text{GA} = i\,\sigma p\,H^2, \tag{4}$$

where H^2 = heritability in broad sense, i = efficacy of selection which is 2.06 at 5% selection intensity, and σp = phenotypic standard deviation.

2.7.4. Genetic Advance as a Percent of the Mean.

$$\text{GA as a percent of the mean} = \left(\frac{\text{GA}}{\overline{x}}\right) \times 100, \qquad (5)$$

where GA = genetic advance and $\overline{x}$ = general mean of the trait.

According to Johnson et al. [22], the genetic advance as a percent of the mean was grouped as high, moderate, and low as follows.

High: 20% and above, moderate: 10–20%, and low: 0–10%.

2.8. Association of Traits and Path Coefficient Analysis

2.8.1. Coefficient of Correlation (r). Phenotypic correlations were calculated by using the formula given by the authors in [23].

$$\text{rp} = \frac{\text{Covxyp}}{\left(\text{Varx}_p \times \text{Vary}_p\right)^{1/2}}, \qquad (6)$$

where Covxyp = phenotypic covariance between the traits x and y, Varxp and Varyp = phenotypic variance of the traits x and y, respectively, and rp = phenotypic correlation. rg = Covxyg/(Varxg × Varyg)1/2, where r_g = genotypic correlation, Covxy$_g$ = genotypic covariance between the traits x and y, and Varx$_g$ and Vary$_g$ = genotypic variance of the traits x and y, respectively.

2.8.2. Path Coefficient Analysis. Path analysis is a straightforward standardized partial regression coefficient that divides the correlation coefficient into the direct and indirect effects of the yield components on yield using the formula given in [24].

$$\text{r} = \text{pij} + \sum r_{ik} p_{ik}, \qquad (7)$$

where Pij is a component of a direct effect of the independent variable (j) as measured by the phenotypic and genotypic path coefficients.

$\sum r_{ik} p_{ik}$ is the summation of components of the indirect effect of a given independent variable (i) on a given dependent variable (j) through all the other independent variables.

r_{ij} is an association between independent variables (i) and dependent variable j as measured by phenotypic and genotypic correlation coefficients.

3. Results

3.1. Range and Mean Values. The range and mean values of the different traits are indicated in Table 3 and shown as follows.

Among the genotypes, the range of days to tasseling significantly varied from 91.49 to 114.51 with a mean of 103.55. The inbred lines AMH169-22, AMH169-87, and AMH169-98 took the longest days to tasseling of 114.51, 109.18, and 109.18, respectively, after sowing. The inbred lines AMH169-5 and AMH169-8 took the shortest days to tasseling of 91.49 and 91.8 days, respectively. Days to silking differed significantly among genotypes, with a mean of 105.99 and a range of 89.61–113.89. The inbred lines AMH169-22 and AMH169-87 took the longest days to silking of 113.89 and 112.69 days after sowing, respectively. Sixty-eight percent of the genotypes under the study took a relatively long time for both tasseling and silking.

Significant variations in genotypes were detected for plant height, which ranged from 111.45 cm for AMH169-12 to 200.86 cm for AMH169-22, with an overall mean of 145.17. Ear height ranged from 44.06 to 118.64 cm for AMH169-12 and AMH169-22, respectively, with a mean of 67.29 cm.

The recorded range for number of leaves per plant is 11.2–16.73, with a mean of 14.42. The inbred lines AMH169-115 and AMH169-28 had the highest and least number of leaves per plant, respectively. The leaf length ranged from 54.99 to 83.05 cm with an average of 67.83, demonstrating wide variation among the genotypes for this trait. The inbred lines AMH169-81 and AMH169-33 had the longest and shortest leaf length, respectively. Leaf width varied from 8.35 to 11.27 cm, with an overall mean of 9.61. The inbred lines AMH169-87 and AMH169-75 had the largest and smallest leaf width, respectively.

The average value of the number of tassel branches per plant varied from 6.84 to 23.04 with an overall mean of 14.79. The inbred lines AMH169-22 and AMH169-8 had the largest and smallest number of tassel branches per plant, showing the presence of significant differences among the genotype.

Ear length varied from 8.25 to 15.1 cm, with a total mean of 11.59. The inbred line AMH169-28 had the highest ear length which is superior among all the genotypes while the inbred line AMH169-114 is the least of all genotypes. Ear diameter varied among the genotypes from 3.29 to 4.6 cm, with an overall mean of 3.83. The inbred lines AMB169-86 and AMB169-1 had maximum and minimum ear diameters, respectively, as shown in Table 3.

The number of kernel rows per ear varies from 10.67 to 13.78, with an overall mean of 12.22. The inbred lines AMH169-33 and AMH169-55 had the maximum and minimum values of the number of kernel rows per ear among the tested genotypes of the maize inbred line. The number of kernels per row significantly ranged from 15.76 to 31.86, with an overall mean of 22.92. The inbred line AMH169-28 had a maximum number of kernels per row (31.86), followed by AMH169-51 (29.11), AMH169-16 (28.48), AMH169-81 (28.05), and AMH169-55 (26.92), while the inbred lines AMH169-75, AMH169-1, and AMH169-12 had a minimum number of kernels per row of 15.76, 15.91, and 16.04, respectively. The number of ears per plant varied from 0.97 to 1.64, with an overall mean of 1.2. The inbred lines AMH169-51, AMH169- 55 AMH169-114,

TABLE 3: Maize inbred lines exhibiting minimum and maximum values for the traits evaluated with the means and standard deviations.

| S/N | Traits | Minimum | | Maximum | | Mean | SD (±) |
		Value	Line	Value	Line		
1	DT	91.49	AMH169-5	114.51	AMH169-22	103.55	1.84
2	DS	89.61	AMH169-8	113.89	AMH169-22	105.99	1.73
3	PH	111.45	AMH169-12	200.86	AMH169-22	145.17	7.54
4	EH	44.06	AMH169-12	118.64	AMH169-22	67.29	7.03
5	NLPP	11.2	AMH169-28	16.73	AMH169115	14.42	0.51
6	LL	54.99	AMH169-33	83.05	AMH169-81	67.83	2.79
7	LW	8.35	AMH169-75	11.27	AMH169-87	9.61	0.5
8	NTB	6.84	AMH169-8	23.04	AMH169-22	14.79	1.37
9	EL	8.25	AMH169-114	15.1	AMH169-28	11.59	1.09
10	ED	3.29	AMH169-1	4.6	AMH169-86	3.83	0.39
11	NKRPE	10.67	AMH169-55	13.78	AMH169-33	12.22	0.69
12	NKPR	15.76	AMH169-75	31.87	AMH169-28	22.92	2.77
13	NEPP	0.97	AMH169-75	1.64	AMH169-51	1.2	0.25
14	TKW	160.19	AMH169-28	354.32	AMH169-87	228.91	24.43
15	GYPP	47.37	AMH169-116	111.78	AMH169-55	75.48	15.79
16	GYPH	824.15	AMH169-1	3384.52	AMH169-55	2137.57	450.19
17	AGBYPP	414.94	AMH169-33	893.82	AMH169-87	657.98	127.26
18	HI	13.39	AMH169-22	36.78	AMH169-55	24.97	3.46

Note. AGBYPP = aboveground biomass yield per plant (g), DT = days to 50% tasseling, DS = days to 50% silking, ED = ear diameter (cm), EH = ear height (cm), EL = ear length (cm), GYPH = grain yield per hectare (kg), GYPP = grain yield per plant (g), HI = harvest index, LL = leaf length (cm), LW = leaf width, NEPP = number of ear per plant, NLPP = number of leaves per plant, NTB = number of tassel branches, NKRPE = number of kernel rows per ear, NKPR = number of kernel per row, PH = plant height (cm), SD = standard deviation, S/N = serial number, and TKW = thousand kernel weight (g).

and AMH169-33 had a maximum number of ears per plant of 1.64, 1.59, 1.59, and 1.48, respectively, while the inbred lines AMH169-75, AMH169-16, and AMH169-1 all had a minimum number of ears per plant (0.97).

Thousand kernels' weight varied from 160 to 354.32 g, with a mean of 228.91 g. The inbred line AMH169-87 had the highest thousand kernel weight (354.22 g), followed by AMH169-75 (290.65), AMH169-98 (287.41), and AMH169-22 (278.84) while the inbred lines AMH169-28, AMH169-33, and AMH169-51 had thousand kernels weight of 160, 173.92, and 177.56 g, respectively.

The mean grain yield per plant ranged significantly from 47.37 to 111.78 g, with a mean of 75.48 g. The inbred line AMH169-55 showed the highest grain yield per plant (111.78 g), followed by AMH169-87 (110.76), AMH169-51 (92.43), and AMH169-114 (91.47) while the inbred lines AMH169-116 (47.37), AMH169-33 (49.48), and AMH169-54 (54.78) showed poor performance for the grain yield per plant.

The data recorded for grain yield per hectare showed significant differences among the studied genotypes with a variation of range from 824.15 to 3384.52 kg, with a mean of 2137.57 kg. According to the mean values, the inbred line AMH169-55 showed the highest performance for the grain yield per hectare (3384.52 kg) followed by AMH169-86 (3150.6), AMH169- 81 (2999.92), AMH169-50 (2986.22), and AMH169-56 (2914.33) while the inbred lines AMH169-1 and AMH169-116 showed the least performance for the grain yield per hectare.

The mean aboveground biomass yield per plant ranged significantly from 414.94 to 893.82 g, with a mean of 657.98 g. The maximum value for aboveground biomass yield per plant was shown by the inbred line AMH169-87 (893.82 g), while the minimum value was recorded in the inbred line AMH169-33 (414.94 g). The harvest index significantly ranged from 13.39 to 36.78, with a mean of 24.94. According to the mean values, the inbred line AMH169-55 showed the highest harvest index followed by AMH169-56 (31.46), AMH169-28 (29.66), and AMH169-86 (28.63) while the inbred lines AMH169-22 (13.39) and AMH169-116 (17.75) had the lowest harvest index.

3.2. Analysis of Variance.
The mean square from the analysis of the variance of grain yield and other related traits in 25 inbred lines of maize is presented in Table 4.

The analysis of variance showed that genotypic mean squares were highly significant ($p \leq 0.01$) for days to 50% tasseling, days to 50% silking, plant height, ear height, number of leaves per plant, leaf length, leaf width, number of tassel branches, ear length, number of kernel rows per ear, number of kernels per row, thousand kernels weight, grain yield per plant, grain yield per hectare, aboveground biomass yield per plant, and harvest index and significant ($p \leq 0.05$) for ear diameter and number of ears per plant.

3.3. Estimates of Variance Components.
Data given in Table 5 showed that there was sufficient genetic variability in most of the traits. For example, the GCV indicated a wide range of variation from 4.52 to 28.49% while the PCV ranged from 4.86 to 35.43% for the different traits studied. The maximum coefficient of genotypic and phenotypic variation was recorded in the grain yield per hectare (28.49 and 35.43) followed by the number of tassel branches (23.14 and 24.92)

TABLE 4: Mean square from analysis of variance of the grain yield and other relevant parameters in 25 inbred lines of maize.

S/N	Trait	Mean squares			LSD 0.05	CV
		Replications df = 2	Genotypes df = 24	Error df = 74		
1	DT	32.173	69.054**	3.397	3.24	1.78
2	DS	38.653	100.959**	3.005	3.06	1.64
3	PH	1628.013	809.597**	56.813	13.20	5.19
4	EH	1081.693	521.860**	49.471	12.38	10.45
5	NLPP	0.272	4.048**	0.257	0.83	3.52
6	LL	146.574	134.865**	7.795	4.97	4.12
7	LW	4.330	1.709**	0.248	0.88	5.18
8	NTB	18.150	37.023**	1.872	2.38	9.25
9	EL	11.658	10.924**	1.184	1.96	9.39
10	ED	0.894	0.339*	0.155	0.65	10.29
11	NKRPE	2.850	2.357**	0.478	1.14	5.66
12	NKPR	65.924	51.344**	7.683	4.85	12.09
13	NEPP	0.726	0.124*	0.061	0.43	20.59
14	TKW	1395.160	4806.707**	596.586	40.10	10.67
15	GYPP	1290.933	836.471**	249.423	27.97	20.92
16	GYPH	7581467.05	1315159.660**	202674.4	811.68	21.06
17	AGBYPP	64332.907	38985.843**	16195.18	227.57	19.34
18	HI	99.581	59.893**	11.991	5.68	13.88

*and ** = significant and highly significant at 5% and 1%, respectively. *Note.* DT = days to 50% tasseling, DS = days to 50% silking, PH = plant height (cm), EH = ear height (cm), NLPP = number of leaves per plant, LL = leaf length (cm), LW = leaf width, NTB = number of tassel branches, EL = ear length (cm), ED = ear diameter (cm), NKRPE = number of kernel rows per ear, NKPR = number of kernel per row, NEPP = number of ear per plant, TKW = thousand kernel weight (g), GYPP = grain yield per plant (g), GYPH = grain yield per hectare (kg), AGBYPP = aboveground biomass yield per plant (g), HI = harvest index, and S/N = serial number.

TABLE 5: Estimate of phenotypic variance ($\delta^2 p$), genotypic variance ($\delta^2 g$), phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV) for the grain yield and other related traits among 25 inbred lines of maize.

S/N	Traits	$\delta^2 g$	$\delta^2 p$	$\delta^2 e$	PCV	GCV
1	DT	21.89	25.28	3.39	4.86	4.52
2	DS	32.65	35.66	3.01	5.63	5.39
3	PH	250.93	307.74	56.81	12.08	10.91
4	EH	157.46	206.93	49.47	21.38	18.65
5	NLPP	1.26	1.52	0.26	8.55	7.80
6	LL	42.36	50.15	7.79	10.44	9.60
7	LW	0.49	0.73	0.24	8.92	7.26
8	NTB	11.72	13.59	1.87	24.92	23.14
9	EL	3.25	4.43	1.18	18.17	15.55
10	ED	0.06	0.22	0.16	12.15	6.46
11	NKRPE	0.63	1.10	0.47	8.60	6.47
12	NKPR	14.55	22.24	7.69	20.57	16.64
13	NEPP	0.02	0.08	0.06	23.84	12.03
14	TKW	1403.37	1999.96	596.59	19.54	16.37
15	GYPP	195.68	445.11	249.43	27.95	18.53
16	GYPH	370828.42	573502.82	202674.40	35.43	28.49
17	AGBYPP	7596.89	23792.07	16195.18	23.44	13.25
18	HI	15.97	27.96	11.99	21.20	16.02

Note. DT = days to 50% tasseling, DS = days to 50% silking, PH = plant height (cm), EH = ear height (cm), NLPP = number of leaves per plant, LL = leaf length (cm), LW = leaf width, NTB = number of tassel branches, El = ear length (cm), ED = ear diameter (cm), NKRPE = number of kernel rows per ear, NKPR = number of kernel per row, NEPP = number of ear per plant, TKW = thousand kernel weight (g), GYPP = grain yield per plant (g), GYPH = grain yield per hectare (kg), AGBYPP = aboveground biomass yield per plant (g), HI = harvest index, and S/N = serial number.

while high PCV and moderate GCV were detected in the grain yield per plant (27.95 and 18.53), ear height (18.65 and 21.38), and number of kernel per row (16.64 and 20.57), respectively.

In the present study, moderate PCV and GCV were observed in thousand kernel weights (16.37 and 19.54), ear height (18.17 and 15.55), and plant height (10.91 and 12.08), respectively. The smallest PCV and GCV were found in days

to 50% of tasseling (4.86 and 4.52) and days to 50% of silking (5.63 and 5.39), respectively.

3.4. Heritability and Genetic Advance.
Various plant traits under investigation were shown to have low, medium, and high broad-sense heritability estimates, as indicated in Table 6. High magnitude of broad-sense heritability was

TABLE 6: Estimate of heritability (H^2), genetic advance, and genetic advance percent of the mean for grain yield and other related traits among 25 inbred lines of maize at APPRC.

S/N	Traits	H^2	GA	GA (%)
1	Days to 50% tasseling	86.56	3.29	3.17
2	Days to 50% silking	91.57	3.27	3.09
3	Plant height	81.54	12.66	8.72
4	Ear height	76.09	11.03	16.38
5	Number of leaves per plant	83.10	0.87	6.02
6	Leaf length	84.46	4.86	7.16
7	Leaf width	66.27	0.68	7.07
8	Number of tassel branches	86.22	2.43	16.43
9	Ear length	73.28	1.64	14.18
10	Ear diameter	28.25	0.23	5.99
11	Number of kernel rows per ear	56.69	0.81	6.61
12	Number of kernels per row	65.45	3.74	16.31
13	Number of ears per plant	25.45	0.13	10.79
14	Thousand kernel weight	70.17	35.31	15.42
15	Grain yield per plant	43.96	14.30	18.95
16	Grain yield per hectare	64.66	59.66	28.05
17	Aboveground biomass yield per plant	31.93	83.71	12.72
18	Harvest index	57.11	4.07	16.33

Note. H^2 = heritability, GA = genetic advance, GA% = genetic advance as a percent of the mean, and S/N = serial number. Plant height (8.72), leaf length (7.16), leaf width (7.07), number of kernel rows per ear (6.61), number of leaves per plant (6.02), ear diameter (5.99), days to 50% silking (3.09), and days to 50% tasseling (3.17) all showed low genetic advance as a percent of the mean.

estimated in the number of leaves per plant (83.10), days to 50% silking (91.57), number of tassel branches (86.22), days to 50% tasseling (86.56), leaf length (84.46), plant height (81.54), number of kernel per row (65.45), ear height (76.09), ear length (73.28), thousand kernels weight (70.17), leaf width (66.27), and grain yield per hectare (64.66).

Moderate heritability was observed in the harvest index (57.11), the number of kernel rows per ear (56.69), grain yield per plant (43.96), and aboveground biomass yield per plant (31.93) while low heritability was observed in ear diameter (28.25) and the number of ears per plant (25.45).

The highest genetic advance was observed in the grain yield per hectare (59.66) followed by the aboveground biomass yield per plant (83.8) and thousand kernels weight (35.31) showing additive gene effects.

High, moderate, and low estimates of genetic advance as a percent of the mean were detected in different plant traits under study in Table 6. For grain yield per hectare (28.05), a high genetic advance as a percent of the mean was observed. Grain yield per plant (18.95), number of tassel branches (16.43), ear height (16.38), harvest index (16.33), number of kernels per row (16.31), thousand kernel weight (15.42), ear length (14.18), aboveground biomass per plant (12.72), and number of ears per plant (10.79) all showed moderate genetic advance as a percent of the mean.

3.5. Phenotypic and Genotypic Correlations of the Grain Yield with Other Traits.

The phenotypic and genotypic coefficients among various traits are given in Tables 7 and 8, respectively.

At both the phenotypic and genotypic levels, there was a strong and positive correlation of the grain yield with the number of kernels per row (rp = 0.386** and rg = 0.462*), the number of ears per plant (rp = 0.438** and rg = 0.435*), and grain yield per hectare (rp = 0.698 and rg = 0.787),

respectively. Ear length (rp = 0.314**) and number of tassel branches (rp = 0.280*) showed a positive and significant correlation with the grain yield per plant at the phenotypic level.

At both the phenotypic and genotypic levels, there was no significant correlation between grain yield per plant and days to 50% silking and tasseling, number of leaves per plant, plant and ear height, number of rows of kernels per ear, ear diameter, and weight of 1,000 kernels per ear.

3.6. Correlation among Yield Components.

At the phenotypic and genotypic levels, the number of kernel rows per ear exhibited a significant positive correlation with the ear diameter (rp = 0.426** and rg = 0.491*), thousand kernels weight (rp = −0.286* and rg = −0.438*), leaf length (rp = 0.453** and rg = 0.498*), ear length (rp = 0.801** and rg = 0.806**), grain yield per hectare (rp = 0.467** and rg = 0.471*), and grain yield per plant (rp = 0.386** and rg = 0.462*) but significant negative correlation with the thousand kernel weight (rg = −0.494** and rp = −0.361**) as shown in Table 8.

The phenotypic and genotypic correlation analysis revealed that the yield per plant had significant positive correlation with the grain yield per hectare (rp = 0.698** and rg = 0.787**), number of ears per plant (rp = 0.438* and rg = 0.435*), and number of kernels per row (rp = 0.386** and rg = 0.462*) at both phenotypic and positive genotypic correlations, respectively.

3.7. Path Analysis of the Grain Yield and Other Traits.

Table 9 presents the path coefficient analysis that demonstrates the direct and indirect effects on grain production per plant at the phenotypic level in the maize inbred line.

Table 7: Analysis of the phenotypic correlation for the maize grain yield and other agronomic traits.

N/S	Traits	DT	DS	PH	EH	NLPP	LL	LW	NTB	EL	ED	NKRPE
1	DT	1	0.930**	0.296*	0.486**	0.571**	0.053	0.115	0.343**	0.142	−0.093	−0.060
2	DS		1	0.230*	0.428**	0.600**	0.040	0.180	0.289*	0.217	−0.029	0.006
3	PH			1	0.805**	0.411**	0.457**	0.162	0.455**	0.157	0.071	0.087
4	EH				1	0.557**	0.294*	0.319**	0.586**	0.280*	−0.021	−0.017
5	NLPP					1	−0.044	0.218	0.330**	0.042	0.139	0.060
6	LL						1	0.225	0.199	0.459**	−0.016	0.127
7	LW							1	0.248*	0.410**	0.294*	0.134
8	NTB								1	0.183	−0.006	−0.018
9	EL									1	−0.010	0.055
10	ED										1	0.426**
11	NKRPE											1

S/N	Traits	NKPR	NEPP	TKW	GYPH	AGBYPP	HI	GYPP
1	DT	0.066	0.238	0.154	−0.066	0.080	−0.279*	−0.051
2	DS	0.128	0.006	0.148	−0.054	0.083	0.229*	−0.055
3	PH	0.267*	0.121	0.030	0.274*	0.345**	−0.224	0.137
4	EH	0.269*	0.163	0.203	0.276*	0.408***	−0.208	0.199
5	NLPP	0.134	0.125	0.050	0.105	0.295*	−0.268*	0.051
6	LL	0.453**	−0.053	−0.126	0.332**	0.404**	−0.029	0.321**
7	LW	0.348**	0.026	0.186	0.491**	0.351**	0.131	0.284*
8	NTB	0.159	0.258*	0.178	0.215	0.415**	−0.159	0.280*
9	EL	0.801**	−0.080	−0.046	0.354**	0.235*	0.248*	0.314**
10	ED	0.081	−0.133	0.142	0.188NS	0.028	−0.024	0.005
11	NKRPE	0.284*	0.060	−0.286*	0.201	−0.081	0.112	0.028
12	NKPR	1	0.075	−0.361**	0.467**	0.258*	0.314**	0.386**
13	NEPP		1	−0.139	0.367**	0.379**	0.389**	0.438**
14	TKW			1	0.074	0.208	−0.086	0.163
15	GYPH				1	0.585**	0.677**	0.698**
16	AGBYPP					1	0.149	0.761**
17	HI						1	0.473**
18	GYPP							1

*and **significant and highly significant at 5% and 1%, respectively. *Note.* DT = days to 50% tasseling, DS = days to 50% silking, PH = plant height (cm), EH = ear height (cm), NLPP = number of leaves per plant, LL = leaf length (cm), LW = leaf width, NTB = number of tassel branches, El = ear length (cm), ED = ear diameter (cm), NKRPE = number of kernel rows per ear, NKPR = number of kernel per row, NEPP = number of ear per plant, TKW = thousand kernel weight (g), GYPP = grain yield per plant (g), GYPH = grain yield per hectare (kg), AGBYPP = aboveground biomass yield per plant (g), HI = harvest index, and S/N = serial number.

Table 8: Analysis of the genotypic correlation for maize grain yield and other agronomic traits.

S/N	Traits	DT	DS	PH	EH	NLPP	LL	LW	NTB	EL	ED	NKRPE
1	DT	1	0.944**	0.431*	0.712**	0.643**	0.141	0.311	0.475*	0.271	−0.110	−0.011
2	DS		1	0.339	0.616**	0.667**	0.122	0.360	0.398*	0.350	−0.024	0.090
3	PH			1	0.785**	0.430*	0.389	−0.062	0.465*	0.070	−0.018	−0.039
4	EH				1	0.616**	0.178	0.132	0.591**	0.262	−0.140	−0.164
5	NLPP					1	−0.090	0.212	0.355	0.041	0.135	0.026
6	LL						1	0.055	0.159	0.522**	−0.086	0.054
7	LW							1	0.198	0.434*	0.381	0.068
8	NTB								1	0.174	−0.009	−0.070
9	EL									1	−0.222	−0.107
10	ED										1	0.491*
11	NKRPE											1

N/S	Traits	NKPR	NEPP	TKW	GYPH	AGBYPP	HI	GYPP
1	DT	0.173	0.107	0.222	0.073	0.350	−0.312	0.074
2	DS	0.224	0.075	0.209	0.070	0.339	−0.267	0.071
3	PH	0.196	0.123	−0.029	0.057	0.359	−0.437*	−0.018
4	E H	0.227	0.082	0.164	0.046	0.371	−0.426*	−0.001
5	NLPP	0.140	0.144	0.038	0.084	0.426*	−0.381	0.040
6	LL	0.498*	−0.197	−0.188	0.205	0.476*	−0.113	0.340
7	LW	0.312	−0.118	0.178	0.353	0.196	0.044	0.162

TABLE 8: Continued.

S/N	Traits	DT	DS	PH	EH	NLPP	LL	LW	NTB	EL	ED	NKRPE
8	NTB	0.166	0.234	0.186	0.171		0.456*		−0.244		0.251	
9	EL	0.806**	−0.067	−0.080	0.349		0.360		0.168		0.391	
10	ED	−0.151	−0.144	0.165	0.149		0.015		−0.129		−0.008	
11	NKPE	0.199	0.092	−0.438*	0.002		−0.241		−0.024		−0.105	
12	NKPR	1	0.197	−0.494*	0.471*		0.290		0.284		0.462*	
13	NEPP		1	−0.307	0.497*		0.225		0.520**		0.435*	
14	TKW			1	−0.011		0.266		−0.181		0.077	
15	GYPH				1		0.581**		0.683**		0.787**	
16	AGBPP						1		0.066		0.748**	
17	HI								1		0.582**	

*and **= nonsignificant and significantly different at 5% and 1%, respectively. *Note.* DT = days to 50% tasseling, DS = days to 50% silking, PH = plant height (cm), EH = ear height (cm), NLPP = number of leaves per plant, LL = leaf length (cm), LW = leaf width, NTB = number of tassel branches, El = ear length (cm), ED = ear diameter (cm), NKRPE = number of kernel rows per ear, NKPR = number of kernel per row, NEPP = number of ear per plant, TKW = thousand kernel weight (g), GYPP = grain yield per plant (g), GYPH = grain yield per hectare (kg), AGBYPP = aboveground biomass yield per plant (g), HI = harvest index, and S/N = serial number.

TABLE 9: Path coefficient analysis showing direct (diagonal bold) and indirect (off-diagonal) effects on the grain yield per plant at the phenotypic level in maize inbred lines.

N/S	Traits	LL	LW	NTB	EL	NKPR	NEPP	GYPH	AGBYPP	HI	r_P
1	LL	**−0.0410**	−0.0144	0.0004	−0.0824	−0.0051	−0.0173	0.0005	−0.0991	0.0199	0.321**
2	LW	−0.0037	**−0.1580**	0.0004	−0.0729	−0.0058	−0.0197	0.0006	−0.1125	0.0226	0.284*
3	NTB	−0.0037	−0.0126	**0.0050**	−0.0719	−0.0021	−0.0073	0.0020	−0.0419	0.0084	0.280*
4	EL	−0.0041	−0.0141	0.0004	**−0.8180**	−0.0092	−0.0313	0.0010	−0.1793	0.0360	0.314**
5	NKPR	−0.0051	−0.0173	0.0005	−0.0991	**1.0570**	−0.0096	0.0242	0.2567	0.0199	0.386**
6	NEPP	−0.0058	−0.0197	0.0006	−0.1125	0.1787	**−0.0570**	0.0275	0.2913	0.0226	0.438**
7	GYPH	−0.0092	−0.0313	0.0010	−0.1793	0.2848	−0.0174	**0.0900**	0.4642	0.0360	0.698**
8	AGBYP	−0.0100	−0.0341	0.0011	−0.1955	0.3105	−0.0190	0.0478	**0.8740**	0.0392	0.761**
9	HI	−0.0062	−0.0212	0.0007	−0.1215	0.1930	−0.0118	0.0297	0.3146	**0.1090**	0.473**

*and **= significant and highly significant at 5% and 1%, respectively. *Note.* LL = leaf length (cm), LW = leaf width, NTB = number of tassel branches, El = ear length (cm), NKPR = number of kernel per row, NEPP = number of ears per plant, GYPP = grain yield per plant (g), GYPH = grain yield per hectare (kg), AGBYPP = aboveground biomass yield per plant (g), HI = harvest index, and S/N = serial number. Bold values represents the direct effects of different traits on the grain yield per plant.

The grain yield is primarily controlled by an independent variable's direct effects and its indirect effects through other yield components. In the current study, the path analysis only included 9 out of the 17 traits at the phenotypic level and 5 out of the 17 at the genotypic level that had a direct association with the grain yield per plant. The grain yield per plant is used as a dependent variable to divide the phenotypic and genotypic correlations into direct and indirect effects.

According to the path coefficient analysis at the phenotypic level, the number of kernels per row (1.0570) had the highest positive direct effect on the grain yield, followed by grain yield per hectare (0.0900) and the number of tassel branches (0.0050). However, the traits such as ear length (−0.8180) and number of ears per plant (−0.057) had a negative direct effect on the grain yield per plant.

The negative direct effect of the number of ears per plant on grain yield per plant was counterbalanced by its indirect effect via the number of kernels per row, which finally resulted in a positive and highly significant phenotypic correlation with the grain yield per plant.

Table 10 presents the path coefficient analysis for maize inbred lines, which illustrates the direct and indirect effects on the grain yield per plant at the genotypic level.

The number of kernels per row (0.8250) and number of ears per plant (0.1280) were found to have the strongest direct positive effects on the grain yield at the genotypic level according to the path coefficient analysis but the grain yield per hectare (−0.1160) had a negative direct effect on the grain yield per plant. However, the number of kernels per row had a positive and highly significant phenotypic correlation with the grain yield per plant, balancing out the direct effect of the grain yield per hectare on the grain yield per plant that was negative.

4. Discussion

Days to tasseling, plant height, leaf length, days to silking, number of leaves per plant, number of tassel branches per plant, leaf width, ear diameter, ear length, number of ears per plant, number of kernel rows per ear, weight of thousand kernels, grain yield per hectare, and grain yield per plant all differed significantly between the inbred line genotypes. This suggests that there is a lot of genetic variation among the genotypes for the improvement of these traits. The findings of the current study are consistent with the findings reported by Tadesse et al. [25] and Gebre et al. [1].

The results of the analysis of variance revealed that genotypic mean squares were highly significant for each of

Table 10: Path coefficient analysis showing direct (diagonal bold) and indirect (off diagonal) effects of different traits on the grain yield per plant in maize inbred lines at the genotypic level.

S/N	Traits	NKPR	NEPP	GYPH	AGBYPP	HI	r_g
1	NKPR	**0.8250**	0.0257	−0.0422	0.2606	0.0820	0.4620*
2	NEPP	0.1658	**0.1280**	−0.0397	0.2453	0.0772	0.4350*
3	GYPH	0.3000	0.0438	**−0.1160**	0.4439	0.1397	0.7870**
4	AGBYPP	0.2851	0.0416	−0.0683	**0.7540**	0.1328	0.7480**
5	HI	0.2218	0.0324	−0.0531	0.3282	**0.3050**	0.5820**

*and **Significant and highly significant at 5% and 1%, respectively. *Note.* NKPR = number of kernels per row, NEPP = number of ears per plant, TKW = thousand kernel weight (g), GYPP = grain yield per plant (g), GYPH = grain yield per hectare (kg), AGBYPP = aboveground biomass yield per plant (g), HI = harvest index, and S/N = serial number. Bold values represents the direct effects of different traits on the grain yields.

the traits under study, showing that the inbred lines had a higher level of genetic diversity. Similar findings were reported by Bartaula et al. [26], Mahmood et al. [27], Prakash et al. [28], and Kumsa et al. [29] for plant height, days to 50% tasseling, number of kernel per row, days to 50% silking, thousand kernel weight, ear height, and grain yield per plant; Kumar et al. [30] for the ear diameter, number of tassel branches, and ear length; and the author in [31] for the grain yield per hectare. The reasonable coefficient of variation for each trait under study demonstrated the experiment's high level of precision.

All of the traits' phenotypic variances and phenotypic coefficients of variation were slightly larger than their genotypic counterparts, showing that the environment has an impact in the expression of these traits. Similar findings were reported by the authors in [32], Mahmood et al. [27, 33], Rafiq et al. [34], Bello et al. [35], Hepziba et al. [36], Begum et al. [37], Tadesse et al. [25], Bartaula et al. [26], and Prakash et al. [28, 38].

The highest results of PCV and GCV obtained in the number of tassel branches and grain yield per hectare reveal that there is sufficient variation for the traits in the available material and suggest that selection can be successful for these traits. The present results correspond with results reported by Shakoor et al. [39], Rafiq et al. [34] for the number of kernels per row, Kabdal et al. [40] for grain yield per plant, Hepziba et al. [36] for ear height, Tadesse et al. [25] for the grain yield, ear height, ear diameter, and 1000 kernel weight, Prakash et al. [28] for traits such as grain yield per plant, ear height, number of tassel per branches, and the number of kernel per row, and the authors in [38] for the grain yield per plant.

The thousand kernel weights, ear heights, and plant heights in the current study all showed moderate GCV and PCV values. The findings of the present study are consistent with findings from several studies on the variability of maize by the author in [33], Kumar et al. [41], and Prakash et al. [28].

In days to 50% of silking and days to 50% of tasseling, the lowest GCV and PCV were recorded. This finding indicated that genotypes' genetic diversity for these traits was extremely low and that these genotypes should be eliminated from breeding programs. The findings obtained in the present study correspond with results reported by the authors in [31, 33], Bello et al. [35], and [38] in the maize genetic diversity.

The presence of high heritability values in the traits demonstrates that genetics mostly governed the variation seen and that environmental factors had a little effect. This suggested that these traits might be genetically improved through efficient selection. A similar finding was reported by Begum et al. [37], Tadesse et al. [25] for ear length, plant height, and 1000 kernel weight [33], Prakash et al. [28] for the number of tassel branches, days to 50% silking, and the number of kernel per row, and the authors in [38] for the grain yield per plant.

The grain yield per hectare and thousand kernel weight have strong heritability and reasonably high genetic advance, demonstrating that these traits are regulated by additive gene action and that phenotypic selection for these traits will be successful for maize improvement. For 1000-grain weight, similar findings were recorded by Begum et al. [37] and Tadesse et al. [25].

The grain yield per hectare, the number of kernels per row, and the number of tassel branches all had high phenotypic and genotypic coefficients of variation, high heritability, and moderate genetic advance as a percentage of the mean. Similar observations were reported by Prakash et al. [28] for the number of tassel branches and the number of kernels per row. This demonstrates that these parameters were governed by additive gene effects and that these traits might be improved through efficient selection.

The complicated trait of the yield is discovered as being quantitatively inherited. Thus, its efficient improvement could be achieved only through improving the associated traits. Consequently, a very significant positive correlation among yield attributes suggests that an increase in one trait will result in an increase in the linked trait, which would then result in an increase in the yield (Hepziba et al. [36]).

At the phenotypic and genotypic levels, there was a strong and positive association between grain yield and the number of ears per plant, ear length, and number of kernels per row. This suggests that traits that boost grain production in maize will be chosen for future maize breeding efforts. Similar findings were reported by Hepziba et al. [36] for plant height, days to silking, and 50% tasseling; the author in [31] for days to silking and 50% tasseling, and ear and plant height; Ojo et al. [42]; Wannows et al. [43] for the number of kernels rows per ear, ear diameter, and plant and ear height; Golam et al. [44] for thousand kernels weight and days to 50% tasseling and silking; Prakash et al. [28] for ear diameter, number of kernels rows per ear, plant, ear height,

and thousand kernels weight; Bartaula et al. [26] for the number of kernels rows per ear, grain yield, and ear diameter; and Abera et al. [7] for the number of kernels rows per ear, plant height, and thousand kernels weight.

The number of kernels per row and the number of kernel rows per ear significantly correlated negatively with thousand kernel weight at phenotypic and genotypic levels. Malik et al. [13] and Nastasić et al. [45] reported similar findings in their maize study.

The phenotypic and genotypic path coefficient analysis showed that parameters including the grain yield per hectare and number of kernels per row may be utilized as selection criteria to increase maize grain yield. Kumar et al. [41], Hepziba et al. [36], and Prakash et al. [28] for the number of kernels per row and Begum et al. [37] for kernel per row reported findings that were similar.

5. Conclusions

The results of the analysis of variance revealed that genotypic mean squares were significant for all traits, demonstrating that the inbred lines under study exhibited a higher level of genetic diversity. The grain yield per hectare and the number of tassel branches exhibited the highest coefficients of genotypic and phenotypic variation. These GCV and PCV estimations imply that selection can be successful for these traits.

The number of tassel branches, leaf length, number of leaves per plant, ear length, plant height, thousand kernels weight, leaf width, number of kernels per row, days to 50% silking, ear height, days to 50% tasseling, and grain yield per hectare were all estimated to have high magnitudes of broad-sense heredity. The values for these traits show that the variance was mostly under genetic control and was less affected by the environment. This suggested that these traits might be genetically improved through efficient selection.

AMH169-55 and AMH169-86, two inbred lines, were discovered to be superior in terms of the grain yield as well as in other crucial yield components. Therefore, it is advised that these lines be applied to the maize crop in order to improve it further.

Furthermore, we recommend studying the genetic diversity of these 25 maize inbred lines using DNA-based molecular markers to identify the genetic diversity among and within maize populations.

Data Availability

The corresponding author can provide the data utilized in this study upon request.

Disclosure

A thesis has been previously published as Korsa et al. (2014) by Haramaya University on its website.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Authors' Contributions

F.K., O.D., H.Z., and Y.P. contributed to conceptualization, investigation, and reviewing and editing; F.K. contributed to formal data analysis and writing the original draft; and F.K. and H.Z. contributed to funding acquisition. Furthermore, O.D., H.Z., and Y.P. were involved in the supervision of the study.

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Supplementary Materials

Supplementary figures that showed the different growth stages of maize inbred lines samples evaluated at the Ambo Plant Protection Research Center during 2013/14. (*Supplementary Materials*)

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