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Review of the genetic variability in maize genotypes (*Zea mays* L)

Werkissa Yali
Chiro National Sorghum Research and Training Centre, P.O.BOX 190, Chiro, Ethiopia
Email: workissayali@gmail.com

Abstract

Maize (Zea mays L.) is the world's third most important cereal crop, with a high yield potential. Most authorities believe that Central America and Mexico, where many different species of maize can be found, are the primary sources of maize. It is one of the world's most important economic crops. Maize is a priority and strategic crop to react to the world's need for alternate energy sources, in addition to its usage as food and feed. It is the staple crop for millions of people in Ethiopia, where it ranks #1 in total output and yield per unit area. The genetic heterogeneity in the existing germplasm is used to select for high yield with desirable features. In order to be successful, breeding programs must have enough genetic variation to allow for selection and improvement. Knowing the extent of genetic variability, heritability, and genetic gains in the selection of desirable traits could aid the plant breeder in determining breeding program requirements. Many research on genetic variability have been conducted using appropriate biometrical instruments such as variability, heritability, and genetic progress to determine the level of genetic diversity in the population. Genetic advance aids in crop development via selecting for specific features, and heritability is a useful measure for estimating the amount of the genetic portion of overall variability. The purpose of this review study was to evaluate the genetic variability, heritability, and genetic progress of maize genotypes.

Keywords: maize, genetic variability, heritability, genotypes, correlation

1. Introduction

One of the oldest domesticated crops is maize (Zea mays L, 2n=2x=20), a member of the Gramineae (Poaceae) family. Wind pollinates maize most of the time, but self-pollination is also possible (Sleper and Poehlman, 2006). Maize is the world's most significant crop and a staple item in the diets of millions of people in Sub-Saharan Africa. Maize is currently farmed in most parts of the world, across a wide variety of environmental conditions spanning 50 degrees north and south of the equator. Maize adapts to a wide range of environments and is an important cereal crop in Ethiopia, providing both food and cash (Woreda et al., 2018).

Following wheat and rice, maize is one of the world's most significant cereal crops. In many regions of the world, it is widely utilized for food, feed, fuel, and fiber. Because of its cross-pollinated nature, maize has a wide range of morphological variety and geographic adaptation. According to the Food and Agriculture Organization of the United Nations (FAO), maize covered 197 million hectares of land in 2017 and produced 1,134 million tons of maize grain. One of the most important crops in Ethiopia's agricultural and food economy is maize.When compared to other cereals, it has the highest coverage of smallholder farmers, as well as the highest production and consumption (Central Statistical Agency [CSA], 2018). Maize outperforms teff, sorghum, and wheat by 58.9%, 62.4 percent, and 80.7 percent, respectively, according to the CSA 2017/18, with a total production of 8.4 million tons grown on 2.1 million hectares. Maize production and productivity were aided by around 11 million formers (3.9-ton \ha).

The Portuguese brought maize to Ethiopia in the 16th or 17th centuries (Haffangel, 1961). It has grown in importance as a primary food and feed crop since its introduction. Mid-altitude sub-humid (1000-1800 m.a.s.l.), highland sub-humid (1800-2400 m.a.s.l.), lowland moisture stress zones (300-1000 m.a.s.l.), and lowland sub-humid (1000 m.a.s.l.) are the four primary groups of maize-growing agro-ecologies in Ethiopia. The national maize research program now has three primary breeding stations, all of which are located within the three major agro-ecologies mentioned above, with the exception of the lowland sub-humid agro-ecology.

Several enhanced OPVs and hybrids with tolerance to particular biotic stressors were released for huge scale production across various agro-ecologies by these breeding sites of the Ethiopian Institute of Agricultural Research's National Maize Research Program (EIAR). In Ethiopia, the high altitude sub-humid agro ecology, which includes the highland transition and real highlands, is located next to the mid-altitude agro ecology, which has more maize acreage and productivity. This agro-ecology encompasses almost 20% of the land allocated to yearly maize growing and includes over 30% of small-scale farmers who rely on maize production for their livelihood (Demissew et al., 2018)

Maize breeding has been going on in Ethiopia since the 1950s, and it has gone through three major stages of study and development. From 1952 to 1980, the majority of activities revolved around the introduction and evaluation of maize materials from various parts of the world for adaptation to local conditions, while from 1980 to 1990, the focus was on the evaluation of inbred lines and the development of hybrid and open-pollinated varieties. The most common operations between 1990 and now have been (a) significant inbreeding and hybridization, (b) production of early maturing or drought-tolerant cultivars, and (c) collecting and improvement of maize with adaptation to highland agro-ecologies.As a result, a number of enhanced hybrids and open-pollinated cultivars, particularly for mid-altitude zones, have been produced for large-scale cultivation. In 1998, the international maize and wheat development center launched a high-altitude maize breeding initiative (Shengu, 2019).

The primary goal of all maize breeding projects is to develop new open-pollinated varieties (OPVs), inbred lines, hybrids, and synthetics that outperform existing cultivars in a range of attributes. Grain yield is the most important agronomic attribute to consider when working toward this goal (EARO, 2015).

Genetic diversity refers to the variation in genotypes across individuals in a population belonging to the same species.Variation could be found across the genome, on chromosomes, in genes, or at the nucleotide level. Maize has a wide range of phenotypes and genetics. Individual genetic heterogeneity in a population allows for successful selection. Morphological features are frequently used to support genetic variability among maize lines.Days to 50% anthesis, days to 50% silk emergence, days to maturity, ear height, days to silking, percent tryptophan content, cob length, and 1000-seed weight; ear length and diameter; days to 50% anthesis, days to 50% silk emergence, days to maturity, ear aspects, grain yield, plant height, ear height, and the number of diseased cobs (Muchie and Fentie, 2016) are variables that will c It is vital to characterize the available maize genotypes and phenotypes in order to make the best use of the resources (Ferdoush et al., 2017).

The amount and character of genetic diversity among genotypes influences the breeding procedures used to improve a crop's genetics. Genetic diversity is the probability that two randomly chosen alleles are different. The distance between the genotypes reflects a significant amount of genetic variation. These figures are frequently derived from morphological parameters and/or the use of molecular markers.Despite the fact that phenotypic parameters are important for classifying inbred lines and populations, genotype by environment interaction makes it difficult to differentiate variance in highly related genotypes and elite breeding germplasm (GEI).Advances in molecular technology have resulted in a trend toward employing genetic markers to discover individual differences. Although the type and extent of genetic variability of each elite maize inbred line are essential, only a small number of highland maize inbred lines have been characterized thus far due to the fact that only a few studies for agro-ecology have been done (Terefe et al., 2019).

In general, understanding the nature and degree of genotype variation is critical for creating genotypes for high yield and other desirable features. The quantity of genetic variability, heritability, and genetic improvements in the selection of desirable traits are important and mandatory considerations for the plant breeder during the breeding program's crossing. It is critical to keep track of genetic advancements in crop improvement initiatives in order to ensure the program's effectiveness.The effectiveness of the latest technology introduced into a program can also be measured via periodic measurements of genetic advances. Estimation of genetic progress in variety development aids breeders in making decisions about productivity increases as well as future breeding methods (Ferede, 2020). As a result, the purpose of this paper is to examine maize genotype genetic diversity and future trends.

2. Review Literature

2.1 Maize's origin, distribution, and adaptability

Maize evolved from a low-yielding progenitor species into its present variants, with an outsized rachis (cob) of the feminine inflorescence carrying up to 1,000 seeds, amid the warm, seasonally dry environment of Mesoamerica (Watson &Dallwitz, 1992). Most authorities believe that Central America and Mexico, where many different types of maize may be found, are the initial centers of origin for maize. The discovery of fossil maize pollen in Mexico, along with other archaeological data, suggests that maize originated in Mexico. When Columbus arrived, it was the primary food crop of the American Indians, and it is now the most significant cereal food crop in Mexico, Central America, and many nations in South America and Sub-Saharan Africa. The highlands of Peru, Ecuador, and Bolivia, and hence the region of southern Mexico and Central America, have been cited as plausible centers of origin for maize. Poehlman (Poehlman, 1987).

Maize is now grown in almost every corner of the world, in a wide range of environmental circumstances, between 500 degrees north and south of the equator. It rises from the water's edge to more than 3000 meters above sea level. Maize is thought to have been brought to West Africa by Portuguese traders in the early 1500s and reached Ethiopia in the 1860s (Dowswell et al., 1996). After the European discovery of America in the 15th century, it spread over the planet, especially in temperate zones (Dowswell et al., 1996, Farnham et al., 2003).Maize was introduced to Southeast Asia by the Portuguese from America in the 16th century. After Columbus' return from America, the maize was introduced to Spain, and from there it spread to France, Italy, and Turkey. During the seventeenth century, the Portuguese brought maize to India. It was first introduced in India, then in China, and last in the Philippines.

Maize cultivation was not documented in Africa until the 16th century (Miracle 1966), when it was introduced from America along the western and eastern coasts, gradually spreading interior as a ration with the slave trade. Prior to 1965, the following driving factors influenced maize production in African countries to a greater or lesser extent: maize's agronomic suitability, the British starch market, milling technology, and thus Africans' integration into the settler wage economy; and market and trade policies promoted by settler farm lobbies (Miracle, 1966).

2.2 Taxonomy, Reproductive, Biology and Genetics of Maize

Maize is a member of the Gramineae Poaceae tribe Maydeae. The word "Zea" (zela) comes from a Greek word that means "food grass." Z. diploperennis, Z. perennis, Z. luxurians, Z. nicaraguensis, and Z. mays are the five species of Zea. Corn is divided into four subspecies: huehuetenangensis, mexicana, parviglumis, and mays, with mays being the most economically significant. Teosintes, which are wild grasses in Mexico and Central America, are the first three subspecies on the opposite side (Doeblay, 2004; Mangelsdorf et al., 1974).Maize was thought to have been created by natural hybridization between two wild forms of grass, a Tripsacum species and a perennial subspecies of teosinte, according to one early theory (Zeadiploperennis). Furthermore, teosinte was crossed with wild maize, resulting in the development of modern maize (Mangelsdorf, 1974). Except for Zeaperennis, which has a total of 40 chromosomes, all Zea species have 20. (Doebley, 2004).

Table 1: Taxonomy and classification of maize

Classification	Taxonomy
Kingdom	Plantae
Division	Magnoliophyta
Class	Liliopsida
Order	Poales
Family	Poaceae
Subfamily	Panicoideae
Genus	Zea L.
Species	Zea mays L.

Source: Verheye (2010).

Maize could be a monoecious species, with female and male reproductive organs on the same plant. The female reproductive component of the plant is the ear or stalk, and the silks are elongated stigmas that develop from and prod the cob (Fulton et al., 2011). The male reproductive portion of the plant, the tassel, is positioned near the top of the plant and generates pollen grains. Pollen grains are the small bodies that house a plant's male germ cell. Normally, maize is a cross-pollinated crop, with around 95% of the ovules on a shoot being cross-pollinated and 5% being self-pollinated.

2.3 Production, Importance, and utilization of maize

Maize is cultivated throughout the year in almost every part of the planet. About 875,226,630 plenty of maize was produced in 2016 alone and production has increased by 600 million metric tons since 1990 (Incarbon and Dunoyer, 2013). World maize production has grown at roughly an equivalent rate to consumption. One mechanism which will be wont to increase maize production is increasing the quantity of land dedicated to producing it and therefore the area of harvested maize has increased at a rate of 1.32% annually since 1990. Similarly, world maize yield increased at the speed of 1.3% per annum from 1990-2016 (FAO, 2017).

Many African countries, in addition to producing maize locally, import additional maize for food and feed usage (Trevor et al., 2015). Some African countries, however, such as South Africa, Uganda, Tanzania, Rwanda, and Namibia, are major maize exporters. Africa accounted for 20% of global maize flour exports in 2013, with the United States and France accounting for 14.9 percent and 10.5 percent, respectively (Daly et al., 2016). Small-scale farmers account for more than 75 percent of maize output in Africa, while large-scale farmers primarily labor for global export (Nuss and Tanumihardijo, 2010).Smallholder farms account for over 95 percent of all attempts to use draft animals for land preparation and agriculture in Ethiopia. Approximately 88 percent of Ethiopian maize is consumed as food, in both green and dry grain form (Demeke, 2012).

According to Abayneh (2019), the Ethiopian Institute of Agricultural Research (EIAR) has generated a total of forty improved maize varieties, including hybrids and OPVs, in conjunction with the International Maize and Wheat Improvement Center-CIMMYT over the last four decades.OPVs are more common in drought-prone areas thanks to farmers in the central valley, and a number of other nitrogen-efficient maize varieties, such as Melkassa II, III, IV, and V, were developed in the 1990s as part of the African Maize Stress (AMS) project, a collaboration between the International Maize and Wheat Improvement Center (CIMMYT) and national agricultural research organizations.

Maize is an important part of many small farmers' livelihoods, as they grow it for food, animal feed, and money. In Ethiopia, for example, over 9 million households are now involved in maize agriculture (Tsedeke et al., 2015). Maize is the world's most popular feed, and it's used as the primary source of calories in both developed and developing countries' animal feed and feed formulation. Animal feed accounts for approximately 60% of all maize produced worldwide.Because of its outstanding qualities, maize might become a major food supply wherever on the planet: it's easy to reproduce from single plants or tiny nurseries to several hectares, and the ears with their kernels are easy to harvest. It's one of the cereals that fulfills the majority of the calorie needs in the typical Ethiopian diet. Matzo, roasted and boiling green ears, parched mature grain porridge, and native drinks are all made with it (Kebede et al., 1993).

2.4 Genetic variability

A breeding program must first understand the genetic variability, heritability, and genetic progress of features in every plant population. In most maize breeding projects, the defined goal is usually genetic improvement in economically important traits while keeping a suitable amount of diversity (Hallauer, 1972). For numerous variables, Grzesiak (2001) found significant genotypic heterogeneity among maize genotypes. Bernardo (1995) and Ihsan et al., (2005) both found significant genetic differences in maize genotype morphological features. Crop improvement may be aided by this heterogeneity (Welsh, 1981).

Genetic diversity refers to the variation in genotypes across individuals in a population belonging to the same species. Variation could exist throughout the genome, chromosomes, and genes, as well as at the nucleotide level. Maize has a wide range of phenotypes and genetics. Individual genetic heterogeneity in a population allows for successful selection. Often, physical features are used to support genetic variation among maize lines (Ferdoush et al., 2017).

Shengu (2019) studied the genetic diversity of twelve maize genotypes in Ethiopia's Humid Tropic. The number of ears per plant (45.44 and 41.77) and ear diameter (24.60 and 23.83) had strong phenotypic and genotypic coefficients of variation, respectively. For the phenotypic and genotypic coefficients of variation in that order, reasonably modest values were obtained for grain yield per hectare (16.93 and 16.70), ear length (15.06 and 10.49), and number of rows per ear (14.29 and 13.38). The number of kernels per row had a moderate phenotypic coefficient of variation (10.49).

In that study, the number of ears per plant and ear diameter had high phenotypic and genotypic coefficients of variation, implying that these traits have a higher chance of effective selection, whereas grain yield per hectare, ear length, and the number of rows per ear had moderate genotypic and phenotypic coefficients of variation, implying that these traits have an average chance of selectionOn the other hand, thousand kernel weights (2.62 and 2.44), days to maturity (3.92 and 3.83), plant height (4.17 and 3.62), days to silking (6.18 and 5.43), days to anthesis (6.21 and 5.47) and ear height (7.47 and 4.36) had the least amount of phenotypic and genotypic coefficients of variation, and thus these traits provide less chance for selection. Genetic traits with a high GCV, according to Mansir (2010), imply a strong potential for effective selection.

Ghosh et al. (2014) evaluated the varied parameters of genetic variability and nature of associations among traits affecting grain yield in thirty-three inbred lines of maize (Zea mays L.) and located the presence of considerable variability among the genotypes for all the 11 traits studied. The equivalence between the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was close for all traits indicating that these characters were less influenced by the environment.For the traits of number of grains per cob, grain yield per plant, number of grains per row, plant height, and ear height, high GCV, heritability, and comparatively high genetic advance were observed, indicating that selection for these characters would be quite effective because these characters appeared to be governed by additive gene action.

Kumar et al. (2014) used newly produced eighty-six maize genotypes to study genetic variability, heritability, and genetic advance in order to determine the various aspects of genetic variability, broad-sense heritability, genetic advance, and genetic variability. The mean sum of squares due to genotypes indicated significant differences for all 12 features tested, according to analysis of variance.The traits yield per plant, plant height, ear height, number of kernels per row, and 100-kernel weight all had high heritability, as well as high to moderate genotypic and phenotypic coefficients of variation and genetic advance, indicating that the majority of the heritability is due to additive gene effects, and selection may be effective in early generations for these traits. Days to 50% tasseling, days to 50% silking, shelling percentage, ear length, days to maturity ear girth, and number of kernel rows per ear all showed high to moderate heritability with modest estimates of genetic progress.

Bhusal, Marker, and Synrem (2017) also estimated the extent of genetic diversity and trait association in maize, using fifty-five genotypes available in India, and found significant differences for 18 of the features evaluated using analysis of variance. Grain yield/plant, biological yield/plant, and cob weight all had strong genotypic and phenotypic coefficients of variation, as well as high heritability and genetic progress. At both the genotypic and phenotypic levels, strong positive relationships were found between grain yield per plant and plant height, ear height, leaf area index, cobs/plant, cob weight, cob length, cob girth, grains/row, and biological yield/plant.

Ferdoush et al. (2017) investigated the genetic variability of 20 maize genotypes in Bangladesh and found that there was a lot of variance among the genotypes used. Yield plant1 (g) demonstrated a positive and significant relationship with ear girth (cm), 1000-kernel weight (g), yield plot1 (g), grain yield (t/ha), and dry weight, according to correlation coefficient analysis. For many phenotypic features, the genotypes differed significantly. All of the traits tested had a phenotypic coefficient of variation (PCV) greater than the genotypic coefficient of variation (GCV), indicating that they interacted with the environment.The traits under investigation showed a wide range of heritability estimates (26.81 percent to 99.95 percent). The 1000-kernel weight has the highest heritability of all the traits (g). The 1000-kernel weight (g), yield plot 1 (g), and grain yield (t/ha) all had substantial heritability and genetic progress.

Abe and Adelegan (2019) studied the extent of genetic variability, heritability, and genetic advance of thirteen agronomic and fresh yield traits among twelve shrunken-2 super-sweet corn populations in Ibadan, Nigeria, over the course of two years, and found that all of the traits had significant genotypic differences. For the number of marketable cobs, yield of cobs, number of cobs, number of kernel rows, husk cover, ear height, and days to anthesis, genotypic variance was significant, while environmental variance was significant for all traits. For all traits, phenotypic coefficients of variance were greater than genotypic coefficients of variation.

At Jimma Agricultural Research Center (JARC), Jilo et al. (2018) conducted an experiment to investigate the degree of genetic diversity, heritability, and genetic progress of 24 maize inbred lines for 16 quantitative variables. With the exception of tassel size, analysis of variance revealed strong significance (P0.01) differences between genotypes for all parameters investigated. The genotypic coefficient of variation (GCV) was lower than the phenotypic coefficient of variation (PCV) for all traits studied, showing that the environment plays a substantial influence in the expression of the traits analyzed.Grain yield, thousand kernel weight, ear height, ear diameter, anthesis and silking interval, and plant appearance all had high PCV and GCV estimates. Also, (Maruthi and Rani, 2015) studied the genetic divergence and various genetic parameters of forty-three maize genotypes for eleven traits, and the analysis of variance revealed a significant (P0.01) difference between genotypes for all the characters, revealing a wide range of variability and high heritability for all the characters.

2.5 Heritability and genetic advance

Stanfield (1988) defined heritability as the percentage of phenotypic variance that can be explained by genetic factors. Heritability estimates are extremely important to breeders since their size reflects how well a genotype can be identified by its phenotypic expression. High heritability does not always imply a high genetic gain; in anticipating the last word effect for selecting improved varieties, heredity should be employed alongside genetic improvements (Muchie and Fentie, 2016).Bello et al. (2012) found that plant height, number of kernels ear1 and yield plot1 had larger genetic advances, indicating the predominance of additive gene action for the development of those traits that can be fixed in later generations.

According to Jilo et al. (2018), broad-sense heritability (H2) ranged from 24.44 for the anthesis-silking interval to 96.02 for 1000-kernel weight, and was an estimate of the overall contribution of genetic variance to the entire phenotypic variance. The 1000-kernel weight (96.02), leaf length (74.79), plant height (69.47), days to 50% anthesis (69.46), days to 50% silking (68.75), leaf width (64.70), ear length (64.62), and leaf area all had higher heritability estimates (63.95).Grain yield per hectare (58.42), ear height (52.99), days to maturity (50.07), number of kernels per row (47.38), plant aspect (33.38), and kernel row per ears all had moderate heritability estimates (32.26). Ear diameter (29.82), anthesis, and silking interval (24.45), on the other hand, had modest heritability values.

Days to maturity had a genetic advance of 2.76 percent, whereas grain yield had a genetic advance of 50.69 percent at a selection intensity of 5%. The high heritability estimates suggest that choosing such a feature should be simple. As a result, 1000-kernel weight, leaf length, plant height, days to 50% anthesis, days to 50% silking, leaf breadth, and leaf area could readily be conveyed from one generation to the next, increasing the efficiency of maize improvement selection. This demonstrated that the features are genetically determined, and that environmental variables have little impact on their phenotypic variance.

Grain yield per hectare, 1000-seed weight, and ear height all had increased genetic advance (GA) as a percentage of the mean, indicating that additive gene action is in charge of these parameters. The findings of Atnafu and Rao (2014), who demonstrated strong genetic advances for plant height, kernel rows per ear, 1000 kernel weight, ear height, and grain production per hectare, back up this theory. Days to maturity and days to 50% silking exhibited minimal genetic progress as a percentage of mean, indicating limited genetic variation for the attributes as demonstrated by low GCV and PCV values.This emphasizes the importance of genetic heterogeneity in selection-based improvement. Fekadu's findings corroborate this conclusion (2014). The genetic advance as a percent of mean was high for grain yield per plant (73.19 percent), ear height (51.05 percent), number of kernels per row (44.40 percent), plant height (43.46 percent), 100-grain weight (42.88 percent), ear length (30.79 percent), and number of kernel rows per ear (25.23 percent), according to Maruthi and Rani (2015). The outcome is likewise consistent with Abe and Adelegan's findings (2019). The anthesis-silking interval's broad sense heritability ranged from 22.2 percent to 85.1 percent for husk cover.For husk cover, the genetic progress was high (32.7%), medium (12.0%) for cob yield, and low for all other parameters.

2.6 Analyzing correlations

The correlation coefficients of various plant features are useful criterion for identifying desired traits that lead to the variable's enhancement (grain yield). For the simultaneous enhancement of numerous traits in breeding programs, knowledge of connections between seed production and its attributing characters is essential. Pleiotropic gene activity, linkage, or both are responsible for correlation. The phenotypic correlation is a visible link between two traits, whereas the environmental correlation is solely due to environmental factors.

The correlation value indicates the nature and extent of the relationship between two characters. Correlation is also a metric that suggests which attributes should be examined in order to increase yield.Ferdoush et al. (2017) looked at the genetic variability of 20 maize genotypes and found some significant positive correlations: yield plant1 (g) with ear girth (cm), 1000-kernel weight (g), yield plot1 (g), grain yield (t ha1) with dry weight; plant height (cm) with ear length (cm), ear girth (cm), no. of kernel ear1; ear length (cm) with ear girth (cm), no. of kernel ear1; ear length (cm) with ear girth (cm).

Grain yield (0.68), grains per row (0.74), grains per ear (0.80), ear height (0.46), ear-down leaves (0.40), total leaves (0.58), grain depth (0.81), grain dry matter weight (0.87), and 1000-grain weight (0.56) were all found to have a significant and direct correlation, according to Khodarahmpour (2012). If comparable research is undertaken in the future using additional morphological qualities, this association is frequently used as the basis for character selection.

3. Summary and Conclusion

The success of a crop improvement program is determined by the breeding material chosen, the degree of variability present, and hence the understanding of quantitative traits associated with yield and yield-related factors. The genetic variety in the materials at hand is critical to the success of any breeding enterprise. The larger the genetic variety, the higher the heritability and, as a result, the higher the chances of success through selection. Within the materials chosen, there was a great deal of variation.

Variability is necessary for resistance to biotic and abiotic stimuli, as well as for extensive adaptation among genotypes. When there is genetic heterogeneity among individuals in a group, selection is successful. As a result, a plant breeder's understanding of the extent of genetic variability existing in a population is critical for establishing a prudent breeding program. The potential to grow a character through selection is determined by heredity and the character's genetic advancement. Heritability estimates combined with genetic improvements are usually more useful than heritability estimates alone in estimating the gain under selection.Further varietal improvement is unlikely without genetic variety.

The fact that the populations had a bigger genotypic difference and high heritability estimates for many variables suggests that they could be used in future maize breeding projects. Furthermore, because the populations had significant genetic diversity and heritability estimates for many of the variables, they could be used as a base or source population in future maize breeding projects to derive superior inbred lines through recurrent selection, S1 line selection, and other methods.

The primary prerequisite for a crop improvement program is information regarding the level of variation, heritability estimates, and predicted genetic advance in terms of maize grain yield and yield contributing characters. Broad sense heritability is useful for determining the relative importance of additive genetic variance that will be passed down to offspring. When additive gene effects controlled a trait, it usually resulted in high heritability and genetic advance, but non-additive gene actions could result in high heritability but poor genetic advance.

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