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Review on Genetic Variability in different Genotypes of Maize (zea mays L)

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ABSTRACT

Maize (Zea mays L.) is that the world's third most vital cereal crop that has remarkable productive potential. The primary center of origin of maize is considered by most authorities to be Central America and Mexico, where many diverse types of maize are found. It is one of the leading economic crops of the world. Besides its uses as food and feed, maize is a priority and strategic crop to respond to the world's quest for alternative energy sources. In Ethiopia, it ranks first in total production and yield per unit area and it is the staple crop for millions of people. The selection for high yield with desirable traits depends on the genetic variability in the existing germplasm. Successful breeding programs need adequate genetic variation for selection and improvement supported necessity. Knowledge of the magnitude of genetic variability, heritability, and genetic gains in the selection of desirable characters could assist the plant breeder in ascertaining criteria to be used for the breeding programs. Many studies on genetic variability with the help of suitable biometrical tools such as variability, heritability, genetic advance gives an idea about the extent of genetic variability present in the population. Heritability is a suitable measure for assessing the magnitude of the genetic portion of total variability and genetic advance aids to make improvements in the crop by selection for various characters. This review paper was prepared to assess the genetic variability, heritability, genetic advance of maize genotypes.

Key words: Maize, Genetic variability, Heritability, Genotypes, Correlation

Introduction

Maize (*Zea mays L*, 2n=2x=20), a member of the Gramineae (Poaceae), is one of the oldest cultivated crops. Maize is predominately cross-pollinated by wind, but self-pollination is also possible [1]. Maize is the most important crop worldwide and a basic trade product recurring ingredient for millions of people in Sub-Saharan Africa. Currently, maize is widely grown in most parts of the planet over a good range of environmental conditions ranging between 50° latitude north and south of the equator. Maize has a wide range of adaptations and is an important cereal crop in Ethiopia as a source of both food and cash [2].

Maize is one of the foremost important cereal crops in the world following wheat and rice. It is widely used for food, feed, fuel, and fiber in many parts of the world. Maize has broad morphological variability and geographical adaptability thanks to its cross-pollinated nature. According to World Food and Agriculture, 197 million hectares of land were covered by maize and produced 1,134 million tons of maize grain in the 2017 production season [3]. Maize is one of the main cereals that play a core role in Ethiopia's agriculture and food economy. It has the largest smallholder farmers' coverage and greatest production and consumption compared to other cereals [4]. According to the CSA 2017/18, maize exceeds teff, sorghum, and wheat by 58.9, 62.4, and 80.7%, respectively, with a total production of 8.4 million tons produced over 2.1 million hectares. About 11 million formers contributed to maize production and productivity (3.9-ton\ha).

Maize was introduced to Ethiopia by the Portuguese within the 16th or 17th century [5]. Since its introduction, it's gained importance as the main food and feed crop. In Ethiopia, maize growing agro-ecologies are broadly classified into four major categories: mid-altitude sub-humid (1000-1800 m.a.s.l), highland sub-humid (1800-2400 m.a.s.l.), lowland moisture stress areas (300-1000 m.a.s.l.) and lowland sub-humid (<1000 m.a.s.l.). Currently, the national maize research program has three main breeding stations located within the above three major agro-ecologies

excluding the lowland sub-humid agro ecology. Several improved OPVs and hybrids with resistance to certain biotic stresses were released for giant scale production across different agro-ecologies by these breeding centers of the National Maize Research Program of the Ethiopian Institute of Agricultural Research (EIAR). The high altitude sub-humid agro ecology, including the highland transition and true highlands, is next to the mid-altitude agro ecology with greater maize area and production in Ethiopia. This agro-ecology covers an estimated 20% of the land dedicated to annual maize cultivation and consisted of quite 30% of small-scale farmers who depend upon maize production for his or her livelihoods [6].

Maize breeding in Ethiopia has been ongoing since the 1950s and has skilled three distinctive stages of research and development. These are from 1952 to 1980, the most activities were the introduction and evaluation of maize materials from different a part of the planet for adaptation to local condition, from 1980 to 1990, the work was focused on the evaluation of inbred lines and development of hybrid and open-pollinated varieties. From 1990 to this, the most activities were (a) extensive inbreeding and hybridization, (b) development of early maturing or drought-tolerant cultivars, and (c) collection and improving maize with adaptation to highland agro-ecologies. As a result, various improved hybrids and open-pollinated varieties were released for large-scale production, especially for mid-altitude zones. The high land maize breeding program was also started in 1998 together with the international maize and wheat improvement center [7].

The main goal of all maize breeding programs is to get new open-pollinated varieties (OPVs), inbred lines, and from their hybrids and synthetics which will outperform the prevailing cultivars with reference to a variety of traits. In working toward this goal, attention must be paid to grain yield because the most vital agronomic trait [8].

Genetic diversity is that the existed variability within the genotypes of the individuals of a population that belongs to the same species. The variation could prevail within the entire genome, chromosomes, gene, or within the nucleotide levels. Maize is both phenotypically and genetically diverse. Genetic variability among individuals in population offers effective selection. Genetic diversity among maize lines is often examined supported by morphological traits. Grain weight and grain yield; kernel weight and days to maturity, ear height, days to silking, % 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 a number of diseased cobs are variables which will contribute to genetic diversity assessment [9]. Characterization of obtainable maize genotypes supported phenotypes is critical to utilize the resources [10].

The existing magnitude and nature of genetic variability among genotypes matters the preference of approaches of breeding for genetic improvement of a crop. The probability that two randomly sampled alleles are different is genetic diversity. The space reflects a definite amount of genetic difference present among the genotypes. These measures are often calculated by measuring morphological characteristics and/or using molecular markers. Albeit, phenotypic evaluation has useful attributes for grouping inbred lines and populations, these phenotypic traits have limitations in distinguishing variation in highly related genotypes and elite breeding germplasm thanks to genotype by environment interaction (GEI). Advances in molecular technology have produced a shift towards detecting individual differences using molecular markers. the character and magnitude of genetic variability of each elite maize inbred line is an important however limited number of highland maize inbred lines are characterized thus far due to only certain researches are conducted for the agro-ecology [11].

Generally, knowledge of the nature and magnitude of variation in genotypes is of great importance to developing genotypes for top yield and other desirable traits. The magnitude of genetic variability, heritability, and genetic advances in the selection of desirable traits are pertinent and compulsory issues for the plant breeder to think about the traits during the crossing in the breeding program. Monitoring of genetic advances in crop improvement programs is important to live the efficiency of the program. Periodic measurement of genetic advances also allows the efficiency of the latest technologies incorporated into a program to be quantified. Estimation of genetic progress in variety development helps breeders to form a choice on the increment of productivity also on considers the breeding strategies within the future [12]. Therefore the target of this paper is to review the genetic variability and future trends of maize genotypes.

Literature Review

Origin, Distribution and Adaptableness of Maize

Maize originated under warm, seasonally dry conditions of Mesoamerica, and was by human selection converted from a low-yielding progenitor species into its modern forms, with an outsized rachis (cob) of the feminine inflorescence

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bearing up to 1,000 seeds [13]. The first center of origin of maize is taken into account by most authorities to be Central America and Mexico, where many diverse sorts of maize are found. The invention of fossil maize pollen with other archaeological evidence in Mexico indicates Mexico to be the native of maize. It had been the principal food crop of the American Indians when Columbus arrived and still remains the foremost important cereal food crop in Mexico, Central America, and lots of countries in South America and Sub-Saharan Africa. Two locations are suggested as the possible center of origin for maize, namely, the highlands of Peru, Ecuador, and Bolivia, and therefore the region of southern Mexico and Central America [14].

Today, maize is widely grown in most parts of the planet, over a good range of environmental conditions, between latitudes of 500 North and South of the equator. It grows from water level to over 3000 m above sea level. It's believed that maize was introduced to West Africa within the early 1500s by Portuguese traders and reached Ethiopia within the 1860s [15]. It spread around the world, particularly in temperate zones, after the European discovery of America within the 15th century.

The Portuguese introduced maize to Southeast Asia from America within the 16th century. The maize was introduced into Spain after the return of Columbus from America and from Spain it visited France, Italy, and Turkey. In India, the Portuguese introduced maize during the seventeenth century. From India, to China and later it had been introduced in the Philippines.

There is no evidence of maize cultivation in Africa until the 16th century. When it had been introduced from America to Africa along the western and eastern coasts, gradually moving inward as a ration with the slave traffic. Before 1965, the increase of maize production altogether of African countries was propelled to a greater or lesser extent by the subsequent driving factors: the agronomic suitability of maize, British starch market, milling technology, and therefore the integration of Africans into the settler wage economy; and market and trade policies promoted by settler farm lobbies [16].

Taxonomy, Reproductive, Biology and Genetics of Maize

Maize belongs to the tribe Maydeae of the Gramineae Poaceae. "Zea" (zela) was derived from an old Greek name for food grass. The Zea consists of 5 species including *Z. diploperennis, Z. perennis, Z. luxurians, Z. nicaraguensis,* and *Z. mays.* The species corn is split into four subspecies: huchuetenangensis, mexicana, parviglumis and mays of which the subspecies mays is economically important. The opposite first three subspecies are teosintes which are wild grasses in Mexico and Central America [17]. An early hypothesis on the origin of maize proposed that maize was produced by natural hybridization between two wild types of grass, a species of Tripsacum and a perennial subspecies of teosinte (Zeadiploperennis). Further, teosinte was crossed with wild maize and therefore the modern maize was produced as a result [18]. Species of Zea have a chromosome number of 20 apart from Zeaperennis which features a total of 40 (Table 1).

Maize may be a monoecious species having separate female and male reproductive parts on an equivalent plant. The ear or shoot is that the female reproductive part of the plant; the silks are elongated stigmas, each growing from and prod the cob [19]. The tassel, which is found at the highest of the plant, is that the male reproductive part that produces pollen grains. Pollen grains are the microscopic body that contains the male germ cell of a plant. Maize may be a cross-pollinated crop normally, about 95% of the ovules on a shoot are cross-pollinated and 5% self-pollinated.

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 [20]. World maize production has grown at roughly an equivalent rate to consumption. One mechanism which will be wont to increase

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

Table 1: Taxonomy and classification of maize Source: Verheye (2010).

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.

In addition to producing maize locally, many African countries import additional maize for food and feed consumption [21]. In contrast, some African countries like South Africa, Uganda, Tanzania, Rwanda, and Namibia are important exporters of maize. In 2013, 20% of the worldwide export of maize flour came from Africa, while the USA and France accounted for 14.9% and 10.5%, respectively [22]. More than 75 you look after maize production in Africa is completed by small-scale farmers, while some large-scale farmers mainly work for global export [23]. In Ethiopia, smallholder farms account for quite 95 attempts to use draft animals for land preparation and cultivation. Approximately 88% of maize produced in Ethiopia is consumed as food, both as green and dry grain [24].

According to the Ethiopian Institute of Agricultural Research (EIAR) has while collaboration with the International Maize and Wheat Improvement Center-CIMMYT and it's developed a complete of quite forty improved maize varieties including hybrids and OPVs within the last four decades. OPVs are more common in the drought-prone areas through the farmers within the central valley and a number of other nitrogen use efficient maize varieties, namely, Melkassa II, III, IV and V were developed within the 1990s under the primary phase of the African Maize Stress (AMS) project, a joint undertaking of the International Maize and Wheat Improvement Center (CIMMYT) and national agricultural research institutes across Eastern and Southern Africa.

Maize plays a crucial role within the livelihoods of many small farmers, who grow maize for food, animal feed and income. For example, about 9 million households in Ethiopia are currently engaged in maize cultivation [25]. Maize is that the world's favorite feed and is employed because the main source of calories in animal feed and feed formulation in both developed and developing countries. Approximately 60% of the maize produced globally is employed for animal feed. Everywhere on the planet, maize may be a major food source thanks to its excellent properties: it's easy to propagate from single plants or small nurseries to many hectares, and therefore the ears with their kernels are easy to reap. It's one of the cereals that provide most of the calorie requirements within the traditional Ethiopian diet. it's prepared and used as matzo, roasted and boiled green ears, parched mature grain porridge, and in local drinks [26].

Genetic Variability

Understanding the genetic variability, heritability and genetic advance of traits in any plant population is a crucial pre-requisite for a breeding program. Genetic improvement in traits of economic importance alongside maintaining a sufficient amount of variability is usually the specified objective in maize breeding programs observed considerable genotypic variability among various maize genotypes for various traits [27,28]. It also reported significant genetic differences for the morphological parameters for maize genotypes [29]. This variability may be a key to crop improvement [30].

Genetic diversity is that the existed variability within the genotypes of the individuals of a population that belongs to the same species. The variation could prevail within the entire genome, chromosomes, and gene or within the nucleotide levels. Maize is both phenotypically and genetically diverse. Genetic variability among individuals in population offers effective selection. Genetic diversity among maize lines is often examined supported by morphological traits.

It conducted genetic diversity research on, twelve maize genotypes in the Humid Tropic of Ethiopia. The high phenotypic and genotypic coefficient of variations were observed from the number of ears per plant (45.44 and 41.77), and ear diameter (24.60 and 23.83) therein order. On the opposite hand, relatively moderate values were recorded for grain yield per hectare (16.93 and 16.70), ear length (15.06 and 10.49), number of rows per ear (14.29 and 13.38) for the phenotypic and genotypic coefficient of variation therein order. A moderate phenotypic coefficient of variation was observed from the number of kernels per row (10.49).

In that study, the number of ears per plant, and ear diameter had high phenotypic and genotypic coefficients of variation and hence these traits provide a greater chance for effective selection whereas grain yield per hectare, ear length, and a number of rows per ear had moderate genotypic and phenotypic coefficients of variation, and hence these traits provide an average chance for selection. On the contrary, 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 smallest amount phenotypic and genotypic coefficients of variation therein order, and hence these traits provide less chance for selection. Consistent with genetic traits having high GCV indicate high potential for effective selection [31].

It 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 [32]. 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. High GCV, heritability, and the comparatively high genetic advance were observed for the traits viz., number of grains per cob, grain yield per plant, number of grains per row, plant height and ear height indicating that selection for these characters would prove quite effective since these characters appeared to be governed by additive gene action.

They conducted research on genetic variability, heritability and genetic advance studies on newly developed eightysix maize genotypes to work out the varied parameters of genetic variability, broad-sense heritability, genetic advance, and Analysis of variance revealed that the mean sum of squares thanks to genotypes showed significant differences for all the 12 characters studied [33]. Traits yield per plant, plant height, ear height, number of kernels per row, 100-kernel weight were showed high heritability accompanied with high to the moderate genotypic and phenotypic coefficient of variation and genetic advance which indicates that the majority likely the heritability is thanks to additive gene effects and selection could also be effective in early generations for these traits. Whereas high to moderate heritability alongside low estimates of genetic advance were observed for days to 50 percent tasseling, days to 50 percent silking, shelling percentage, ear length and days to maturity ear girth and number of kernel rows per ear.

It also estimate the extent of genetic variability and traits association in maize, fifty-five genotypes available in India and analysis of variance revealed significant differences for 18 characters studied among the genotypes [34]. High genotypic and phenotypic coefficient of variation was recorded for grain yield/plant, biological yield/plant and cob weight including high heritability and genetic advance. Strong positive associations were displayed to grain yield per plant with plant height, ear height, leaf area index, cobs/plant, cob weight, cob length, cob girth, grains/row and biological yield/plant both at genotypic and phenotypic levels.

It conducted research to work out the existing genetic variability of 20 maize genotypes in Bangladesh and observed a high degree of variation among the genotypes used. Correlation coefficient analysis revealed that yield plant-1 (g) had a positive and significant association with ear girth (cm), 1000-kernel weight (g), yield plot-1 (g), grain yield (t/ ha) with dry weight. The genotypes differed significantly for many of the phenotypic traits. The phenotypic coefficient of variation (PCV) was above the genotypic coefficient of variation (GCV) altogether traits studied indicating that those traits interacted with the environment. The traits under study expressed wide heritability estimates (26.81% to 99.95%). Among the characters, the highest heritability was recorded for the 1000-kernel weight (g). High heritability alongside high genetic advance was noticed for the 1000-kernel weight (g), yield plot-1 (g) and grain yield (t/ha).

They 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 for 2 years in Ibadan, Nigeria and therefore the shows all the traits exhibited significant genotypic differences [35]. The genotypic variance was significant for the number of marketable cobs, the yield of cobs, number of cobs, number of kernel rows, husk cover, ear height and days to anthesis, while environmental variance was significant for all the traits. Phenotypic coefficients of variation were above the corresponding genotypic coefficients of variation for all traits.

It conducted an experiment to assess the magnitude of genetic variability, heritability and genetic advance of 24 maize inbred lines for 16 quantitative traits at Jimma Agricultural Research Center (JARC) and Analysis of variance showed high significance (P<0.01) differences among genotypes for all traits studied except tassel size. The genotypic coefficient of variation (GCV) for all traits studied was smaller than the phenotypic coefficient of variation (PCV), indicating the significant role of environment in the expression of traits studied [36]. The estimates of PCV and GCV were high for grain yield, thousand kernel weight, ear height, ear diameter, anthesis and silking interval and plant aspect. Also evaluated forty-three genotypes of maize for eleven traits to study their genetic divergence and various genetic parameters and the analysis of variance showed a significant (P<0.01) difference between genotypes for all the characters [37].

Heritability and Genetic Advance

Stanfield (1988) defined heritability because the proportion of the entire phenotypic variance that happens thanks to gene effects. Heritability estimates are of tremendous significance to the breeder, as their magnitude indicates the accuracy with which a genotype is often recognized by its phenotypic expression. High heritability doesn't always indicate a high genetic gain; heritability should be used alongside genetic advances in predicting the last word effect for choosing superior varieties. They recorded higher genetic advances for plant height, number of kernels ear–1 and yield plot–1 which indicated the preponderance of additive gene action for the expression of those traits which is fixable in subsequent generations [38].

According to broad-sense heritability (H2), an estimate of the entire contribution of genetic variance to the entire phenotypic variance and ranged from 24.44 for the anthesis-silking interval to 96.02 for 1000-kernel weight. Higher heritability estimates were scored for 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 (63.95). Moderate heritability estimates were observed for 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 (32.26). In contrast, ear diameter (29.82), anthesis and silking interval (24.45) had low heritability estimates. Estimates of genetic advance as percent of mean at 5% selection intensity ranged from 2.76% for days to maturity to 50.69% for grain yield. The high heritability estimates suggest a selection of such character might be fairly easy. Therefore, 1000-kernel weight, leaf length, plant height, days to 50% anthesis, days to 50% silking, leaf width, and leaf area could easily be passed from one generation to subsequent then enhancing the efficiency of selection in the maize improvement program. This indicated that the traits are under genetic control and therefore the environmental factors didn't greatly affect their phenotypic variation.

Genetic advance (GA) as a percentage of the mean was higher for traits like grain yield per hectare, 1000-seed weight and ear height showing that these traits are under the control of additive gene action. This is supported by the findings of who reported high genetic advances for plant height, kernel rows per ears, 1000 kernel weight, ear height, and grain yield per hectare [39]. The traits like days to maturity and days to 50% silking indicated low values of genetic advance as percent of mean and which correspondingly indicated low value of genetic variation for the traits as indicated by low GCV and PCV values. This suggests the importance of genetic variability in improvement through selection. This result's also confirmed by the results observed the genetic advance as percent of mean was high for grain yield per plant (73.19%), ear height (51.05%), number of kernels per row (44.40%), plant height (43.46%), 100-grain weight (42.88%), ear length (30.79%), number of kernel rows per ear (25.23%), which is usually similar with these result. The result's also in line with the findings of Abe and broad sense heritability ranged from 22.2% for the anthesissilking interval to 85.1% for husk cover [40]. The genetic advance was high (32.7%) for husk cover, medium (12.0%) for a yield of cobs and low for other traits.

Correlation Analysis

Studies on correlation coefficients of various plant traits are useful criteria to spot desirable traits that contribute to enhance the variable (grain yield). The knowledge of correlations between seed yield and its attributing characters is vital for the simultaneous improvement of several characters in breeding programs. Correlation is either thanks to pleiotropic gene action or thanks to linkage or both. The phenotypic correlation refers to the observable association between two characters while the environmental correlation is entirely thanks to environmental effects. The correlation value denotes the character and extent of association existing between pairs of characters. Correlation is additionally a measure that indicates traits to be considered to extend yield. They evaluated the genetic variability of 20 maize genotypes and observe some positive significant correlation: yield plant–1(g) with ear girth(cm), 1000-kernel weight(g), yield plot–1(g), grain yield(t ha–1) with dry weight; plant height(cm) with ear length(cm), ear girth(cm), no. of kernel ear–1; ear height(cm) with ear length(cm); ear length(cm) with ear girth(cm), no. of kernel ear–1; with dry weight; yield plot–1(g) with grain yield(t ha–1) with dry weight; 1000-kernel weight(g) with yield plot–1 (g), grain yield(t ha–1) with dry weight; 1000-kernel weight(g) with yield plot–1 (g), grain yield(t ha–1) with dry weight; yield plot–1(g) with grain yield(t ha–1) with dry weight; 1000-kernel weight(g) with yield plot–1 (g), grain yield(t ha–1) with dry weight; yield plot–1(g) with grain yield(t ha–1) with dry weight; yield plot–1(g) with grain yield(t ha–1) with dry weight; 14,42].

It also reported that 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) had significant and direct correlation. This correlation is often used as the basis for character selection if similar research is conducted in the future using additional morphological traits [43-45].

Summary and Conclusion

The progress of the crop improvement program depends on the selection of the breeding material, the extent of variability and therefore the knowledge of quantitative traits with yield and yield-related traits. The success of any breeding program depends upon the genetic variation within the materials at hand. The greater the genetic variability, the upper would be the heritability and hence the higher the probabilities of success to be achieved through selection. There was considerable variability present within the materials used.

The existence of variability is important for resistance to biotic and abiotic factors also for wide adaptability within the genotypes. Selection is effective when there's genetic variability among the individuals during a population. Hence, insight into the magnitude of genetic variability present during a population is of paramount importance to a plant breeder for stating a judicious breeding program. Knowledge of heritability and the genetic advance of the character indicates the scope for the development through selection. Heritability estimates alongside genetic advances are

normally more helpful in predicting the gain under selection than heritability estimates alone. Without having genetic diversity further varietal improvement is unexpected.

The presence of greater genotypic difference and high heritability estimates for various traits among the populations indicates that the populations might be utilized in future maize breeding programs. Moreover, high genetic variability and heritability estimates for many of the traits show a greater amount of additive gene action thus the populations might be utilized in future maize breeding programs as a base or a source population for deriving superior inbred lines through recurrent selection, S1 line selection, etc.

Generally information about the extent of variation, estimates of heritability and expected genetic advance in respect of maize grain yield and yield contributing characters constitutes the essential requirement for a crop improvement program. Broad sense heritability is beneficial for measuring the relative importance of additive portion of genetic variance which will be transmitted to the offspring. The preponderance of additive gene effects controlling a trait usually resulted in both high heritability and genetic advance, while those governed by non-additive gene actions could give high heritability with low genetic advance.

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