

Review of Sorghum [*Sorghum bicolor* (L.) Moench] Genetic Variability Genotypes

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Abstract: Sorghum [*Sorghum bicolor* (L.) Moench] is a tropical C4 crop that originated in Ethiopia and was domesticated there. It is the fifth most widely grown cereal crop in the world. It is a vital staple crop for more than 500 million people in 30 Sub-Saharan African and Asian nations, although it is mostly farmed as a feed crop in the developed world. In a breeding program, the presence of genetic variety is critical. For sorghum breeding and novel cultivar deployment, the genetic variation present in sorghum germplasm collections is frequently investigated. Effective breeding and genetic conservation may need a well-characterized sorghum genetic resource. The level of trait heritability is linked to the genetic development of breeding populations for yield and its component traits. The amount of genetic variability contained in a population and how it is used determines the success of a crop improvement effort. A breeder's understanding of a crop's genetic diversity usually aids them in selecting desirable parents for breeding programs. As a result, it's critical to examine genetic diversity, heritability, and genetic progress since they provide information that can be used to improve grain yield as well as quality qualities to increase crop production and productivity.

Keywords: Sorghum, Genetic Variability, Heritability, Yield

1. Introduction

Sorghum (*Sorghum bicolor* (L.) Moench) is a major grain crop grown throughout the world, especially in the semi-arid tropics. After wheat, rice, maize, and barley, it is the most essential cereal [10]. Sorghum is grown on 40 million hectares in over 105 countries, with 60 percent of the area in Africa, and it plays a significant role in food security [35]. It is classified as a tropical crop with a $2n = 20$ chromosome and a genomic size of 750 megabytes. It is a member of the Gramineae family [25]. Sorghum is a naturally self-pollinated plant with up to 20% spontaneous cross pollination under certain conditions, depending on panicle kinds. Ethiopia is regarded as the birthplace and diversification hub for sorghum [17, 32]. It is primarily produced in a country's mid- and lowlands. It withstands heat and drought better than most planted crops [4].

Sorghum is the fifth most extensively grown cereal crop in

the world, with 57.89 million metric tons produced and 40 million hectares harvested [20]. Sorghum is grown in practically every region of Ethiopia, and ranks third in terms of area coverage behind tef and maize, with a national average production of 2.80 tons/ha [13]. It is very essential crop in the country's arid lowlands, accounting for roughly 66 percent of total farmed acreage. Improved cultivars and production procedures have the potential to increase sorghum yield from 3 to 6 tons per hectare, according to research [49]. However, there have been a lot of roadblocks in the path of sorghum production. "The main issues are a lack of early maturing types that can withstand drought, poor soil fertility, poor stand establishment due to reduced emergence in often crusty soils, and insect pests such as spotted stalk borers and birds" [21].

In Ethiopia, sorghum is the second most significant food crop after teff, for preparing injera (leavened local flat bread). Porridge, "injera," "Kitta," "Nifro," infant food, syrup, and native beverages like "Tella" and "Areke" are all made using

it [33]. "With 70-80 percent carbohydrate, 11- 13 percent protein, 2-5 percent fat, 1-3 percent fiber, and 1-2 percent ash, sorghum grain has a good nutritional value." Sorghum protein is gluten-free, making it a specialist diet for celiac disease (gluten sensitivity) sufferers, including diabetics, and a viable substitute for cereal grains like wheat, barley, and rye" [15].

The genetic diversity of cultivated crops and their wild counterparts provides a potential and long-term foundation for developing new and better crop kinds [46]. The breeder can use information on a crop's genetic diversity to help pick required parents for a breeding program and gene introgression from distantly related germplasm. With the availability of various genotypes, superior cultivars with tolerance to biotic and abiotic stressors can be created. Knowing more about sorghum's genetic diversity will help to improve the crop's genetic architecture [38]. Sorghum yield improvement is determined by the nature and degree of genetic variability, heritability, and genetic progress existing in the base population.

Because Ethiopia is the origin of the sorghum crop, there is a great deal of variation in the country. Previous research has demonstrated that within Ethiopian sorghum collections, there is a lot of phenotypic heterogeneity in terms of grain production and yield-related features [8, 6]. National and regional sorghum development initiatives have released a number of sorghum varieties for the moisture deficient arid lowland parts of Ethiopia, utilizing the existing diversity [33]. Furthermore, unless the genetic variability is properly understood, the presence of variety in the population is insufficient for enhancing relevant qualities. Exact assessments of phenotypic coefficients of variation, genotypic coefficients of variation, heritability, and genetic progress are essential for future breeding programs [7]. As a result, the goal of this review paper is to examine the genetic variability, heritability, and genetic progress of sorghum genotypes.

2. Review of the Literature

2.1. Origin and Domestication of Sorghum

The original domestication of sorghum and geographic place of origin is in Africa. Sorghum [*Sorghum bicolor* (L.) Moench] is thought to have originated and been domesticated in Ethiopia [47, 17]. The early domestication of farmed sorghum [*Sorghum bicolor* (L.) Moench] is thought to have occurred in north-eastern Africa. Some scholars believe there are many origin centers for the crop. Stemler et al. [44] found no indication that sorghum was domesticated or originated in Ethiopia, based on biogeographic, morphological, historical, or evolutionary evidence. Some scholars believe sorghum originated in India, while others believe it originated and was domesticated in southern and northern China. However, the time and location are not guaranteed to be correct [30].

According to Doggett [17], sorghum originated in the

north-eastern African countries of Ethiopia, Sudan, and East Africa. These areas have the greatest variety of wild and domesticated species. Wider variety emerged through early domestication and crop selection in response to environmental variables and human needs. Day length, height, temperature, rainfall, and soil characteristics were among the environmental parameters. Larger panicles, non-shattering habits, huge grain, tall plant height, and early crop duration are typical human requirements. As a result, the increased diversity is attributable in part to the region's different physical settings and in part to man's interaction with the environment [37]. As a result of selection, adaptability, intercrossing, and migration of plant material from place to place, new and stable sorghum biotypes have arisen.

2.2. Sorghum Botany and Taxonomy

Sorghum is a grass that belongs to the Poaceae family and the genus Sorghum [39]. It has a root system that is twice as large as maize and a C4 photosynthetic pathway. Sorghum bicolor is an erect plant with a sturdy stem that is sweet, dry, or juicy and grooved, with a length of 0.8m to 5m [12]. Under favorable conditions, the stem grows longer and more internodes, which are covered with a thick waxy layer that gives it its blue hue. The leaf has a noticeable mid-rib; typical leaf blades are 8-12 cm wide and 50-90 cm long while the leaf sheaths are 15-55 cm long and wrap the stem [36]. Panicle refers to the sorghum inflorescence that produces bisexual flowers with stamens and pistil encased in the glumes. Its shape and color vary depending on the race; kernel numbers range from 800-3000 per panicle; the color of sorghum seeds can be red, yellow, white, pink, or brownish; the shape of sorghum seeds can range from roundish to ovoid to flat; and it is made up of testa, embryo, and endosperm [26].

Subgenera of the genus Sorghum include Heterosorghum, Parasorghum, Eu-sorghum, Chaetosorghum, and Stiposorghum. While this classification is correct, it does not take into account evolutionary ties [16]. *Sorghum bicolor* (L.) Moench is a cultivated species with subspecies drummondii and arundinaceum, while wild species include Sorghum xalum Parodi, Sorghum halepense (L.) Pers., and Sorghum propinquum [14]. The Eu-sorghum section is African or Asian in origin. *S. macrospermum* and *S. laxiflorum*, which are both annuals and polyploids, make up the sections Chaetosorghum and Heterosorghum. The Stiposorghum Section has ten species, while the Para-sorghum Section has seven species from Africa, Asia, Australia, and Central America.

Sorghum halepense, *Sorghum propinquum*, and *Sorghum bicolor* make up the crop. Johnson grass, commonly known as *Sorghum halepense*, is a natural cross between *Sorghum arundinaceum* and *Sorghum propinquum*. The majority of tropical sorghums have short day lengths, and their response to this is a crucial adaptation [36]. Grain sorghum is a member of the Poaceae family, the tribe Andropogoneae, the sub-tribe Sorghinae, and the genus Sorghum. In 1794,

Moench identified the genus *Sorghum* and designated the sorghums as *S. bicolor*. All farmed sorghum belongs to the *Sorghum bicolor* subspecies.

"The five principal races of sorghum are durra, kafir, guinea, bicolor, and caudatum. Grain size, yield potential, panicle form, and other characteristics vary. Durra sorghums originated in Ethiopia and the Horn of Africa, then expanded to Nigeria and the West African savanna region. Domesticated Kafir species in eastern and southern Africa. Guinea sorghums are largely produced in West and Central Africa, with bicolor varieties playing a minor role in African output and cultivation in East Africa. Caudatum cultivars were thought to have originated in Kenya or Ethiopia" [2].

2.3. Study of Genetic Parameters in Sorghum

2.3.1. Genetic Variability

The occurrence of variances in performance among individuals due to differences in their genetic composition and/or the environment in which they are raised is called genetic variation [48]. Senbetay, [21] similarly define genetic variability as the change in genetic makeup of organisms within a population. For breeding program understanding the genetic variation of traits in any plant population is a vital precondition. In breeding programs, the goal is always to develop economically important features while keeping a sufficient degree of genetic variability [23]. Once the presence of genetic variability ensured for traits of interest, crop improvement would be under taken through selection or combining of desirable genes.

The extent of phenotypic and genotypic variability existing in species is the most important determinant issues toward initiating breeding program for developing better varieties in a crop. Genetic variability is of immense importance to breeders because it could be transmitted to the progeny and the proper management of diversity can indorse stability in the performance of the plant. Information on the nature and magnitude of genetic variability is critical for developing a sound crop breeding program. It is of particular importance to plant breeders because correct management of this diversity can result in long-term improvements in plant performance. Genotypic value and environmental deviance make up phenotypic variation [48].

Rayaprolu *et al.* [38] did an experiment on a total of 242 germplasm accessions of sorghum to assess the quantity of variability, trait associations, genetic diversity and observed large variability for agronomic traits and powerful associations between the traits studied. This result's similar to the study of Chavan [11] which analyzed 24 genotypes of sorghum lines and reported important differences among genotypes for all characters indicating the presence of variability among the lines being estimated and ample scope of enhancement selectively.

Genetic variability within a population is essential for biodiversity because without it, a population's ability to adjust to environmental changes is hampered, making it more vulnerable to extinction. Variability is a crucial think about evolution because it affects a person's response to

environmental stress and thus can cause differential survival of organisms within a population thanks to survival of the fit variants. Crop genetic variability not only helps varieties to adopt to diverse environments, but also to supply the range and to urge better yield and quality of product to serve the requirements of individuals [42]. According to Sivasubramanian and Menon, [43] PCV and GCV levels were classified as low (0-10 %), moderate (10-20 %), and high (>20 %).

Chaudhary *et al.* [10] investigated 34 sorghum genotypes for 12 quantitative characters in order to assess genetic diversity, heritability, and genetic progress among genotypes, and found substantial differences for all of the characters studied. Their findings revealed that the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for variety of leaves per plant, leaf stem ratio, and green fodder yield were the best, indicating that these traits may be exploited to boost crop productivity.

Amare *et al.* [5] assessed sixteen sorghum varieties to determine the genetic diversity, associations among the variables, and the direct and indirect effect of the traits on grain production of kinds across the two locations, using analysis of variance. Senbetay, [41] also conducted an experiment at Jimma on 84 newly introduced sorghum accessions, and the analysis of variance revealed that there was significant diversity among genotypes for the variables evaluated. Plant height, head weight, grain yield, rust, and days to 50% flowering all showed a high degree of heritability.

Endalamaw and Semahegn [18] conducted an experiment to determine genotypic and phenotypic variations, as well as yield performance of early maturing sorghum genotypes, and found that the combined analysis of variance across locations revealed a very highly significant (P0.0001) difference in grain yield between locations, as well as significant (P0.05) differences among genotypes and highly significant (P0.0001) differences among interactions for most of the traits studied. These findings were similar to those of Adane *et al.* [3] who evaluated 14 sorghum genotypes at the Bako, Jimma, and Mechara research centers to study genetic variability and interrelationships of traits with grain yield. They found that the combined analysis of variance (ANOVA) across years and locations revealed highly significant differences among genotypes for all traits, signifying the occurrence of adequate variability between genotypes.

In sorghum, Abraha *et al.* [1] reported phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) above 20% for productive tillers, plant height, and grain yield, while Khandelwal *et al.* [29] reported moderate to high GCV and PCV for all agronomic traits studied except number of days to maturity, which was low. The existence of slightly higher PCV than GCV for the agronomic traits of plant height and grain yield and little for days to flowering, maturity and productive tillers studied of sorghum suggesting small environmental influence on the phenotypic expression of the traits [1]. Using the equations provided by Johnson *et al.* [28] and genetic parameters were

evaluated using the relevant mean square values.

Environmental variance (σ^2_e): $\sigma^2_e = MS_e$

Genotypic variance (σ^2_g): $\sigma^2_g = MS_g - MS_e/r$

Phenotypic variance (σ^2_p): $\sigma^2_p = \sigma^2_g + \sigma^2_e$

Genotypic Coefficient of Variation (GCV) = $\sqrt{\sigma_g}/\bar{x} * 100$

Phenotypic Coefficient of Variation (PCV) = $\sqrt{\sigma_p}/\bar{x} * 100$

Where: PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, \bar{x} = population mean of the character being evaluated.

2.3.2. Heritability

Heritability is defined as the ratio of genetic to all other factors (including non-genetic ones) that influence variability. It is frequently characterized, in a general sense, as the ratio of genotypic variability to total variation. It refers to the proportion of phenotypically expressed variation that exists within a given environment and quantifies how frequently a trait is modified selectively. The ratio of additive genetic variance to phenotypic variance is known as narrow sense heritability.

Heritability refers to the ability of qualities to be passed down from one generation to the next. A breeder's understanding of heritability influences the strategies he or she can employ to develop characteristics in plants. Heritability is a determining element that reveals the consistency of a phenotypic observation that leads a breeding value [19]. A trait's high heritability indicates that it will progress in its development. Broad sense heritability, on the other hand, may not be dependable in the absence of genetic progress. As a result, for a more realistic assessment, broad sense heritability calculation must include estimates of genetic progress, as indicated [24]. A trait's heritability is crucial in determining how well it responds to selection. Estimates of heritability help breeders organize the resources needed to efficiently select for desirable traits and obtain the most genetic gain with the least amount of time and effort. Individual examination of the factors is less reliable and relevant than heritability assessments with genetic advancement [27].

Because broad sense heritability does not provide a clear picture of variation transmissibility from generation to generation (because genetic variation contains fixable and non-fixable dominance as well as epistatic variation), its utility in plant development programs is constrained [19]. According to Robinson et al. [40], heritability values are classified as low (0-30%), moderate (30-60%), and high (>60%). (60 percent and above).

The following formula, proposed by Falconer and Mackay [19], was used to estimate broad sense heritability:

$$\text{Heritability in broad sense } H^2_b = \sigma^2_g / \sigma^2_p * 100$$

Where: - H^2_b = Heritability in broad sense, σ^2_p = phenotypic variance, σ^2_g = genotypic variance.

2.3.3. Genetic Advance

Another significant genetic parameter is the genetic advance (GA), which assesses the expected response to selection. The most successful condition for selection is high genetic advancement, which includes high heritability [31]. On the other hand, GA refers to the evolution of features in genotypic value for the new population vs the prior population. It's an estimate of the predicted gain from selection for a certain character. Genetic progress is determined by genetic variability, heritability, and the degree of selection. It calculates the difference between the genotypic values of generations produced from the selected population and the population mean. With an increase in variance, genetic progress would accelerate. As a result, the utility of heritability estimates is boosted when they are combined with the choice difference, the amount by which the mean of the chosen lines exceeds the mean of the entire group [28].

Various studies have demonstrated that prime heritability alone isn't enough for selection in advanced generations unless there has been a significant degree of genetic progress. When a trait is regulated by non-additive gene action, it has a high heritability but a low genetic advance, but when a character is controlled by additive gene action, it has a high heritability and a high genetic advance. With an increase in variance, genetic progress would accelerate. As a result, the utility of heritability estimates is boosted when they are combined with the choice difference, the amount by which the mean of the chosen lines exceeds the mean of the entire group [28]. Genetic advancements, according to Burton and DeVane [9], provide an estimate of the projected gain for a certain character through selection. According to Johnson et al. [28] the GA can be classified as low (0-10%), moderate (10-20%), or high (>20%).

High heritability combined with high genetic progress suggests additive gene control, and early selection may also be helpful for this feature [18]. "Only high broad sense heritability does not always give high forecast of genetic gain to ensure effective selection for improvement," Johnson et al. [28] argued, "rather higher heredity including higher estimation of GCV and GAM." This recommendation implies that, in order for these traits to be successful for sorghum grain yield improvement, they must be accompanied by estimates of higher GCV and GAM [22].

Taking into consideration the importance of heritability, different studies have done to estimate the heritability in sorghum genotypes. According to Chaudhary et al. [10], high heritability was observed for plant height, leaf length, leaf area, number of leaves per plant, leaf stem ratio, and green fodder yield among 34 sorghum genotypes, indicating a predominance of additive gene effects and the possibility of effective selection for the development of those characters. Gebregergs and Mekbib [22] conducted an experiment on 258 advanced sorghum lines and found that plant height, panicle yield, grain yield, head weight, and biomass had prime heritability combined with significant genetic advance (as percent of mean). High heritability estimates combined

with a high GA indicate that these traits' variance is due to additive gene effects, implying that there is greater room for improvement through selection.

Swamy et al. [45] investigated the genetic variability and nature of character association in 122 Rabi sorghum genotypes and found a high magnitude of heritability, as well as a high magnitude of genetic advance over the mean, for the characters days to 50% flowering, plant height, panicle length, panicle girth, panicle weight, stover weight, grain yield, and 1000-grain weight. For grain filling rate, plant height, grain yield, panicle weight, panicle exertion, and stay green, Endalamaw and Semahegn [18] reported strong heritability (H percent) and high genetic advance as percentage of mean (GAM percent).

Plant height, thousand seed weight, panicle length, and rachis number had the highest heritability, according to Mofokeng et al. [34]. The genetic progress ranged from 0.39 to 17655.04, resulting in a genetic gain (of the mean percent) of 3.27 to 372.52. Greater broad sense heritability, as well as higher genetic progress in the traits investigated, indicated that these were under the control of additive genetic effects, implying that selection within the germplasm should result in rapid trait development.

Estimation Genetic advance and genetic advance as percent of means were estimated as described by Johnson *et al.* [28] as:

$$\text{Genetic Advance (GA)} = K \sigma_p H^2 b$$

Where: - K= the standardized selection differential at 5 % (2.063), σ_p = phenotypic standard deviation and, $H^2 b$ =heritability in broad sense. Genetic advance as percent of mean (GAM) = $GA/x \times 100$ Where: GA= genetic advance, and x = mean of population.

3. Conclusion

In a plant breeding program, the magnitude of genetic diversity and the degree of association between yield and other agronomic characteristics are significant because they provide the basis for selection. The presence of high diversity among genotypes suggested that direct and indirect selection may be used to improve the characteristics, as variety within populations is a necessary requirement for crop development.

Characters with high heritability and genetic advancement are significant traits to pay attention to in order to improve the grain yield of the concerned variety. Heritability estimates combined with genetic progress are usually more useful in projecting selection gain than heritability estimates alone. 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, for many of the variables, high genetic variability and heritability estimates indicate a greater amount of additive gene impact. As a result, in order to boost grain output effectively, more emphasis should be paid to features with strong positive phenotypic and

genotypic correlation coefficients and a significant direct and indirect effect on grain yield.

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