



# Exploring Genetic Variability, Path Analysis and Divergence in Sorghum (*Sorghum bicolor* (L.) Moench)

**Kancham Reddy Anush Kumar Reddy<sup>a++\*</sup>**  
**and Chetariya Chana Pitha<sup>a#</sup>**

<sup>a</sup> Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara-144411, Punjab, India.

## **Authors' contributions**

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

## **Article Information**

DOI: <https://doi.org/10.9734/jeai/2024/v46i82679>

## **Open Peer Review History:**

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/119918>

**Review Article**

**Received: 09/05/2024**

**Accepted: 12/07/2024**

**Published: 15/07/2024**

## **ABSTRACT**

The grain crop known as sorghum [*Sorghum bicolor* (L.) Moench], which belongs in the Poaceae family, is said to have evolved from Ethiopia or Sudan. This is a crucial crop for food security, especially within the tropical and semi-arid regions in African nations. By terms of long-term domestication and genetic diversity, this crop was native from Ethiopia. showed differences between the crop's cultivated and wild ancestors that gathered within the nation. Due to its enormous diversity of sorghum, which shows innate biological resistant to disease, dryness, and insects in addition to having large lysine content and excellent quality of grain, Ethiopia has become the world's top contributor of germplasm for the sorghum breeding

<sup>++</sup> M.Sc. Student;

<sup>#</sup> Assistant Professor;

<sup>\*</sup>Corresponding author: E-mail: [iamanush06@gmail.com](mailto:iamanush06@gmail.com);

**Cite as:** Reddy, Kancham Reddy Anush Kumar, and Chetariya Chana Pitha. 2024. "Exploring Genetic Variability, Path Analysis and Divergence in Sorghum (*Sorghum Bicolor* (L.) Moench)". *Journal of Experimental Agriculture International* 46 (8):49-62. <https://doi.org/10.9734/jeai/2024/v46i82679>.

programmes. Ethiopian landraces referred to as "zera zera" sorghum and the generations that sprang of those were used in ICRISAT along with other nations' contemporary sorghum breeding programmes for hybrids creation. Sorghum is at present Ethiopia's second most significant cereal crop after the tef with regard to of its combined area covered and productivity, which means it's used to make injera. Sorghum genotype from Ethiopia is varied and has responded to a variety of rainfall conditions and elevations. Plant breeding starts with the characterisation and recognition of sorghum seeds that offer desired features for improved genetics. When contrast with field trial evaluation, DNA-based molecular markers and PCR-based methods were most effective in characterising and identifying sorghum genotypes which offer desired features since they are unaffected by duration or climate. The most economical method of increasing sorghum production for many applications is genetic enhancement. Gaining more knowledge about sorghum's genetic diversity could be extremely beneficial for improving the crop in terms of quality of food along with other crucial agronomic characteristics. Sorghums from the Ethiopian Centre of Crop Diversity have a vast amount of genetic variety. To effectively gather and conserve this genetic variety before it is overrun and lost, some serious work is required.

*Keywords: Sorghum; genetic diversity; genetic variability; genotype; germplasm.*

## 1. INTRODUCTION

The fifth-most significant cereals crop farmed worldwide was sorghum [*Sorghum bicolor* (L.) Moench], a tropical cereal C4 type of grass that is cultivated and diploid ( $2n = 20$ ). It is a tropical monocotyledon plant that is a member of the family Poaceae [1]. Because of its remarkable resistance to heat and stress from water as well as its outstanding capacity of photosynthesis, sorghum is known to be the "camel of crops" and is valued as a vital species in dry and semi-arid areas [2].

For a lot domesticated and wild agricultural species, involving sorghum, Ethiopia is recognised as one among the Vavilovian centres of origin, or diversity. Sorghum, which constitutes one in the cereal crops in which Ethiopia is recognised to be a centre of origin and/or diversity. In high-latitude regions, the landrace sorghum germplasm has frequently been the most readily available, well-suited materials [3]. Since both varieties largely grow in resonance with their wild and invasive cousins in the majority of Ethiopia's sorghum-growing regions, namely on the south-eastern and south-western regions of the nation, there's a larger likelihood that genetic material interchange will take place among the wild and cultivated sorghum [4]. A higher level of genetic variety in a species is frequently interpreted as an indicator of that species' capacity for environmental adaptation. Ethiopia is the world's sixth-largest producer of sorghum, accounting for 16.4% of the total overall yearly output of cereal grains and is placed third in terms of productivity and total area covered. Ethiopia's current national average sorghum production is 2.5 tons/ha [5].

According to Admas and Tesfaye [2], sorghum is indigenous to Ethiopia and possesses a great variety of genes, as demonstrated by several landrace collections established inside the nation. In semi-arid Africa, this is perfectly suited to a variety of ecological circumstances. Ethiopia's middle and lowlands are where it is mostly grown. It is more resilient to dry and hot weather than the majority of Ethiopia's planted crops. Sorghum is cultivated to grow its grain, which can be utilised to make food and regional drinks. These days, the stalk itself is utilised as well as biofuel and an alternative source of feed for animals. The typical yield is trending lower, though [6-9].

The crop germplasm with the highest diversity offers more room for development in terms of climate tolerance and obtaining superior agricultural characteristics unique to the crop species. The promise of food supply in any given nation greatly depends on the identification and selection of the finest cultivars from this enormous biodiversity that fulfil particular local dietary and industrial needs [10].

Varietal development requires genetic variety within current populations. The current and next plant breeding initiatives have a higher focus on germplasm gathering and characterisation due to a shortage in genetic variety that causes the loss of genetic diversity [11]. Understanding a crop's diversity in genes often aids in the breeding program's parental selection process and facilitates the introduction of genes from somewhat related germplasm. The greater the varied genetic makeup or according to Elangovan and Babu [12], accession numbers

could be mated to create better hybrids that are resistant to both biotic and abiotic stressors. It will become easier to modify sorghum's genetic structure going forward if its rich genetic variety is recognised.

The crop species genetic variety was a gift from environment that results from geographic isolation or genetic obstacles to cross-pollination. Traditional techniques for evaluating genetic diversity include morphological characteristics [13]. In most cases, morphological tests don't need complex tools or advance preparation. In overall, scoring them is easy and affordable. These readily apparent quantitative morphological characteristics are a helpful tool for first assessment since they provide a quick and practical method for determining the degree of variety. Several investigations have been conducted over time to estimate genetic diversity in farmed sorghum through the use of physical features. The most popular method for estimating connections among genotypes is through the application of morphological features. A possible and ongoing basis for the creation of enhanced crop varieties is the genetic diversity of both farmed species and varieties and the wild equivalents [14].

Gaining more knowledge about sorghum's genetic diversity might be very beneficial for improving the crop in terms of quality of food along with other crucial agronomic characteristics. Consequently, it is necessary to assess the genetic diversity of the accessible additions and determine which ones are most suitable based on what they did [46]. The Ethiopian Biodiversity Institute gene bank contains approximately 11,353 sorghum accessions that have been gathered and preserved. Of these, 8,913 accessions have been characterised by breeders of plants and other researchers, and 2,440 more sorghum accessions have not yet been examined to identify their possibly beneficial features [15]. As a result, the purpose of writing this review was to evaluate the genetic variability, path analysis and divergence of sorghum.

## 2. REVIEW OF LITERATURE

Sorghum originated and is most diverse in Ethiopia (Vavilov, 1951). Around 5000 and 7000 years ago, in what is now known as Ethiopia, sorghum evolved in Africa [16]. Subsequently, it was dispersed throughout the Middle East and

Africa's trading and transportation routes. Approximately 3000 years ago, east to India. After that, it travelled to China via the Silk Road [17]. By the slave trade, it was initially brought to the Americas in the 1700s–1800s from West African countries. In the latter part of the nineteenth century, it was once again brought to Africa to use for commercial cultivation, and it eventually expanded to South America as well as Australia [43].

Nowadays, arid lowland regions of Africa, Asia (including China and India), the Americas, and Australia are home to a large population of sorghum growers [17]. This crop holds significant financial, social, and cultural value, and is cultivated throughout many biological areas in Ethiopia, spanning from 400 to 3000 metres above sea level. In 2007 [44]. Because of its resistance to drought, sorghum is a special kind of cereal crop that grows well in lowland settings [18].

### 2.1 significance of Sorghum

Ethiopia and the neighbouring Eastern regions of Africa are the birthplace and domestication centres of Sorghum [*Sorghum bicolor* (L.) Moench], a C4 tropical crop that coexists alongside its farmed and wild relatives [19]. Sorghum is a crop that can tolerate droughts better than other cereals and can survive poor fertility in the soil [45]. Over 500 million individuals in the poor globe, mostly in the thirty countries of sub-Saharan Africa and Asia, depend on it as their primary crop [20]. However, in the industrialised world, it is additionally grown as a feed crop. Furthermore, because of its high biomass output and excellent water usage efficiency, sorghum is a favoured feedstock for the manufacturing of biofuels [21].

The geographical distribution of sorghum has exhibited a heterogeneous pattern worldwide. Although the cultivation area of sorghum has consistently decreased annually, primarily in the United States, China, and India, it has been steadily increasing in most African countries, particularly those in Sub-Saharan Africa, as well as the nation of Australia [22]. Over the last forty years, sorghum production has improved by 1 to 4% annually in various nations, such as China, Australia, and the United States [22]. Sorghum's greater efficiency has kept up overall output, making it the world's fifth-most significant cereal crop in terms of total production of grains [20].

According to FAOSTAT [23], 2.7 percent of the top five main cereal grains produced worldwide throughout the last ten years have come from sorghum production.

Better cultivars and enhanced methods of management have led to an improvement in sorghum production. Many industrialised plus some developing nations have seen production gains thanks to the deployment of hybrid crop varieties with better management [20]. According to Rakshit et al. [22], improved cultivars, particularly hybrids, have been planted in over 85 percent of sorghum cultivation areas in China and India, while hybrids currently make up the entirety of the sorghum cultivation region in the USA and Australia. Many nations have seen increases in sorghum production as a result of the adoption of hybrids; for example, output has improved by 2. percent year in India and by 3.9% annually in China [22].

## 2.2 Sorghum's Significance in India

Sorghum, often referred to by the name "jowar" in India, is an important staple crops that is appreciated because of its resistance to drought and adaptability as a food source, animal feed, and commercial material of manufacture, especially in semi-arid settings [48]. Madras, Karnataka, Telangana, Andhra Pradesh, and Tamil Nadu are the states where sorghum is grown most commonly in India, which is one of the world's biggest producers of the grain [49]. Geographical variations, farming methods, and environmental factors all contribute to production variances. Environmental factors, fertility of the soil, farming methods, consumer demand, and government regulations are some of the factors that impact productivity as well as output [50]. Development of high- yielding and drought-resistant cultivars, encouragement of improved agronomic techniques, and government programmes assisting farmers are the main focuses of current attempts to increase sorghum

production [51]. Notwithstanding its significance, sorghum farming confronts obstacles like a shortage of facilities rivalry with different crops, and changes in the climate [52]. Possibilities for increasing sorghum production and efficiency in the future include better extension services, more research and development, and supportive policies [53]. Sorghum is still important for the economy of rural India and food security, but in order to realise its full potential, these issues must be resolved [57].

Here is the national production data for sorghum in India over recent years:

According to the most recent statistics, the yearly region under the cultivation of sorghum remains fairly constant, ranging from a 4.5 to 4.8 millions of hectares of land Production have been found to fluctuate among 3.8 and 4.4 million tonnes, and yields have been found to vary between 844 and 917 kg per hectare, depending on factors such as soil fertility, methods of cultivation, and climate [59]. A significant portion of the country's production is guaranteed by the main contributing states, with Maharashtra being the top generator, next to Telangana, Karnataka, Tamil Nadu, and Andhra Pradesh [54]. Through enhanced agronomic techniques and commercial connections, government programmes like the National Food Security Mission (NFSM) and the Sub-Mission on Millets (SMM) seek to advance sorghum planting. Considering its significance, India's sorghum industry has difficulties due to poor infrastructure, competing with different crops, and rising temperatures. Notwithstanding, prospects exist for augmenting productivity via the advancement of high-yielding and drought-tolerant cultivars, enhanced services for extension, and advantageous governmental backing [55]. The rural economy of India and food security depend heavily on sorghum, therefore addressing these issues and realising its full potential would need concentrated efforts [56].

**Table 1. Sorghum Production in India (2019-2023)**

Year	Area (Million Hectares)	Production (Million Tonnes)	Yield (Kg/Hectare)
2019-2020	4.7	4.2	893
2020-2021	4.8	4.4	917
2021-2022	4.6	4.0	870
2022-2023*	4.5	3.8	844

*\*Data for 2022-2023 are provisional*

## 2.3 Genetic Variability in Sorghum

### 2.3.1 Races and taxonomic classifications

Up until recently, the genus *Sorghum* was thought to consist of between 20 and 30 species, which are divided in five categories: Stipo sorghum, Para sorghum, Eu-sorghum, Hetero sorghum, and Chaeto sorghum. Three species are recognised under the Eu-sorghum section: *Sorghum halepense* (L.) Pers., that is found in India; *Sorghum propinquum* (Kunth) Hitchc, which is situated in Southeast Asia; and *Sorghum bicolor* (L.) Moench, which is native to Africa [24]. All categorised under the *Sorghum* genus. Two rhizomatous species, *S. halepense* as well as *S. propinquum*, as well as most yearly grown, wild, and weedy sorghums were represented by De Wet's identified *S. bicolor* (L.) Moench. Every variety of *S. bicolor*, or the primitive species spread by seeds, including the exception of rhizomatous species, which reproduce by producing seeds as well and rhizomes. Three subspecies of *Sorghum bicolor* were identified: *Sorghum bicolor* sub sp. *bicolor*, *Sorghum bicolor* sub sp. *drummondii*, and *Sorghum bicolor* sub sp. *verticilliflorum*. The cultivated sorghums, which include Sudan grass, broom corn, sweet sorghum, and grain sorghum, are categorised as *S. bicolor* sub sp. *bicolor*.

According to their inflorescence type, grains, and legumes, all among the world's farmed sorghum species can be divided into five races: Durra, Bicolor, Caudatum, Kaffir, and Guinea; moreover, there are intermediary race that include all possible paired combinations among the fundamental race [24,25]. The blooms, grains, and the glumes of each race allowed for morphological differentiation. The race *bicolor*'s grains is longer and is clasped by glumes, which can either cover the grain entirely or uncovered. In addition to being farmed on a small scale nearly everywhere in Africa, this race grows mainly to the west in the Rift Valley [58]. Guinea is mostly in West Africa, with Tanzania and Malawi serving as its secondary centres. When fully grown, the grain flattens dorso-ventrally and twists at 90 degrees among the glumes which are either the same length or longer than that of the grain itself. Asymmetry glumes that are at least 1/2 the length of a grains characterise the *caudatum* grains. In Uganda, Sudan, and east Nigeria, this type of race is the most common. East and Southern Africa are home to the majority of the Kafir people. With the glumes of varying lengths holding the grain, it exhibits

symmetric grain. For Durra covers the driest regions of the continent west of the Sahara, with a predominance in Ethiopia [60]. House (1985) reported that the plant has a spherical grain and broad glumes.

With the exception of Kaffir, Ethiopia is home to 4 of the 5 sorghum races as well as wild forms [61]. On the basis of Ethiopian data, Stemler et al. [26] detailed and examined the variety of sorghum cultivated in Ethiopia including the races Bicolor, Durra, Durra-Bicolor, Caudatum, and Guinea. outdoors observations and sorghum collections. Ethiopia's geography and varying climate seem to have an impact on each race's geographical distribution patterns. Consequently, sorghum race Whereas *caudatum* race is mostly cultivated in warm, arid valley and lowlands savanna in the south and west of the country, durra is the main agricultural product of the eastern highlands area and the middle elevation terraces in the north. Ethiopia. In the southwestern highlands, where temperatures are lower and precipitation is more than that of the eastern and northern regions, the middle race Durra-Bicolor is more prevalent. On the other hand, the Rift Valley area is home to the majority of the Bicolor and Guinea races, which together account for a relatively minor portion of Ethiopian sorghum variety.

These several panicle forms' disparate distribution is further demonstrated by qualitative morphological characterization studies conducted on Ethiopian landraces, foreign-introduced lines of sorghum, and nearby Eritrean accessions. This demonstrated the adaptive importance of panicle form and compactness. Represented the patterns of dispersal of several sorghum races in Ethiopia. The distribution patterns of the various panicle forms in their research seemed to correspond with Ethiopian and Eritrean rainfall, humidity, and temperature trends. In Ethiopia, particularly in the more arid and hot districts of Hararge, Tigray, and Wello, compact as well as semi-compact panicle kinds were more common. In generally chilly and moist areas of Ethiopia like Wollega, Illubabor, Shewa, and Sidamo, there were a lot of loose panicle kinds with falling branches [10].

### 2.3.2 Variability in indian sorghum genotypes genetically

Breeding programmes aiming at enhancing disease resistance, drought tolerance, yield, and other agronomic qualities depend heavily on the

genetic heterogeneity present in Indian sorghum genotypes. India has a vast array of landrace sorghum varieties that are bred historically, have distinct genetic characteristics, and are acclimated to the local environment. Several enhanced sorghum cultivars with increased production potential, superior quality, and better resilience to biotic and abiotic stressors have been produced by research agencies like the Indian Institute of Millets Research (IIMR) [62]. Drought tolerance is one of the most important genetic features; several genotypes of Indian sorghum thrive in arid places because of quantifiable trait loci (QTLs) that have been found. Furthermore, genetic heterogeneity exists for resistance to pathogens such as grain mould, anthracnose, and downy mildew, which prompts breeding initiatives combining several resistance alleles. There are attempts to improve grain protein density, iron, as well as zinc levels by biofortification, although nutritional quality varies as well. To detect and select desired characteristics, speed up breeding and increase efficiency, molecular approaches like marker-assisted selection (MAS) along with genomic selection—which includes next-generation sequencing as well as genome-wide association studies (GWAS)—are widely utilised [63].

Organisations that handle genetic preservation of resources include the International Crops Research Institute in the Semi-Arid Tropics (ICRISAT), which collaborates internationally with other organisations, and the National Bureau of Plant Genetic Resources (NBPGR), that maintains a vast variety of sorghum germplasm. In order to generate high-yielding, climate-resilient cultivars that are also adaptable to marginal areas, breeding efforts must be ongoing due to challenges such as soil salinity, developing disease and insect pressures, and climate change. Indian sorghum genotypes possess a great deal of genetic variability, which presents a great opportunity for breeding programmes that target improving traits like yield, stress tolerance, and nutritional quality. To fully utilise this variability and address future agricultural challenges, sophisticated molecular methods and conservation approaches are crucial [64].

Nine sorghum genotypes were assessed for five quantitative characteristics, including plant height (cm), leaves/plant, leaf length (cm), leaf width (cm), and green fodder output (t/ha), in Andaman and Nicobar Island during the rabi conditions (dry season). For each of the five characteristics

under investigation, the analysis of variance revealed very significant variations between the kinds. The variety CSV24SS was determined to be the most promising based on the average fodder yield performance; it was followed by CHS 22SS and CHS 13 [63]. Regarding the estimated genotypic and phenotypic coefficient of variation, the values for leaf width, leaves per plant, leaf area, leaf stem ratio, and green fodder yield were high, while the values for leaves length, internode length, stem girth, total soluble solids, and protein content were moderate (10–25%), and the values for days to 50% flowering were low (<10%) [27].

40 genotypes of fodder sorghum were used in the experiment. The current study demonstrated that forage sorghum exhibits significant levels of GCV, PCV, heritability, as well as genetic progress as a percentage of mean for a variety of features, including leaf: stem ratio, the number of leaves per plants, green fodder production per plant, stem width, as well as dry matter yield per plant [65]. demonstrated a higher proportion of genotypic and phenotypic variance than environmental variance, indicating that the population's characteristics were genetically regulated and might be used in breeding initiatives. For the majority of the characteristics, strong genetic advancement as a percentage of mean and high heritability were observed [28]. strong genetic advancement as a percentage of mean and high heritability were noted for the majority of the characteristics [56].

Eighty sorghum land races were gathered, and their genetic variability was evaluated. High PCV along with GCV were measured for the overall height of the plant, but moderate leaf length and width were found. Significant PCV with moderate GCV were detected by the trait stem diameter [66]. The purpose of the study was to assess 33 genotypes of sweet sorghum, including two tick variants, for various yield and sugar-related characteristics. Every character in the research had a significant difference, according to the analysis of variance. For the majority of the features in the genetic variability research, there was a higher phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV), suggesting the presence of an environmental influence. High PCV and GCV were observed for stem girth, nodes each plant, juice content, biomass weight, the cane weight, total soluble solids, and total sugars. Moderate PCV along with GCV were reported for plant and cane heights [46].

### 2.3.3 Genetic Variability of Sorghum in a Worldwide

Recognition and description of genotypes in sorghum in order to enhance genetics, plant breeding efforts must first bestow significant features. Details of the main global sorghum collections including breeding lines, which together comprise more than 150,000 accessions, were provided by Kimber et al. [29]. morphological Sorghum's diversity has been exploited to create global fundamental collections, which stand in for global collections and are useful for the breeding of plants [30]. However, the usefulness of morphological features for characterising and analysing the variety of germplasm collections is limited by the time needed for phenotyping as well as the influence of environmental factors on trait expression. The development of many DNA-based molecular markers system has made it possible to efficiently organise and characterise an enormous amount of genotypes with no taking seasonality into account. The first DNA marker system discovered that could distinguish between homozygote and heterozygote loci was hybridization-based RFLPs (Restricted Fragment Length Polymorphism) markers [31]. For research on genetic diversity in a variety of crops, including sorghum, RFLP markers are being employed. However, because to its technological complexity, the RFLP markers system is not recommended for low-cost, screening with high throughput. Developed in 1983, [67], polymerase chain reaction, or PCR, technology offers a novel way to boost sample throughput along with sample cost for markers screening.

PCR-based marker systems include amplified fragment length polymorphism (AFLP), simple sequence repeats (SSRs), random amplified polymorphism (RAPDs), and ISSRs (Inter Simple Sequence Repeats) [68]. These systems have been extensively employed in numerous studies on a variety of crops, including sorghum [3]. Being dominant markers, RAPD and AFLP are unable to distinguish between homozygous and heterozygous loci. Furthermore, it has been demonstrated that these marker types are time-consuming and have poor reproducibility among laboratory [69], both of which have reduced their usefulness.

Yet, the uses of SSR markers are limited to certain crops since they need sequence data and the creation of polymorphic markers may be

costly and time-consuming [68]. The uses of PCR-based and hybridised markers for sorghum are numerous. According to a current genetic variability investigation utilising SSR markers on a worldwide standard set of sorghum genotypes, landraces coming in Africa had the highest variability, with Eastern African genotypes having the most polymorphic alleles, which next to western African genotypes . Using several DNA-based markers, researchers have also examined genetic diversity and the genetic foundation of racial groups in sorghum [32]. The agreement among racial groups based on physical features has been shown in earlier research. Moreover, with the sole exception to the bicolor race, the clustering of sorghum genotypes was based on genetic distance determined by molecular markers, which similarly represented the geographic distribution of sorghum [32]. Comparing the bicolor racially type to the other four races, it was discovered that they were most basic and diversified, whilst the kafir race showed the least genetic variety [47]. It has also been documented that breeding lines utilising SSR markers may be derived from several groups of sorghum entry and inbred lines [3].

Next-generation sequencing (NGS) methods have recently become available, opening up new possibilities for whole genome or focused area sequencing and resequencing. In order to find polymorphic markers when genotyping utilising a high-through sequencing techniques at a cheap cost per data point, genotyping by sequencing, or GBS, has been established [63]. Current repeated sequencing of several sorghum genotypes showed unexpected genetic variability that may be helpful for efforts aimed at genetic improvement as well as the structure of genotypes according to racial grouping. Furthermore, genome-wide markers produced by GBS have been used to sorghum for the purpose of diversity analysis and comprehending the genetic foundation of complex characteristics and adaptability [52].

## 2.4 Correlation and Path Analysis of Sorghum

### 2.4.1 Correlation and path analysis importance

Important statistical methods in agricultural research, especially in crop genetics along with breeding, are correlation and route analysis. Understanding the magnitude and trajectory of the link among multiple factors is crucial for

determining how yield relates to different agronomic features like drought tolerance, plant height, and grain size. Correlation analysis can help with this. This knowledge helps pick features that are highly connected with yield, which helps breeders indirectly increase yield in situations when selective breeding is difficult because of environmental uncertainty [41].

Correlation analysis also streamlines breeding programmes by reducing the number of characteristics to concentrate on, which saves time and money. By breaking down the coefficients of correlation into the direct and indirect impacts of predictor factors upon a response variable, path analysis expands on correlation analysis and offers a thorough knowledge of the ways in which different qualities affect yield. By separating characteristics with true causal associations with yield from those that are associated because of their linkage with other qualities, it aids in identifying the most important features and prioritises them in selection programmes. Path analysis also makes it possible to model intricate interactions between a variety of variables, providing insights into the physiological and genetic processes that underlie yield production. These methods are used in the context of sorghum breeding to increase yield, comprehend the effects of drought tolerance traits both directly and indirectly, improve nutritional traits such as grain protein content, iron, alongside zinc levels, and find correlations among disease resistance as well yield, which helps select disease-resistant varieties without sacrificing yield [54].

In general, correlation with path analysis assist discover important qualities for selection, increase the effectiveness of breeding programmes, and offer a greater knowledge of the links between different traits and yield. Through the application of these strategies, researchers may enhance the nutritional quality, stress tolerance, and yields of crops such as sorghum, eventually promoting agricultural sustainability along with food security [65].

#### **2.4.2 Correlation and path analysis in indian sorghum genotypes genetically**

Aruna et al., 2015 found that in a research of forage sorghum improvement, there was a significantly substantial correlation between fresh fodder output and dry fodder yield. Therefore, in the following studies on association and combining ability, only fresh fodder yield was

used. The number of leaves per plant, plant height, days to 50% blooming, and feed yield were all correlated. Utilising rabi sorghum advanced breeding lines, the experiment examined the relationship between yield and its constituent characteristics as well as the direct and indirect impacts of features on yield. According to association studies, plant height at both the phenotypic and genotypic levels significantly positively correlated with seed yield per plot [33]. A correlation analysis showed that there was an inherent relationship between the examined traits, with genotypic correlation being higher than phenotypic correlation. At the both the genotypic as well as phenotypic levels, the amount of green forage produced by each plant was extremely important and exhibited a positive association with stem width, leaf in length. leaf width, as well as dry matter output per plant. These traits might be thought of as crucial sorghum yield components [34].

The amount of dry and green feed produced by each plant was positively and significantly correlated with the measured plant height, stem girth, and leaf length. Plant height, the quantity of leaves on each plant, and leaf length all showed a positive and significant correlation with leaf breadth. Plant height, number of leaves per plant, stem girth, and dry fodder production per plant all had a strong direct impact on the amount of green fodder produced by each plant, according to the path coefficient analysis, which also showed a positive and significant relationship [35]. While HCN content showed a negative significant correlation with green forage yield per plant, other plant characteristics such as plant height, 50% flowering, leaf number, leaf width, leaf length, and crude protein yield per plant all showed positive and significant relationships with this yield. According to path analysis, the number of leaves per plant, tiller count, leaf length, leaf stem ratio, and thickness were the factors that significantly influenced the yield of green forage, followed by the crude protein output per plant, days to 50% blooming, and left length [36].

40 sorghum genotypes with respect to grain yield, forage, and other attributes. The genotypic levels correlations are significantly bigger than the phenotypic level correlations. The study found a strong and positive relationship between several plant characteristics, such as height of the plant, stem width, the number of leaves per plant, days till blooming, and length and width of leaves, and the amount of dry feed produced by each plant. Overall genotypic path coefficient



evaluation revealed that the total number of leaves per plant, leaf breadth, leaf length, and days till blooming all had significant and positive direct effects on the amount of dry feed produced by each plant [37]. In 47 germplasm lines, the correlation of the characteristics along with their effects both direct and indirect were examined. The results of the association research showed a positive and substantial link between the number of grains in the primary panicle, plant height, panicle breadth, and seedling vigour and the grain production per plant in the days till 50% blooming [38]. Dual variety sorghum genotypes were investigated using correlation along with path coefficient investigations. Thus, the goal of this research was to find correlations and path coefficients among green fodder production, stover production, yield of grains, and quality attributes [39].

## 2.5 Genetic Diversity in Sorghum

### 2.5.1 Importance of genetic diversity in India

Sorghum's genetic diversity in India is important, indicating its lengthy history of agriculture and adaptability to varied agro-ecological zones, as well as is critical for breeding programmes aiming at increasing yield, resiliency, and nutritional value. India has a vast collection for sorghum landraces as well as traditional cultivars that have developed over ages, exhibiting a wide variety of characteristics like as tolerance to drought, resistance to disease, and nutritional quality. Furthermore, the existence of wild cousins of sorghum in India adds to the genetic diversity by providing unique features that might boost the resilience and adaptation of cultivated forms. Research institutions, which include the Indian Institute of Millets Research (IIMR), developed multiple enhanced sorghum varieties that are grown for higher yield, higher quality, and greater resilience to biotic and abiotic challenges, therefore increasing the genetic pool [40].

Drought tolerance, which includes multiple quantitative trait loci (QTLs), resistance to key sorghum diseases such as downy mildewing, anthracnose, and grain mould, as well as substantial variations in nutritional characteristics such as grain amount of protein, iron, and zinc levels, constitute all helpful reproduction targets. advanced molecular and genomic tools, such as marker-assisted selection (MAS), selection for genomes with sequencing of the next generation, as well as genome-wide association studies

(GWAS), are frequently utilised to find and choose desirable traits, thus speeding up the breeding process and increasing efficiency. Conservation initiatives by institutions that include the National Bureau of Plant Genetic Resources (NBPGR) as well as international collaborations with organisations like as the International Crop Research Institute for the Semi-Arid Tropics, or ICRISAT, ensure the genetic diversity's preservation and use [41]. However, concerns like as climate change, developing diseases and pest pressures, and abiotic factors such as soil salinity necessitate ongoing breeding efforts to generate climate-resilient and high-yielding cultivars while retaining flexibility in marginal conditions. As a result, India's sorghum genetic variety is a precious asset that, via targeted breeding and conservation initiatives, may assist address future agricultural problems, assuring food security as well as agricultural sustainability.

To classify sorghum genotypes, morphological divergence was assessed using Mahalanobis generalised distance (D<sub>2</sub>) analysis. Variations were noted regarding the number of days till 50% blooming. Days till maturity, plant height, quantity of seeds per panicle, 100-seed weight, and grain production per plant. Grain yield was highest (124.95g) in genotype BD-755 and lowest (4.50g) in genotype BD-736 [5]. I made an effort using D<sub>2</sub> statistics and the tocher approach, with 25 selected small central accessions and 16 potential variety divided into six and five clusters, respectively. Selected micro core selection showed a wide range of seed hardness, from hard (33.33%) to extremely hard (66.67%), which is the principal source of enhancement variation, whereas successfully release varieties had seeds that seemed spherical and glossy (62.5%) [34].

Sixteen Sorghum genotypes were tested in a Randomised Block Design using three replications. The study's goal was to quantify genetic divergence across yield and yield-related components using the Mahalanobis D<sub>2</sub> approach. The observations were made for 13 different features, and the findings showed that seven distinct clusters were formed. Cluster I was the largest and had the most genotypes (9), next to cluster IV (2), while clusters II, III, V, VI, and VII only had one genotype apiece (Pal et al., 2022). A randomised block design was used with three replications to assess the genetic divergence within 30 sorghum genotypes over 14 characters in order to identify genetic diversity

via D2 analysis as well as principal component analysis. D2 values varied among D2 = 80.0061 while D2 = 3471544.8770, indicating high genetic divergence among the genotypes. Based on the D2 values, 30 genotypes were classified into seven clusters [42].

Plant survival and agricultural improvement are both dependent on genetic diversity. Plant genetic diversity allows breeders to create cultivars with desired qualities, such as high production potential and huge size. Breeder-preferred features include pest and disease resistance, photosensitivity, and so forth [43]. Crop species' natural genetic variety has been used to fulfil subsistence food needs from the beginning of agriculture. Later, the focus moved to producing excess food for expanding populations. Currently, the focus is on improving the productivity and quality of important food crops to ensure a balanced diet for humans [15].

### 3. CONCLUSION AND RECOMMENDATION

The challenge for new plant breeders is to generate enough genetic variety to continuously improve genetic yield potential. Plant breeders may use exotic non-adapted material, exotic adapted material, or current elite material as a source of novel alleles to safeguard and promote genetic gain via selection. Plant breeding poses a difficulty in feeding a growing population on limited land. Current plant breeding has seen considerable progress in this direction. However, this has led to genetic fragility due to the limited genetic diversity of cultivated variants in many crops. Hence, there is a need for a paradigm change in plant breeding to focus on different genetic resources. Genetic diversity has been identified as a key factor in ensuring security of nutrition and food. Gaining a better grasp of genetic diversity can guide conservation efforts. Crop plant genetic diversity enables sustained creation of new types. To effectively utilise heterogeneous genetic resources in breeding programmes, it is necessary to characterise them using various statistical approaches. Morphological data combined with molecular data are used to precisely characterise germplasm resources. High throughput molecular marker technologies enable faster and more efficient characterization of germplasm.

The Indian Centre of Crop Diversity has a vast amount of genetic diversity in sorghum.

Collecting and preserving genetic diversity is crucial to prevent it from being wiped out by uniform variations and contemporary technologies.

### DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that generative AI technologies such as Large Language Models, etc have been used during writing or editing of manuscripts. This explanation will include the name, version, model, and source of the generative AI technology and as well as all input prompts provided to the generative AI technology

Details of the AI usage are given below:

1. Google scholar
2. Krishi kosh

### ACKNOWLEDGEMENT

The reviewer recognised researchers that researched improving sorghum genetic variability and divergence.

### COMPETING INTERESTS

Authors have declared that no competing interests exist.

### REFERENCES

1. Abdie A, Bekele E, Asfaw Z, Teshome A. Pattern of morphological variation of sorghum (*Sorghum bicolor* (L) Moench) landraces in qualitative characters in North Showa and south Wello. *Hereditas*. 2002; 137:161–172
2. Admas S, Tesfaye K. 'Genotype-by-environment interaction and yield stability analysis in sorghum (*Sorghum bicolor* (L.) Moench) genotypes in North Shewa, Ethiopia', *Acta Universitatis Sapientiae, Agriculture and Environment*. 2018;9(1): 82–94. DOI: 10.1515/ausae-2017-0008.
3. Agrama HA, Tunistra MR. Phylogenetic diversity and relationships among sorghum accessions using SSRs and RAPDs. *Afr J Biotech*. 2003;2:334-340.
4. Ahalawat NK et al. 'Genetic divergence in forage sorghum (*Sorghum bicolor* L. Moench). 2018;10(1):439–444.
5. Ahmad Akram, Gulfray M, Khan KS, Iqbal MS, Mahmood T. Character association and inheritance studies of different

- sorghum genotypes for fodder yield and quality under irrigated and rainfed conditions. *African J. Biotechnol.* 2015; 11(38):9189-9195.
6. Prajwal V, Krishnamoorthi A, Riya Thakur, Ruchitha T, Manish Kapoor, Anushi, Abhishek Singh, Karthik Chittibomma. From Code to Crop: How bioinformatics is transforming crop genomics in modern agriculture and bettering environment. *Journal of Advances in Biology & Biotechnology.* 2024;27(4):27-49. Available:<https://doi.org/10.9734/jabb/2024/v27i4737>.
  7. Pavan Kumar N, Biradar BD, Hanamaratti NG, Nethra P, Prashant Kariyannanavar, Revannasiddayya, Prajwal RS. Differential expression of restorer gene on different nuclear background with maldandi cytoplasm in Sorghum (*Sorghum Bicolor* (L.) Moench). *Journal of Scientific Research and Reports.* 2024; 30(6):365-72. Available:<https://doi.org/10.9734/jsrr/2024/v30i62051>.
  8. Michael TP, VanBuren R. Progress, challenges and the future of crop genomes. *Current Opinion in Plant Biology.* 2015, Apr 1;24:71-81.
  9. Schreiber M, Stein N, Mascher M. Genomic approaches for studying crop evolution. *Genome Biology.* 2018, Sep 21;19(1):140.
  10. Amsalu Ayana, Endashaw Bekele. Geographical patterns of morphological variation in sorghum (*Sorghum bicolor* (L.) Moench) germplasm from Ethiopia and Eritrea: qualitative characters. *Hereditas.* 1998;129:195–205.
  11. Anagholi A, Kashiri A, Mokhtar poor H. The study of comparison between inside forage sorghum cultivars and speed feed hybrids. *Agricultural Science and Natural Resources Journal.* 2000;7(4):73-83.
  12. Elangovan M, Babu PK. Genetic variability and diversity of sorghum land race collected from Uttar Pradesh India. *Indian Journal of Plant Genetic Re- Sources.* 2015;28(2):213-22.
  13. Anonymous. Reports on cereal crops, Ministry of Agriculture, Government of India. 2018;245.
  14. Ayana A, Bryngelsson T, Bekele E. Genetic variation of ethiopian and eritrean sorghum (*Sorghum bicolor* (L.) Moench) germplasm assessed by random amplified polymorphic DNA (RAPD). *Genet Resour Crop Ev.* 2000;47:471-482.
  15. Bhandari HR et al. Assessment of genetic diversity in crop plants - An overview. 2017;7(3):279– 286. DOI: 10.15406/apar.2017.07.00255.
  16. ICRISAT (International Crop Research Institute for Semi-Arid Tropics). Sorghum report; 2005. Available:<http://www.icrisat.org/text/research/grep/homepage/sorghum/sorghumhomepage.htm> Online. Patancheru, India
  17. Dicko MH, Gruppen H, Traore AS, Alphons GJ, Voragen AGJ, Berkel WJH van. Sorghum grain as human food in Africa: Relevance of content of starch and amylase activities. *African Journal of Biotechnology.* 2006;5:384-395
  18. Kebede H, Subudhi PK, Rosenow DT, et al. Quantitative trait loci influencing drought tolerance in grain sorghum (*Sorghum bicolor* L. Moench). *Theor Appl Genet.* 2001;103:266-276.
  19. Dillon SL, Shapter FM, Henry RJ, Cordeiro G, Izquierdo L, Lee LS. Domestication to crop improvement: Genetic resources for sorghum and saccharum (Andropogoneae). *Ann Bot.* 2007;100:975-989
  20. Kumar AA, Reddy BVS, Sharma HC, Hash CT, Rao PS, Ramaiah B, Reddy PS. Recent advances in sorghum genetic enhancement research at ICRISAT. *Am J Plant Sci.* 2011;2:589-600.
  21. Packer DJ, Rooney WL. High-parent heterosis for biomass yield in photoperiod-sensitive sorghum hybrids. *Field Crop Res.* 2014;167:153-158.
  22. Rakshit S, Hariprasanna K, Gomashe S, Ganapathy KN, Das IK, Ramana OV, Dhandapani A, Patil JV. Changes in area, yield gains, and yield stability of sorghum in major sorghum producing countries, 1970 to 2009. *Crop Sci.* 2014;54:1571–1584
  23. Food and Agriculture organization of the United Nation statistical division (FAOSTAT); 2015. Available:<http://faostat3.fao.org/home/E>
  24. De Wet, JMJ. Systematics and evolution of Sorghum Sect. sorghum (Graminae). *American Journal of Botany.* 1978;65:477.
  25. Harlan JR, de Wet JMJ. Simplified classification of cultivated sorghum. *Crop Science.* 1972;12:172-176

26. Stemler ABL, Harlan JR, de Wet JMJ. The sorghums of Ethiopia. *Economic Botany*. 1977;31:446–460.
27. Malik A, Singh SK, Chand P, Singh B, Singh DK. Genetic variability, heritability and genetic advance studies on forage sorghum. *Progressive Agriculture*. 2015; 15(1):92-94.
28. Jimmy MLF Nzuve, Florence O, Manyasa E, Muthomi J. Genetic variability, heritability, genetic advance and trait correlation in selected sorghum (*sorghum bicolor* L. Moench) varieties. *International Journal of Agronomy and Agricultural Research*. 2017;11(5):47-56.
29. Kimber CT, Dahlberg JA, Kresovich S. The gene pool of *Sorghum bicolor* and its improvement. In: Paterson A.H. (ed.) *genomics of the saccharinae, plant genetics and genomics: Crops and model*. Springer Science, Media New York. 2013;23-41.
30. Dahlberg JA, Burke JJ, Rosenow DT. Development of a sorghum core collection: Refinement and evaluation of a subset from Sudan. *Econ Bot*. 2004;58: 556-567
31. Botstein D, White RL, Skolnick MH, Davies RW. Construction of a genetic map in man using restriction fragment length polymorphism. *Am J Hum Genet*. 1980; 32:314–331
32. Brown PJ, Myles S, Kresovich S. Genetic support for phenotype-based racial classification in sorghum. *Crop Sci*. 2011; 51:224-230.
33. Girish G, Kiran SB, Lokesh R, Vikas V, Kulkarni V, Rachappa LN Yogesh, Talwar AM. Character association and path analysis in advanced breeding lines of rabi sorghum J. *Appl. Nat. Sci*. 2016;8(1):35-39.
34. Karadi, ST Kajjidoni. Genetic variability and diversity for productivity traits and grain quality including nutritional quality traits in selected mini core and promising released varieties of sorghum. *Journal of Pharmacognosy and Phytochemistry*. 2019;8(4):2091-2097.
35. Bisne R, Sarawgi AK, Verulkar SB. Study of heritability, genetic advance and variability for yield contributing characters in rice. *Bangladesh Journal of Agricultural Research*. 2009;34(2):175-179.
36. Borell AK, Hammer GL, Douglas ACI. Does maintaining green leaf area in sorghum improve yield under drought. *Leaf growth and senescence*. *Crop Science*. 2000;40:11026-103.
37. Central Statistical Agency of Ethiopia (CSA) *Agricultural Sample Survey 2013/2014*. *Stat Bull*. 2014;532.
38. Chakraborty I, Kumari PUMMY, Pahuja SK, Tokas J, Kumar VINOD. Elucidation of combining ability and fodder potential of sorghum hybrids. *Forage Res*. 2020;46: 132-140.
39. Chala CB. 'Sorghum [*Sorghum bicolor* ( L .)] Breeding in Ethiopia: Review. 2018; 8(21):81–94.
40. Chittapur Rekha, Biradar BD. Association studies between quantitative and qualitative traits in rabi sorghum. *Indian J. Agric. Res*. 2015;49(5):145-148.
41. Dhutmal RR, Kalpande HV, More AW. Correlation and path analysis in drought tolerant *rabi sorghum*. *Ann. Pl. soil Res*. 2015;17(4):404-408.
42. Diwakar A, Ranwah BR, Diwakar P, Namrata, Bisen P. Genetic divergence study in forage sorghum [*sorghum bicolor* (L.) Moench]. *Indian Journal of Ecology*. 2018;44:834-837.
43. Doggett H. *Sorghum*. 2nd ed. Longman Group UK Limited; 1988.
44. Engida CE. Genetic diversity in yield traits and kernel composition of selected Ethiopian sorghum landraces (Doctoral dissertation, University of the Free State); 2023.
45. Frew Mekbib. Genetic erosion of sorghum (*Sorghum bicolor* (L.) Moench) in the centre of diversity, Ethiopia. *Genetic Resources and Crop Evolution*. 2008; 55:351–364.
46. Geleta N, Labuschagne MT, Viljoen C. Genetic diversity analysis in sorghum germplasm as estimated by AFLP, SSR and Morpho agronomical markers. *Biodivers Conserv*. 2006;15:3251-3265
47. Hossain MH. Effect of spacing and variety on biomass production and quality of *Moringa oleifera* L; 2021.
48. Hundekar R, Kamatar MM, Brunda SM. Correlation and path analysis in rainy season Sorghum. *Electronic J. Plant Breed*. 2016;7(3):666-669.
49. IBC (Institute of Biodiversity Conservation). *Third Country Report on the State of Plant Genetic Resources for Food and Agriculture*, Adis Abeba, Ethiopia. 2012;10-15.

50. Khandelwal V, Shukla M, Jodha BS, Nathawal VS, Dashora SK. Genetic parameters and character association in sorghum [*sorghum bicolor* (L.) Moench]. Indian J. Sci. Tech. 2015;9(22): 231-235.
51. Mekbib F. Farmer and formal breeding of sorghum (*Sorghum bicolor* (L.) Moench) and the implications for integrated plant breeding. Euphytica. 2006;152:163–176.
52. Nagara GO. 'Genetic diversity analysis of sorghum [*Sorghum bicolor* (L.) Moench] Races in Ethiopia Using SSR Markers'; 2017.
53. Paterson AH, Bowers JE, Chapman BA. Ancient polyploidization predating divergence of the cereals, and its consequences for comparative genomics. Proc Natl Acad Sci USA. 2004;101:9903–9908.
54. Prasada Rao KE, Mengesha MH. A pointed collection of zera-zera sorghum in the Gambella area of Ethiopia. Genetic Resources Units Progress Rep. No. 33. ICRISAT, Patancheru, India; 1981.
55. Prasanna BM. Phenotypic and molecular diversity of maize landraces: Characterization and utilization. The Indian Journal of Genetics and Plant Breeding. 2010;70:315- 327
56. Rafiul amin Iascar. Assessment on induced genetic variability and divergence in the mutagenized lentil populations of microsperma and macrosperma cultivars developed using physical and chemical mutagenesis. Plos One; 2017, sep18.
57. Rangare NR, Reddy GE, Kumar SR. Study of heritability, genetic advance and variability for yield contributing characters in pigeonpea (*Cajanus cajan* L. Millspaugh). Trends in Biosciences. 2013; 6(5):660-662.
58. Reddy BVS, Rao P, Deb UK, Stenhouse JW, Ramaiah B, Ortiz R. Global sorghum genetic enhancement processes at ICRISAT. Pp.65–102 in Sorghum genetic enhancement: research process, dissemination and impacts (Bantilan MCS, Deb UK, Gowda CLL, Reddy BVS, Obilana AB and Evenson RE, eds.). Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropic; 2004.
59. Rooney WL. Sorghum Improvement-Integrating Traditional and New Technology to Produce Improved Genotypes. In: Advance in agronomy. 2004; 83:37-109
60. Rosenow DT, Dahlberg JA, Paterson GC, Clark LE, Sotomayor RA, Miller FR, Hamburger AJ, Madera-Torres P, Quiles-Belen A, Woodfin CA. Release of 50 converted sorghum lines and 253 partially converted sorghum bulks. International Sorghum and Millets Newsletter. 1995; 36:19–31
61. Shehzad T, Okuno K. Review article diversity assessment of sorghum germplasm and its utilization in genetic analysis of quantitative traits-A review. 2014;8(6):937–944.
62. Singh R, Axtell JD/ High lysine mutant gene (hl) that improves protein quality and biological value of grain sorghum. Crop Sci. 1973;13:535-539.
63. Singh PK, Gautam RK, Roy SD, Singh AK, Ahmed SZ. Performance of sorghum varieties for fodder yield during Rabi season in Andaman & Nicobar Islands. Journal of the Andaman Science Association. 2014;19:174-176.
64. Sujatha K, Pushpavalli SN. Genetic divergence for yield attributing traits in rabi sorghum Germplasm. Electron. J. Plant Breed. 2015;6(2):521-527.
65. Suthakar V, Mullainathan L. Studies on effect of physical and chemical mutagens in sorghum (*sorghum bicolor* L. Moench) in M2 generation International Letters of Natural Sciences. 2015;37: (2):41-49.
66. Tesfamichael A, Githiri SM, Kasili R, Woldeamlak A, Nyende AB. Genetic variation among sorghum (*sorghum bicolor* L. Moench) landraces from Eritrea under post-flowering drought stress condition. American J. Pl. Sci. 2015;6: 1410-1424.
67. Tesfaye K. Genetic diversity study of sorghum (*Sorghum bicolor* (L.) Moench) genotypes, Ethiopia. 2017;9:44–54. DOI: 10.1515/ausae-2017-0004.
68. Venkateswaran K., Muraya M, Dwivedi SL, Upadhyaya. Wild sorghum- their potential use in crop improvement. IN; Wang YH,

- Upadhyaya HD, Kole C (eds) Genetics, Genomics and Breeding of sorghum. CRC Press, New York. 2015;56-81.
69. Zinzala S, Davda BK, Modha KG, Pathak VD. Studies on variability, correlation and path analysis in sorghum (*sorghum bicolor* L. Moench). Int. J. Agri. Sci. 2018; 10(19):7285-7287.

**Disclaimer/Publisher's Note:** The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of the publisher and/or the editor(s). This publisher and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.

---

© Copyright (2024): Author(s). The licensee is the journal publisher. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

*Peer-review history:*

*The peer review history for this paper can be accessed here:*

<https://www.sdiarticle5.com/review-history/119918>