

**Genetic Variability Character Association and Clustering
Pattern of Sweet Sorghum (*Sorghum bicolor* (L.) Moench)
Genotype for Agronomic Traits in Rainfed Conditions**

THESIS



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By

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CERTIFICATE – I

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This is to certify that the thesis entitled “**Genetic Variability character association and clustering pattern of sweet sorghum (*Sorghum bicolor* (L.) Moench) genotype for agronomic traits in rainfed conditions**” Submitted in partial fulfilment of the requirement for the Degree of **MASTER OF SCIENCE** in **AGRICULTURE (Genetics and Plant Breeding)** of **Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior** is a record of the bona-fied research work carried out by Mr. **ANIL BAGHEL** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee and Director of Instruction.

No part of the thesis has been submitted for any other degree or diploma or has been published. All the assistance and help received during the course of this investigation has been acknowledged by the scholar.

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This is to certify that thesis the entitled “**Genetic Variability Character Association and Clustering Pattern of Sweet Sorghum (*Sorghum bicolor* (L.) Moench) Genotype for Agronomic Traits in Rainfed Conditions**” submitted by Mr. **ANIL BAGHEL** to the Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE** in **AGRICULTURE** in the department of **Genetics and Plant Breeding, College of Agriculture, Indore** has been accepted after evaluation by the External Examiner and approved by the Student’s Advisory Committee after an oral examination of the same.

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Place: Indore

Date:

(ANIL BAGHEL)

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List of Abbreviations

Abbreviations/ Acronyms	Meaning
Ag.	Agriculture
a.i.	Active ingredient
&	And
<i>et al.</i>	And co-workers
@	At the rate of
BCR	Benefit: cost ratio
AGR	Absolute growth rate
CD	Critical difference
CGR	Crop growth rate
Cm	Centi meter
DAS	Days after sowing
DAT	Days after transplanting
dSm ⁻¹	Deci Siemens per meter
°C	Degree centigrade
Dist.	District
E	East
ELS	Early leaf spot
EC	Electrical conductivity
F	Fertility
Fig.	Figure
FYM	Farm yard manure
G	Gram
Ha	Hectare
H. I.	Harvest index
HW	Hand weeding
i.e.	In reference to; that is
INM	Integrated nutrient management
Kg	Kilogram
kg ha ⁻¹	Kilogram per hectare
LAI	Leaf area index
LAR	Leaf area ratio
Max.	Maximum

Mg m ⁻³	Mega gram per cubic meter
M	Meter
mg kg ⁻¹	Milli gram per kilogram
Min	Minimum
Mm	Milli meter
M.P.	Madhya Pradesh
Mt	Metric tones
Viz	Namely
N	Nitrogen
No.	Number
OC	Organic carbon
O.M.	Organic manure
%	Per cent
K	Potassium
LLS	Late leaf spot
P	Phosphorus
PE	Pre-emergence
PoE	Post emergence
PSB	Phosphorus Solubilizing Bacteria
RDF	Recommended dose of fertilizer
RGR	Relative growth rate
RH	Relative humidity
Rs.	Rupees
R.V.S.K.V.V.	Rajmata Vijayaraje Scindia Krishi Vishwa Vidhyalaya
pH	Soil reaction
Q	Quintal
S	Sulphur
S.E.m (d)	Standard error mean of difference
Sy.	Symbol
Temp.	Temperature
t ha ⁻¹	Tonnes per hectare
U.P.	Uttar Pradesh
VC	Vermicompost
Wt.	Weight

CHAPTER – I

INTRODUCTION

Botanical name of Sorghum is- *Sorghum bicolor* (L.) Moench having $2n = 20$ chromosomes. It is an annual and short-term perennial plant belonging to the family Poaceae. It is originated from Africa, particularly in Ethiopia and surrounding countries (Kimber, 2000). Today, sorghum is widely cultivated around the world and 5th most important cereal crop in the world after rice, wheat, maize & barley in terms of production and acreage (FAOSTAT, 2020). In India, Sorghum is grown in an area of 4.82 million hectares with a production 4.77 million tonnes and productivity 989 kg/ha (Directorate of economics & statistics, DAC&FW (2019-20 final deta).

In Madhya Pradesh, it is cultivated in an area of 0.11 million hectares with an annual production of 0.17 million tonnes and productivity of 1529 kg per ha. (Directorate of Economics & Statistics, DAC&FW, (2019-20 Final Deta).

Sorghum can be grown in both Kharif and Rabi season. It can be cultivated on wide range of soils but grows well in sandy loam soils having well drainage. Soil pH range of 6 to 7.5 is ideal for its cultivation and better growth. Sorghum is a tropical crop. It grows well at a temperature between 25°C and 32°C. Sorghum crop requires rainfall about 40 cm annually. Sorghum is extreme drought tolerant crop and recommended for dry regions so it is called “**Camel Crop**”. Sorghum is an extreme C4 crop, it utilizes water more efficiently, making it highly adaptable to semi-arid or arid environments where drought is a serious problem (Buchanan et al., 2005; Ghannoum, 2009; Xin et al., 2009).

Some sorghum genotype also possess the ability to accumulate sugar in the culm while producing starch in grains and high amounts of biomass. Sorghum with 10 to 15 percent sugar in the stalk juice near the period of grain maturity, is called Sweet sorghum. Sweet sorghum is tall, juicy stem with high biomass and most important contains high stem sugar concentration. Sweet sorghum is closely related to sugarcane, and the commercial value of these crops are based on their stem which contains high amount of sugar and brix.

Sweet sorghum similar to grain sorghum with sugar rich stalk and water use efficiency and it is an alternative feed stalk for ethanol production as an industrial crop. Sweet sorghum is mainly used for high biomass production and other used to sugar, jaggery, syrup or fodder, sucrose and lignocellulose. The ethanol production

by sweet sorghum will help boost biofuel production at a lesser cost than the sugarcane molasses.

Recently, high-sucrose sweet sorghum genotype has been developed with potential as a sugar crop. Because of the rapid increase in crude oil prices, sweet sorghum has been investigated as a potential source of fermentable sugars for ethanol fuel production as an **industrial crop**. This is because of the crops high sugar content and biomass production, wide geographic and climatic adaptation, and relatively low water and fertilizer requirements and costly effective. Considering all these aspects it is clear that sweet sorghum possesses considerable potential as an alternative crop to sugarcane. The full potential of crop can be exploited by following optimum agronomic practices. Further, this crop has bright prospects and efforts are required in developing and identifying the varieties possessing higher sugar content and higher ethanol production potential for different agro-ecological conditions. It is also necessary to understand the variations in sugar and biomass yield among different sweet sorghum genotypes.

The use of advanced, novel techniques of plant improvement will be certainly helpful in twenty first century; however, the conventional plant breeding tools such as characters associations, path analysis and genetic variability will also play an important role in crop improvement. Further, sweet sorghum has a potential to overtake sugarcane, if efforts are directed in developing genotype with high sugar content and grain yield. There is a possibility of regaining the lost area under kharif sorghum. However, limited information is available on the genetics and inheritance pattern of sugar content in sweet sorghum.

The largest diversity of the crop germplasm provides greater opportunities for improvement regarding its environmental adaptability and acquiring better agronomic traits from the crop varieties. The genetic variability of cultivated varieties and their wild relatives together form a potential and continued source for the development of improved crop species (Ahalawat et al., 2018). Identifying and selecting the best genotype meeting specific local food and industrial requirements from this great biodiversity of high importance for the food security assurance of any given country (Dahlberg et al., 2002). Genetic variability is important in the existing population for varietal improvement. Loss of genetic diversity leading to genetic erosion has lead to greater emphasison germplasm collection and characterization for present and future plant breeding programmes (Prasanna, 2010). The study of variability

provides an opportunity for selecting the desirable species. Estimation of diversity parameters in a population is an important for breeding programme aimed at improving yield, quality and other important traits under consideration. To bring about any correction in any crop, the knowledge of association of yield with other characters will be of immense help. Correlation coefficient is an important statistical constant, which show the degree of association among the various traits. The genotypic correlation was generally higher than phenotypic correlation indicating the inherent association between various characters. The Yield is a complex character, which depends upon many independent contributing traits. Knowledge on type of association between yield and its components themselves greatly help in evaluating the contribution of different components towards yield information on the nature of association between yield and its components help in simultaneous selection for many traits related with yield improvements. It is essential to find out the relative contribution of each of the component trait in relation to yield so as give weightage during selection.

Knowledge of genetic diversity of a crop usually helps the breeder in choosing desirable parents for the breeding program and gene introgression from distantly related germplasm. The more diverse genotypes or accessions can be crossed to produce superior genotype with resistance to abiotic and biotic stresses (Elangovan and Babu, 2015). To understanding the wealth of genetic diversity in sorghum will facilitate the further improvement of this crop for its genetic architecture. Genetic diversity in the crop species is the gift of nature and arises due to geographical separation or due to genetic barriers to cross ability. Morphological traits are conventional tools to analyze the genetic diversity (Prasanna, 2010). Morphological assays generally require neither sophisticated equipment nor preparatory procedures. The use of morphological traits is the most common approach utilized to estimate relationships between varieties. Among the several multivariate analyses, the Mahalanobis D^2 (1936) technique is a unique tool for identifying the degree of genetic diversity in a biological population. To better understanding of the genetic diversity in sorghum would greatly contribute to crop improvement with a view to food quality grain yield and other important agronomic characters.

Therefore, there is a need to evaluate the available accessions for genetic diversity and identify the best accessions according to their performance. An attempt in the present study has been made to study the nature and magnitude of genetic

divergence and identify promising parents for biofuel related traits like brix (%), Juice%, juice yield, green cane yield and other characters in sweet sorghum genotypes.

Objectives:

- 1) To estimate genetic variability among twenty five sweet sorghum genotypes.
- 2) To establish correlation between different agronomic and quantitative traits of sweet sorghum.
- 3) To assess the genetic divergence in genotypes of sweet sorghum using clustering Patterns.

To identify desirable sweet sorghum genotypes to be utilized in crop improvement programme to develop high brix and high biomass and improved variety.

CHAPTER-II

REVIEW OF LITERATURE

Considerable knowledge on the genetic diversity aspect of sweet stalk sorghum during *kharif* is essential to identify superior genotypes. Present review is an attempt to compile the recent findings on genetic diversity aspect of sweet stalk sorghum. Nevertheless, scanty literature is available on sweet stalk sorghum during *kharif* season. In order to illustrate these aspect, some of findings in rabi sorghum have also quoted. A brief review of available information on the above aspects in sorghum is presented in this section under the following headings.

2.1 Parameters of variability.

2.2 Correlation coefficient studies.

2.3 Genetic divergence.

2.4 Variability & genetic parameters:

2.1. Genetic variation:

Possibility of achieving improvement in any crop plants depends heavily on the magnitude of genetic variability. The phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and phenotypic components. The genotypic component being the heritable part of the total variability, it's magnitude on yield and it's component characters influences the selection strategies to be adopted by the breeders. The genetic variability in relation to environmental variability was first studied by Fisher (1918). Next to Fisher, several workers discovered many techniques for the estimation of components of variance (Wright, 1921; Lush, 1949; Robinson *et al.*, 1951 and Weber and Moorthy, 1952).

Chaudhary and Arora (2001) studied genetic variability and interrelationships of characters in 23 genotypes of sorghum in four environments. Estimates of GCV and PCV were higher for stover yield, biological yield and panicle weight.

Arunkumar *et al.* (2004) observed high phenotypic coefficient of variation and genotypic coefficient of variation for grain yield per plant (g/plant), plant height (cm), earhead length (cm), number of primaries/earhead and leaves per plant.

Deepalakshmi and Ganesamurthy (2007) observed high heritability accompanied with high GA as percent of mean for the characters - days to fifty per cent flowering, plant height, leaves per plant, leaf length, earhead weight, number of primaries per panicle, 100 grain weight, grain mould score and single plant yield.

Chavan *et al.* (2010) recorded high genotypic and phenotypic variances for plant height, number of grains per panicle, grain yield per panicle and number of primary branches per panicle. Also on the basis of mean, the GCV and PCV observed to be high for harvest index (36.10) pursued by grain yield per plant (34.23), panicle width (27.67). The highest value of GCV (35.49) and PCV (36.72) were observed for harvest index. The least values for GCV and PCV were recorded by days to maturity (27.10 and 5.97).

Godbharle *et al.* (2010) studied the genetic variability and nature of character association in 20 B lines and 16 R lines of *kharif* sorghum. The genotypic variance was lower than the phenotypic variance for all the characters. High genotypic and phenotypic variance, heritability and genetic advance were observed for the characters panicle length, fodder yield, primary branches per panicle, grains per primary branches, harvest index, grain yield and plant height.

Zou *et al.* (2011) studied differences and relationship between stalk yield related traits and sugar concentration of stalk juice in a large recombinant inbred (RI) population derived from a grain sorghum × sweet sorghum. A large proportion of the phenotypic variance for PH, HSL, PL and SC was attributed by genotypic variance. Highest ratio of genotype × environment ($G \times E$) interaction variance to phenotypic variance was observed for SD. Moderate proportion of phenotypic variances for HD, NN and PNL were explained by genotypic variances.

Tomar *et al.* (2012) observed that phenotypic co-efficient of variation (PCV) was greater than genotypic co-efficient of variation (GCV) for most of the characters studied indicating influence of the environmental effect on the characters. But the GCV was near to PCV for the characters like days to fifty per cent flowering, days to physiological maturity, plant height, juice yield and sucrose yield.

Bhusal *et al.* (2013) recorded significant variations among the genotypes for various morphological traits in 20 sorghum genotypes. High values for phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for neck of panicle visible above sheath pursued by panicle length of branches, panicle length without peduncle and dry fodder yield.

Iraddi Vemanna *et al.* (2013) observed Wide range of variability for plant height, total biomass, fresh stalk yield, grain yield, juice yield and juice extraction per cent.

Sami *et al.* (2013) estimated genetic variability in thirty genotypes of sweet sorghum. Significant mean squares were obtained for 10 traits in the individual analysis and also for the combined analysis across locations, suggesting that this sweet sorghum population was highly variable for some of the characters.

Rana *et al.* (2016) studied variability parameters in forty diverse genotypes of forage sorghum. A wide range of phenotypic variability was recorded for green fodder yield per plant and its component traits. The magnitude of genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded high for various characters like leaf stem ratio, number of leaves per plant, green fodder yield per plant, stem girth and dry matter yield per plant.

Mahanthasha *et al.* (2017) observed that genotypic coefficient of variation for all the characters studied was lesser than the phenotypic coefficient of variation indicating the effect of environment. High GCV and PCV values were observed for grain yield per plot pursued by grain yield per plant, no. of basal tillers per plant, productive tillers per plant, main ear width

and finger length.

Kalpande *et al.* (2018) evaluated sweet grain sorghum land races for grain yield and per cent threshable grains at dough (milky) stage. High GCV and PCV values were recorded for the traits % threshable grains, seed yield per plant, fodder yield, taste score, 100-seed weight, whereas, days to 50% flowering recorded low estimates of GCV and PCV. The PCV was relatively greater than GCV for all the traits; however, the magnitude of the difference was low.

More *et al.* (2018) reported significant variability for all the traits studied and suggesting presence of wide range of variation among the genotypes for all the characters. The genotypic coefficient of variation was lower than the phenotypic coefficient of variation for all the characters, indicating the importance in hybridization programme for generating variability.

Wadikar *et al.* (2018) studied genetic variability in forty five genotypes of sweet sorghum for fifteen characters. For all characters studied, phenotypic co-efficient of variation (PCV) was higher than the genotypic co-efficient of variation (GCV) indicating the influence of environment on the expression of these traits.

Karadi and Kajjidoni (2019) assessed nature and magnitude of genetic variability for productivity, grain and nutritional quality traits in selected mini core collection and promising varieties of sorghum. High estimates of PCV and GCV were recorded for most of the characters in selected mini core accessions except for seed bulk density and seed true density. Similarly, among promising varieties observed in grain yield per plant and fodder yield per plot.

Yücel *et al.* (2020) Forty-nine sweet sorghum genotypes. The experiment was carried out in a randomized complete block design with four replications in Turkey. Analysis of variance revealed that there are highly significant differences among the genotypes in all investigated traits indicating the presence of variability. The genotypes Smith and Batem-3 with high juice, sugar and ethanol yield can be used for breeding of biofuel

production in the Mediterranean region of Turkey. High heritability accompanied with high genetic advance was observed for the flowering day, fresh biomass weight, stem fresh weight, juice volume, estimated sugar yield, and estimated ethanol yield. Therefore, these characters could be used for the development of high yielding sorghum varieties through selection in a breeding program.

de Oliveira *et al.* (2021) evaluated Twenty-five sweet sorghum genotypes were evaluated in randomized blocks design with three repetitions and studied variables were: number of days to flowering; plant height; number of stems; weight of green mass; weight of dry mass; number of leaves; diameter of stems; volume of extracted juice and percentage of total soluble solids. In order to verify the existence of variability among the genotypes. Subsequently, genetic parameters were determined, as soon as genetic correlation estimator's method, performed by t-test, to determine phenotypic correlation and bootstrap method for determining environmental and genetics correlation coefficient. The results of genetic correlation and path analysis point weight of green mass as the main variable influencing the juice volume, allowing these characters in indirect selection for increasing juice volume.

2.2. Heritability and Expected Genetic Advance

Heritability in broad sense, refers to the functioning of the whole genotype as a unit is used in contrast with environment effects. The narrow sense heritability includes only the average effects of genes transmitted adaptively from parent to progeny .

The heritability estimates along with genetic advance are more useful than the heritability value alone in predicting the resultant effect for selecting the best individual (Johnson *et al.*, 1955). According to Ramanujan and Tirumalachar (1967) broad sense heritability is more reliable if accompanied by high genetic advance.

Chaudhary and Arora (2001) evaluated 23 genotypes of sorghum and found that high heritability was associated with high genetic advance for

stover yield and biological yield which reflected that additive gene effect were important in genetic control of these characters.

Arunkumar *et al.* (2004) evaluated 138 genotypes of rabi sorghum, high heritability coupled with genetic advance over mean was observed for, earhead length, earhead diameter and number of leaves per plant indicating that additive gene effects were operating for these traits and selection for superior genotype was possible.

Godbharle *et al.* (2010) studied the genetic variability and nature of character association in 20 B lines and 16 R lines of kharif sorghum. High heritability coupled with high genetic advance was observed for the characters panicle length, fodder yield, primary branches per panicle, grains per primary branches, harvest index, grain yield and plant height indicating that additive gene effects were operating for these traits.

Rani and Umakanth (2012) evaluated F₁ hybrids of sweet sorghum and reported that grain yield exhibited high heritability coupled with high genetic advance implying additive gene effects.

Tomar *et al.* (2012) observed high heritability combined with high genetic advance (as per cent of mean) for sucrose yield, juice yield, cane yield, juice extraction percent, sucrose per cent, juice volume, juice weight, millable cane weight, fresh cane weight, stay green trait, stem girth and plant height.

Bhusal *et al.* (2013) recorded high heritability coupled with high genetic advance for neck of panicle visible above sheath followed by 1000 grain weight, panicle length of branches and dry fodder yield.

Subi and Idris (2013) observed high estimates of heritability and high genetic advance for days to 50% flowering and days to maturity indicating that these characters were under the control of additive genetic effects. The genotypes ICMV155 and SADC (long) scored the most minimum days to maturity (68) days whereas, the genotypes ICMW221 and Ugandi scored the highest yield values of 2.20 t/ha and 2.05 t/ha, respectively.

Mahanthasha *et al.* (2017) observed high heritability coupled with high genetic advance as per cent of mean for plant height, number of basal tillers per plant, no. of productive tillers per plant, main ear length, main ear

width, finger length, grain yield per plant and grain yield per plot.

Kalpande *et al.* (2018) observed high heritability accompanied with high genetic advance in case of plant height, per cent threshable grains, seed yield per plant 100-seed weight, fodder yield and taste score. This indicated that these traits were highly heritable and selection of high performing genotypes is possible to the improvement of the characters.

Wadikar *et al.* (2018) reported that characters like green cane yield, total biomass, total soluble sugar, non-reducing sugar, reducing sugar and juice demonstrated high estimates of heritability and expected genetic advance indicating presence of additive gene effect.

Mofokeng *et al.* (2019) found low, medium and high estimates of broad sense heritability in different plant characters under study. Highest heritability estimates were found in plant height, thousand seed weight, panicle length and rachis number. Values of genetic advance ranged between 0.39 to 17655.04 and the genetic gain (of the mean percent) ranged from 3.27 to 372.52.

Gebregergs *et al.* (2020) demonstrated significant difference for yield and yield attributing traits among genotypes. Higher range of genotypic coefficient of variation (GCV) (3.13–37.44) and phenotypic coefficient of variation (PCV) (5.11–38.08) values were observed. Yield per panicle (YPP) (97%) and harvest index (HI) (31%) were the highest and lowest broad sense heritable (H₂) traits, respectively. Higher estimate of GAM observed for YPP (75.93%) followed by head weight (HW) (62.36%). Moreover, plant height (PH) (23.51, 83, and 44.22), YPP (37.44, 97, 75.93), HW (31.88, 89, 62.36), biomass (BM) (29.21, 74, 51.94), and grain yield (GY) (32.99, 78, 60.25) were traits with higher estimate of GCV, H₂ (%) and GAM, respectively. This study demonstrated wider genetic variability in the tested genotype.

Navya *et al.* (2021) estimated the genetic variability and diversity in 20 sorghum genotypes. A wide range of variation for 14 yield attributing traits. High to moderate phenotypic and genotypic coefficient of variation were recorded for yield, panicle weight, panicle length, 1000 seed weight, total chlorophyll, and total flavonoids. High heritability accompanied by relatively high genetic advance as percent of mean was observed for yield, panicle length, panicle weight, leaf length, plant height, 1000 seed weight, days to

50% flowering, total chlorophyll, total flavonoids, and total antioxidants. Panicle weight (72.11%) followed by 1000 seed weight (9.98%) and total chlorophyll (2.63%) demonstrated maximum contribution towards total divergence among the genotypes. Genotypes of cluster IV were the best performing in correspond to yield and its components while, cluster II was finest in respect of maturity and biochemical characters.

2.3. Correlation coefficient studies and path analysis:

Association between yield and yield components as determined by correlation coefficient is useful for selecting desirable plant types. The efficiency of selection depends on the direction and magnitude of association between yield and its components. Thus, correlation coefficient enables to identify characters or combination of characters which might be useful as indicator of high yield by way of evaluating the relative influence of various characters on grain yield and among themselves as well.

Almodares *et al.* (2007) studied the relationship between growth analysis and carbohydrate contents to recognize the best growth stages for sweet sorghum harvesting. Five sweet sorghum cultivars and four sweet sorghum lines were evaluated for leaf area index (LAI), net assimilation rate (NAR), relative growth rate (RGR) and stem crop growth rate (CGR) in relation to sucrose content, invert sugars and total sugar at booting, soft-dough, hard dough and post grain maturity. Except at post grain maturity stage, the correlations among LAI, NAR and RGR for sucrose content and total sugar were positive and for invert sugars were negative. The relationship between invert sugars including glucose, fructose, maltose and xylose at hard dough stage regarding LAI, NAR and GRG were negative. As plant grows LAI, NAR and RGR increases which consequently increases sucrose content and decrease invert sugar.

Godbharle *et al.* (2010) observed positive and significant correlation between grain yield and harvest index, total biomass, fodder yield and leaf area index was observed both at phenotypic and genotypic level, while the characters field grade score, threshed grade score and days to fifty per cent flowering exhibited negative correlation with grain yield.

Prakash *et al.* (2010) investigated parents and their 35 hybrids (L x T mating design) of sorghum to assess association of fodder yield components and their direct and indirect effects on green fodder yield per plant. Results of correlation analysis indicated that the green fodder yield per plant was found to be appreciably and positively correlated with plant height, number of tillers, leaf length, leaf breadth, stem diameter, hydrocyanic acid and crude fibre. Days to fifty per cent flowering, crude protein, and in vitro dry matter digestibility demonstrated a negative association with green fodder yield per plant.

Warkad *et al.* (2010) determined correlation between yield and yield contributing components and to assess the direct and indirect effects of yield components on yield in sorghum. 1000 Seed weight demonstrated highly significant association with grain yield per plant at both genotypic and phenotypic level. Among the yield components themselves, days to fifty per cent flowering exhibited highly significant positive association with days to maturity, plant height, dry fodder weight per plant and number of leaves per plant. The character number of internodes per plant exhibited very strong positive correlation with number of leaves per plant and stem girth while number of leaves exhibited moderately significant positive association with stem girth.

Sandeep *et al.* (2010) In a study of 20 sweet sorghum genotypes, observed maximum positive direct effect of juice volume and cane weight on ethanol yield and positive indirect effect of cane height via cane weight, juice volume on ethanol yield.

Sandeep *et al.* (2011) studied the interrelationship of sugar yield and its attributing traits in F₂ population of two crosses of sweet sorghum viz., '27 B × BJ 248' and 'CSV 17 × BJ 248'. Correlation studied in F₂ generation in both the crosses revealed high significant positive correlation of stalk yield, Brix, juice volume, juice yield, juice extraction per cent and total soluble sugar with sugar yield in the crosses.

Shinde *et al.* (2012) revealed that green stalk yield exhibited highly significant and positive correlation at genotypic and phenotypic levels with plant height, number of internodes, stem girth and juice extraction

percentage which indicated that selection for these traits would lead to an improvement in green stalk yield in sweet sorghum

Tomar and Sivakumar (2012) analysed fifty two diverse genotypes of sweet sorghum in order to understand the interrelationship of sugar yield and its attributing quantitative traits and found that sucrose yield exhibited highly significant positive phenotypic (P) and genotypic (G) correlation with stem girth, millable cane weight, sucrose percentage, juice extraction percentage, cane yield, juice yield and significant correlation to days to physiological maturity.

Bhusal Nabin *et al.* (2013) observed that dry fodder yield/plant exhibited positive significant correlation with green fodder yield/plant, 1000-grain weight and plant height.

Sowmy *et al.* (2013) observed that days to maturity at genotypic level and days to flowering at both genotypic and phenotypic levels exhibited highly significant negative correlation with grain yield in F₃ generation of sorghum. At both phenotypic and genotypic levels, plant height exerted highly significant positive correlation with grain yield.

Singh *et al.* (2015) computed correlation coefficient to elucidate inter relationship on sweet sorghum among growth parameters (plant height, leaf area index, mid stem diameter; leaf : stem ratio) with yield parameters (stalk, juice, sugar, ethanol, fodder, crude protein content and in vitro dry matter digestible yield). Quality parameters (juice percent, brix percent, juice purity coefficient and sucrose percent) were also correlated to each other and yield parameters (cane yield, sugar yield, juice yield and ethanol yield). Positive correlations were observed between growth, yield and quality parameters.

Hundekar *et al.* (2016) observed that grain yield had expressed highly significant and positive correlation with plant height, panicle length, days to maturity and test weight at both genotypic and phenotypic levels.

Rana *et al.* (2016) observed that the magnitude of genotypic correlation was higher as compared to their corresponding phenotypic correlations indicating the inherent relationship among the characters studied. Green forage yield per plant was highly significant and positively

correlated with stem girth, leaf length, leaf width and dry matter yield per plant at both genotypic and phenotypic level. These characters may be considered as important yield component in sorghum.

Shukla *et al.* (2016) observed that high sugar concentration in sweet sorghum is not conditional on the plants being tall, making the development of short, sweet inbred lines feasible. This information will also significantly benefit studies aimed at identifying QTL for sugar yield in sweet sorghum.

Endalamaw *et al.* (2017) observed that panicle weight and width, dry matter yield, thousand kernel weight and harvest index had significant positive correlation with grain yield and exerted favourable direct effects both at phenotypic and genotypic levels. Ethanol yield was also correlated with juice yield, sugar yield and fresh stalk yield. Moreover, days to maturity had negative correlation and imposed negative direct effect on grain yield, which may indicate the possibility to select high yielding, early maturing dualpurpose varieties for dry environments where terminal drought is rampant.

Makanda (2017) studied correlations and path-coefficients between grain yield and stem sugar traits. Grain yield, the dependent variable, was positively and significantly ($P < 0.05$) correlated with stem sugar, stem biomass, days to 50% flowering, number of leaves per plant, plant height and stem diameter. Grain yield was negatively appreciably ($P < 0.05$) correlated with stem juice score ($r = -0.049$), suggesting that high grain yielding cultivars are generally low in stalk juice. However, the significance of the positive correlation coefficient between grain yield and stem sugar ($r = 0.071$) suggested that the traits are not mutually exclusive.

Soujanya *et al.* (2018) analysed 48 hybrids of sweet sorghum to understand the interrelationship between green fodder yield and its attributing traits. Character association analysis revealed significant positive association of green fodder yield with early vigour, leaf length, leaf breadth and internodal length.

Prasad *et al.* (2019) studied 40 ICRISAT sorghum germplasm lines. Path coefficient analysis revealed plant height exhibited positive direct effect

coupled with positive significant correlation with grain yield per plant. Days to 50% flowering exhibited negative direct and negative indirect effects via., days to maturity, number of leaves per plant and leaf length. Number of leaves per plant exhibited positive direct effect as well as positive significant correlation with grain yield per plant.

Kanbar *et al.* (2020) evaluated 12 genotypes of sorghum originated from different countries (five sweet, four grain and three forage). These different genotypes and types of sorghum were evaluated for the agro-morphological traits that are associated with the estimated sugar and bioethanol yield to estimate their phenotypic diversity. A positive significant correlation was observed between plant height, leaf number, leaf area, biomass yield, cane and bagasse yields, and the predicted bioethanol yield. Both, cluster and principal component analysis were performed to group the genotypes according to their agro-morphological and molecular similarity coefficients. For analytical approaches, the Iranian grain and forage genotypes clustered separately from the other genotypes.

2.4. Genetic divergence:

The concept of D^2 statistic for measuring the divergence between two populations was introduced by Mahalanobis (1936). It gives a result based on the magnitude of divergence and is independent of size of the sample. Mahalanobis *et al.* (1949) employed D^2 statistic in detailed study of Anthropometric data of Uttar Pradesh classifying in 23 groups and into three major clusters *i.e.* Brahmin (B-cluster) of the top of the Hindu social hierarchy comprising nine groups, the Artisan (A-cluster) in the middle consisting of four groups and the Trivial (T-cluster) at the bottom consisting of ten groups.

Mahajan and Wadikar (2012) assessed genetic divergence among twentyfour sorghum genotypes using Mahalanobis D^2 statistic. The genotypes were grouped in to eight clusters, which revealed wide diversity in the experimental material. The maximum inter cluster distance was observed between clusters VII and VIII followed clusters II and VI.

Elangovan *et al.* (2013) observed that large variations was found for

traits viz., field brix (4–22 %), stem fresh weight/5 plants (1,667–6,250 g) and stem dry weight/5 plants (833–5,000 g), juice brix (12.4–24 %), juice volume/5 plants (142–1,667 ml), total soluble sugars (9.35–20.82 %), reduced sugars (0.11–3.74 %) and juice purity (49.33–80.72 %).

Shinde *et al.* (2012) studied genetic diversity among 46 genotypes of sweet sorghum against the thirteen growth characters mostly at maturity that has effect on ethanol production. Based on D^2 statistics, grouped 46 genotypes into 11 clusters, out of which cluster I shows the highest intra cluster value (13.79) followed by cluster II (13.64) while maximum inter cluster distance (i.e. 34.72) was observed between cluster V and cluster IX, indicating there is presence of wide range of genetic diversity among the sweet sorghum genotypes.

Jain, S. K. and Patel, P.R. (2013) observed that green and dry fodder yield contributed enormously (33.25 and 28.80 per cent) to the total variation followed by plant height (13.00 percent) and days to 50 percent flowering (9.21 percent). Thus, the considerable degree of divergence existed in the present sorghum material.

Bahadure *et al.* (2014) analysed thirtyfive sweet sorghum genotypes and depending on the D^2 values, these were grouped in to six clusters. Cluster II was the largest and consisted of 10 genotypes and cluster VI was the least with one genotype. The inter-cluster distances were higher than the intracluster distances reflecting wider genetic diversity among the genotypes.

Sujatha and Pushpavalli (2015) carried out D^2 analysis in 62 genotypes of sorghum and grouped them into 15 clusters where cluster I was the largest comprising of 41 genotypes followed by cluster III with 7 genotypes and cluster XI with 2 genotypes. Based on the inter cluster distance and performance, the elite variety Phule Anuradha, the landraces RSV 1426, SSRG 147, Pusegaon local and the advanced breeding line RSV 1420. Seed yield contributed maximum to divergence (31.84 %) followed by plant height (20.62 %) and days to 50% flowering (14.38 %).

Meena *et al.* (2016) analyzed sixty-two sorghum genotypes for

genetic divergence which resulted in 10 clusters having maximum inter-cluster distance between clusters II and IX and least between clusters VI and VIII. Maximum intra-cluster distance was exhibited by cluster IX followed by cluster VII.

Damor *et al.* (2017) carried out D^2 analysis in sixty genotypes of forage sorghum and revealed considerable genetic diversity among the genotypes. The genotypes grouped into 5 clusters. Cluster I contains forty genotypes followed by sixteen in cluster II, while cluster III and V were contain solitary genotype and cluster IV had only two genotypes.

Ahalawat *et al.* (2018) studied thirty genotypes of forage sorghum for generating information on nature and magnitude of genetic variability and diversity. Based on D^2 — Statistics, 30 genotypes were grouped into six clusters. The highest inter-cluster distance was observed between cluster III and VI followed by IV and VI, indicating genotypes included in these clusters had wide genetic diversity.

Swamy *et al.* (2018) applied Mahalanobis D^2 statistics to assess the divergence among one hundred and twenty-two rabi sorghum genotypes. All the genotypes were grouped into nine clusters and cluster I was largest with 88 genotypes, followed by cluster IV, II and V (17, 10 and 2 genotypes respectively) and remaining clusters (III, VI, VII, VIII and IX) were solitary in nature.

More *et al.* (2018) carried out multivariate analysis based on Mahalanobis's D^2 statistic (D^2 values) grouped the 26 accessions in to 6 clusters. The intra and inter cluster distances among the 26 accessions revealed that the maximum divergence were observed between the clusters III and IV ($D=34.11$) followed by I and VI ($D=32.17$), II and IV (31.51).

Khandelwal *et al.* (2019) grouped 150 genotypes into 6 clusters based on D^2 values, out of which cluster 1 shows the highest intra cluster value (142.62) followed by cluster 2 (119.47). While maximum inter cluster distance (i.e.652.68) was observed between cluster 5 and cluster 6.

Yuvaraja *et al.* (2019) evaluated sorghum germplasm for forage traits during the Rabi to study the divergence using multivariate (D^2) analysis. Result revealed four distinct cluster indicates that the germplasm had variation between group of clusters. The intra-cluster distances in all the four clusters were registered low, indicating that the genotypes within the same cluster were closely related for its forage value. The highest inter-cluster distance was observed between cluster I (14 genotypes) and cluster IV (2 genotypes) and the lowest between the cluster II (25 genotypes) and III (85 genotypes).

Kavya *et al.* (2020) assessed the genetic diversity among 110 sorghum genotypes using D^2 statistics. 4 clusters were formed, highest no of genotypes are in cluster –I with 91 and lowest in cluster-III having solitary genotypes. The highest inter cluster distance was observed between cluster II & IV (4018.74) and lowest between cluster III and IV (235.21). Based on the mean values no single genotype possessed all desirable characters, most yield and yield related attributes is-2834 performed for biomass type's NSJB-6652.

Sejake *et al.* (2020) assessed One hundred sorghum accessions were evaluated based on five qualitative and 14 quantitative traits. Analysis of variance revealed highly significant ($p \leq 0.01$) differences for all quantitative traits measured indicating the existence of a wide genetic variation among accessions. Hierarchical cluster analysis grouped the 100 accessions into four clusters. The clustering patterns of accessions was not entirely based on geographic origin and/or breeding status, probably due to gene flow. This study exhibited the existence of wide genetic diversity within the sorghum accessions, which could be exploited in the improvement of the crop. Accessions SA 2020 and SA 0700 with brown midrib colour could be used to improve the fodder quality in livestock. Accessions SA 2097, SA 3710, SA 0954 and Maseka a swere that recorded high grain yield per panicle were characterised by a semi-loose erect panicle type and brown grain colour, traits preferred by farmers.

de Oliveira *et al.* (2022) studied 10 sweet sorghum genotypes were installed in 2015/16 at the municipalities of Sinop, in the state of Brazil. The

variables evaluated in this assessment comprised fresh mass production, dry mass production, soluble solid contents, plant height and flowering. The sweet sorghum performance and genetic diversity was estimated. Five genetic groups were observed. Fresh mass, flowering and height were significant for both locations, demonstrating the influence of environment on hybrid behavior. Crosses between genotypes 4x8 at Passo Fundo, and 9x10 at Sinop are favorable, as these genotypes exhibit good agronomic characteristics, especially for the main variable employed in the sugar-alcohol industry. Flowering contributed the most to genotype separation in both locations.

Andiku, *et al.* (2022) studied 348 sorghum germplasm was field evaluated Data were collected on 20 sorghum agro-morphological traits. A significant ($P \leq 0.05$) variation was detected amongst the test genotypes for all the assessed traits, suggesting the presence of sufficient genetic diversity for selection. High heritability ($H^2 > 0.60$) and genetic advance as percent of the mean ($GA > 20\%$). Cluster analysis based on phenotypic traits resolved the test sorghum genotypes into four distinct genetic groups. Six genotypes with superior agronomic traits were identified for production or potential parents for quality breeding.

Chapter III

MATERIAL AND METHODS

The experimental materials used and the methods applied during the course of present investigation entitled “**Genetic Variability character association and clustering pattern of sweet sorghum (*Sorghum bicolor* (L.) Moench) genotype for agronomic traits in rainfed conditions**”.

3.1. Experimental site

The experiment was conducted Research field of all India Coordinated Research Project on Sorghum, College of Agriculture, Indore - (M.P.) 452001

3.2. Experimental material

The experimental material used in the present study comprised of 25 genotypes of Sweet sorghum. Details of genotypes used in present investigation are given in Table 3.2.

3.3. Experimental details

Table 3.1: Detail of experimental material used for present investigation:

Crop	Sorghum [<i>Sorghum bicolor</i> (L.) Moench]
Season	Kharif season (2021-22)
Year	2021-22
Number of genotypes	25
Replications	3
Experimental design	RBD (Randomized Block Design)
Plot size gross	5m x 3.6m (18 m ²)
Net plot size	4.6m x 2.40m (11.04 m ²)
Row length	4.0 m
No. Of Rows	6
Spacing	60 cm x 12 cm (R x P)

Table: 3.2. Meteorological information (Standard week) during entire crop growth of the year 2021-22 at Indore (M.P.)

SM W	Week	Total Rainfall (mm)	Temperature (°C).		Relative Humidity (%)		Wind Velocity	No. of Rain in Days
			Maximum	Minimum	Morning	Evening		
14	April 2 – 8, 2021	0.00	38.14	19.29	78.46	76.79	0.58	0.00
15	April 9 – 15	0.00	38.57	22.00	84.81	73.56	0.87	0.00
16	April 16 – 22	0.00	38.00	22.43	77.06	71.10	1.24	0.00
17	April 23-29	0.00	39.86	22.14	75.36	77.27	0.65	0.00
18	April 30–6 May	0.00	38.79	24.57	12.26	72.03	0.94	0.00
19	May 7 – 13	0.00	40.00	25.86	0.00	73.27	1.07	0.00
20	May 14 – 20	3.00	37.86	25.00	0.00	77.81	2.58	1.00
21	May 21 – 27	0.00	38.43	26.71	0.00	71.06	3.05	0.00
22	May 28 – June 3	18.50	38.86	24.86	37.54	76.00	2.64	3.00
23	June 4– 10	100.70	35.64	24.00	88.21	71.83	1.64	3.00
24	June 11– 17	84.00	36.43	25.29	86.44	81.31	3.82	1.00
25	June 18– 24	50.70	32.93	23.14	87.29	79.60	2.78	3.00
26	June 25– July 01	2.00	32.29	24.29	88.51	82.14	2.72	0.00
27	July 02– 08	0.00	34.14	24.86	88.44	79.69	3.73	0.00
28	July 09 – 15	64.00	31.79	24.57	89.13	90.68	0.89	2.00
29	July 16 – 22	54.40	30.00	24.29	88.16	90.56	1.89	5.00
30	July 23 – 29	82.20	25.57	23.29	93.64	93.30	3.21	7.00
31	July 30 – Aug.05	22.20	24.93	23.14	92.20	92.04	5.25	5.00
32	Aug. 06 – 12	83.00	27.00	22.71	91.89	86.27	1.42	5.00
33	Aug. 13 – 19	9.30	29.14	23.00	91.89	87.56	0.88	2.00
34	Aug. 20 – 26	82.50	26.86	22.71	90.69	88.49	0.46	3.00
35	Aug. 27– Sep.02	128.60	28.86	23.21	90.96	85.69	0.14	4.00
36	Sept. 03 – 09	40.00	29.79	23.43	91.90	83.21	0.06	4.00
37	Sept 10 – 16.	86.70	28.71	23.29	92.04	82.21	0.40	4.00
38	Sept. 17 – 23	103.40	27.14	21.86	90.74	88.44	0.95	5.00
39	Sept 24 – 30	45.30	29.14	22.29	90.97	85.49	0.19	4.00
40	Oct. 01 – 07	17.10	32.00	22.86	88.57	86.36	0.01	3.00
41	Oct. 08 – 14	0.00	32.71	22.00	86.83	74.81	0.01	0.00
42	Oct. 15 – 21	49.70	30.43	17.71	87.81	78.44	0.05	2.00
43	Oct. 22 – 28	0.00	29.36	15.71	81.06	84.47	0.01	0.00
44	Oct. 29 – Nov. 04	0.00	28.21	11.71	82.44	85.40	0.01	0.00
45	Nov. 5-11	0.00	28.50	10.57	78.07	80.49	0.01	0.00
46	Nov. 12-18	0.00	28.00	12.00	74.40	83.41	0.07	0.00
47	Nov. 19-25	0.00	29.00	17.43	85.86	85.56	0.05	0.00
48	Nov. 26- 2 Dec	13.10	26.86	11.71	76.16	80.54	0.04	0.00
49	03 Dec -09 Dec	4.20	22.86	12.57	86.33	86.89	0.02	0.00

50	10 Dec -16 Dec	0.00	25.57	13.57	84.31	85.26	0.01	0.00
51	17 Dec -23 Dec	0.00	22.79	7.00	86.01	85.69	0.04	0.00
52	24 Dec -31 Dec	0.00	22.50	9.25	81.83	88.47	0.05	0.00
1	Jan. 1 – 7, 2022	4.30	24.21	13.71	87.00	88.39	0.05	0.00
2	Jan. 8 – 14	27.10	19.07	9.57	83.01	85.67	0.02	0.00
3	Jan. 15 – 21	0.00	24.14	10.43	78.16	83.99	0.01	0.00
4	Jan. 22 – 28	0.00	19.43	7.57	75.57	86.29	0.02	0.00
8	Jan. 29 – Feb. 4	0.00	25.86	8.00	79.47	79.33	0.27	0.00
9	Feb. 5 – 11	0.00	27.43	9.14	81.96	81.11	0.10	0.00
7	Feb. 12 – 18	0.00	25.14	8.86	84.81	82.33	0.20	0.00
8	Feb. 19 – 25	0.00	29.86	12.43	83.57	77.47	0.16	0.00
9	Feb. 26 – 4 March	0.00	13.43	4.97	38.30	31.40	0.12	0.00
10	March 5 – 11	0.00	0.00	0.00	0.00	0.00	0.00	0.00
11	March 12 – 18	0.00	0.00	0.00	0.00	0.00	0.00	0.00
12	March 19 – 25	0.00	0.00	0.00	0.00	0.00	0.00	0.00
13	March 26 - 01 April, 2022	0.00	0.00	0.00	0.00	0.00	0.00	0.00

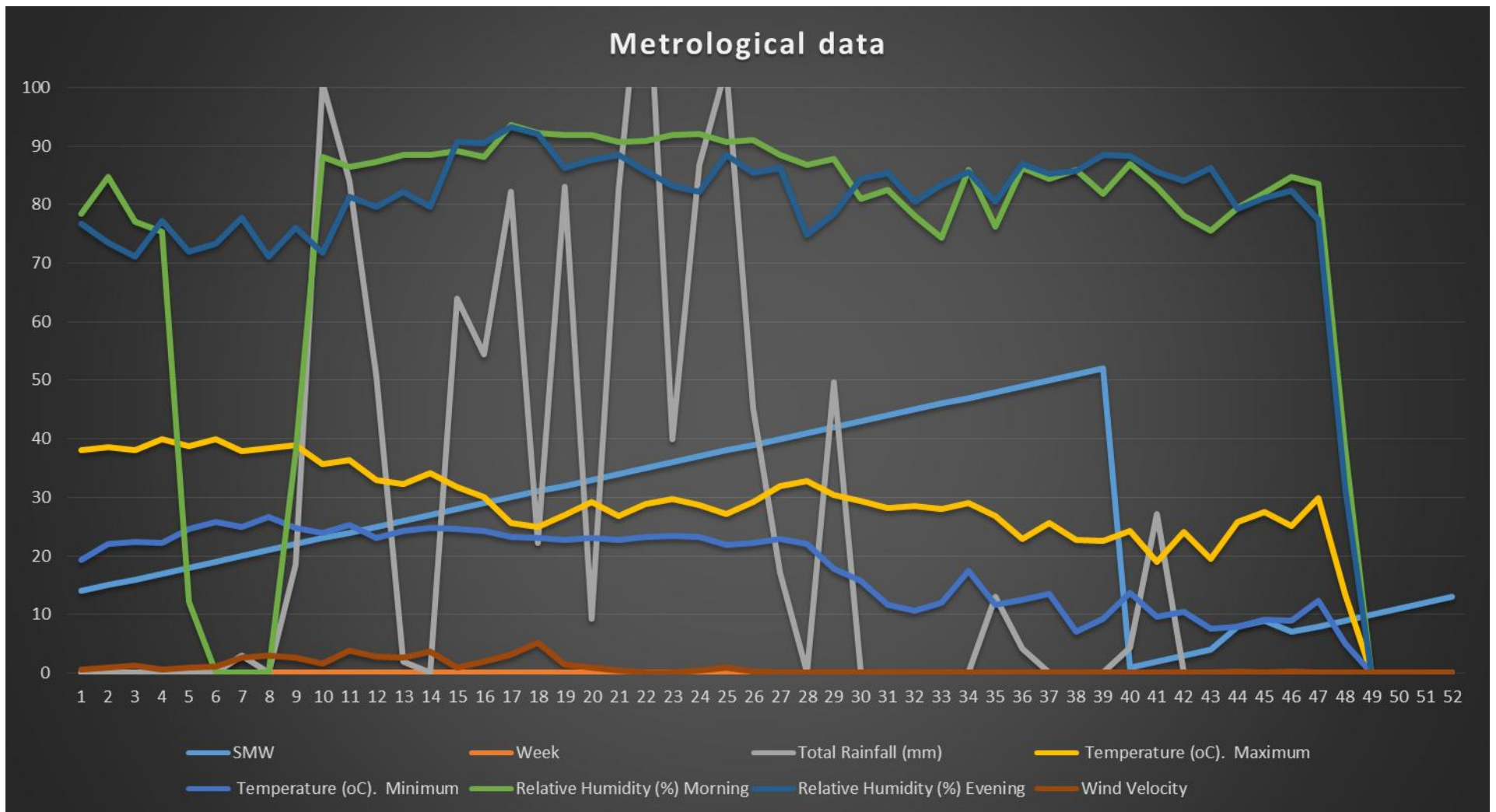


Fig 3.1: Weekly Metrological Data for the crop growing period.

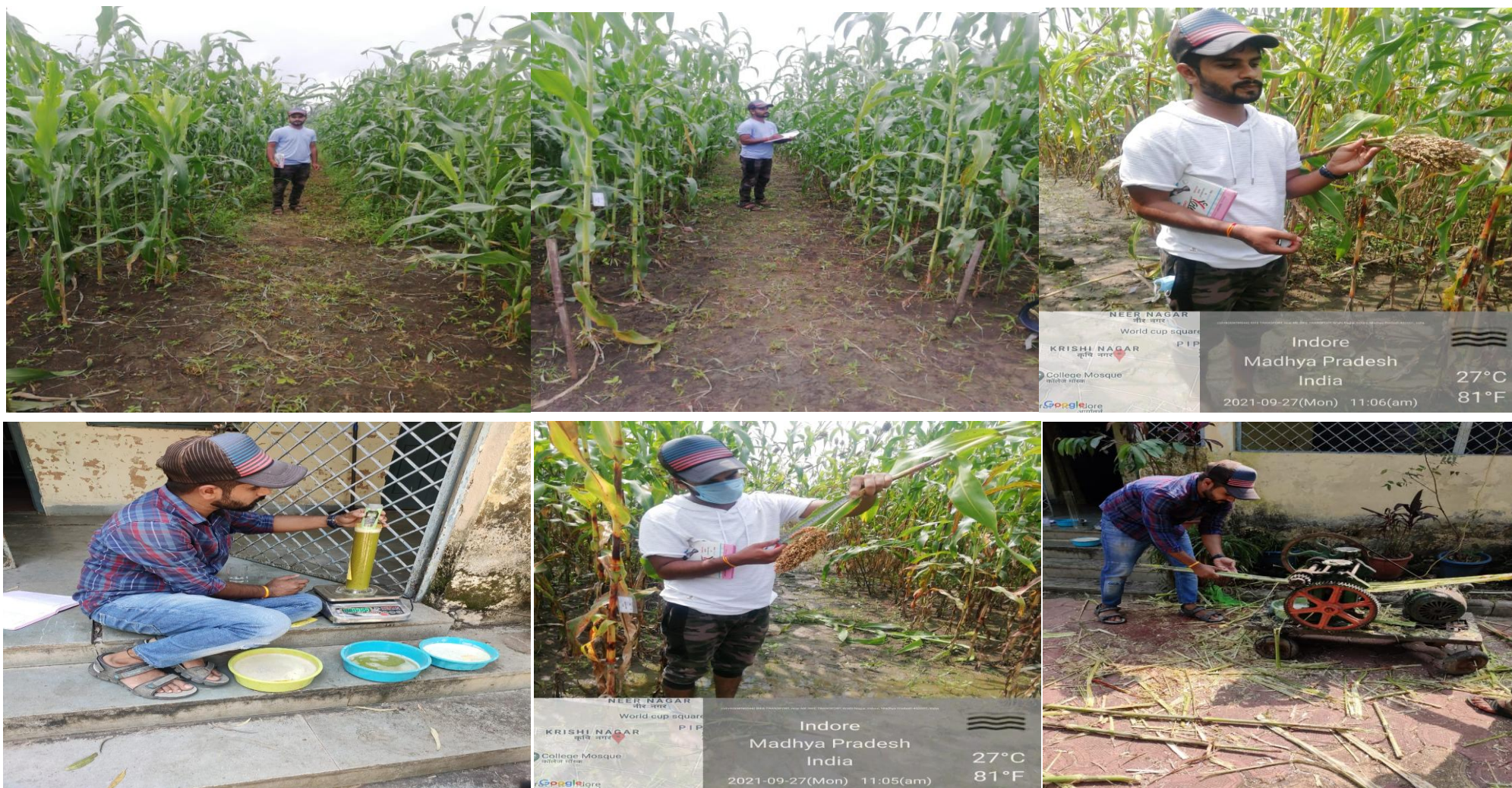


Plate 1. Field view of 25 Sorghum genotypes experimental material used for present investigation.

3.4.1 Observational procedure:

Five competitive plants were selected randomly from each plot and tagged for recording the observations the following observations were recorded on the five selected plants in each plot.

3.4.1.1 Days to 50% flowering:

Number of days taken from the date of sowing to the day on which 50% of the plants in a genotype initiate first flower was recorded as days to flowering.

3.4.1.2 Plant population

Plant population is calculated by formula:

$$\frac{1}{\text{Row to Row (m)} \times \text{Plant to Plant (m)}}$$

3.4.1.3 Number of internodes / plant

Number of internodes of randomly selected plants were counted (average 11.25) at physiological maturity stage.

3.4.1.4. Flag leaf Length (cm)

Length of the flag leaf measured in cm.

3.4.1.5 Plant height (cm)

The height of plant was measured in centimeter from the ground level to the top of the main axis at the time of maturity.

3.4.1.6 Stem girth (cm)

Stem girth in centimeter of each observational plant was recorded at maturity stage with help of Vernier caliper.

3.4.1.7 100 seed weight (g)

100 seed weight was computed by weighing 100 seeds which are randomly chosen filled seeds from a complete sample made by mixing the seeds of all the five plants in each replication and recorded in grams.

3.4.1.8 Number of seeds per pod

Number of seeds per pod was counted from fifty randomly selected pods in each of the five selected plants.

3.4.1.9 Juice P^H

Juice pH was determined by using portable pH meter.

3.4.1.10 Juice extraction %

Recorded by using formula:

$$\text{Juice extraction (\%)} = (\text{juice weight} / \text{Fresh stem weight}) \times 100$$

3.4.1.11 4th leaves length (cm)

The length of 4th number leaves counted from stem 1st leave.

3.4.1.12 4th leaves width (cm)

Width of the flag leaf measured in cm.

3.4.1.13 Leaf Area (cm²)

Area of the third leaf from the flag leaf, computed as (leaf length x leaf width x 0.747) suggested by Stickler *et al.* (1961).

3.4.1.14 Fresh biomass (leaves + stem + cob)

Total fresh biomass above ground including panicle was recorded at physiological maturity in g/plant.

3.4.1.15 Brix at physiological maturity (%)

Brix at physiological maturity was measured by hand refractometer/ brixmeter.

3.4.1.16 Grain yield (g/plant)

Earhead from randomly selected five plants in net plot was harvested, dried and threshed. The grain was thoroughly sun dried before weighing and finally grain weight (g) per plant was recorded.

Table 3.3: Detail of experimental material used for present investigation

S.NO.	Name of genotype	S.NO.	Name of genotype
1	SPH2009	13	SPV2894
2	SPV2697	14	SPV2895
3	SPV2789	15	CSH22SS
4	SPV2793	16	CSV19SS
5	SPV2794	17	CSV24SS
6	SPV2795	18	SPV2714
7	SPV2888	19	SPV2812
8	SPV2889	20	SPV2896
9	SPV2890	21	SPV2897
10	SPV2891	22	SPV2898
11	SPV2892	23	SPV2899
12	SPV2893	24	SPV2900
		25	CSH25

3.5 Statistical analysis:

1. Analysis of variance:

The data on yield and its contributing traits were statistically analyzed on the basis of model described by Cochran and Cox (1950) for randomized block design. In order to test the significance of treatments Critical difference was computed (Fisher and Yates, 1963).

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

Where,

Y_{ij} = value of the variate for the i^{th} treatment in the j^{th} block

($i=1, 2, 3, \dots, t$; $j=1, 2, 3, \dots, b$)

μ = General mean effect

b_j = effect due to j^{th} block

t_i = effect due to i^{th} treatment

e_{ij} = Random errors which is assumed to be independently and normally distributed with mean zero and variance σ_e^2 .

Table 3.4: ANOVA table for RBD

Source	Degree of freedom	Mean sum of squares	Variance ratio
Replication	(r-1)	M_r	M_r/M_e
Treatment	(t-1)	M_t	M_t/M_e
Error	(r-1) (t-1)	M_e	-
Total	rt-1	-	-

Where, r = Number of replications, t = Number of treatments

2. Estimation of phenotypic and genotypic coefficients of variation:

The phenotypic and genotypic coefficients of variation in per cent were computed by the following formulae given by Burton (1952).

$$\text{Phenotypic Coefficient of Variation (PCV)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Genotypic Coefficient of Variation (GCV)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

The PCV and GCV values are ranked as low, medium and high (Shivasubramanian and Menon, 1973) and are mentioned below:

0-10%	- Low
10-20%	- Moderate
>20%	- High

3. Estimation of heritability and genetic advance:

Heritability in per cent in broad sense was estimated by the following formula given by Singh and Choudhary (1977):

$$\text{Heritability (h}^2\text{)} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

Heritability values are categorised as low, moderate and high (Robinson *et al.*, 1949) and are given below,

0-30%	- Low
30-60%	- Moderate
60% and above	- High

The estimates of expected genetic advance from selection, G(s), was obtained by the formula suggested by Robinson *et al.* (1949).

$$G(s) = k \times h^2 \times \sigma_p$$

where,

k = Selection differential in standard deviation units which is 2.06 for 5% selection intensity,

h^2 = Heritability in broad sense, and

σ_p = Phenotypic standard deviation

Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson *et al.* (1955).

$$\text{Genetic advance as percentage of mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

Genetic advance as percent of mean was classified as low, moderate and high (Johnson *et al.*, 1955) and values are given below:

0-10%	- Low
10-20%	- Moderate
20% and above	- High

4. Estimation of correlations coefficients:

Phenotypic and genotypic correlation coefficients between characters were computed utilizing respective components of variance and co-variance, by following formula suggested by Miller *et al.* (1958).

$$r_{xy} = \frac{\text{Covariance x, y}}{\sqrt{(\text{Variance x}) \times (\text{Variance y})}}$$

where,

r_{xy} = Correlation coefficient between character x and y,

To test the significance of correlation coefficients, the estimated values were compared with the tabulated values of Fisher and Yates (1938) at n-2 d.f. at two levels of probability, viz., 5% and 1%.

5. Path coefficient analysis:

The proportion of direct and indirect contributions of various traits to the total correlation coefficients with seed yield per plant was estimated through path coefficient analysis as suggested by Wright (1921, 1934) and elaborated by Dewey and Lu (1959).

Path coefficient is a standardized partial regression, which measures the direct influence of one variable upon another and allows partition of correlation coefficient into components of direct and indirect effects.

To estimate various direct and indirect effects, the following set of simultaneous equations were formed and solved.

$$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \dots + r_{1l}P_{ly}$$

$$r_{2y} = r_{2y}P_{1y} + P_{2y} + r_{23}P_{3y} + \dots + r_{2l}P_{ly}$$

.

.

$$r_{ly} = r_{l1}P_{1y} + r_{l2}P_{2y} + r_{l3}P_{3y} + \dots + P_{ly}$$

where,

r_{1y} to r_{ly} = Coefficient of correlation between causal factor 1 to l and dependent character y,

r_{12} to $r_{l-1,l}$ = Coefficient of correlation among causal factors themselves, and

P_{1y} to P_{ly} = Direct effects of characters 1 to l on character y.

Residual effect, which measures the contribution of the characters not considered in the causal scheme, was obtained as:

$$\text{Residual effect } (P_{RY}) = \sqrt{1 - R^2}$$

where,

$$R^2 = \sum_{iy} P_{iy}^2 + 2 \sum_{\substack{i \neq j \\ i > j}} P_{iy} P_{jy} r_{ij}$$

6. Multivariate analysis:

(a) Estimation of Wilk's (Λ) criterion:

To test the significance of difference between lines, taking all the characters simultaneously, 'V' statistic was calculated which was based on Wilk's (Λ) criterion (Wilk, 1932). The sum of squares and sum of products of error and error + variety were utilized for estimation of " Λ ".

To calculate the value of " Λ " following relationship was used:

$$\Lambda = \frac{|E|}{|E + V|}$$

where,

$|E|$ was the determinant of error sum of squares and sum of products matrix and $|E + V|$ was the determinant of the 'error + variety' sum of squares and sum of products matrix.

χ^2 was used to test the significance of Λ as

$$\chi^2_{pq} = -m \log_e \Lambda$$

where,

$$m = n - \frac{p+q+1}{2} \text{ with } pq \text{ degree of freedom.}$$

where,

n = total number of observations – 1,

p = number of characters,

$q = k - 1$, and

k = number of lines

(b) Estimation of D^2 -statistic:

To estimate divergence between two lines Mahalanobis (1936) D^2 - statistic was used. He defined generalized distance between two lines as:

$$\Delta^2 = \sum \sum \lambda^{ij} \delta_i \delta_j$$

where,

λ^{ij} = Reciprocal matrix of the common dispersion matrix λ_{ij} ,

δ_i = Difference between mean values of two lines for the i^{th} character,
and

δ_j = Difference between mean values of two lines for the j^{th} character.

D^2 -statistic is the sample estimate of the generalized distance which is estimated as:

$$D^2 = \sum_{i,j=1}^p s^{ij} d_i d_j$$

where, s^{ij} and d_i are the sample estimates of λ^{ij} and δ_i , respectively. For calculating D^2 values inversion of matrix was required which is quite cumbersome. To overcome this difficulty original correlated, unstandardized character means (X_i) were transformed to uncorrelated, standardized variables (Y_i) by Pivotel condensation method (Rao, 1952). D^2 between any pairs of populations, for example population 1 and 2, was then estimated as:

$$D_p^2 = \sum_{i=1}^p (Y_{i1} - Y_{i2})^2$$

where, p = number of characters used for estimation of divergence.

(c) Determination of population constellations:

Population constellations were determined by Tocher's method described by Rao (1952). A cluster or constellation may be explained as a group of populations or genotypes such that any two populations belonging to the same cluster showed, on the average, a smaller D^2 value than those belonging to different clusters.

Tocher suggested that two closely related populations of low D^2 value be pooled together and then a third population of similar D^2 value be added to this group such that it did not increase the average D^2 value appreciably. This process is continued. Any population, which sharply increases the average D^2 value, should not be included in that group.

After formation of first cluster, the process is repeated to form second, third clusters, using remaining populations until all populations are included in one or the other cluster. After cluster formation average intra and inter-cluster distances were calculated. The square root of corresponding average D^2 values represents the distance within and between groups.

Chapter – IV

RESULTS

The experimental data investigation entitled “**Genetic Variability Character Association and Clustering Pattern of Sweet Sorghum (*Sorghum Bicolor* (L.) Moench) Genotype for Agronomic Traits in Rainfed Conditions**” has been statistically analyzed. A total of 25 varieties were evaluated during Kharif season 2021-22.

4. Experimental data were analyzed statistically and results described as under:

4.1 Analysis of variance

4.2 Mean performance

4.3 Genetic parameters: Genotypic and phenotypic coefficient of variation, heritability and genetic advance

4.4 Association analysis: Genotypic and phenotypic correlation coefficient & path coefficient analysis.

4.1 Analysis of variance:

Analysis of variance of grain yield per plant and its contributing traits mean sum of square due to genotypes exhibited highly significant variation for all 19 characters, viz., plant population, days 50% flowering, number of leaves per plant, 4th leaves length, 4th leaves width, leaves area, flag leaves length, plant height, brix per cent, stem girth, total fresh biomass in grams per plant, fresh biomass in grams per plant, juice yield (lit/plant), juice yield (g/plant), juice pH, juice extraction per cent, number of internode per plant, 100 seed weight and grain yield g/plant. It indicated that there was considerable variability for these characters in present germplasms (Table 4.1a & 4.1b) and (Fig 4.1).

4.2. Mean performance:

The mean performance of 25 genotypes have been described for different characters and presented in (Table 4.2a & Table 4.2b). Range values graph of different morphological characters of sweet sorghum genotypes are presented in Fig. (4.1)

Plant population

Genotypes were appreciably varied for plant population which ranged from SPV2899 (35) to SPV2890 (200) followed by genotype SPV2795 (199) and SPV2888 (178) had the maximum plant population. The genotype SPV2899 (35) and SPV2812 (67) had the lowest Plant population with a grand mean value of 133.52.

Days 50% flowering

The variation for days to 50 per cent flowering ranged from 73 days (SPV2889), (SPV2891) to 89 days (SPV2899), (SPV2900). The genotypes namely SPV2889, SPV2891 (73 days), SPV2892, SPV2812 (74 days) and SPV2893 (75 days) were earliest in days to fifty per cent flowering and variety SPV2888 (87 days), SPV2793 (88 days) and (SPV2899), (SPV2900) (89 days) were late in flowering. 14 out of 25 genotypes were appreciably earlier with the grand mean of 80 days to fifty per cent flowering.

Number of leaves per plant

Number of leaves were associated ranged from 7.67 (SPV2889) to 10.00 (SPV2793), (SPV2892), (SPV2897) followed by genotype CSH22SS, SPV2812 and SPV2899 (9.67) had the maximum number of leaves per plant. The genotype SPV2894 (8) and SPV2890 and SPV2891 (8.33) had the minimum number of leaves per plant with a grand mean value of 9.04.

4th leaves length

4th leaves length was associated ranged from 65 cm (SPV2794), (SPV2795) to 100cm (SPV2895), (SPV2714) followed by genotype SPV2697, SPV2891 and CSH22SS (95 cm) had the maximum 4th leaves length. The genotype CSV19SS (70 cm) had the least 4th leaves length with a grand mean value of 81.60 cm.

4th leaves width

4th leaves width was associated varied from 8 cm (SPV2894) to 12 cm (CSH22SS) followed by genotype SPV2789 and SPV2899 (11 cm) had the maximum 4th leaves width. The genotype SPV2794, SPV2795, SPV2888, SPV2889, SPV2892, SPV2893, CSV19SS, CSV24SS, SPV2896 and SPV2900 (9 cm) had the least 4th leaves width with a grand mean value of 9.68 cm.

Leaves area

Leaves area were remarkably varied from 432.90 cm² (SPV2794), (SPV2795) and (SPV2893) to 843.60 cm² (CSH22SS) followed by genotype CSV24SS (766.10 cm²) and SPV2714 (747.00 cm²) had the maximum leaves area. The genotype CSV19SS (466.20 cm²) and SPV2894 (473.60 cm²) had the least leaves area with a grand mean value of 597.24 cm².

Flag leaf length

Flag leaves length were remarkably ranged from 30 cm (SPV2794) to 55 cm (SPV2714) followed by genotype CSH22SS, SPV2900 (50 cm) and SPV2891 (48 cm) had the maximum Flag leaves length. The genotype SPH2009, SPV2697, SPV2789, SPV2793, SPV2890, SPV2894 and SPV2899 (35 cm) had the least Flag leaves length with a grand mean value of 40.92 cm.

Plant height

Plant height was remarkably varied from 199.83 cm (CSH25) to 359.83 cm (CSH22SS), (SPV2888) followed by genotype SPV2893, SPV2795, SPV2793 (339.83 cm) and SPV2697, SPV2892, SPV2895, SPV2896, SPV2900 (329.83 cm) had the maximum Plant height. The genotype SPV2889 (204.83 cm), SPV2898 (249.83 cm) and SPV2714 (269.83 cm) had the minimum Plant height with a grand mean value of 304.63 cm.

Brix per cent

Brix percent was associated differ from 10 % (CSH25) to 19 % (SPV2895), (SPV2893), (SPV2894) pursued by genotype SPV2789, SPV2890, SPV2891 (18 %) and SPV2897, SPV2812, CSH22SS, SPV2795, SPV2888 (17 %) had the maximum Brix percent. The genotype SPV2898 (11 %), SPV2899 (14 %) and SPV2714, SPV2697 (15 %) had the minimum Brix percent with a grand mean value of 16.20%.

Stem girth

Stem girth was associated differently from 14 cm (SPV2898), (SPV2894), (SPV2892) to 22 cm (SPV2899), (CSH22SS), (SPV2789) pursued by genotype CSH25, CSV24SS, SPV2889, SPV2793 (20 cm) and SPV2900, SPH2009 (19 cm) had the maximum Stem girth. The genotype SPV2714, CSV19SS, SPV2895, SPV2794 (15 cm) and SPV2896, SPV2891, SPV2888 (16 cm) had the least Stem girth with a grand mean value of 17.64 cm.

Total fresh biomass in grams per plant

Total fresh biomass was associated varied from 511.11 g (SPV2898) to 1311.11 g (SPV2794), (SPV2895) pursued by genotype SPV2789 (1277.77 g) and SPH2009 (1188.88 g) had the maximum Total fresh biomass. The genotype SPV2896, SPV2888 (577.77 g) and SPV2897 (655.55 g) had the lowest Total fresh biomass in grams per plant with a grand mean value of 904.44 g.

Fresh biomass (without leaves) in grams per plant

Fresh biomass in grams per plant was associated ranged from 311.11 g (SPV2888) to 1511.11 g (SPV2891) pursued by genotype SPV2889 (844.44 g), SPV2895 (800 g) and SPV2697, SPV2793, SPV2714 (711.11 g) had the maximum Fresh biomass. The genotype SPV2898 (344.44 g), SPV2892 (411.11 g) and SPV2896 (444.44 g) had the lowest Fresh biomass in grams per plant with a grand mean value of 623.55 g

Juice yield (lit/plant)

Juice yield was associated varied from 23.33 (SPV2896) to 1600 (SPV2789) chased by genotype SPV2697 (1540), CSV24SS (1510) and SPV2895 (1460) had the maximum Juice yield. The genotype SPV2898 (24.44), SPV2900 (41.11) and SPV2812 (72.22) had the minimum Juice yield with a grand mean value of 682.04.

Juice yield (g/plant)

Juice yield (g/plant) was appreciably varied from ranges from 23.33 g (SPV2896) to 222.22 g (CSH25) chased by genotype SPV2789 (188.88 g), CSV24SS (175.55 g) and SPV2895 (170 g) had the maximum Juice yield (g/plant). The genotype SPV2898 (26.66 g), SPV2897 and SPV2892 (32.22 g) had the lowest Juice yield (g/plant) with a grand mean value of 103.15 g.

Juice Ph

Juice Ph was associated ranges from 5.50 (SPV2714) to 6.50 (SPV2892), (SPV2897), (SPV2898) chased by genotype SPV2789 and SPH2009 (6.40) had the maximum Juice yield. The genotype SPV2894, SPV2895 and SPV2899 (6.30) had the minimum Juice Ph with a grand mean value of 6.38.

Juice extraction per cent

Juice extraction per cent was appreciably varied from 4 % (SPV2896), (SPV2900) to 25 % (CSH25) chased by genotype SPV2890 (23 %) and CSV24SS (18 %) had the maximum Juice extraction per cent. The genotype SPV2898 (4.20 %) and SPV2795 (4.50 %) had the lowest Juice extraction per cent with a grand mean value of 10.73 %.

Number of internodes per plant

Number of internodes per plant were associated varied from 10 (SPV2714), (SPV2890) to 13 (SPV2892), (SPV2897) chased by genotype SPV2889, SPV2898 and SPV2899 (12.00) had the maximum Juice yield. The genotype SPV2697, SPV2789 and SPV2793 (11.00) had the minimum Number of internodes per plant with a grand mean value of 11.36.

100 seed weight

100 seed weight was remarkably varied from 1.50 g (SPV2898) to 3.20 g (SPV2789) pursued by genotype SPV2890 (3.06 g), SPV2789 (3.20 g) and CSH22SS (3.03 g) had the maximum 100 seed weight. The genotype SPV2897, SPV2899 (1.60 g) and SPV2898 (1.50 g) had the lowest 100 seed weight with a grand mean value of 2.33 g.

Grain yield (gram per plant)

Grain yield per plant (g) was remarkably varied from 2.50 g (SPV2896) to 77.50 g (CSH25) pursued by genotype SPV2895 (68.88 g) and SPV2812 (62.50 g) had the maximum Grain yield (gram per plant). The genotype SPV2899 (3.75 g), SPV2900 (6.25 g) and SPV2789 (7.70 g) had the minimum Grain yield with a grand mean value of 34.09 g.

Table 4.1 a Analysis of Variance for 19 characters of 25 Sorghum genotypes.

Source	DF	PP	DF 50%	NLP	4LL	4LW	LA	FLL	PH	BRIX
Rep	2	6.25	6.25	0.04	6.8	7.2	6.25	6	2.08	6.25
Genotypes	24	4610.03**	74.23**	1.314444**	317**	2.18**	39491.4**	108.4.8**	5053.03**	13.75**
Error	48	0.128	1.78	0.442778	2.356	3.71	2.77	1.55	3.4	0.05

** = Significance at 1% values less than 0.001 (highly significant)

PP = Plant population, **DF 50%** = Days to 50% flowering, **NLP** = Number of leaves/plant, **4LL** = 4th leaves length (cm), **4LW** = 4th leaves width (cm), **LA** = leaves area (cm²), **FLL** = Flag leaves length (cm), **PH** = plant height (cm), **BRIX** = Brix%.

Table 4.1 b Analysis of Variance for 19 characters of 25 Sorghum genotypes.

Source	DF	STG	TFB	TFBWL	JY1	JY2	JP	JE	NIPP	SW	GYPP
Rep	2	6.25	5.32	4.23	5.58	6.53	7.59	6.45	6.32	5.63	5.41
Genotypes	24	19.97**	159413.57**	157665.53**	1010810.85**	10842.85**	3.078**	107.5**	2.2**	1.742**	1495.54**
Error	48	2.55	1.23	1.53	1.23	1.56	1.23	2.3	1.56	1.42	1.78

** = Significance at 1% values less than 0.001 (highly significant)

STG = stem girth (cm), **TFB** = total fresh biomass (without leaves) in g/plant, **JY1** = Juice yield (lit/plant), **JY2** = juice yield (g/plant), **JP** = juice ph, **JE** = juice extraction %, **NIPP** = number of internode/plant, **SW** = 100 seed weight (g) and **GYPP** = grain yield (g/plant)

Table: 4.2 (a). Mean Performance of 25 Sorghum genotypes for agronomic traits evaluated under field conditions in Kharif 2021-22.

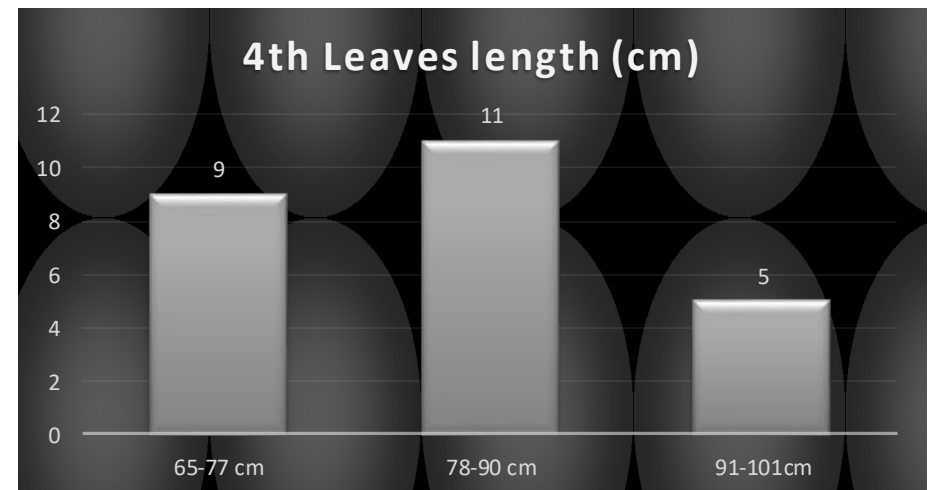
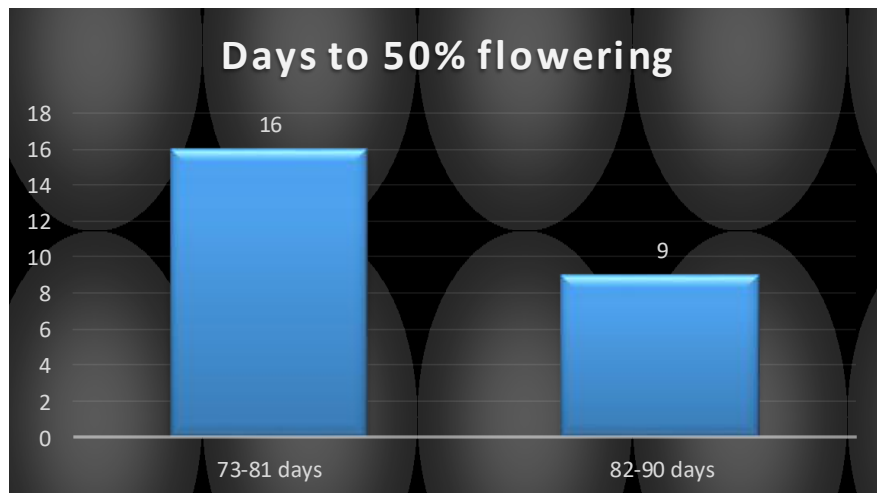
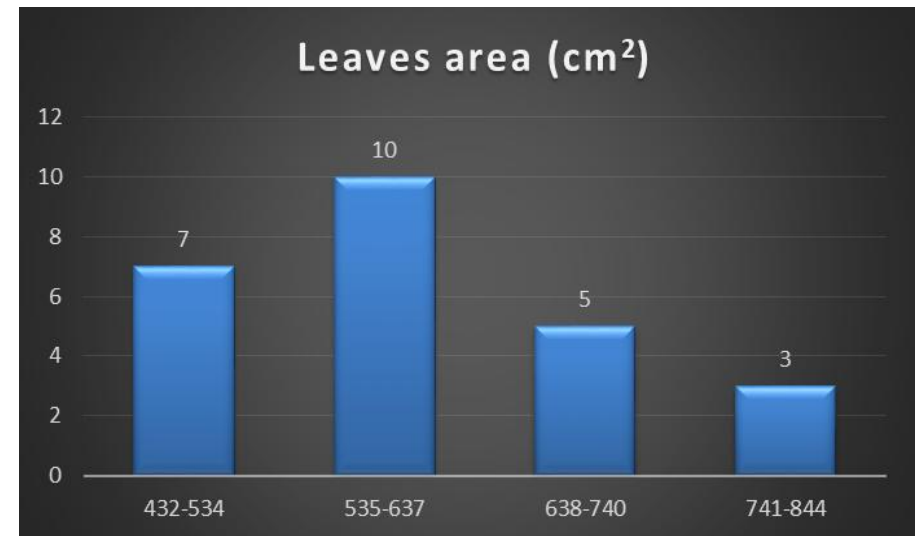
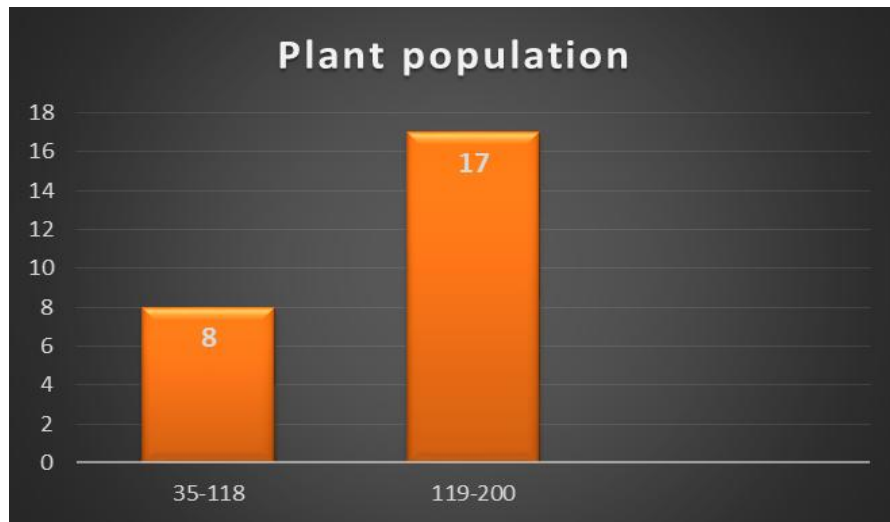
Sr. no.	Genotypes	plant population	Days to 50% flowering	NO. of leaves/plant	4th leaves length (cm)	4th leaves width (cm)	leaves area (cm ²)	Flag leaves length(cm)	plant height (cm)	Brix%
1	SPH2009	145	81	9.33	80	10	592	35	319.8333	16
2	SPV2697	110	79	9.33	95	10	703	35	329.8333	15
3	SPV2789	113	83	9	85	11	691.9	35	279.8333	18
4	SPV2793	149	88	10	85	10	629	35	339.8333	16
5	SPV2794	121	79	9	65	9	432.9	30	309.8333	16
6	SPV2795	199	84	9.33	65	9	432.9	45	339.8333	17
7	SPV2888	178	87	9	90	9	599.4	45	359.8333	17
8	SPV2889	163	73	7.66	75	9	499.5	40	204.8333	16
9	SPV2890	200	84	8.33	75	10	555	35	279.8333	18
10	SPV2891	165	73	8.33	95	10	703	48	309.8333	18
11	SPV2892	143	74	10	75	9	499.5	40	329.8333	16
12	SPV2893	158	75	9	65	9	432.9	40	339.8333	19
13	SPV2894	170	77	8	80	8	473.6	35	304.8333	19
14	SPV2895	130	81	9.33	100	10	740	45	329.8333	19

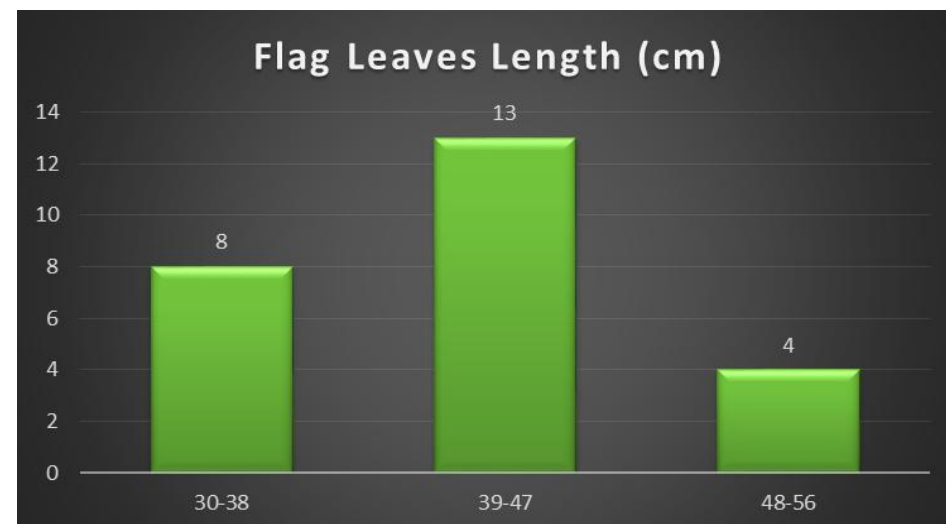
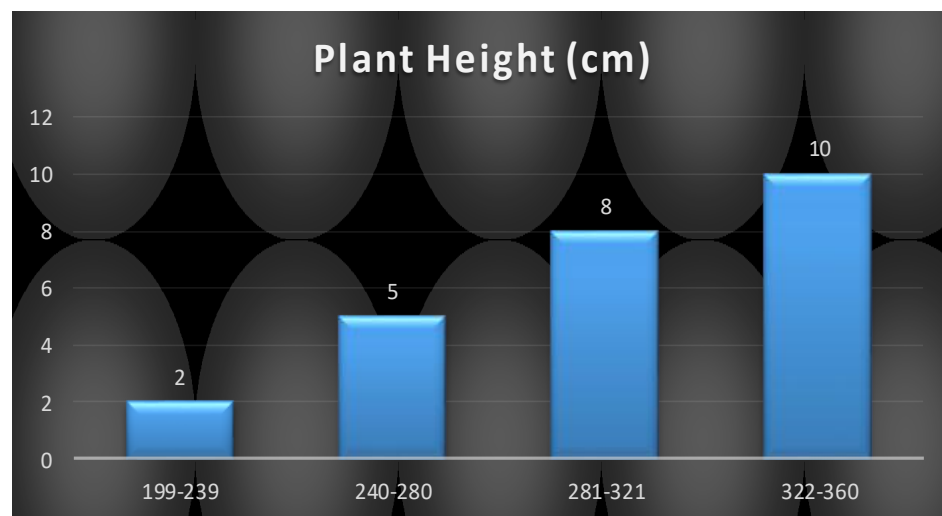
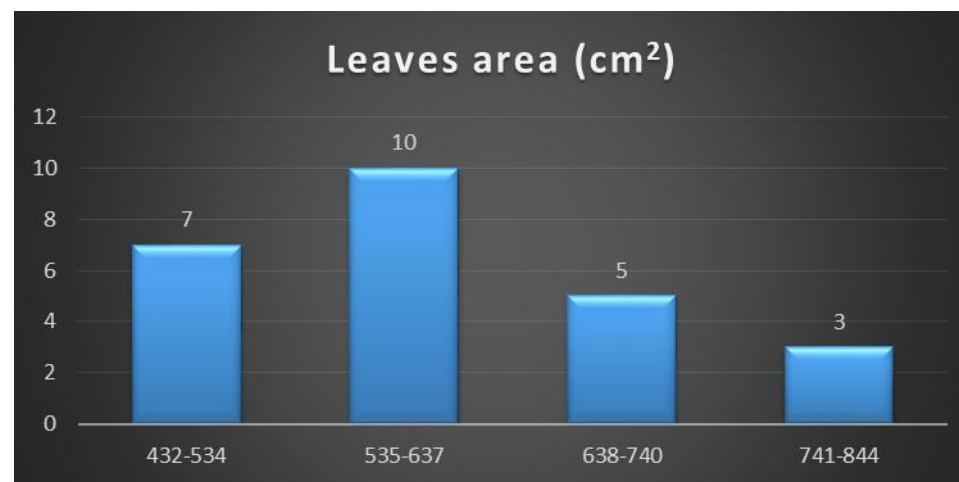
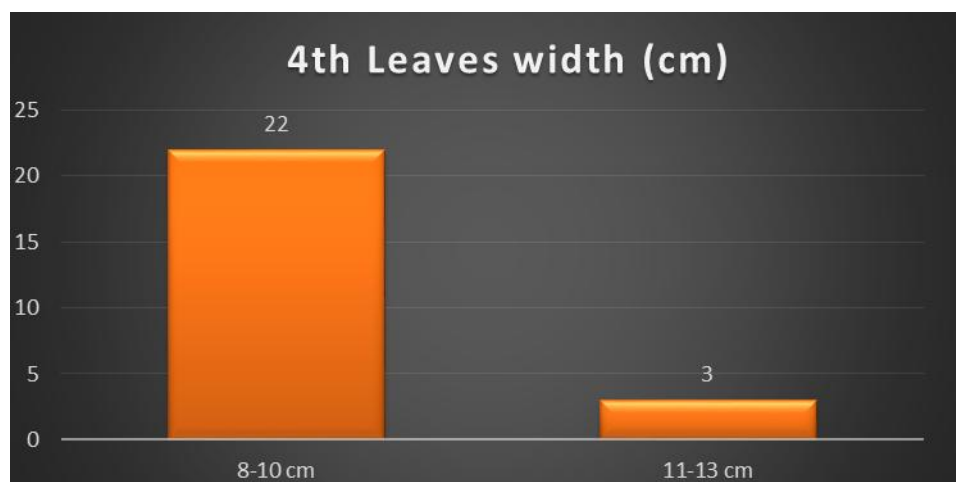
15	CSH2 2SS	145	82	9.66	95	12	843.6	50	359.8333	17
16	CSV19 SS	123	83	8.66	70	9	466.2	45	314.8333	16
17	CSV24 SS	140	76	8.66	85	9	766.1	40	304.8333	16
18	SPV27 14	92	79	9	100	10	747	55	269.8333	15
19	SPV28 12	67	74	9.66	80	10	597.6	40	299.8333	17
20	SPV28 96	100	76	7.66	80	9	537.84	45	329.8333	16
21	SPV28 97	139	78	10	75	10	560.25	40	299.8333	17
22	SPV28 98	110	78	9	80	10	597.6	40	249.8333	11
23	SPV28 99	35	89	9.66	85	11	698.445	35	279.8333	14
24	SPV29 00	158	89	9.33	85	9	571.455	50	329.8333	16
25	CSH2 5	85	76	9	75	10	560.25	40	199.8333	10
	Mean	133.52	80	9.04	81.60	9.68	597.24	40.92	304.63	16.20
	S. E.	0.12	0.12	0.38	0.32	0.12	1.20	3.60	0.12	0.12
	C. D. 5%	0.34	0.34	1.09	0.90	0.34	2.30	5.30	0.34	0.34
	cv	0.34	0.57	1.46	11.18	4.78	5.30	2.30	0.15	2.83

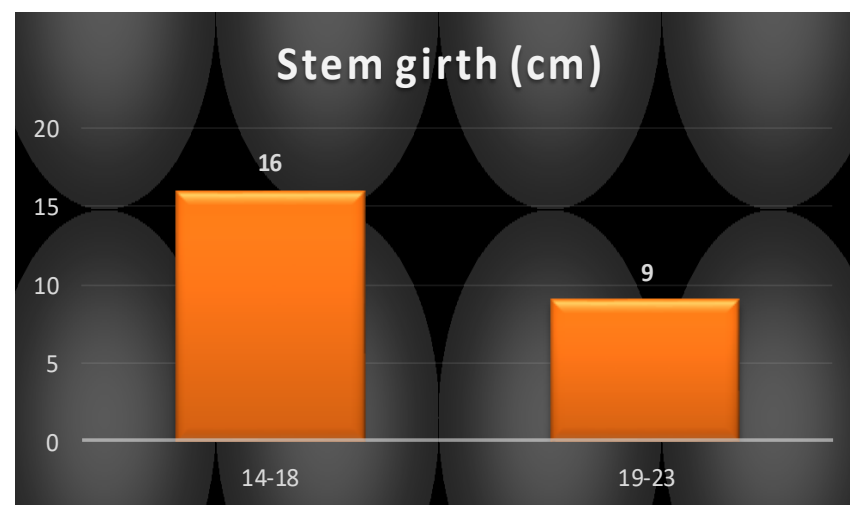
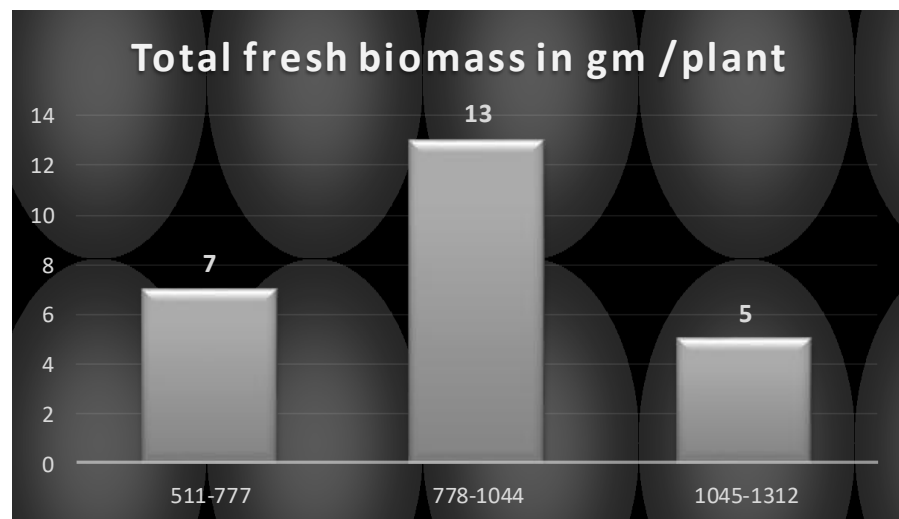
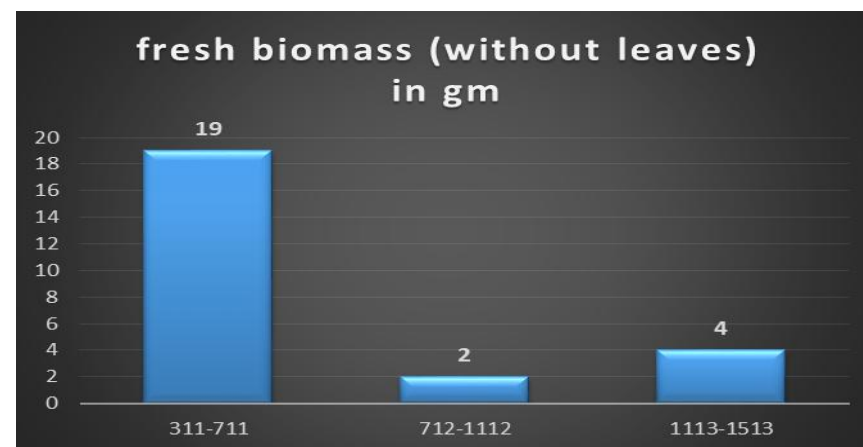
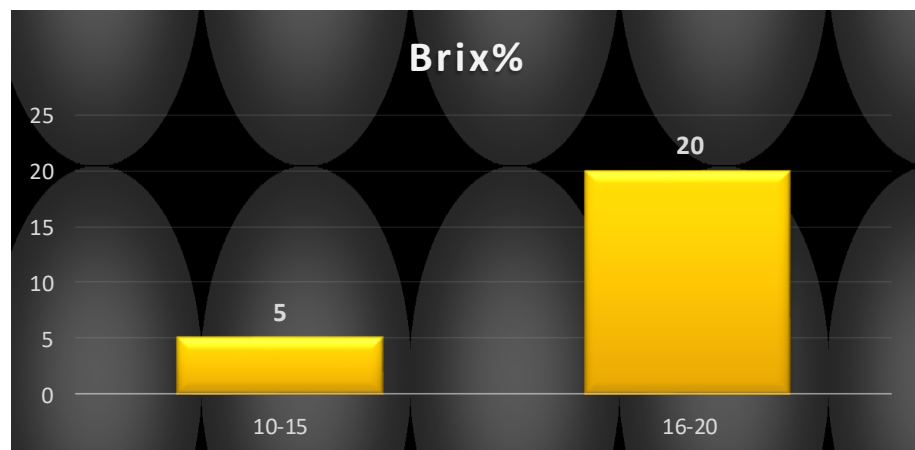
Table: 4.2 (b). Mean Performance of 25 Sorghum genotypes for agronomic traits evaluated under field conditions in Kharif 2021-22.

Sr. no.	Genotypes	stem girth (cm)	total fresh biomass in g/plant	fresh biomass (without leaves) in g/plant	juice yield(lit/plant)	juice yield (g/plant)	juice pH	juice extraction %	no.of internode/plant	100 seed weight (g)	grain yield (g/plant)
1	SPH 2009	19	1188.88	700	1440	168.88	6.4	14.2	12	2.36	55.6
2	SPV2 697	18	1155.55	711.11	1540	121.11	6.5	15.6	11	2.92	15.5
3	SPV2 789	22	1277.77	700	1600	188.88	6.4	14.7	11	3.2	7.7
4	SPV2 793	20	811.11	711.11	480	165.55	6.4	8	11	2.03	10
5	SPV2 794	15	1311.11	688.88	700	83.33	6.3	6.5	11	2.51	10
6	SPV2 795	18	866.66	488.88	340	38.88	6.4	4.5	10	2.66	46.11
7	SPV2 888	16	577.77	311.11	300	34.44	6.5	6	11	2.39	22.22
8	SPV2 889	20	700	844.44	1000	115.55	6.5	16	12	2.29	23.32
9	SPV2 890	18	700	455.55	1380	161.11	6.4	23	10	3.06	40.33
10	SPV2 891	16	844.44	1511.11	1100	128.88	6.3	15	11	2.13	45
11	SPV2 892	14	688.88	411.11	280	32.22	6.5	4.8	13	2.25	37.22
12	SPV2 893	18	800	477.77	500	57.77	6.4	7.2	12	2.41	24.44
13	SPV2 894	14	1011.11	577.77	740	87.77	6.3	8.6	11	2.94	40
14	SPV2 895	15	1311.11	800	1460	170	6.3	13	11	2.23	68.88

15	CSH 22SS	22	1033.33	622.22	1360	162.22	6.4	15.5	11	3.03	49.44
16	CSV 19SS	15	866.66	488.88	680	78.88	6.4	9	13	1.64	16.11
17	CSV 24SS	20	977.77	544.44	1510	175.55	6.4	18	11	2.72	59.22
18	SPV2 714	15	933.33	711.11	100	104.44	5.5	11	10	2.6	31.25
19	SPV2 812	18	1022.22	633.33	72.22	74.44	6.5	7.2	12	1.8	62.5
20	SPV2 896	16	577.77	444.44	23.33	23.33	6.5	4	11	2.3	2.5
21	SPV2 897	17	655.55	577.77	131.11	32.22	6.5	4.8	13	1.6	35
22	SPV2 898	14	511.11	344.44	24.44	26.66	6.5	4.2	12	1.5	62.5
23	SPV2 899	22	944.44	600	76.66	81.11	6.3	8.5	12	1.6	3.75
24	SPV2 900	19	1033.33	666.66	41.11	43.33	6.4	4	11	2.4	6.25
25	CSH 25	20	811.11	566.66	172.22	222.22	6.4	25	11	1.7	77.5
	Mean	17.64	904.44	623.55	682.04	103.15	6.38	10.73	11.36	2.33	34.09
	S. E.	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12
	C. D. 5%	0.34	0.34	0.34	0.34	0.34	0.34	0.34	0.34	0.34	0.34
	cv	2.59	0.05	0.07	0.07	0.43	7.24	4.23	3.99	2.35	1.31







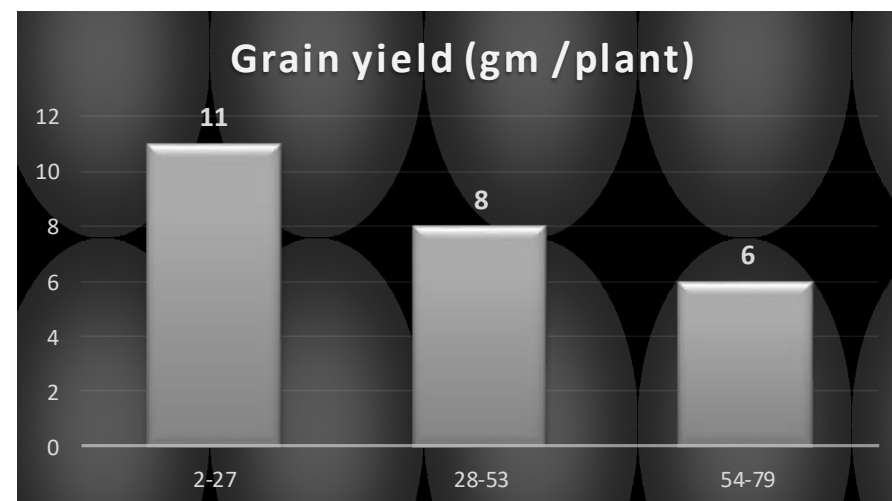
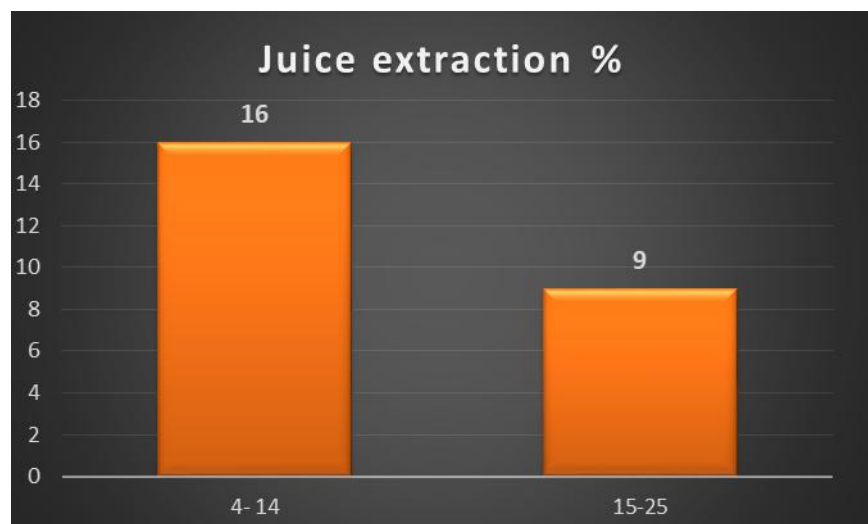
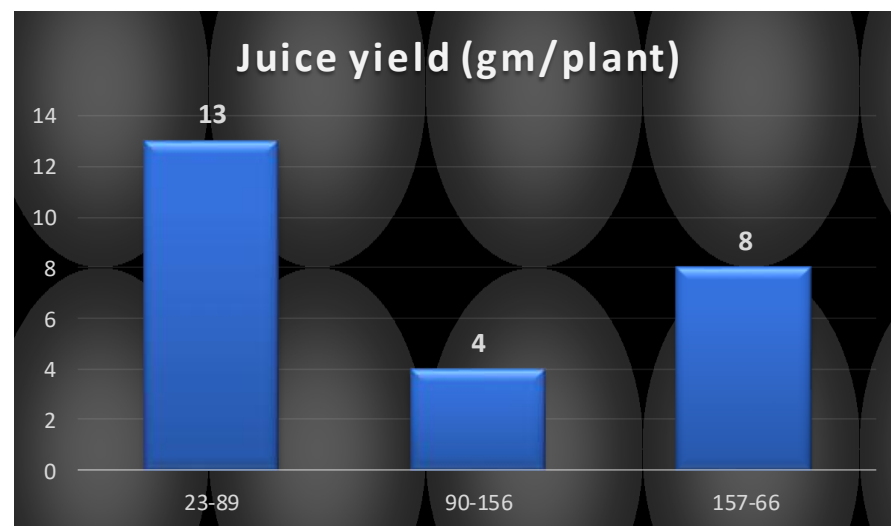
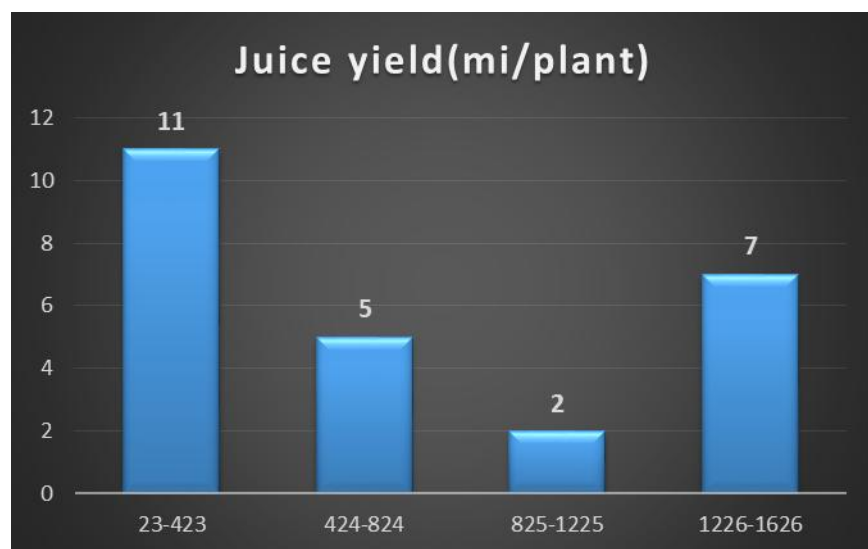


Fig. 4.1. Range values of some of the important morphological observations of Sorghum genotypes.

4.3. Genetic parameters:

4.3.1. Phenotypic and Genotypic coefficient of variation:

Variance plays an important role in crop breeding. The magnitude of variance present in crop species is importance as it provides the basis for selection. The total variation present in a population arises due to genotypic and environmental effects. Presence of genetic variance in the breeding materials is essential for a successful plant breeding program. During present investigation, genotypic coefficient of variation was lower than phenotypic coefficient of variation for all traits studied.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were categorized as low (<10%), moderate (10-20%) and high (> 20%) as suggested by Sivasubramanian and Madhavamenon (1973). juice yield (lit/plant) had the highest PCV and GCV content (85.106, 84.106), pursued by grain yield (65.489, 64.523), juice yield (58.283, 57.145), juice extraction % (55.78, 53.72), fresh biomass (36.765, 35.452), plant population (29.359, 28.124), total fresh biomass (25.487, 23.541), 100 seed weight (g) (21.344, 20.452) and moderate for leaves area (19.211, 18.214), Flag leaves length (14.695, 13.542), stem girth (14.626, 13.523), plant height (13.472, 12.345), Brix% (13.215, 12.210), 4th leaves length (12.597, 11.145) and low for 4th leaves width (8.806, 7.128), number of internode/plant (7.572, 6.523), days to 50% flowering (6.224, 5.236), number of leaves/plant (5.963, 4.236) and juice ph (3.08, 2.103) (Table 4.3) and (Fig 4.3).

4.3.2. Heritability in Broad Sense (%)

Heritability in broad sense was presented in Table 4.3. Heritability estimates were classified as high (> 70%), moderate (50- 70%) and low (< 50%). 2 out of 19 characters have higher heritability estimates including juice yield lit/plant (83.381) and plant population (73.096), moderate for days to 50% flowering (65.782), plant height (63.361), juice yield g/plant (62.202), total fresh biomass (61.137), stem girth (53.532), and grain yield (50.817).

The low heritability was observed for juice extraction % (49.627), 100 seed weight (g) (45.326), leaves area (43.609), 4th leaves length (40.30), number of leaves/plant (37.508), 4th leaves width (36.563), Brix% (35.756), fresh biomass (32.513), Flag leaves length (21.272), number of internode/plant (17.99) and juice pH (10.143).

4.3.3. Genetic advance as percentage of mean:

Genetic advance as percentage of mean was estimated for all the characters under study. The genetic advance was classified as suggested by Johnson *et al.* (1955) *i.e.*, high ($> 20\%$), moderate (10-20%) and low ($< 10\%$). The high genetic advance as percentage of mean (at 5% selection intensity) was recorded for juice yield lit/plant (175.319), grain yield (134.907), juice yield (g/plant) (120.062), juice extraction % (114.906), fresh biomass (75.736), plant population (60.48), total fresh biomass (52.504), 100 seed weight (43.968), leaves area (39.574), flag leaves length (30.272), stem girth (30.13), plant height (27.753), Brix% (27.223), 4th leaves length (25.951), moderate for 4th leaves width (18.141), number of internode/plant (15.599), days to 50% flowering (12.822) and number of leaves/plant (10.003) low for juice pH (6.345). (Table 4.3).

4.4. Identified desirable sweet sorghum genotypes

Total of ten genotypes out of 25 genotypes were identified as desirable sweet sorghum genotypes based on Brix percentage, total fresh biomass juice yield (lit/plant) and juice extraction %. Genotype SPV2890 was highest in juice extraction (16.00%) with 1380 lit/plant of juice yield, 700g of total fresh biomass and with 18% of Brix percentage. Genotypes namely SPV2789, SPV2889, SPV2891, SPV2893, SPV2894, SPV2895 CSH22SS, CSV19SS and CSV24SS were found superior among 25 genotypes in sweetness index based on above parameters. (Table 4.4)

4.5. Association analysis:

4.5.1 Correlation coefficient analysis

Genotypic and phenotypic correlation coefficient among grain yield and its contributing characters are presented in [Table 4.5(a) & 4.5 (b)].

4.5.2 Phenotypic correlation coefficient

4th leaves length (cm)

4th leaves length exhibited significant and highly positive association with days to 50% flowering (0.291).

4th leaves length (cm)

4th leaves length exhibited significant and positive association with days to 50% flowering (0.234). It exhibited highly significant positive correlation with number of leaves/plant (0.397) and 4th leaves length (0.584).

Leaves area (cm²)

Leaves area exhibited significant positive correlation with Days to 50% flowering (0.258) and number of leaves/plant (0.287). It had highly significant positive correlation with 4th leaves length (0.814) and 4th leaves width (0.862).

Flag leaves length (cm)

Flag leaves length demonstrated highly significant positive association with Days to 50% flowering (0.314), 4th leaves length (0.525) and leaves area (cm²) (0.417). It also had demonstrated significant positive association with 4th leaves width (0.263).

Plant height (cm)

Plant height exhibited significant positive association with Plant population (0.246) and number of leaves/plant (0.239)

Brix%

Brix% exhibited highly positive and significant association with Plant population (0.461). It also had demonstrated significant positive association with plant height (0.227).

Stem girth (cm)

Stem girth demonstrated highly significant positive association with Days to 50% flowering (0.314), number of leaves/plant (0.349), 4th leaves length (0.298) 4th leaves width (0.562) and leaves area (0.518).

Total fresh biomass in g/plant

Total fresh biomass exhibited significant positive association with number of leaves/plant (0.271) and highly positive association with 4th leaves length (0.373), 4th leaves width (0.431), leaves area (0.463) and stem girth (0.534).

Total fresh biomass (without leaves) in g/plant

Total fresh biomass demonstrated highly significant positive association with 4th leaves length (0.413), 4th leaves width (0.391), leaves area (0.449), stem girth (0.435) and total fresh biomass (0.676).

Juice yield (lit/plant)

Juice yield (lit/plant) exhibited highly significant positive association with Plant population (0.396), Brix% (0.344), total fresh biomass (0.523) and fresh biomass (0.329). It also had exhibited significant positive association with stem girth (0.261).

Juice yield (g/plant)

Juice yield g/plant exhibited significant positive association with 4th leaves length (0.275). It also had exhibited highly significant positive association with 4th leaves width (0.350), leaves area (0.393), stem girth (0.580), total fresh biomass (0.569), fresh biomass (0.497) and juice yield (lit/plant) (0.633).

Juice pH

Juice pH exhibited significant positive association with Plant population (0.258). It also had demonstrated significant negative association with total fresh biomass (-0.226), fresh biomass (-0.256) and juice yield (g/plant) (-0.224).

Juice extraction %

Juice extraction % demonstrated significant positive association with 4th leaves width (0.264), leaves area (0.235), total fresh biomass (0.242) and highly significant negative association with plant height (-0.373). It also had demonstrated highly significant positive association with stem girth (0.406), fresh biomass (0.304), juice yield (lit/plant) (0.486) and juice yield (g/plant) (0.813).

Number of internode/plant

Number of internode/plant demonstrated significant positive association with number of leaves/plant (0.287). It also had demonstrated highly significant negative association with juice yield (lit/plant) (-0.325) and negative association with juice extraction % (-0.226).

100 seed weight (g)

100 seed weight demonstrated significant positive association with 4th leaves length (0.245), leaves area (0.284), Brix% (0.288), stem girth (0.256) and juice extraction % (0.257) and highly positive association with total fresh biomass (0.381), juice yield (lit/plant) (0.396) and juice yield (g/plant) (0.382).

Grain yield (g/plant)

Grain yield demonstrated negative significant association with days to 50% flowering (-0.272). It also had demonstrated significant positive association with number of leaves/plant (0.224) and highly significant positive association with 4th leaves width (0.311), leaves area (0.299), juice yield (g/plant) (0.326) and juice extraction % (0.392).

Table 4.3. Estimation of range, mean and different genetic parameters for different characters in 25 genotypes of Sorghum.

Sr. No.	Character	Mean	Range		PCV (%)	GCV (%)	Heritability (Broad sense)	Genetic advance as % of mean 5%
			min	max				
1	plant population	133.52	35	200	29.359	28.124	73.096	60.48
2	Days to 50% flowering	80	73	89	6.224	5.236	65.782	12.822
3	NO. of leaves/plant	9.04	7.67	10	5.963	4.236	37.508	10.003
4	4th leaves length (cm)	81.60	65	100	12.597	11.145	40.3	25.951
5	4th leaves width	9.68	8	12	8.806	7.128	36.563	18.141
6	leaves area (cm ²)	597.24	432.9	843.6	19.211	18.214	43.609	39.574
7	Flag leaves length(cm)	40.92	30	55	14.695	13.542	21.272	30.272
8	plant height (cm)	304.63	199.83	359.83	13.472	12.345	63.361	27.753
9	Brix%	16.20	10	19	13.215	12.210	35.756	27.223
10	stem girth (cm)	17.64	14	22	14.626	13.523	53.532	30.13
11	total fresh biomass in g/plant	904.44	511.11	1311.11	25.487	23.541	61.137	52.504
12	fresh biomass (without leaves) in	623.55	311.11	1511.11	36.765	35.452	32.513	75.736

	g/plant							
13	juice yield(lit/plant)	682.04	23.33	1600	85.106	84.106	83.381	175.319
14	juice yield (g/plant)	103.15	23.33	222.22	58.283S	57.145	62.202	120.062
15	juice ph	6.38	5.50	6.50	3.08	2.103	10.143	6.345
16	juice extraction %	10.73	4	25	55.78	53.72	49.627	114.906
17	no.of internode/plant	11.36	10	13	7.572	6.523	17.99	15.599
18	100 seed weight (g)	2.33	1.50	3.20	21.344	20.452	45.326	43.968
19	grain yield (g/plant)	34.09	2.50	77.50	65.489	64.523	50.817	134.907

PP = Plant population, **DF 50%** = Days to 50% flowering, **NLP** = Number of leaves/plant, **4LL** = 4th leaves length (cm), **4LW** = 4th leaves width (cm), **LA** = leaves area (cm²), **FLL** = Flag leaves length (cm), **PH** = plant height (cm), **BRIX** = Brix%. **STG** = stem girth (cm), **TFB** = fresh biomass (without leaves) in g/plant, **JY1** = juice yield (lit/plant), **JY2** = juice yield (g/plant), **JP** = juice ph, **JE** = juice extraction %, **NNP** = number of internode/plant, **HSW** = 100 seed weight (g) and **GLYD** = grain yield (g/plant).

Table 4.4. Identified desirable sweet Sorghum genotypes to be utilized in crop improvement programme to develop high brix and high biomass.

Sr.no.	Sweet Sorghum genotypes	Brix%	total fresh biomass in gm /plant	juice yield (lit/plant)	juice extraction %
1	SPV2890	18.00	700.00	1380	23.00
2	CSV24SS	16.00	977.77	1510	18.00
3	CSH22SS	17.00	1033.33	1360	15.50
4	SPV2891	18.00	844.44	1100	15.00
5	SPV2889	16.00	700.00	1000	16.00
6	SPV2789	18.00	1277.77	1600	14.70
7	SPV2895	19.00	1311.11	1460	13.00
8	SPV2894	19.00	1011.11	740	8.60
9	CSV19SS	16.00	866.66	680	9.00
10	SPV2893	19.00	800.00	500	7.20

Table 4.5 (a). Phenotypic correlation coefficient for grain yield and its 19 attributing characters in Sorghum.

Charact ers	PP	DF 50%	NLP	4LL	4LW	LA	FLL	PH	BRIX	STG	TFB	TFB WL	JY1	JY2	JP	JE	NN P	HS W	GLY D
PP	1																		
DF 50%	0.04 9	1																	
NLP	- 0.22 1	0.14 2	1																
4LL	- 0.09 1	0.29 1**	0.12 3	1															
4LW	- 0.18 8	0.23 4*	0.39 7**	0.58 4**	1														
LA	- 0.17 5	0.25 8*	0.28 7*	0.81 4**	0.86 2**	1													
FLL	- 0.10 6	0.31 4**	0.03 8	0.52 5**	0.26 3*	0.41 7**	1												
PH	0.24 6*	0.22	0.23 9*	0.15 7	0.02 6	0.04 3	0.12 2	1											
BRIX	0.46 1**	0.16 3	- 0.22 1	0.08 5	- 0.09 3	0	0.04 4	0.22 7*	1										
STG	- 0.20 7	0.31 4**	0.34 9**	0.29 8**	0.56 2**	0.51 8**	0.16 7	- 0.06 7	- 0.03 9	1									
TFB	- 0.12 8	0.20 7	0.27 1*	0.37 3**	0.43 1**	0.46 3**	0.15 4	0.06 9	0.19 1	0.53 4**	1								
TFBWL	- 0.13 2	0.07 5	0.14 9	0.41 3**	0.39 1**	0.44 9**	0.18 8	-0.01	0.14	0.43 5**	0.67 6**	1							

JY1	0.39 6**	0.05 6	- 0.07 9	0.16 6	0.12 1	0.18 4	- 0.12 1	0.05 1	0.34 4**	0.26 1*	0.52 3**	0.329*	1						
JY2	- 0.01 3	0.02 7	0.06 8	0.27 5*	0.35 0**	0.39 3**	- 0.08 5	- 0.20 8	- 0.00 5	0.58 0**	0.56 9**	0.497*	0.63 3**	1					
JP	0.25 8*	- 0.07 3	0.15 8	- 0.13 3	- 0.01 8	- 0.14 5	- 0.21 3	0.18 5	0.05 4	- 0.03 4	- 0.22 6	- 0.256*	0.06 7	- 0.22 4	1				
JE	- 0.05 1	- 0.14 4	- 0.03 9	0.08 7	0.26 4*	0.23 5*	- 0.17 2	- 0.37 3**	-0.1	0.40 6**	0.24 2*	0.304*	0.48 6**	0.81 3**	- 0.11 6	1			
NNP	- 0.19 4	0.06 3	0.28 7*	-0.08	- 0.04 7	- 0.07 3	0.10 3	0.11 3	- 0.08 1	0.00 4	0.01 8	0.125	- 0.32 5**	- 0.15 8	0.04 4	- 0.22 6*	1		
HSW	0.21 7	0.01	0.00 8	0.24 5*	0.20 8	0.28 4*	0.04 5	0.19	0.28 8*	0.25 6*	0.38 1**	0.209	0.39 6**	0.38 2**	- 0.14 4	0.25 7*	- 0.21 6	1	
GLYD	- 0.12 3	- 0.27 2*	0.22 4*	0.13	0.31 1**	0.29 9**	0.02 2	- 0.20 1	- 0.12 8	0.21 3	0.21 4	0.202	0.02 4	0.32 6**	0.00 8	0.39 2**	0.10 7	0.09 3	1

*, Significant at the 0.05 level (2-tailed). **, Significant at the 0.01 level (2-tailed).

PP = Plant population, **DF 50%** = Days to 50% flowering, **NLP** = Number of leaves/plant, **4LL** = 4th leaves length (cm), **4LW** = 4th leaves width (cm), **LA** = leaves area (cm²), **FLL** = Flag leaves length (cm), **PH** = plant height (cm), **BRIX** = Brix%. **STG** = stem girth (cm), **TFB** = fresh biomass (without leaves) in g/plant, **JY1** = juice yield (lit/plant), **JY2** = juice yield (g/plant), **JP** = juice ph, **JE** = juice extraction %, **NNP** = number of internode/plant, **HSW** = 100 seed weight (g) and **GLYD** = grain yield (g/plant)

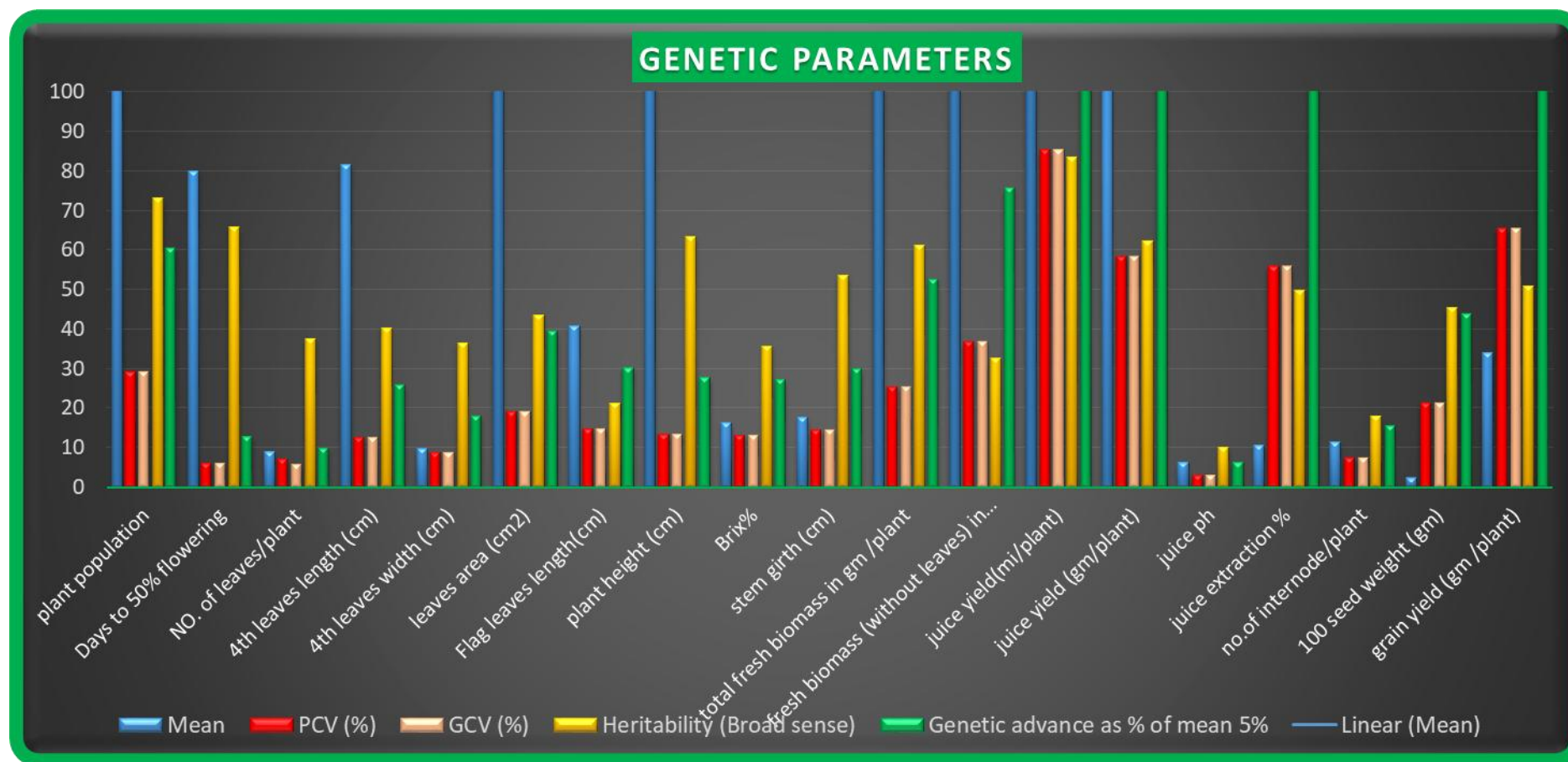


Fig. 4.2. Genetic parameter summary graph of 25 Sorghum genotypes.

4.5.2 Genotypic correlation coefficient

Number of leaves/plant

Number of leaves/plant demonstrated highly negatively associated with Plant population (-0.407). It had highly positive association with Days to 50% flowering (0.392).

4th leaves length (cm)

4th leaves length demonstrated highly significant positive association with Days to 50% flowering (0.560).

4th leaves width (cm)

4th leaves width highly negatively associated with Plant population (-0.391). It had positive correlation with Days to 50% flowering (0.239), highly positive association with number of leaves/plant (0.520) and 4th leaves length (0.642).

Leaves area (cm²)

Leaves area highly negatively associated with Plant population (-0.329). It had highly positive and significant association with Days to 50% flowering (0.432), NUMBER of leaves/plant (0.317), 4th leaves length (0.841) and 4th leaves width (0.959).

Flag leaves length (cm)

Flag leaves length highly negatively associated with Plant population (-0.415). It also had demonstrated highly significant positive association with Days to 50% flowering (0.502), 4th leaves length (0.662) and leaves area (0.491).

Plant height (cm)

Plant height exhibited significant and positive association with Plant population (0.287) and 4th leaves length (0.227). It also had exhibited highly positive association with NUMBER of leaves/plant (0.438).

Brix %

Brix% exhibited significant and highly positive association with Plant population (0.870), Days to 50% flowering (0.434) and plant height (0.491).

Stem girth (cm)

Stem girth highly negatively associated with Plant population (-0.340). It also had exhibited highly positive association with Days to 50% flowering (0.478), NUMBER of leaves/plant (0.391), 4th leaves length (0.697), 4th leaves width (1.060) and leaves area (0.941) and significant positive association with Flag leaves length (0.245). It also had demonstrated negative association with plant height (-0.231).

Total fresh biomass in g/plant

Total fresh biomass manifested significant and highly positive association with Days to 50% flowering (0.296), Number of leaves/plant (0.391), 4th leaves length (0.700), 4th leaves width (0.933), leaves area (0.902) and stem girth (0.877). It also had demonstrated positive association with Brix% (0.277).

Fresh biomass (without leaves) in g/plant

Fresh biomass negatively associated with Plant population (-0.239). It also had manifested highly positive association with Days to 50% flowering (0.336), Number of leaves/plant (0.360), 4th leaves length (0.751), 4th leaves width (1.096), leaves area (1.009), stem girth (0.956) and total fresh biomass (0.948).

Juice yield (lit/plant)

Juice yield (lit/plant) demonstrated significant and highly positive association with Plant population (0.524), 4th leaves length (0.344), 4th leaves width (0.305), leaves area (0.352), Brix% (0.538), stem girth (0.375), total fresh biomass (0.664) and fresh biomass (0.545). It also had manifested negative association with Number of leaves/plant (-0.252) and highly negative association with Flag leaves length (-0.345).

Juice yield (g/plant)

Juice yield manifested significant and highly positive association with 4th leaves length (0.817), 4th leaves width (0.907), leaves area (0.930), stem girth (0.756), total fresh biomass (0.871), fresh biomass (0.954) and juice yield (lit/plant) (0.722). It also had demonstrated negative association with plant height (-0.241).

Juice pH

Juice pH expressed significant and highly positive association with Plant population (0.677). It also had expressed highly negative association with Days to 50% flowering (-0.540), Number of leaves/plant (-0.640), 4th leaves length (-1.502), 4th leaves width (-1.555), leaves area (-1.462), Flag leaves length (-1.012), stem girth (-0.989), total fresh biomass (-1.028), fresh biomass (-1.391) and juice yield (g/plant) (-0.817).

Juice extraction %

Juice extraction % expressed significant and highly positive association with 4th leaves length (0.569), 4th leaves width (0.722), leaves area (0.739), stem girth (0.747), total fresh biomass (0.700), fresh biomass (0.903), juice yield (lit/plant) (0.536) and juice yield (g/plant) (0.961). It also had expressed highly negative association with plant height (-0.504) and juice Ph (-0.803).

Number of internode/plant

Number of internode/plant highly negatively associated with Plant population (-0.318), Brix% (-0.761), total fresh biomass (-0.297), fresh biomass (-0.430), juice yield (lit/plant) (-0.856), juice yield (g/plant) (-0.728) and juice extraction % (-0.756). It also had expressed highly positive association with Days to 50% flowering (0.555), Number of leaves/plant (1.170), 4th leaves width (0.379), flag leaves length (0.527) and plant height (0.321).

100 seed weight (g)

100 seed weight revealed significant and positive association with Plant population (0.256) and 4th leaves length (0.227). It also had revealed highly positive association with 4th leaves length (0.467), 4th leaves width (0.428), leaves area (0.509), Brix% (0.869), stem girth (0.451), total fresh biomass (0.815), fresh biomass (0.579), juice yield (lit /plant) (0.568), juice yield (g/plant) (0.617), juice extraction % (0.437).

It also had revealed highly negative association with juice Ph (-0.594) and number of internode/plant (-0.470).

Grain yield (g/plant)

Grain yield revealed highly negatively associated with Plant population (-0.318), Days to 50% flowering (-0.298), Brix% (-0.452), juice pH (-0.610) and negatively associated with plant height (cm) (-0.229). It also had revealed highly positive association with number of leaves/plant (0.442), 4th leaves length (0.336), 4th leaves width (0.767), leaves area (0.727), stem girth (0.449), total fresh biomass (0.417), fresh biomass (0.577), juice yield (g/plant) (0.506), juice extraction % (0.435) and number of internode/plant (0.394).

Table 4.5 (b). Genotypic correlation coefficient for grain yield and its 19 attributing characters in Sorghum.

Charact ers	PP	DF 50%	NLP	4LL	4L W	LA	FLL	PH	BRI X	STG	TFB	TFB WL	JY1	JY2	JP	JE	NNP	HS W	GLY D
PP	1																		
DF 50%	-0.036	1																	
NLP	-0.407**	0.392**	1																
4LL	-0.198	0.560**	0.079	1															
4LW	-0.391**	0.239*	0.520**	0.642*	1														
LA	-0.329**	0.432**	0.317**	0.841*	0.959**	1													
FLL	-0.415**	0.502**	0.046	0.662*	0.214	0.491*	1												
PH	0.287*	0.201	0.438**	0.227*	0.162	-0.045	0.112	1											
BRIX	0.870**	0.434**	-0.031	0.213	0.065	0.072	0.216	0.469*	1										
STG	-0.340**	0.478**	0.391**	0.697*	1.060**	0.941*	0.245*	-0.231*	0.053	1									
TFB	-0.136	0.296**	0.391**	0.700*	0.933**	0.902*	0.193	0.068	0.277*	0.877**	1								
TFBWL	-0.239*	0.336**	0.360**	0.751*	1.096**	1.009*	-0.047	-0.167	-0.057	0.956**	0.948*	1							
JY1	0.524**	0.126	-0.252*	0.344*	0.305**	0.352*	-0.345**	0.089	0.538**	0.375**	0.664*	0.545*	1						
JY2	0.002	0.159	-0.125	0.817*	0.907**	0.930*	-0.102	-0.241*	0.066	0.756**	0.871*	0.954*	0.722*	1					
JP	0.677**	-0.540**	-0.640**	1.502*	1.555**	1.462*	-1.012**	0.209	0.192	0.989**	1.028*	1.391*	0.158	0.817*	1				
JE	-0.109	-0.038	-0.204	0.569*	0.722**	0.739*	-0.146	0.504*	-0.222	0.747**	0.700*	0.903*	0.536*	0.961*	-0.803*	1			

NNP	-0.318**	0.555**	1.170**	-0.026	0.379**	0.209	0.527**	0.321*	-0.761**	0.204	-0.297*	-0.430*	-0.856*	-0.728*	-0.143	-0.756*	1		
HSW	0.256*	0.034	-0.18	0.467*	0.428**	0.509*	0.079	0.256*	0.869**	0.451**	0.815*	0.579*	0.568*	0.617*	-0.594*	0.437*	-0.470*	1	
GLYD	-0.318**	-0.298**	0.442**	0.336*	0.767**	0.727*	0.111	-0.229*	-0.452**	0.449**	0.417*	0.577*	-0.059	0.506*	-0.610*	0.435*	0.394*	0.206	1

*. Significant at the 0.05 level (2-tailed). **. Significant at the 0.01 level (2-tailed).

PP = Plant population, **DF 50%** = Days to 50% flowering, **NLP** = Number of leaves/plant, **4LL** = 4th leaves length (cm), **4LW** = 4th leaves width (cm), **LA** = leaves area (cm²), **FLL** = Flag leaves length (cm), **PH** = plant height (cm), **BRIX** = Brix%, **STG** = stem girth (cm), **TFB** = fresh biomass (without leaves) in g/plant, **JY1** = juice yield (lit/plant), **JY2** = juice yield (g/plant), **JP** = juice ph, **JE** = juice extraction %, **NNP** = number of internode/plant, **HSW** = 100 seed weight (g) and **GLYD** = grain yield (g/plant).

4.6. Path coefficient analysis:

The association of different component characters among themselves and with yield is quite important for planning an efficient selection criterion for yield. Path analysis is a Bio-metrical tool and it is a standardized partial regression coefficient. Path analysis used to split the correlation coefficient into the measures of direct and indirect effects on dependent variables by a set of independent variables if the correlation between yield and character is due to the direct effects of character or indirect effect of character. Direct effect reflects true relationship between dependent and independent character and selection can be practiced for such a character in order to improve yield. Indirect effect reflects that independent character indirectly correlated to the dependent character through another component trait. Path coefficient analysis was carried out using phenotypic correlation and grain yield per plant as a dependent variable presented in [Table 4.6 and Table 4.6 (b)].

4.6.1. Genotypic path coefficient analysis:

Direct effect on grain yield per plant:

The genotypic path coefficient analysis of different morpho-physiological and yield traits on grain yield per plant *via* [Table: 4.6 (a) and Fig 4.3] hundred seed weight (1.1591), had considerably higher estimates of positive direct effect pursued by plant population (1.1423), total fresh biomass (0.9439), leaves area (0.5553), number of internode/plant (0.455), juice extraction % (0.4488), 4th leaves width (0.3252), juice ph (0.1005), 4th leaves length (0.0846), Brix% (0.0636) and number of leaves/plant (0.0527). Whereas negative direct effect on grain yield per plant manifested by days to 50% flowering (-0.91), fresh biomass (-0.8098), juice yield (-0.3916), plant height (-0.1421), stem girth (-0.1202), juice yield (-0.0757) and flag leaves length (-0.0157).

Plant population 50%

Plant population 50% manifested remarkably positive indirect effect on grain yield per plant *via* Brix% (0.6003), hundred seed weight (0.521), plant height (0.378), juice yield (0.3516), juice ph (0.2239), flag leaves length (0.0987), Days to 50% flowering (0.0815), juice extraction % (0.0337) and fresh biomass (0.0293). Whereas negative direct effect on grain yield per plant exhibited by 4th leaves width (-0.4513), leaves area (-0.3481), number of leaves/plant (-0.3203), number of internode/plant (-

0.2889), 4th leaves length (-0.2239), total fresh biomass (-0.2191), stem girth (-0.1715) and juice yield (-0.0556).

Days to 50% flowering

Days to 50% flowering exhibited appreciably positive indirect effect on grain yield per plant *via* number of internode/plant (0.2329), fresh biomass (0.2145), juice extraction % (0.1409), juice ph (0.0446) and flag leaves length juice yield (0.0434). Whereas negative direct effect on grain yield per plant exhibited by number of leaves/plant (-0.3971), plant height (-0.3017), stem girth (-0.2933), 4th leaves width (-0.2268), leaves area (-0.1366), 4th leaves length (-0.1358), total fresh biomass (-0.1355), hundred seed weight (-0.0684), plant population (-0.065), juice yield (-0.0183), brix% (-0.0085) and flag leaves length (-0.0011).

Number of leaves/plants

Number of leaves/plants exhibited remarkably positive indirect effect on grain yield per plant *via* Days to 50% flowering (0.023), 4th leaves width (0.0286), plant height (0.0222), number of internode/plant (0.0172), leaves area (0.0151), total fresh biomass (0.0132), 4th leaves length (0.0066), and juice ph (0.0026). Whereas negatively indirect effect shown by days to maturity (-0.0170), biological yield per plant (-0.0256) and pods per plant (-0.0351).

4th leaves length

4th leaves length exhibited remarkably positive indirect effect on grain yield per plant *via* leaves area (0.0743), 4th leaves width (0.0394), flag leaves length (0.0361), fresh biomass (0.0347), juice yield (g/plant) (0.0277), juice yield(lit/plant) (0.0241), total fresh biomass (0.021), juice extraction % (0.0193), 100 seed weight (0.0163), days to 50% flowering (0.0126), No. of leaves/plant (0.0106), stem girth (0.0066) and brix% (0.0043) Whereas negative direct effect on grain yield per plant exhibited by plant population (-0.0166), no. of internode/plant (-0.0277) and juice ph (-0.0324).

4th leaves width

4th leaves width exhibited remarkably positive indirect effect on grain yield per plant *via* leaves area (0.2313), stem girth (0.1856), no. of leaves/plant (0.1756), 4th leaves length (0.1512), juice yield (g/plant) (0.1483), juice extraction % (0.1138), juice yield(lit/plant) (0.0821), days to 50% flowering (0.081), total fresh biomass (0.076), fresh biomass (0.0701), flag leaves length (0.0195) and 100 seed weight

(0.0018) while negatively indirect effect shown by no. of internode/plant (-0.0207), plant height (-0.0219), juice pH (-0.0317), brix% (-0.0549) and plant population (-0.1285).

Leaves area

Leaves area manifested significantly positive indirect effect on grain yield per plant *via* 4th leaves length (0.4877), 4th leaves width (0.395), juice yield (g/plant) (0.2771), juice yield(lit/plant) (0.2187), juice extraction % (0.2144), stem girth (0.2112), fresh biomass (0.1869), flag leaves length (0.1704), total fresh biomass (0.1641), no. of leaves/plant (0.159), 100 seed weight (0.1027), days to 50% flowering (0.0833) and plant height (0.0392) while negatively indirect effect shown by brix% (-0.0292), no. of internode/plant (-0.1501), juice pH (-0.1636) and plant population (-0.1692).

Flag leaves length

Flag leaves length manifested remarkably positive indirect effect on grain yield per plant *via* juice pH (0.0065), juice yield(lit/plant) (0.0039), total fresh biomass (0.0033), juice yield (g/plant) (0.0031), no. of internode/plant (0.0029), stem girth (0.0024), juice extraction % (0.002), no. of leaves/plant (0.0009), 100 seed weight (0.0006) and days to 50% flowering while negatively indirect effect shown by brix% (-0.0006), 4th leaves width (-0.0009), plant population (-0.0014), fresh biomass (-0.0023), plant height (-0.0027), leaves area (-0.0048) and 4th leaves length (-0.0067).

Plant height

Plant height manifested remarkably positive indirect effect on grain yield per plant *via* juice extraction % (0.0647), juice yield (g/plant) (0.04), stem girth (0.0191), fresh biomass (0.0141), 4th leaves width (0.0096) and no. of internode/plant (0.0081) while negatively indirect effect shown by leaves area (-0.01), juice yield(lit/plant) (-0.0153), juice pH (-0.0197), 4th leaves length (-0.0212), total fresh biomass (-0.0244), flag leaves length (-0.0245), 100 seed weight (-0.041), plant population (-0.047), days to 50% flowering (-0.0471), no. of leaves/plant (-0.0598) brix% (-0.0803).

Brix%

Brix% indicated remarkably positive indirect effect on grain yield per plant *via* plant height (0.0359), plant population (0.0334), 100 seed weight (0.0321), juice yield(lit/plant) (0.0258), total fresh biomass (0.0174), fresh biomass (0.0144), 4th leaves length (0.0032), flag leaves length (0.0023), juice Ph (0.0008) and days to 50% flowering (0.0006), while negatively indirect effect shown by juice yield (g/plant) (-0.0025), leaves area (-0.0033), stem girth (-0.0054), no. of internode/plant (-0.0069), juice extraction % (-0.0079), no. of leaves/plant (-0.0089) and 4th leaves width (-0.0107).

Stem girth

Stem girth indicated significantly positive indirect effect on grain yield per plant *via* flag leaves length (0.0186), plant population (0.018), plant height (0.0162), no. of internode/plant (0.0153) and brix% (0.0102) while negatively indirect effect shown by 4th leaves length (-0.0093), fresh biomass (-0.0126), juice pH (-0.0216), 100 seed weight (-0.0218), total fresh biomass (-0.0271), no. of leaves/plant (-0.0289), juice yield(lit/plant) (-0.0338), days to 50% flowering (-0.0378), leaves area (-0.0457), juice extraction % (-0.0518), juice yield (g/plant) (-0.0622) and 4th leaves width (-0.0686).

Total fresh biomass

Total fresh biomass indicated remarkably positive indirect effect on grain yield per plant *via* juice yield(lit/plant) (0.5127), juice yield (g/plant) (0.4554), 100 seed weight (0.3778), fresh biomass (0.3379), leaves area (0.279), brix% (0.2586), no. of leaves/plant (0.2354), 4th leaves length (0.234), 4th leaves width (0.2206), stem girth (0.2128), juice extraction % (0.2071), plant height (0.1618) and days to 50% flowering (0.1406) while negatively indirect effect shown by plant population (-0.181), flag leaves length (-0.1968), no. of internode/plant (-0.2085) and juice pH (-0.2178).

Fresh biomass (without leaves)

Fresh biomass indicated appreciably positive indirect effect on grain yield per plant *via* juice pH (0.1918), days to 50% flowering (0.1909), no. of leaves/plant (0.1409), no. of internode/plant (0.1218) and plant height (0.0801) while negatively indirect effect shown by plant population (-0.0208), 100 seed weight (-0.0295), stem

girth (-0.085), flag leaves length (-0.1176), 4th leaves width (-0.1745), brix% (-0.1836), juice extraction % (-0.2422), leaves area (-0.2726), juice yield(lit/plant) (-0.2896), total fresh biomass (-0.2899), juice yield (g/plant) (-0.3056), and 4th leaves length (-0.3317).

Juice yield (lit/plant)

Juice yield(lit/plant) indicated remarkably positive indirect effect on grain yield per plant *via* flag leaves length (0.0965), no. of internode/plant (0.087), no. of leaves/plant (0.0869) and days to 50% flowering (0.0187) while negatively indirect effect shown by juice pH(-0.0356), plant height (-0.0422), 4th leaves width (-0.0989), stem girth (-0.1102), 4th leaves length (-0.1114), plant population (-0.1205), fresh biomass (-0.14), leaves area (-0.1542), brix% (-0.1589), total fresh biomass (-0.2127), 100 seed weight (-0.2427), juice extraction % (-0.2498) and juice yield (g/plant) (-0.2674).

Juice yield (g/plant)

Juice yield (g/plant) indicated remarkably positive indirect effect on grain yield per plant *via* no. of internode/plant (0.0257), plant height (0.0213), flag leaves length (0.0148), juice pH (0.011), plant population (0.0037), no. of leaves/plant (0.0031) and brix% (0.003) while negatively indirect effect shown by days to 50% flowering (-0.0015), 100 seed weight (-0.023), 4th leaves length (-0.0248), fresh biomass (-0.0285), 4th leaves width (-0.0345), total fresh biomass (-0.0365), leaves area (-0.0377), stem girth (-0.0391), juice yield(lit/plant) (-0.0517) and juice extraction % (-0.0657).

Juice pH

juice pH indicated remarkably positive indirect effect on grain yield per plant *via* no. of internode/plant (0.0425), plant population (0.0197), stem girth (0.018), plant height (0.014), juice yield(lit/plant) (0.0091), no. of leaves/plant (0.0049) and brix% (0.0012) while negatively indirect effect shown by days to 50% flowering (-0.0049), juice extraction % (-0.0084), 4th leaves width (-0.0098), juice yield (g/plant) (-0.0146), 100 seed weight (-0.0162), total fresh biomass (-0.0232), fresh biomass (0.0238), leaves area (-0.0296) and 4th leaves length (-0.0384).

Juice extraction %

Juice extraction % exhibited appreciably positive indirect effect on grain yield per plant *via* juice yield (g/plant) (0.39), juice yield(lit/plant) (0.2863), stem girth (0.1936), leaves area (0.1733), 4th leaves width (0.157), 100 seed weight (0.139), fresh biomass (0.1342), 4th leaves length (0.1025), total fresh biomass (0.0985) and plant population (0.0132) while negatively indirect effect shown by juice pH (-0.0375), brix% (-0.0561), flag leaves length (-0.0584), days to 50% flowering (-0.0695), no. of leaves/plant (-0.1439) and no. of internode/plant (-0.1474).

No. of internode/plant

No. of internode/plant exhibited notably positive indirect effect on grain yield per plant *via* 100 seed weight (0.2816), juice yield (g/plant) (0.1546), juice extraction % (0.1494), 4th leaves length (0.1488), leaves area (0.1229), days to 50% flowering (0.1164), plant population (0.1151), juice yield(lit/plant) (0.1011), total fresh biomass (0.1005), flag leaves length (0.0853), fresh biomass (0.0684), stem girth (0.0577), brix% (0.0494), 4th leaves width (0.029) and plant height (0.0259) while negatively indirect effect shown by no. of leaves/plant (-0.1488),

100 seed weight

100 seed weight exhibited notably positive indirect effect on grain yield per plant *via* no. of internode/plant (0.7174), no. of leaves/plant (0.3507), juice pH (0.1866), flag leaves length (0.0455), stem girth (0.0024), juice extraction % (0.002), no. of leaves/plant (0.0009) and 100 seed weight (0.0006) while negatively indirect effect shown by 4th leaves width (-0.0064), fresh biomass (-0.0422), days to 50% flowering (-0.0871), stem girth (-0.2106), leaves area (-0.2144), 4th leaves length (-0.223), plant height (-0.3341), juice yield (g/plant) (-0.353), juice extraction % (-0.359), total fresh biomass (-0.464), plant population (-0.5286) and brix% (-0.5861).

Table: 4.6. Genotypic path coefficients for yield and its attributing traits of Sorghum genotypes.

Characters	PP	DF 50%	NLP	4LL	4LW	LA	FLL	PH	BRIX	STG	TFB	TFBWL	JY1	JY2	JP	JE	NNP	HSW	Partial R ²
PP	1.1423	0.0815	-0.3203	-0.2239	-0.4513	-0.3481	0.0987	0.378	0.6003	-0.1715	-0.2191	0.0293	0.3516	-0.0556	0.2239	0.0337	-0.2889	0.521	0.0595
DF 50%	-0.065	-0.91	-0.3971	-0.1358	-0.2268	-0.1366	-0.0011	-0.3017	-0.0085	-0.2933	-0.1355	0.2145	0.0434	-0.0183	0.0446	0.1409	0.2329	-0.0684	0.3732
NLP	-0.0148	0.023	0.0527	0.0066	0.0286	0.0151	-0.0031	0.0222	-0.0074	0.0127	0.0132	-0.0092	-0.0117	-0.0021	0.0026	-0.0169	0.0172	-0.016	0.006
4LL	-0.0166	0.0126	0.0106	0.0846	0.0394	0.0743	0.0361	0.0126	0.0043	0.0066	0.021	0.0347	0.0241	0.0277	-0.0324	0.0193	-0.0277	0.0163	0.0078
4LW	-0.1285	0.081	0.1765	0.1512	0.3252	0.2313	0.0195	-0.0219	-0.0549	0.1856	0.076	0.0701	0.0821	0.1483	-0.0317	0.1138	-0.0207	0.0018	0.0396
LA	-0.1692	0.0833	0.159	0.4877	0.395	0.5553	0.1704	0.0392	-0.0292	0.2112	0.1641	0.1869	0.2187	0.2771	-0.1636	0.2144	-0.1501	0.1027	0.1078
FLL	-0.0014	0.00010	0.0009	-0.0067	-0.0009	-0.0048	-0.0157	-0.0027	-0.0006	0.0024	0.0033	-0.0023	0.0039	0.0031	0.0065	0.002	0.0029	0.0006	-0.002
PH	-0.047	-0.0471	-0.0598	-0.0212	0.0096	-0.01	-0.0245	-0.1421	-0.0803	0.0191	-0.0244	0.0141	-0.0153	0.04	-0.0197	0.0647	0.0081	-0.041	0.0344
BRIX	0.0334	0.0006	-0.0089	0.0032	-0.0107	-0.0033	0.0023	0.0359	0.0636	-0.0054	0.0174	0.0144	0.0258	-0.0025	0.0008	-0.0079	-0.0069	0.0321	-0.0111
STG	0.018	-0.0387	-0.0289	-0.0093	-0.0686	-0.0457	0.0186	0.0162	0.0102	-0.1202	-0.0271	-0.0126	-0.0338	-0.0622	-0.0216	-0.0518	0.0153	-0.0218	0.0139
TFB	-0.181	0.1406	0.2354	0.234	0.2206	0.279	-0.1968	0.1618	0.2586	0.2128	0.9439	0.3379	0.5127	0.4554	-0.2178	0.2071	-0.2085	0.3778	0.0052
TFBWL	-0.0208	0.1909	0.1409	-0.3317	-0.1745	-0.2726	-0.1176	0.0801	-0.1836	-0.085	-0.2899	-0.8098	-0.2896	-0.3056	0.1918	-0.2422	0.1218	-0.0295	-0.0293
JY1	-0.1205	0.0187	0.0869	-0.1114	-0.0989	-0.1542	0.0965	-0.0422	-0.1589	-0.1102	-0.2127	-0.14	-0.3916	-0.2674	-0.0356	-0.2498	0.087	-0.2427	-0.0575
JY2	0.0037	-0.0015	0.0031	-0.0248	-0.0345	-0.0377	0.0148	0.0213	0.003	-0.0391	-0.0365	-0.0285	-0.0517	-0.0757	0.011	-0.0657	0.0257	-0.023	-0.0257
JP	0.0197	-0.0049	0.0049	-0.0384	-0.0098	-0.0296	-0.0416	0.014	0.0012	0.018	-0.0232	-0.0238	0.0091	-0.0146	0.1005	-0.0084	0.0425	-0.0162	0.0016
JE	0.0132	-0.0695	-0.1439	0.1025	0.157	0.1733	-0.0584	-0.2043	-0.0561	0.1936	0.0985	0.1342	0.2863	0.39	-0.0375	0.4488	-0.1474	0.139	0.1761
NNP	0.1151	0.1164	-0.1488	0.1488	0.029	0.1229	0.0853	0.0259	0.0494	0.0577	0.1005	0.0684	0.1011	0.1546	-0.1926	0.1494	0.455	0.2816	0.0156
HSW	-0.5286	-0.0871	0.3507	-0.223	-0.0064	-0.2144	0.0455	-0.3341	-0.5861	-0.2106	-0.464	-0.0422	-0.7183	-0.353	0.1866	-0.359	0.7174	1.1591	0.1676

R SQUARE = 0.9609, RESIDUAL EFFECT = 0.1977

PP = Plant population, **DF 50%** = Days to 50% flowering, **NLP** = Number of leaves/plant, **4LL** = 4th leaves length (cm), **4LW** = 4th leaves width (cm), **LA** = leaves area (cm²), **FLL** = Flag leaves length (cm), **PH** = plant height (cm), **BRIX** = Brix%. **STG** = stem girth (cm), **TFB** = fresh biomass (without leaves) in g/plant, **JY1** = Juice yield (lit/plant), **JY2** = juice yield (g/plant), **JP** = juice ph, **JE** = juice extraction %, **NNP** = number of internode/plant, **HSW** = 100 seed weight (g) and **GLYD** = grain yield (g/plant).

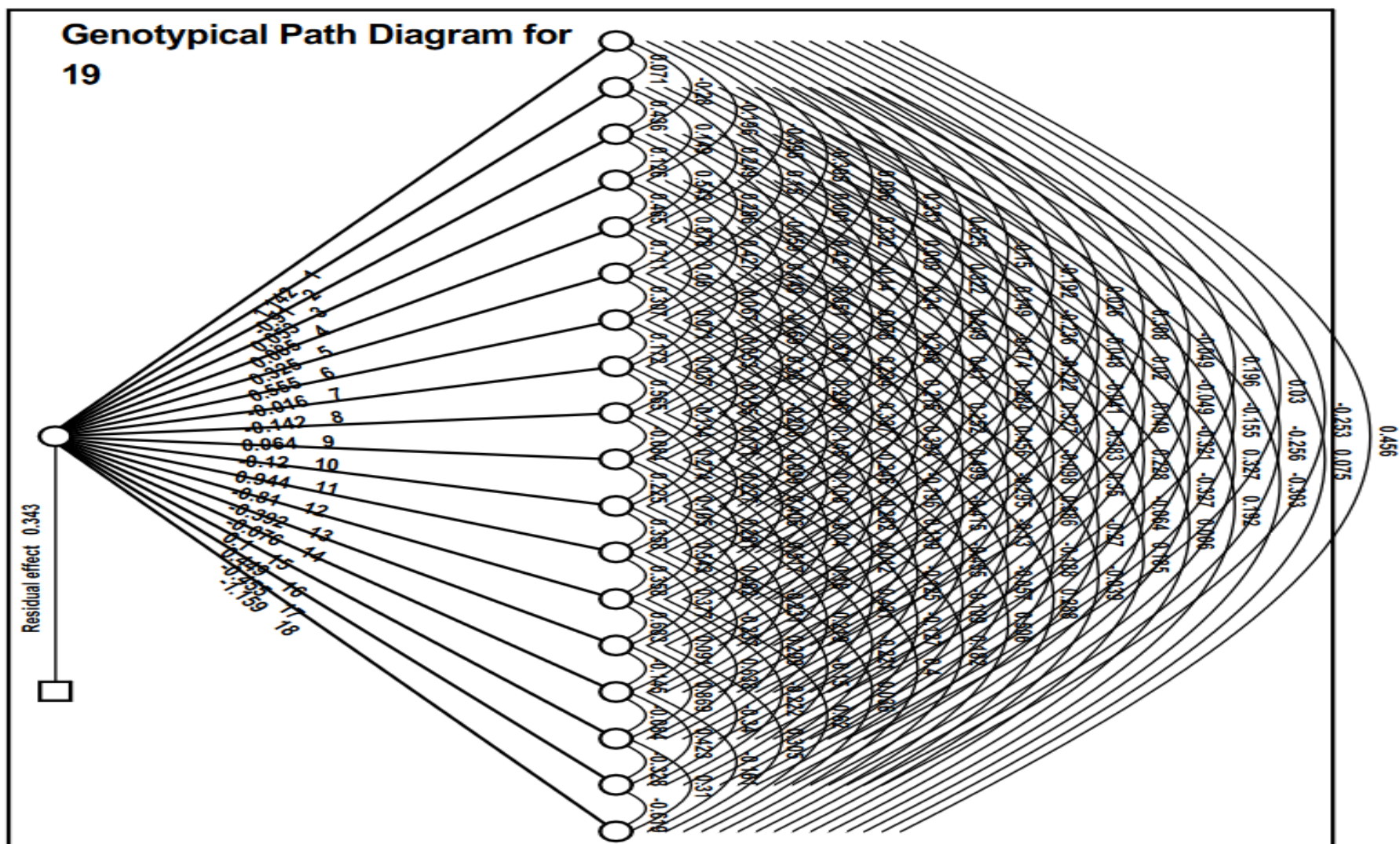


Fig. 4.3. Genotypic path coefficients for yield and its attributing traits of Sorghum genotypes.

4.7. Phenotypic path coefficient analysis:

Direct effect on grain yield per plant:

The Phenotypic path coefficient analysis of different morpho-physiological and yield traits on grain yield per plant via [Table: 4.7 and Fig 4.4] Plant population (1.2868), had considerably higher estimates of positive direct effect chased by 100 seed weight (1.207), total fresh biomass (1.0687), leaves area (0.6205), juice extraction % (0.4867), 4th leaves width (0.4064), no. of internode/plant (0.3939), 4th leaves length (0.102), juice pH (0.0694) and brix% (0.028). Whereas negative direct effect on grain yield per plant exhibited by plant height (-0.0709), No. of leaves/plant (-0.0778), flag leaves length (-0.0824), juice yield (g/plant) (-0.0881), stem girth (-0.1022), juice yield (lit/plant) (-0.5499) and fresh biomass (-0.8566).

Indirect Effects on grain yield per plant:

Plant population

Plant population exhibited associated positive indirect effect on grain yield per plant via brix% (0.6762), 100 seed weight (0.5868), plant height (0.4258), juice yield(lit/plant) (0.3961), juice pH (0.2522), flag leaves length (0.1112), days to 50% flowering (0.0918), juice extraction % (0.038) and fresh biomass (0.033) while negatively indirect effect shown by juice yield (g/plant) (-0.0627), stem girth (-0.1931), total fresh biomass (-0.2468), 4th leaves length (-0.2522), no. of leaves/plant (-0.2938), no. of internode/plant (-0.3254), leaves area (-0.3922) and 4th leaves width (-0.5084).

Days to 50% flowering

Days to 50% flowering revealed associated positive indirect effect on grain yield per plant via no. of internode/plant (0.2417), fresh biomass (0.2227), juice extraction % (0.1462), juice Ph (0.0463) and juice yield(lit/plant) (0.045) while negatively indirect effect shown by flag leaves length (-0.0011), brix% (-0.0089), juice yield (g/plant) (-0.019), plant population (-0.0674), 100 seed weight (-0.071), total fresh biomass (-0.1406), 4th leaves length (-0.141), leaves area (-0.1418), 4th leaves width (-0.2354), stem girth (-0.3045), plant height (-0.3132) and no. of leaves/plant (-0.3356).

No. of leaves/plant

No. of leaves/plant revealed associated positive indirect effect on grain yield per plant via juice extraction % (0.0203), 100 seed weight (0.0192), plant population (0.0178), juice yield(lit/plant) (0.0141), fresh biomass (0.011), brix% (0.0088), flag leaves length (0.0037) and juice yield (g/plant) (0.0026) while negatively indirect effect shown by juice pH (-0.0031), 4th leaves length (-0.008), stem girth (-0.0152), total fresh biomass (-0.0158), leaves area (-0.0181), no. of internode/plant (-0.0207), plant height (-0.0267), days to 50% flowering (-0.0277) and 4th leaves width (-0.0344).

4th leaves length

4th leaves length revealed associated positive indirect effect on grain yield per plant via leaves area (0.2891), stem girth (0.2319), 4th leaves length (0.189), juice yield (g/plant) (0.1853), no. of leaves/plant (0.1797), juice extraction % (0.1422), juice yield(lit/plant) (0.1026), days to 50% flowering (0.1013), total fresh biomass (0.095), fresh biomass (0.0876), flag leaves length (0.0243), 100 seed weight (0.0023) while negatively indirect effect shown by no. of internode/plant (-0.0259), plant height (-0.0274), juice pH (-0.0397), brix% (-0.0687) and plant population (-0.1606).

Leaves area

Leaves area revealed associated positive indirect effect on grain yield per plant via 4th leaves length (0.545), 4th leaves width (0.4414), juice yield (g/plant) (0.3096), juice yield(lit/plant) (0.2444), juice extraction % (0.2396), stem girth (0.236), fresh biomass (0.2089), flag leaves length (0.1904), total fresh biomass (0.1834), no. of leaves/plant (0.1447), 100 seed weight (0.1148), days to 50% flowering (0.0931) and plant height (0.0438) while negatively indirect effect shown by brix% (-0.0326), no. of internode/plant (-0.1677), juice pH (-0.1828) and plant population (-0.1891).

Flag leaves length

Flag leaves length indicated associated positive indirect effect on grain yield per plant *via* juice pH (0.0342), juice yield(lit/plant) (0.0203), total fresh biomass (0.0172), juice yield (g/plant) (0.0161), no. of internode/plant (0.0155), juice extraction % (0.0107), no. of leaves/plant (0.004), 100 seed weight (0.0032) while negatively indirect effect shown by days to 50% flowering (-0.0001), brix% (-0.003), 4th leaves width (-0.0049), plant population (-0.0071), fresh biomass (-0.012), plant height (-0.0142), leaves area (-0.0253) and 4th leaves length (-0.0352).

Plant height

Plant height indicated associated positive indirect effect on grain yield per plant *via* juice extraction % (0.0323), juice yield (g/plant) (0.02), stem girth (0.0095), fresh biomass (0.007), 4th leaves width (0.0048) and no. of internode/plant (0.004), while negatively indirect effect shown by leaves area (-0.005), juice yield(lit/plant) (-0.0076), juice pH (-0.0099), 4th leaves length (-0.0106), total fresh biomass (-0.0121), flag leaves length (-0.0122), 100 seed weight (-0.0204), plant population (-0.0235), days to 50% flowering (-0.0235), no. of leaves/plant (-0.0243) and brix% (-0.04).

Brix%

Brix% indicated remarkably positive indirect effect on grain yield per plant *via* plant height (0.0158), plant population (0.0147) and 100 seed weight (0.0141), juice yield(lit/plant) (0.0113), total fresh biomass (0.0077), fresh biomass (0.0063), 4th leaves length (0.0014), flag leaves length (0.001), days to 50% flowering (0.0003) and juice pH (0.0003) while negatively indirect effect shown by juice yield (g/plant) (-0.0011), leaves area (-0.0015), stem girth (-0.0024), no. of internode/plant (-0.003), no. of leaves/plant (-0.0032), juice extraction % (-0.0035) and 4th leaves width (-0.0047).

Stem girth

Stem girth indicated associated positive indirect effect on grain yield per plant *via* flag leaves length (0.0158), plant population (0.0153), plant height (0.0138), no. of internode/plant (0.013) and brix% (0.0086) while negatively indirect effect shown by 4th leaves length -0.0079), fresh biomass (-0.0107), juice pH (-0.0184), 100 seed weight (-0.0186), no. of leaves/plant (-0.02), total fresh biomass (-0.023), juice

yield(lit/plant) (-0.0288), days to 50% flowering (-0.033), leaves area (-0.0389), juice extraction % (-0.0441), juice yield (g/plant) (-0.0529) and 4th leaves width (-0.0583).

Total fresh biomass

Total fresh biomass indicated remarkably positive indirect effect on grain yield per plant *via* juice yield(lit/plant) (0.5805), juice yield (g/plant) (0.5156), 100 seed weight (0.4278), fresh biomass (0.3826), leaves area (0.3158), brix% (0.2928), 4th leaves length (0.265), 4th leaves width (0.2498), stem girth (0.2409), juice extraction % (0.2345), no. of leaves/plant (0.217), plant height (0.1831) and days to 50% flowering (0.1591), while negatively indirect effect shown by plant population (-0.205), flag leaves length (-0.2228), no. of internode/plant (-0.236) and juice pH (-0.2466).

Fresh biomass (without leaves)

Fresh biomass indicated appreciably positive indirect effect on grain yield per plant *via* juice pH (0.2029), days to 50% flowering (0.202), no. of internode/plant (0.1289), no. of leaves/plant (0.1214) and plant height (0.0847), while negatively indirect effect shown by plant population (-0.022), 100 seed weight (-0.0312), stem girth (-0.0899), flag leaves length (-0.1244), 4th leaves width (-0.1846), brix% (-0.1943), juice extraction % (-0.2562), leaves area (-0.2883), juice yield(lit/plant) (-0.3063), total fresh biomass (-0.3067), juice yield (g/plant) (-0.3233) and 4th leaves length (-0.3509).

Juice yield (lit/plant)

Juice yield(lit/plant) exhibited remarkably positive indirect effect on grain yield per plant *via* flag leaves length (0.1355), no. of internode/plant (0.1222), no. of leaves/plant (0.0993) and days to 50% flowering (0.0262) while negatively indirect effect shown by juice pH (-0.05), plant height (-0.0592), 4th leaves width (-0.1388), stem girth (-0.1548), 4th leaves length (-0.1564), plant population (-0.1693), fresh biomass (-0.1966), leaves area (-0.2166), brix% (-0.2232), total fresh biomass (-0.2987), 100 seed weight (-0.3408), juice extraction % (-0.3508) and juice yield (g/plant) (-0.3755).

Juice yield (g/plant)

Juice yield (g/plant) exhibited remarkably positive indirect effect on grain yield per plant *via* no. of internode/plant (0.0299), plant height (0.0248), flag leaves length (0.0172), juice pH (0.0128), plant population (0.0043), brix% (0.0035) and no. of

leaves/plant (0.0029) while negatively indirect effect shown by days to 50% flowering (-0.0018), 100 seed weight (-0.0268), 4th leaves length (-0.0289), fresh biomass (-0.0333), 4th leaves width (-0.0402), total fresh biomass (-0.0425), leaves area (-0.044), stem girth (-0.0456), juice yield(lit/plant) (-0.0602) and juice extraction % (-0.0766).

Juice pH

Juice pH exhibited associated positive indirect effect on grain yield per plant *via* no. of internode/plant (0.0294), plant population (0.0136), stem girth (0.0125), plant height (0.0096), juice yield(lit/plant) (0.0063), no. of leaves/plant (0.0028) and brix% (0.0008) while negatively indirect effect shown by days to 50% flowering (-0.0034), juice extraction % (-0.0058), 4th leaves width (-0.0068), juice yield (g/plant) (-0.0101), 100 seed weight (-0.0112), total fresh biomass (-0.016), fresh biomass (-0.0164), leaves area (-0.0204), 4th leaves length -0.0266) and flag leaves length (-0.0288).

Juice extraction %

Juice extraction % exhibited outstandingly positive indirect effect on grain yield per plant *via* juice extraction % (0.0323), juice yield (g/plant) (0.02), stem girth (0.0095), fresh biomass (0.007), 4th leaves width (0.0048) and no. of internode/plant (0.004), while negatively indirect effect shown by leaves area (-0.005), juice yield(lit/plant) (-0.0076), juice pH (-0.0099), 4th leaves length (-0.0106), total fresh biomass (-0.0121), flag leaves length (-0.0122), 100 seed weight (-0.0204), plant population (-0.0235), days to 50% flowering (-0.0235), no. of leaves/plant (-0.0243) and brix% (-0.04).

No. of internode/plant

No. of internode/plant exhibited appreciably positive indirect effect on grain yield per plant *via* 100 seed weight (0.2438), juice yield (g/plant) (0.1338), juice extraction % (0.1294), 4th leaves length (0.1288), leaves area (0.1064), days to 50% flowering (0.1008), plant population (0.0996), juice yield(lit/plant) (0.0875), total fresh biomass (0.087), flag leaves length (0.0739), fresh biomass (0.0593), stem girth (0.05), brix% (0.0428), 4th leaves width (0.0251) and plant height (0.0224) while

negatively indirect effect shown by no. of leaves/plant (-0.1049) and juice pH (-0.1667).

100 seed weight

100 seed weight manifested outstandingly positive indirect effect on grain yield per plant via no. of internode/plant (0.7471), no. of leaves/plant (0.2974), juice pH (0.1943) and flag leaves length (0.0474) while negatively indirect effect shown by 4th leaves width (-0.0067), fresh biomass (-0.0439), days to 50% flowering (-0.0907), stem girth (-0.2193), leaves area (-0.2232), 4th leaves length (-0.2323), plant height (-0.348), juice yield (g/plant) (-0.3676), juice extraction % (-0.3738), total fresh biomass (-0.4832), plant population (-0.5505) and brix% (-0.6104).

Table 4.7. Phenotypic path coefficients for yield and its attributing traits of Sorghum genotypes.

Characters	PP	DF 50%	NLP	4LL	4LW	LA	FLL	PH	BRIX	STG	TFB	TFBWL	JY1	JY2	JP	JE	NNP	HSW	Partial R ²
PP	1.2868	0.0918	-0.2938	-0.2522	-0.5084	-0.3922	0.1112	0.4258	0.6762	-0.1931	-0.2468	0.033	0.3961	-0.0627	0.2522	0.038	-0.3254	0.5868	0.067
DF 50%	-0.0674	-0.9446	-0.3356	-0.141	-0.2354	-0.1418	-0.0011	-0.3132	-0.0089	-0.3045	-0.1406	0.2227	0.045	-0.019	0.0463	0.1462	0.2417	-0.071	0.3874
NLP	0.0178	-0.0277	-0.0778	-0.008	-0.0344	-0.0181	0.0037	-0.0267	0.0088	-0.0152	-0.0158	0.011	0.0141	0.0026	-0.0031	0.0203	-0.0207	0.0192	-0.0072
4LL	-0.02	0.0152	0.0105	0.102	0.0474	0.0896	0.0435	0.0152	0.0052	0.0079	0.0253	0.0418	0.029	0.0334	-0.039	0.0233	-0.0334	0.0196	0.0094
4LW	-0.1606	0.1013	0.1797	0.189	0.4064	0.2891	0.0243	-0.0274	-0.0687	0.2319	0.095	0.0876	0.1026	0.1853	-0.0397	0.1422	-0.0259	0.0023	0.0495
LA	-0.1891	0.0931	0.1447	0.545	0.4414	0.6205	0.1904	0.0438	-0.0326	0.236	0.1834	0.2089	0.2444	0.3096	-0.1828	0.2396	-0.1677	0.1148	0.1205
FLL	-0.0071	-0.0001	0.004	-0.0352	-0.0049	-0.0253	-0.0824	-0.0142	-0.003	0.0128	0.0172	-0.012	0.0203	0.0161	0.0342	0.0107	0.0155	0.0032	-0.0106
PH	-0.0235	-0.0235	-0.0243	-0.0106	0.0048	-0.005	-0.0122	-0.0709	-0.04	0.0095	-0.0121	0.007	-0.0076	0.02	-0.0099	0.0323	0.004	-0.0204	0.0172
BRIX	0.0147	0.0003	-0.0032	0.0014	-0.0047	-0.0015	0.001	0.0158	0.028	-0.0024	0.0077	0.0063	0.0113	-0.0011	0.0003	-0.0035	-0.003	0.0141	-0.0049
STG	0.0153	-0.033	-0.02	-0.0079	-0.0583	-0.0389	0.0158	0.0138	0.0086	-0.1022	-0.023	-0.0107	-0.0288	-0.0529	-0.0184	-0.0441	0.013	-0.0186	0.0118
TFB	-0.205	0.1591	0.217	0.265	0.2498	0.3158	-0.2228	0.1831	0.2928	0.2409	1.0687	0.3826	0.5805	0.5156	-0.2466	0.2345	-0.236	0.4278	0.0059
TFBWL	-0.022	0.202	0.1214	-0.3509	-0.1846	-0.2883	-0.1244	0.0847	-0.1943	-0.0899	-0.3067	-0.8566	-0.3063	-0.3233	0.2029	-0.2562	0.1289	-0.0312	-0.031
JY1	-0.1693	0.0262	0.0993	-0.1564	-0.1388	-0.2166	0.1355	-0.0592	-0.2232	-0.1548	-0.2987	-0.1966	-0.5499	-0.3755	-0.05	-0.3508	0.1222	-0.3408	-0.0807
JY2	0.0043	-0.0018	0.0029	-0.0289	-0.0402	-0.044	0.0172	0.0248	0.0035	-0.0456	-0.0425	-0.0333	-0.0602	-0.0881	0.0128	-0.0766	0.0299	-0.0268	-0.0299
JP	0.0136	-0.0034	0.0028	-0.0266	-0.0068	-0.0204	-0.0288	0.0096	0.0008	0.0125	-0.016	-0.0164	0.0063	-0.0101	0.0694	-0.0058	0.0294	-0.0112	0.0011
JE	0.0144	-0.0753	-0.1271	0.1111	0.1703	0.1879	-0.0633	-0.2216	-0.0609	0.2099	0.1068	0.1456	0.3104	0.4229	-0.0407	0.4867	-0.1598	0.1507	0.191
NNP	0.0996	0.1008	-0.1049	0.1288	0.0251	0.1064	0.0739	0.0224	0.0428	0.05	0.087	0.0593	0.0875	0.1338	-0.1667	0.1294	0.3939	0.2438	0.0135
HSW	-0.5505	-0.0907	0.2974	-0.2323	-0.0067	-0.2232	0.0474	-0.348	-0.6104	-0.2193	-0.4832	-0.0439	-0.748	-0.3676	0.1943	-0.3738	0.7471	1.207	0.1745

R SQUARE = 0.8827 RESIDUAL EFFECT = 0.3425

PP = Plant population, DF 50% = Days to 50% flowering, NLP = Number of leaves/plant, 4LL = 4th leaves length (cm), 4LW = 4th leaves width (cm), LA = leaves area (cm²), FLL = Flag leaves length (cm), PH = plant height (cm), BRIX = Brix%. STG = stem girth (cm), TFB = fresh biomass (without leaves) in g/plant, JY1 = Juice yield (lit/plant), JY2 = juice yield (g/plant), JP = juice ph, JE = juice extraction %, NNP = number of internode/plant, HSW = 100 seed weight (g) and GLYD = grain yield (g/plant).

4.8 Genetic Divergence:

To estimate D^2 values, correlated means of characters were transformed to standard uncorrelated means using Tocher's method. The statistical distance between pair of genotypes were obtained as the sum of squares of the difference between the pairs of corresponding uncorrelated value of any two genotypes considered at a time. The genetic divergence has been studied using Mahalanobis' D^2 statistics on 25 genotypes over 14 yield contributing characters. Results are presented as under.

4.9. Mahalanobis generalize distance (D^2)

The analysis of variance manifested highly significant differences among the population for the 14 characters investigated. The D^2 values corresponding to possible comparison among 25 genotypes taking two genotypes at a time were computed separately in the analysis. (Table 4.8 and Fig 4.2).

4.10. Contribution of individual characters towards genetic divergence

The percentage contribution towards genetic divergence by all the characters is presented in (Table 4.9). The character leaves area (27.4%), juice extraction % (12.7%), contributed most towards genetic divergence chased by Days to 50% flowering (11.5%), juice yield (9.5 %), 4th leaves length (9.3%), juice yield (5.4%), fresh biomass (5.2%), Flag leaves length (4.8%), Brix% (4.5%), plant height (4.4%), plant population (4.4%), number of internode/plant (1.6%) and stem girth (0.9%).

4.11. Grouping of genotypes into different clusters:

The study comprised of 25 genotypes based on 14 morpho-physiological and yield related traits following Mahalanobis D^2 statistics. On the basis of D^2 values, the 25 genotypes were grouped into two clusters following Tocher's method. The cluster one had polygenotypic 24 genotypes and cluster II had one genotype respectively. Cluster wise distribution of genotypes is summarized in (Table 4.10.).

4.10. Cluster mean

The cluster mean calculated for seventeen characters under study have been presented in table 4.11. Mean of plant population and Days to physiological maturity was highest in cluster I (135.5) and lowest in cluster II (85.0). Mean of days to 50% flowering was highest in cluster I (80.1) and lowest in cluster II (76.0). Mean of 4th

leaves length was highest in cluster I (81.9) and lowest in cluster II (75.0) Mean of leaves area was highest in cluster I (598.8) and lowest in cluster II (560.3).

Flag leaves length exhibited highest mean for cluster number I (41.0) and lowest mean for cluster number II (40.0)

Plant height exhibited highest mean for cluster number I (309.0) and lowest mean for cluster number II (199.8)

Brix% exhibited highest mean for cluster number I (16.5) and lowest mean for cluster number II (10.0)

Stem girth indicated highest mean for cluster number II (20.0) and lowest mean for cluster number I (17.5)

Total fresh biomass indicated highest mean for cluster number I (908.3) and lowest mean for cluster number II (811.1)

Juice yield (lit/plant) revealed highest mean for cluster number I (703.3) and lowest mean for cluster number II (172.2)

Juice yield (g/plant) revealed highest mean for cluster number II (222.2) and lowest mean for cluster number I (98.2)

Juice extraction % (g/plant) expressed highest mean for cluster number II (25.0) and lowest mean for cluster number I (10.1)

Number of internode/plants demonstrated highest mean for cluster number I (11.4) and lowest mean for cluster number II (11.0)

4.11. Intra and inter cluster divergence D^2 values:

The average intra and inter-cluster D^2 values estimated as per the procedure given by Singh and Choudhary (1979). Cluster No I exhibited maximum intra cluster D^2 value ($D^2 = 1.058$).

From the inter cluster D^2 values among the II clusters, highest inter cluster divergence was observed between genotypes of cluster II ($D^2 = 9.572$). The inter cluster distance in mostly case were larger than the intra cluster distance which indicated that wider diversity is present among the genotypes of distant group. (Table 4.12).

Table 4.8. MANOVA of Mahalanobis generalize distance (D^2).

Source	DF	Pillai	Approxf	Pr (>F)
Rep	2	15	3	
Genotypes	24	15	INFINITY**	2.2***
Error	48			

Significance. Codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 4.9. Percent contribution of characters towards divergence in 25 Sorghum genotypes.

Sr. No.	Characters	Percent contribution
1	Leaves area	27.4%
2	Juice extraction	12.7%
3	Days to 50% flowering	11.5%
4	Juice yield (lit/plant)	9.5 %
5	4th leaves length	9.3%
6	Juice yield (g/plant)	5.4%
7	Fresh biomass (without leaves)	5.2%
8	Flag leaves length	4.8%
9	Brix%	4.5%
10	Plant height	4.4%
11	Plant population	4.4%
12	Number of internode/plants	1.6%
13	Stem girth	0.9%

Table 4.10. Distribution of Sorghum genotypes in different clusters.

S. No.	Cluster No.	No. of genotypes	Genotypes Names
1	I	24	SPH2009, SPV2697, SPV2789, SPV2793, SPV2794, SPV2795, SPV2888, SPV2889, SPV2890, SPV2891, SPV2892, SPV2893, SPV2894, SPV2895, CSH22SS, CSV19SS, CSV24SS, SPV2714, SPV2812, SPV2896, SPV2897, SPV2898, SPV2899 and SPV2900
2	II	1	CSH25

Table 4.11. Cluster Means for 14 characters

Clusters	plant population	Days to 50% flowering	4th leaves length (cm)	leaves area (cm ²)	Flag leaves length(cm)	plant height (cm)	Brix%
I	135.5	80.1	81.9	598.8	41.0	309.0	16.5
II	85.0	76.0	75.0	560.3	40.0	199.8	10.0

Table 4.11. Contd...

Clusters	stem girth (cm)	total fresh biomass in g/plant	juice yield(lit/plant)	juice yield (g/plant)	juice extraction %	Number of internode/plant
I	17.5	908.3	703.3	98.2	10.1	11.4
II	20.0	811.1	172.2	222.2	25.0	11.0

Table 4.12. Average intra and inter cluster D^2 values of 25 genotypes of Sorghum.

Clusters	Cluster1	Cluster 2
Cluster 1	1.058	9.572
Cluster 2		0.000

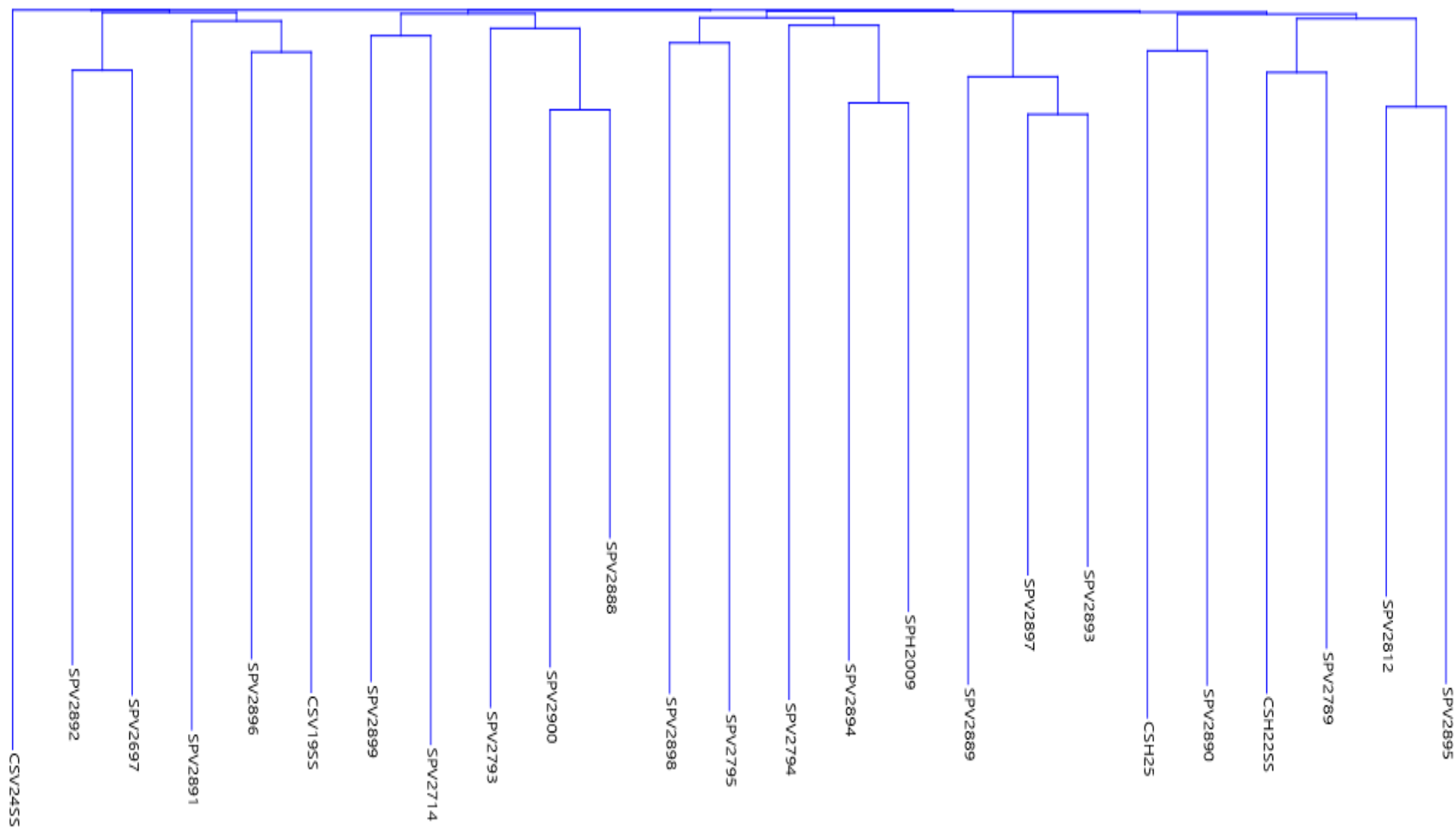


Fig 4.5. Cluster diagram of Sorghum genotypes based on morpho-physiological data by tocher's methods.

Chapter- V

DISCUSSION

The findings of the present investigation have been compared with those of similar research work being done by other researchers in the past and the outcome has been described in this chapter.

GENETIC PARAMETERS:

5.1. Analysis of variance and mean performance:

Sorghum genotypes were highly outstandingly differed for all 19 characters *i.e.* viz., plant population, days 50% flowering, number of leaves per plant, 4th leaves length, 4th leaves width, leaves area, flag leaves length, plant height, brix per cent, stem girth, total fresh biomass in grams per plant, fresh biomass in grams per plant, juice yield (lit/plant), juice yield (g/plant), juice pH, juice extraction per cent, number of internode per plant, 100 seed weight and grain yield g/plant. This suggested that the genotype selected for research were quite variable and constant levels of variability are present among them. Thus, indicating simply scope for selection of different qualitative characters in Sorghum improvement these results were consistent with the results reported by (Bhusal *et al.* 2013; More *et al.* 2018; Yücel *et al.* 2020 and Navya *et al.* 2021).

5.2. Identified desirable sweet sorghum genotypes

Total of ten genotypes out of 25 genotypes were identified as desirable sweet sorghum genotypes based on Brix percentage, total fresh biomass juice yield (lit/plant) and juice extraction %. Genotype SPV2890 was highest in juice extraction (16.00%) with 1380 lit/plant of juice yield, 700g of total fresh biomass and with 18% of Brix percentage. Genotypes namely SPV2789, SPV2889, SPV2891, SPV2893, SPV2894, SPV2895 CSH22SS, CSV19SS and CSV24SS were found superior among 25 genotypes in sweetness index based on above parameters. These genotypes can be utilized in crop improvement programme to develop high brix and high biomass. These results were consistent with the results reported by (Tomar and Sivakumar 2012).

Shukla *et al.* (2016) observed that high sugar concentration in sweet sorghum is not conditional on the plants being tall, making the development of short, sweet inbred lines feasible. Similarly in our study high sugar concentration in sweet sorghum were observed based on Brix percentage, total fresh biomass juice yield (lit/plant) and juice extraction % parameters.

5.3. Genotypic and phenotypic coefficient of variation:

The knowledge about the nature and extent of variability present in genetic material is important to formulate a successful crop improvement programme. The assessment of phenotypic and genotypic coefficients of variation gives a clear idea about amount of variability present in the tested genotypes. In the present study, the phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the traits which demonstrated much influence of environment on expression of all the traits. Similar findings were also reported by (Tomar *et al.* 2012; T Iraddi Vemanna *et al.* (2013; Rana *et al.* 2016; Kalpande *et al.* 2018; and Karadi and Kajjidoni 2019).

High magnitude (> 20%) of PCV and GCV was determined for juice yield (lit/plant), grain yield, juice yield (g/plant), juice extraction %, fresh biomass, plant population, total fresh biomass in g/plant, 100 seed weight indicated that these traits may be improved through selection. (Wadikar *et al.* 2018 and Karadi and Kajjidoni 2019). While the characters primary branches/plant and 100 seed weight exhibited moderate value of PCV and GCV indicating that there could be used as selection indices for yield improvement. (Mahanthesha *et al.* 2017).

Low magnitude of PCV and GCV was recorded for 4th leaves width, number of internode/plant, days to 50% flowering, number of leaves/plant and juice pH. Low magnitude of both PCV and GCV suggested that direct selection will be little effective for improvement of these traits. (Mofokeng *et al.* 2019)

GCV was near to PCV for the characters like days to physiological maturity, total fresh biomass, cane yield and juice yield, indicating that the phenotype is the true representation of its genotype and selection will be effective for further improvement on the basis of per se performance, these results are in conformity with the findings of Tomar *et al.* (2012).

5.4. Heritability (broad sense) and genetic advance:

Heritability is the ability of trait to transmit it from parents to offspring. It partitions the amount of environmental variation from phenotypic variation and provides information in making effective selection. Therefore, existence of high heritability along with wide range of genetic variation is equally important for improvement of population.

Furthermore, heritability is not only responsible for the degree of improvement attained though but also genetic advance as per cent of mean is also important because it is calculated by involving heritability (broad sense), phenotypic standard deviation and selection intensity. Thus, heritability (broad sense) coupled with genetic advance as per cent of mean give clear cut idea regarding the effectiveness of selection for improving the plant traits in breeding population.

High heritability along with high genetic advance as per cent of mean was found for juice yield (lit/plant) and plant population. The existence of high heritability coupled with high genetic advance as per cent of mean clearly indicated that the additive gene action is predominant in the manifestation of these traits and as a result more chance of improving these attributes through simple selection.

On the other hand, high genetic advance with moderate heritability were observed for days to 50% flowering, plant height, juice yield, total fresh biomass, stem girth, and grain yield which indicates the presence of both additive and non-additive gene action for these traits. The above findings are supported with the result of (Tomar *et al.* 2012) and (Gebregergs *et al.* 2020).

Moderate heritability with moderate genetic advance was found for days to 50 per cent flowering Low heritability and low GA were observed low for juice pH. The similar result was found by (Rani and Umakanth 2012).

5.5. Correlation coefficients:

Grain yield is a complex trait and is the final product of yield contributing traits. The genetic gain through direct selection for seed yield is not rewarding because undesirable linkage between grain yield and other undesirable characters. Therefore, selection for grain yield on per se performance may not be much effective without

taking other yield component traits in to consideration. Hence, information regarding direction and magnitude of correlation amongst the traits under investigation is necessary while aiming at a coherent genetic improvement in economic yield through methodologies of selection in a population of genetically dissimilar genotypes.

In present investigation, grain yield was positively and associated correlated with Seed yield/plant at both genotypic and phenotypic level exhibited significant and positive association with number of leaves/plant and highly significant positive association with 4th leaves width, leaves area, juice yield and juice extraction % indicated that this trait was positively associated because of linkages of genes governing the character at coupling phase. These results were conformity with the findings of (Prakash *et al.* 2010); Tomar and Sivakumar 2012; Hundekar *et al.* 2016; Shukla *et al.* 2016 and Kanbar *et al.* 2020).

100 seed weight demonstrated significant positive association with 4th leaves length, leaves area, Brix%, stem girth and juice extraction % and highly positive association with total fresh biomass, juice yield (lit/plant) and juice yield (g/plant). These results were conformity with the findings of (Makanda 2017).

(Singh *et al.* 2015) computed correlation coefficient to elucidate inter relationship on sweet sorghum among growth parameters (plant height, leaves area and juice extraction %) Positive correlations were observed between growth, yield and quality parameters. Similarly in our study also leaves area index and juice extraction % exhibited highly significant positive association with grain yield.

(Makanda 2017) studied correlations found positively and significantly ($P < 0.05$) correlated with number of leaves per plant, similarly in our finding number of leaves/plant were highly positively and significantly ($P < 0.01$)

5.6. Path coefficient:

Path coefficient analysis measures the causal influence of one variable on the other and allows correlation coefficients to partition into direct and indirect effects. The distinction into direct and indirect results of the overall relationship offers authentic knowledge on the contribution of traits and as a result made the basis for selection to improve yield. (Wright 1921) proposed principle of path-coefficient analysis and this technique was first used by Dewey and (Lu 1959) for

plant selection. Path coefficient analysis is basically designed on the assumptions of linearity and additivity and to measure the causes of association between two variables and provides information about the direct and indirect effect of independent variables on dependent variable. Path analysis is an effective tool to measure direct and indirect contribution of yield related traits towards economic yield and therefore, in present investigation it was also aim to calculate direct and indirect effect of yield related traits on yield.

Path coefficient analysis at genotypic level and phenotypic level revealed that hundred seed weight, had considerably higher estimates of positive direct effect chased by total fresh biomass, leaves area, number of internode/plant, juice extraction %, 4th leaves width, juice ph, 4th leaves length, Brix% and number of leaves/plant.

The residual effect values were exhibited very low at genotypic and phenotypic level respectively thus, indicated majority of the factors influencing the grain yield per/plant. This suggests that hundred seed weight total fresh biomass, leaves area, number of internode/plant, juice extraction %, 4th leaves width, juice ph, 4th leaves length, Brix% and number of leaves/plan having significant positive correlation and high direct effect on grain yield explained the true relationship and the direct selection of the genotypes through these traits is effective for improving yield potentiality. This finding of the present study is in confirmation with the outcome of the research work done by (Makanda 2017).

In present investigation, the positive and direct effect were exhibited by hundred seed weig total fresh biomass, leaves area, number of internode/plant (0.455), juice extraction %, 4th leaves width, juice ph, 4th leaves length, Brix% and number of leaves/plant. This clearly indicated that an increase in one of the above traits may increase in grain yield. Whereas negative direct effect on grain yield per plant exhibited by plant height, flag leaves length, juice yield (g/plant), stem girth, juice yield (lit/plant) and fresh biomass at both genotypica and phenotypic level. Similar findings have been reported by (Sandeep et al. 2010; Shinde et al 2012; Prasad et al. 2019 and Kavya et al. 2020).

5.7. Genetic divergence:

On the basis of 14 different morpho-physiological parameters, 25 sorghum genotype were grouped into 2 clusters among them cluster 1 polygenotypic had (24 genotypes) pursued by cluster 2 (1 genotype). Cluster No I exhibited maximum intra cluster D^2 value. Similar results obtained by (Swamy *et al.* 2018) and (Kavya *et al.* 2019). In our finding genotypes were distributed in only two clusters due the small poulaion of 25 genotypes only.

The cluster mean calculated for seventeen characters were studied and mean of plant population and days to physiological maturity was highest in cluster I (135.5) and lowest in cluster II (85.0). Mean of days to 50% flowering was highest in cluster I (80.1) and lowest in cluster II (76.0). Mean of 4th leaves length was highest in cluster I (81.9) and lowest in cluster II (75.0) Mean of leaves area was highest in cluster I (598.8) and lowest in cluster II (560.3). Similar results were observed for days to fifty per cent flowering and days to physiological maturity by Swamy *et al.* (2018) and Khandelwal *et al.* (2019).

Flag leaves length exhibited highest mean for cluster number I (41.0) and lowest mean for cluster number II (40.0). Plant height exhibited highest mean for cluster number I (309.0) and lowest mean for cluster number II (199.8). Brix% exhibited highest mean for cluster number I (16.5) and lowest mean for cluster number II (10.0). Stem girth indicated highest mean for cluster number II (20.0) and lowest mean for cluster number I (17.5). Total fresh biomass indicated highest mean for cluster number I (908.3) and lowest mean for cluster number II (811.1). Juice yield (lit/plant) revealed highest mean for cluster number I (703.3) and lowest mean for cluster number II (172.2). Similar results were observed for Flag leaves length and Plant height by Yuvaraja *et al.* (2019)

Chapter-VI

SUMMARY, CONCLUSION AND SUGGESTIONS FOR FURTHER WORK

6.1 Summary:

The present study entitled as “**Genetic Variability Character Association and Clustering Pattern of Sweet Sorghum (*Sorghum bicolor* (L.) Moench) Genotype for Agronomic Traits in Rainfed Conditions**” was conducted to study the possible presence of variability, association between grain yield and its attributing characters and direct and indirect effects of attributing traits on yield which would be helpful in the identification and selection of major yield attributing traits that can be used for the improvement of grain yield in sorghum. A total of 25 genotypes were evaluated during Kharif 2020-21. The finding has been summarized as under.

Analysis of variance of grain yield per plant and its contributing traits mean sum of square due to genotypes demonstrated highly significant variation for all 19 characters viz., plant population, days 50% flowering, number of leaves per plant, 4th leaves length, 4th leaves width, leaves area, flag leaves length, plant height, brix per cent, stem girth, total fresh biomass in grams per plant, fresh biomass in grams per plant, juice yield (lit/plant), juice yield (g/plant), juice pH, juice extraction per cent, number of internode per plant, 100 seed weight and grain yield g/plant. Indicated that there was considerable variability for these characters in present germplasms.

Total of ten genotypes out of 25 genotypes were identified as desirable sweet sorghum genotypes based on Brix percentage, total fresh biomass juice yield (lit/plant) and juice extraction %. Genotype SPV2890 was highest in juice extraction (16.00%) with 1380 lit/plant of juice yield, 700g of total fresh biomass and with 18% of Brix percentage. Genotypes namely SPV2789, SPV2889, SPV2891, SPV2893, SPV2894, SPV2895 CSH22SS, CSV19SS and CSV24SS were found superior among 25 genotypes in sweetness index based on above parameters. These genotypes can be utilized in crop improvement programme to develop high brix and high biomass.

The phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the traits which demonstrated much influence of environment on expression of all the traits. PCV and GCV demonstrated very little differences indicating the selection for improvement of such characters on the basis of phenotype would be rewarding to improve present Sorghum genotypes. High heritability along with high genetic advance as per cent of mean was found for juice yield (lit/plant) and plant population. The existence of high heritability coupled with high genetic advance as per cent of mean clearly indicated that the additive gene action is predominant in the manifestation of these traits and as a result more chance of improving these attributes through simple selection. On the other hand, high genetic advance with moderate heritability were observed for days to 50% flowering, plant height, juice yield, total fresh biomass, stem girth, and grain yield which indicates the presence of both additive and non-additive gene action for these traits

grain yield was positively and associated correlated with Seed yield/plant at both genotypic and phenotypic level demonstrated significant and positive association with number of leaves/plant and highly significant positive association with 4th leaves width, leaves area, juice yield and juice extraction % indicated that this trait was positively associated because of linkages of genes governing the character at coupling phase.

Positive correlation between desirable traits is supposed to be favorable to the breeder in the selection of suitable yield attributing traits for improvement in the productivity of Sorghum. Thus, selection for these characters will directly follow the immediate improvement of the grain yield for Sorghum crop.

Path coefficient analysis at genotypic level and phenotypic level revealed that hundred seed weight, had considerably higher estimates of positive direct effect chased by total fresh biomass, leaves area, number of internode/plant, juice extraction %, 4th leaves width, juice ph, 4th leaves length, Brix% and number of leaves/plant.

This suggests that hundred seed weight, had considerably higher estimates of positive direct effect pursued by total fresh biomass, leaves area, number of internode/plant, juice extraction %, 4th leaves width, juice ph, 4th leaves length,

Brix% and number of leaves/plant having significant positive correlation and high direct effect on grain yield explained the true relationship and the direct selection of the genotypes through these traits is effective for improving yield potentiality. The positive and direct effect were exhibited by biological yield/plant pods per plant, days to maturity and plant height. This clearly indicated that an increase in one of the above traits may increase in grain yield.

Genetic divergence on the basis of 14 different morpho-physiological parameters, 25 sorghum genotype were grouped into two clusters among them cluster one was polygenotypic had 24 genotypes pursued by cluster two had one genotype. Cluster number I demonstrated maximum intra cluster D^2 value. The cluster I polygenotypic had 24 genotypes and cluster II had one genotype respectively. and lowest mean for cluster number II

Juice yield (lit/plant) demonstrated highest mean for cluster number I and lowest mean for cluster number II. Juice yield (g/plant) demonstrated highest mean for cluster number II and lowest mean for cluster number I. Juice extraction % (g/plant) demonstrated highest mean for cluster number II and lowest mean for cluster number I. Number of internode/plants exhibited highest mean for cluster number I and lowest mean for cluster number II

6.2. Conclusion:

The salient findings of the study are as follows:

6.2.1. Genetic Parameters:

- Analysis of variance of grain yield per plant and its contributing traits mean sum of square due to genotypes demonstrated highly significant variation for all 19 characters.
- Higher PCV and GCV with very little differences were evidenced for juice yield (lit/plant) had the highest PCV and GCV content, pursued by grain yield, juice yield (g/plant), juice extraction %, fresh biomass, plant population, total fresh biomass and 100 seed weight. Emphasized greater role of genetic factors influencing expression of these characters and

selection with these characters may be good approach for enhancing grain yield of the genotypes.

- Higher heritability along with high genetic advance as a percentage of mean was observed was found juice yield (lit/plant) and plant population indicates the presence of additive gene action for improvement of this trait by various selection methods.
- Seed yield/plant at both genotypic and phenotypic level exhibited significant and positive association with number of leaves/plant and highly significant positive association with 4th leaves width, leaves area, juice yield and juice extraction % indicated that this trait was positively associated because of linkages of genes governing the character at coupling phase.
- In present investigation, the positive and direct effect were exhibited by hundred seed weight, total fresh biomass, leaves area, number of internode/plant, juice extraction %, 4th leaves width, juice ph, 4th leaves length, Brix% and number of leaves/plant. This clearly indicated that an increase in one of the above traits may increase in grain yield.
- Total of ten genotypes out of 25 genotypes were identified as desirable sweet sorghum genotypes based on Brix percentage, total fresh biomass juice yield (lit/plant) and juice extraction %. Genotypes namely SPV2789, SPV2889, SPV2891, SPV2893, SPV2894, SPV2895 CSH22SS, CSV19SS and CSV24SS can be utilized in crop improvement programme to develop high brix and high biomass.

6.3. Suggestions for further work:

- The genetic variability reported for different characters in relation in grain yield/plant should be exploited.
- Characters showing high heritability with high genetic advance should be utilized in selection.
- Characters which were found to be governed by additive gene action should be used in the development of high yielding Sorghum varieties in future breeding programmes by fixation of the additive gene action in the early segregating populations.
- Selection should be more effective for the characters viz., Seed yield/plant, pods/plant, juice yield and juice extraction %. High proportion of GCV to

PCV is desirable in process because it depicts that trait are much under the genetic control rather than the environment.

- Genotypes namely SPV2789, SPV2889, SPV2891, SPV2893, SPV2894, SPV2895 CSH22SS, CSV19SS and CSV24SS should be utilized in crop improvement programme to develop high brix and high biomass.

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APPENDIX

i. Morphological data of 25 Sorghum genotypes during study.

S r. n o .	G e n o t y p e s	pl a n t p o p u l a t i o n	Days to 50% flowe ring	NO. of leav es/pl ant	4th leav e s lengt h (cm)	4th leav e s widt h (cm)	leav es area (cm 2)	Flag leav e s lengt h(cm)	plan t heig ht (cm)	B r i x %	ste m girt h (cm)	total fresh biomas s in g/plant	fresh biomass (without leaves) in g/plant	juice yield (mi/ plant)
1	S P H 20 09	145	81	9.33	80.0 0	10.0 0	592 .00	35.0 0	319 .83	1 6 . 0 0	19. 00	1188.8 8	700.00	144 0.00
2	S P V 26 97	110	79	9.33	95.0 0	10.0 0	703 .00	35.0 0	329 .83	1 5 . 0 0	18. 00	1155.5 5	711.11	154 0.00
3	S P V 27 89	113	83	9.00	85.0 0	11.0 0	691 .90	35.0 0	279 .83	1 8 . 0 0	22. 00	1277.7 7	700.00	160 0.00
4	S P V 27 93	149	88	10.0 0	85.0 0	10.0 0	629 .00	35.0 0	339 .83	1 6 . 0 0	20. 00	811.11	711.11	480. 00
5	S P V 27 94	121	79	9.00	65.0 0	9.00	432 .90	30.0 0	309 .83	1 6 . 0 0	15. 00	1311.1 1	688.88	700. 00
6	S P V 27 95	199	84	9.33	65.0 0	9.00	432 .90	45.0 0	339 .83	1 7 . 0 0	18. 00	866.66	488.88	340. 00
7	S P V 28 88	178	87	9.00	90.0 0	9.00	599 .40	45.0 0	359 .83	1 7 . 0 0	16. 00	577.77	311.11	300. 00
8	S P V 28 89	163	73	7.67	75.0 0	9.00	499 .50	40.0 0	204 .83	1 6 . 0 0	20. 00	700.00	844.44	100 0.00
9	S P V 28	200	84	8.33	75.0 0	10.0 0	555 .00	35.0 0	279 .83	1 8 . 0 0	18. 00	700.00	455.55	138 0.00

	90									0				
10	S P V 28 91	165	73	8.33	95.0 0	10.0 0	703 .00	48.0 0	309 .83	18 . 0 0	16. 00	844.44	1511.11	110 0.00
11	S P V 28 92	143	74	10.0 0	75.0 0	9.00	499 .50	40.0 0	329 .83	16 . 0 0	14. 00	688.88	411.11	280. 00
12	S P V 28 93	158	75	9.00	65.0 0	9.00	432 .90	40.0 0	339 .83	19 . 0 0	18. 00	800.00	477.77	500. 00
13	S P V 28 94	170	77	8.00	80.0 0	8.00	473 .60	35.0 0	304 .83	19 . 0 0	14. 00	1011.1 1	577.77	740. 00
14	S P V 28 95	130	81	9.33	100. 00	10.0 0	740 .00	45.0 0	329 .83	19 . 0 0	15. 00	1311.1 1	800.00	146 0.00
15	C S H 22 S S	145	82	9.67	95.0 0	12.0 0	843 .60	50.0 0	359 .83	17 . 0 0	22. 00	1033.3 3	622.22	136 0.00
16	C S V 19 S S	123	83	8.67	70.0 0	9.00	466 .20	45.0 0	314 .83	16 . 0 0	15. 00	866.66	488.88	680. 00
17	C S V 24 S S	140	76	8.67	85.0 0	9.00	766 .10	40.0 0	304 .83	16 . 0 0	20. 00	977.77	544.44	151 0.00
18	S P V 27 14	92	79	9.00	100. 00	10.0 0	747 .00	55.0 0	269 .83	15 . 0 0	15. 00	933.33	711.11	100. 00
19	S P V 28	67	74	9.67	80.0 0	10.0 0	597 .60	40.0 0	299 .83	17 . 0 0	18. 00	1022.2 2	633.33	72.2 2

	12									0				
20	S P V 28 96	100	76	7.67	80.0 0	9.00	537 .84	45.0 0	329 .83	16 · 0 0	16. 00	577.77	444.44	23.3 3
21	S P V 28 97	139	78	10.0 0	75.0 0	10.0 0	560 .25	40.0 0	299 .83	17 · 0 0	17. 00	655.55	577.77	131. 11
22	S P V 28 98	110	78	9.00	80.0 0	10.0 0	597 .60	40.0 0	249 .83	11 · 0 0	14. 00	511.11	344.44	24.4 4
23	S P V 28 99	35	89	9.67	85.0 0	11.0 0	698 .45	35.0 0	279 .83	14 · 0 0	22. 00	944.44	600.00	76.6 6
24	S P V 29 00	158	89	9.33	85.0 0	9.00	571 .46	50.0 0	329 .83	16 · 0 0	19. 00	1033.3 3	666.66	41.1 1
25	C S H 25	85	76	9.00	75.0 0	10.0 0	560 .25	40.0 0	199 .83	10 · 0 0	20. 00	811.11	566.66	172. 22
	M e a n	133 .52	80	9.04	81.6 0	9.68	597 .24	40.9 2	304 .63	16 · 2 0	17. 64	904.44	623.55	682. 04
	S. E.	0.1 2	0.12	0.38	0.32	0.12	1.2 0	3.60	0.1 2	0 · 1 2	0.1 2	0.12	0.12	0.12
	C. D. 5 %	0.3 4	0.34	1.09	0.90	0.34	2.3 0	5.30	0.3 4	0 · 3 4	0.3 4	0.34	0.34	0.34
	cv	0.3 4	0.57	1.46	11.1 8	4.78	5.3 0	2.30	0.1 5	2 · 8 3	2.5 9	0.05	0.07	0.07

ii. Morphological data of 25 Sorghum genotypes during study.

Sr.n o.	Genoty pes	juice yield (g/plant)	juice ph	juice extraction %	no.of internode/plant	100 seed weigh (g)	grain yield (g/plant)
1	SPH20 09	168.88	6.40	14.20	12.00	2.36	55.60
2	SPV26 97	121.11	6.50	15.60	11.00	2.92	15.50
3	SPV27 89	188.88	6.40	14.70	11.00	3.20	7.70
4	SPV27 93	165.55	6.40	8.00	11.00	2.03	10.00
5	SPV27 94	83.33	6.30	6.50	11.00	2.51	10.00
6	SPV27 95	38.88	6.40	4.50	10.00	2.66	46.11
7	SPV28 88	34.44	6.50	6.00	11.00	2.39	22.22
8	SPV28 89	115.55	6.50	16.00	12.00	2.29	23.32
9	SPV28 90	161.11	6.40	23.00	10.00	3.06	40.33
10	SPV28 91	128.88	6.30	15.00	11.00	2.13	45.00
11	SPV28 92	32.22	6.50	4.80	13.00	2.25	37.22
12	SPV28 93	57.77	6.40	7.20	12.00	2.41	24.44
13	SPV28 94	87.77	6.30	8.60	11.00	2.94	40.00
14	SPV28 95	170.00	6.30	13.00	11.00	2.23	68.88
15	CSH22 SS	162.22	6.40	15.50	11.00	3.03	49.44
16	CSV19 SS	78.88	6.40	9.00	13.00	1.64	16.11
17	CSV24 SS	175.55	6.40	18.00	11.00	2.72	59.22
18	SPV27 14	104.44	5.50	11.00	10.00	2.60	31.25
19	SPV28 12	74.44	6.50	7.20	12.00	1.80	62.50
20	SPV28 96	23.33	6.50	4.00	11.00	2.30	2.50
21	SPV28 97	32.22	6.50	4.80	13.00	1.60	35.00
22	SPV28 98	26.66	6.50	4.20	12.00	1.50	62.50
23	SPV28 99	81.11	6.30	8.50	12.00	1.60	3.75
24	SPV29 00	43.33	6.40	4.00	11.00	2.40	6.25
25	CSH25	222.22	6.40	25.00	11.00	1.70	77.50

	Mean	103.15	6.38	10.73	11.36	2.33	34.09
	S. E.	0.12	0.12	0.12	0.12	0.12	0.12
	C. D. 5%	0.34	0.34	0.34	0.34	0.34	0.34
	cv	0.43	7.24	4.23	3.99	2.35	1.31

THESIS ABSTRACT

S. No		
1.	Title of the Thesis	Genetic Variability Character Association and Clustering Pattern of Sweet Sorghum (<i>Sorghum bicolor</i> (L.) Moench) Genotype for Agronomic Traits in Rainfed Conditions
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ABSTRACT

The present investigation entitled, "**Genetic Variability Character Association and Clustering Pattern of Sweet Sorghum (*Sorghum bicolor* (L.) Moench) Genotype for Agronomic Traits in Rainfed Conditions**" was conducted during *Kharif* season of 2020-21 at Research field of all India Coordinated Research Project on Sorghum, College of Agriculture, Indore. Botanical name of Sorghum is- *Sorghum bicolor* (L.) Moench. It is one of the most important cereal crops around the world. It ranked 5th most produced food crops in the world after Wheat, Rice, Maize and Barley. It belongs to grass family, Poaceae with diploid ($2n=20$), tropical and C4 crop. Sorghum is a single most important cereal in the low land area because of extreme resistance to water stress. So it is called "**Camel Crops**". Sorghum is originated and domesticated in Africa continent, particularly east Africa (Ethiopia). In rainfed areas sorghum is truly a dual - purpose crop both grain and stalk are highly valued output. *Sorghum bicolor* growing major state in India - Maharashtra, Karnataka, Andhra Pradesh, Tamilnadu, Gujarat, Madhya Pradesh, Rajasthan. In Madhya Pradesh sorghum is an important for food and feed crop under rainfed conditions. Area of sorghum in India is approximately 4.8 m hac. With production 4.77 m ton and productivity 989 kg per hectare. (Anonymous, 2019-20).

In Madhya Pradesh, it is cultivated in an area of 0.11 million hectares with an annual production of 0.17 million tonnes and productivity of 1529 kg per ha. (Directorate of Economics & Statistics, DAC&FW, (2019-20 Final Data).

Analysis of variance of grain yield per plant and its contributing traits mean sum of square due to genotypes exhibited highly significant variation for all 19 characters *i.e. viz.*, plant population, days 50% flowering, number of leaves per plant, 4th leaves length, 4th leaves width, leaves area, flag leaves length, plant height, brix per cent, stem girth, total fresh biomass in grams per plant, fresh biomass in grams per plant, juice yield (lit/plant), juice yield (g/plant), juice pH, juice extraction per cent, number of internode per plant, 100 seed weight and grain yield g/plant. The phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the traits which demonstrated much influence of environment on expression of all the traits. PCV and GCV exhibited very little differences indicating the selection for

improvement of such characters on the basis of phenotype would be rewarding to improve present Sorghum genotypes.

Grain yield was positively and associated correlated with Seed yield/plant at both genotypic and phenotypic level exhibited significant and positive association with number of leaves/plant and highly significant positive association with 4th leaves width, leaves area, juice yield and juice extraction % indicated that this trait was positively associated because of linkages of genes governing the character at coupling phase. Positive correlation between desirable traits is supposed to be favorable to the breeder in the selection of suitable yield attributing traits for improvement in the productivity of Sorghum. Thus, selection for these characters will directly follow the immediate improvement of the grain yield for Sorghum crop.

Genetic divergence on the basis of 14 different morpho-physiological parameters, 25 sorghum genotype were grouped into 2 clusters among them cluster 1 polygenotypic had (24 genotypes) pursued by cluster 2 (1 genotype). Cluster No I exhibited maximum intra cluster D^2 value. The cluster I polygenotypic had (24 genotypes) and cluster II had (1 genotype) respectively.) and lowest mean for cluster number II.

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