

**STABILITY ANALYSIS IN
SORGHUM [*Sorghum bicolor* (L.)
Moench] GENOTYPES**

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M.Sc. (Ag.)

**DOCTOR OF PHILOSOPHY IN AGRICULTURE
(GENETICS AND PLANT BREEDING)**



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STABILITY ANALYSIS IN SORGHUM
[*Sorghum bicolor* (L.) Moench]
GENOTYPES

By
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M.Sc. (Ag.)

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CHAIRPERSON: Dr. V. SATYANARAYANA RAO



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DECLARATION

I, **PATI KAVYA** hereby declare that the thesis entitled “**STABILITY ANALYSIS IN SORGHUM [*Sorghum bicolor* (L.) Moench] GENOTYPES** submitted to the **Acharya N.G. Ranga Agricultural University** for the degree of **Doctor of Philosophy in Agriculture** is the result of original research work done by me. Part of the thesis has been published by me as “Kavya. P., V. Satyanarayana Rao, B. Vijayalakshmi, B. Sreekanth, Y. Radha Krishna and Naffez Umar. 2020, entitled “Correlation and path coefficient analysis in sorghum [*Sorghum bicolor* (L.) Moench] for ethanol yield”. *Journl of pharmacognosy and phytochemistry*. 9(2):2407-2410.

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CERTIFICATE

Ms. **PATI KAVYA** has satisfactorily prosecuted the course of research and that thesis entitled “**STABILITY ANALYSIS IN SORGHUM [*Sorghum bicolor* (L.) Moench] GENOTYPES**” submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part thereof has been previously submitted by her for a degree of any University.

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CERTIFICATE

This is to certify that the thesis entitled “**STABILITY ANALYSIS IN SORGHUM [*Sorghum bicolor* (L.) Moench] GENOTYPES**” submitted in partial fulfilment of the requirements for the degree of ‘**Doctor of Philosophy in Agriculture**’ of the Acharya N.G. Ranga Agricultural University, Lam, Guntur is a record of the bonafide original research work carried out by Ms. **PATI KAVYA** under our guidance and supervision.

No part of the thesis has been submitted by the student for any other degree or diploma. The published part and all the assistance received during the course of the investigations have been duly acknowledged by the author of the thesis.

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LIST OF SYMBOLS AND ABBREVIATIONS

%	:	Per cent
ANOVA	:	Analysis of Variance
AMMI	:	Additive Main Effects and Multiplicative Interaction
CD	:	Critical Difference
cm	:	Centimeter
contd.	:	Continued
CV	:	Coefficient of variation
DF (50%)	:	Days to 50% flowering
df	:	Degrees of Freedom
EI	:	Environment one (Bapatla)
EII	:	Environment two (Guntur)
EIII	:	Environment three (Garikapadu)
ESS	:	Error Sum of Squares
<i>et al.</i>	:	And co workers
etc.	:	and so on; and other people/things
FICCI	:	Federation of Indian Chambers of Commerce & Industry
F ₁	:	First filial generation
g	:	Grams
µg	:	micrograms
GA	:	Genetic Advance
GAM	:	Genetic Advance as per cent of Mean
GCV	:	Genotypic Coefficient of Variation
GCA	:	General Combining Ability
PCV	:	Phenotypic Coefficient of Variation
$h^2_{(b)}$	:	Heritability (broad sense)
H	:	Hybrid
HC	:	Hybrid check

VC	:	Varietal check
<i>i.e.</i>	:	That is
IPCA	:	Interaction principal component axis
IIMR	:	Indian Institute of Millets Research
ICRISAT	:	International Crops Research Institute for the Semi-Arid Tropics
T ha ⁻¹	:	Tonnes per hectare
L ha ⁻¹	:	litres per hectare
MSS	:	Mean Sum of Squares
M t	:	Million tonnes
Mtr	:	Meter
ml	:	Millilitre
mg	:	Milligram
nm	:	Nanometer
NPK	:	Nitrogen Phosphorous Potassium
No.	:	Number
S	:	Significant
NS	:	Non-significant
PCA	:	Principal Component Analysis
<i>per se</i>	:	As such with mean
RBD	:	Randomized Block Design
S.E.	:	Standard Error
SEm	:	Standard Error of Mean
SS	:	Sum of Squares
SCA	:	Specific Combining Ability
TrSS	:	Treatment Sum of Squares
TSS	:	Total Sum of Squares
<i>Via</i>	:	Through
<i>viz.,</i>	:	Namely
vs.	:	Against

ABSTRACT

Name of the Author : **P. KAVYA**

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The present investigation was carried out at Agricultural College farm, Bapatla, Andhra Pradesh with the following objectives: Study of variability, diversity, correlation and path analysis, combining ability, stability analysis and generation mean analysis for 13 quantitative characters

The data was recorded on Days to 50% flowering (Days), Days to maturity (Days), Plant height (cm), Number of nodes per plant, Stem girth (cm), Panicle weight (g), 1000 grain weight (g), Fresh stalk yield ($T\ ha^{-1}$), Juice yield ($l\ ha^{-1}$), Brix per cent, Total soluble sugars (%), Ethanol yield ($l\ ha^{-1}$), Grain yield ($T\ ha^{-1}$).

The analysis of variance indicated significant differences among the 110 genotypes indicating the existence of variability among the genotypes. Estimates of PCV were narrowly higher than the corresponding GCV values for the characters days to 50 % flowering, days to maturity and stem girth, while number of nodes per plant, fresh stalk yield (t/ha), grain yield (t/ha), brix %, T.S.S, juice yield (t/ha), ethanol yield (t/ha) showed moderate differences between PCV and GCV. Characters plant height (cm), 1000 grain weight, Panicle weight (gm) showed high magnitude of difference. Narrow and moderate difference between PCV and GCV indicating less environment influence on these characters. Therefore, selection based on phenotypic performance could be worth in achieving desired results. High heritability coupled with high genetic advance as percent of mean was observed for all the 13 characters studied.

The diversity study for 110 genotypes were grouped into 8 clusters indicating the presence of a wide range of genetic diversity. Cluster- I, was possessing the highest number of genotypes *i.e.*, 78 indicating the genetic similarity among them followed by Cluster- III with 15 genotypes, Cluster - II with 12 genotypes. Cluster - IV, V, VI, VII, VIII were monogenotypic indicating the uniqueness of the genotypes included in those clusters when compared to other genotypes included in the study. The cluster means for brix %, juice yield, ethanol yield and days to 50 % flowering were considered as criteria and for crossing, diverse parents were selected from various clusters. *i.e.*, from cluster IV, cluster V, cluster VI, cluster VII, and cluster VIII for hybridization programme.

The correlation results in 110 genotypes for 13 characters revealed that ethanol yield has significant positive correlation with brix percent, total soluble sugars, juice yield while negative association with grain yield, plant height, days to 50% flowering and days to maturity.

Path coefficient analysis revealed that juice yield exerted the highest positive direct effect on ethanol yield followed by brix %, total sugar yield along with positive correlation for all the above mentioned characters.

Four lines were crossed with 4 testers selected from the divergence studies in L x T fashion. The pooled analysis of variance for 13 characters measured over three locations in the present investigation revealed significant differences among environments, lines, testers, crosses, environment x line x tester for all the characters studied except panicle weight.

In the line x tester analysis, *sca* variance component estimates were greater than that of *gca* for the characters no of nodes, fresh stalk yield (t/ha), stem girth (cm), 1000 grain weight (g), panicle weight(g), brix%, total soluble sugars, juice yield(l/ha) and grain yield(t/ha) indicating the non-additive control of genetic variation in these traits.

Female line 1 (ICSA-14029) was found to be promising general combiner for fresh stalk yield, brix%, total soluble sugars, juice yield, and ethanol yield with higher positive significant GCA effects, while line 4 (ICSA-14035) was negative significant for all the characters studied except stem girth and plant height indicating this line was poor combiner for all the characters.

Among the testers which are used as male parents, tester 3 (ICSV 15006) has shown positive significant *gca* for all the traits like number of nodes, plant height, fresh stalk weight, stem girth, panicle weight, brix per cent, total soluble sugars, juice yield, ethanol yield followed by tester 2 (GGUB 28) possessing positive *gca* for juice yield and ethanol yield and tester 4 (IS 29308) had positive significant *gca* for brix %, total soluble sugars. Tester 1 (SEVS-08) recorded negative significant association for brix, total soluble solids, juice yield, ethanol yield and grain yield.

Among the hybrids, hybrid ICSA 14029 x ICSV 15006 has excelled with high *sca* effects for brix%, total soluble sugars, juice yield and ethanol yield followed by hybrid ICSA 14029 x GGUB 28 having high *sca* effects for brix %, total soluble sugars, juice yield and ethanol yield, 1000 grain weight, panicle weight. Hybrid ICSA 14030 x IS 29308 showed high *sca* effects for brix, total soluble sugars, juice yield, ethanol yield, days to maturity, 1000 grain weight, panicle weight and negative significant for no. of nodes, days to 50 % flowering, fresh stalk yield, stem girth. Hybrid ICSA 14033 x SEVS-08 was possessing high *sca* effects for brix, total soluble sugars, juice yield and ethanol yield, 1000 grain weight, days to 50% flowering and Number of nodes and negative effects for days to maturity, fresh stalk yield, stem girth and hybrid ICSA 14035 x SEVS-08 showing significant *sca* effects for juice and ethanol yield respectively. Among the Hybrids H-3, H-2, H-8 and H-10 were found to be superior for juice, brix percent and ethanol content. Hence the following hybrids can be used for further improvement.

The range of heterosis over mid parent, better parent and commercial check indicated that it was high with respect to ethanol productivity related traits particularly juice yield and brix per cent. Considering standard heterosis as reference point for viz;

juice yield, brix and ethanol yields the following hybrids have performed well ICSA 14029 x ICSV-15006; ICSA 14030 x ICSV 15006; ICSA 14305 x ICSV-15006; ICSA 14029 x GGUB 28; ICSA 14030 x GGUB 28; ICSA 14033 x ICSV-15006.

Stability analysis was conducted for 16 F₁ hybrids at three different locations. In pooled analysis of variance for stability, the genotypes, environments, genotype-environment interaction, environment (linear) and pooled deviations showed significant differences for most of the characters studied.

Stability analysis through “Eberhart and Russell’s model” resulted that Bapatla location was found to be most favourable location for brix %, total soluble sugars, ethanol yield and seed yield. Guntur was the most favourable location for number of nodes per plant and juice yield. Garikapadu was the favourable for days to fifty percent flowering, days to maturity, plant height, fresh stalk yield, stem girth, 1000 grain weight and panicle weight.

According to AMMI analysis the following hybrids were stable over locations for these characters like H-2 for days to 50% flowering, H-3 and H-5 for days to maturity, H-10 and H-2 for plant height, H-7 and H-5 for no of nodes per plant, H-15 for stem girth, H-3 and H-4 for 1000 grain weight, H-5 for fresh stalk yield, hybrids 12, 10, 11, 2 for grain yield, H -7 for brix%, H- 7 & H-8 for total soluble sugars and H-10 and 11 for juice yield and H-2 and 3 for ethanol yield.

The classification for Eberhart and Russell’s model and AMMI model was similar for the traits Days to 50% flowering, days to maturity, Plant height, number of nodes per plant. For remaining characters the AMMI classification doesn’t present any similarity with the results obtained by Eberhart and Russell’s model. The stable performing hybrids ICSA 14029 x GGUB 28, ICSA 14035 x GGUB 28 and ICSA 14033 x IS 29308 which are tested in 3 locations may be further tested in All India trials before commercial exploitation of ethanol production.

In the generation mean analysis study of ICSB 14029 x ICSV 15006, mean performance of 6 populations indicated that the F₂ means were lesser than the F₁ means except for brix per cent and stem girth and between mid-parental values in respect of all the traits except panicle weight, fresh stalk weight, grain yield indicating high degree of inbreeding depression. These results depict the predominant role of non-additive gene action which includes both dominance as well as epistatic interactions.

The scaling tests as well as chi square test from joint scaling test were highly significant in the cross ICSB 14029 x ICSV 15006’ cross for 11 characters excluding stem girth and 1000 grain weight, indicating inadequacy of simple additive-dominance model and justifying the use of six parameter model for the detection of gene interactions.

The six generation mean analysis carried out for 13 quantitative characters indicated significance of dominance gene effects for days to flowering, plant height, fresh stalk weight, juice yield, grain yield and ethanol yield. Significance of one or more interaction types (additive × additive or additive × dominance or dominance × dominance) in all the 13 traits except nodes per plant, stem girth, 1000 grain weight, total sugars estimation and ethanol yield was observed. Based on the signs of $[h^*]$ and $[I^*]$ gene effects, complementary gene interaction was evident in the inheritance of days to 50% flowering, days to maturity, juice yield, ethanol yield, while, duplicate gene

interaction in the inheritance was evident for plant height, number of nodes per plant, stem girth, panicle weight, 1000 grain weight, fresh stalk weight, brix %, total sugars estimation, grain yield indicating predominantly dispersed alleles at the interacting loci.

CHAPTER –I

INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] is a C₄ crop belonging to family Poaceae with chromosome number 2n=20, possessing different range of products like grain sorghum, forage sorghum, sweet sorghum which is native to semiarid tropics & subtropics. In India and Africa, it is used as food crop while in Europe and United states it is used as feed for livestock. Profuse alternative use of sorghum is not only as food and feed but also as a bioenergy crop which has rich amounts of sugars in stalks (10-20 %) as in sugarcane (Hunter and Anderson, 1997) terming it as sweet sorghum.

One of the important aspect in climate change is the air pollution, which is growing at an alarming rate, primary cause is the industries and secondary source is the exhaust from automobiles using petroleum products, crude oil, gasoline, diesel, *etc.* as raw material. The dependency on fossil fuels is very high and they are depleting day by day, where there is need for other alternate sources like biofuels from plant based products like Sugarcane, Corn, Sweet sorghum (Reddy *et al.* 2005) Sweet potato (Lareo *et al.* 2013) and sugar beet (Duraism *et al.* 2017). The above mentioned crops are food crops, which may hinder the food security if used for biofuels, but there are few crops for biofuel purpose like Sweet sorghum. In south American countries like Brazil it is grown as a source crop for ethanol production (Doggett, 1988). Currently, the ethanol blending with gasoline in Brazil is 18 to 27.5 per cent. (Lopes *et al.* 2016)

The present commercial ethanol production in India is only through sugarcane, where the by-product from sugar refineries *i.e.*, molasses which is utilised for the ethanol production. When compared to sugarcane, the juice from sweet sorghum is possessing high amounts of reducing sugars which aids in the efficient fermentation, producing clear and potable ethanol with low aldehydes (Ratnavathi *et al.* 2003). Both the dry matter yielded from high biomass, juice extracted from sweet sorghum stalks are among the major raw materials for bio-fuel production. Also, the juice extraction and fermentation procedures are similar to sugarcane without much differences. The cultivable land under sugarcane is decreasing year by year. The added advantages of sweet sorghum are four months of crop period when compared to sugarcane 12-13 months of crop period, where three crops can be harvested in a single year with 300 % cropping intensity, while the water consumption is nearly three times lower (8,000 m³ ha⁻¹) than sugarcane (36,000 m³ ha⁻¹). (Vinutha *et al.* 2014).

In India, ethanol is used in three different ways. Of the total available ethanol produced, potable liquor occupies the major share (45 %), the next 40 per cent is used in the chemical industry as a solvent in synthesis of other organic chemicals and the rest is used for blending with petrol and other purposes. The growth of user industries and use of ethanol has been continually increasing year by year which is creating a huge demand, but the production and availability of ethanol has largely lagged behind. The countries viz; Brazil, The United States of America (USA) and China are the top ethanol producing countries respectively, while India stands in 4th position producing around 2000 million litres of ethanol, primarily from sugarcane molasses. (Prasad *et al.* 2018).

The World ethanol production has increased from 13.6 billion gallons in 2007 to 22.3 billion gallons by 2012. (Satyanarayana and Rameshchandra, 2014). India has produced 530.09 million gallons of ethanol in 2019. (www.staista.com). In order to reduce carbon monoxide emission through automobiles, Indian government has mandated for blending of five per cent ethanol with petrol and diesel and could save nearly 80 million liter of petrol annually, if petrol is blended with ethanol by 10 per cent. (GAIN report 2013). The current ethanol production raw material is through sugarcane molasses which is lagging in production and the most of the distilleries (ethanol based) work only for 180 days *i.e.*, during the peak period of sugarcane harvesting stage. The government has no stringent regulations for blending ethanol in petrol (gasoline) due to truncated production of sugarcane crop and it's byproduct in the past decade. The sweet sorghum can be a best alternative for ethanol production to meet up the demand of the country, by providing year the round operations to molasses-based ethanol distilleries and provide an assured income to the farmers.

In any breeding programme, there is need for knowing the available variability present. As yield is influenced by a number of yield contributing characters, which are controlled by polygenes and also influenced by environment. Allard and Bradshaw, (1964) observed that the nature of genotype environment interactions are extremely complex.

Genetic diversity is the basic requirement in any crop improvement programme. It provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936). Sorghum is endowed with high diversity due to its wide range of adaptation in tropical and temperate climates and free gene exchange among various races. In the D^2 statistics enables one to discriminate

between different cultivars according to the diversity present in the genotypes and helps in the selection of genetically divergent parents for their exploitation in hybridization programme (Oliveira *et al.*, 2020)

Correlation refers to the degree and direction of association between two or more variables. (Toor, 2020) Thus, correlation enables to identify the characters or combination of characters which might be useful as indicator of high yield by way of evaluating relative influence of various characters on yield and among themselves as well. The original concept of correlation was given by Galton (1889) and later elaborated by Fisher (1936).

Path coefficient analysis was used to calculate the direct and indirect contribution of various traits to yield (Dewey and Lu, 1959). Thus, path analysis can provide a better insight into the cause and effect relationship between different pairs of characters. (Goswami *et al.*, 2020)

The constant effort of scientists by national and international institutes and SAU's have resulted in excellent sweet sorghum varieties for use in ethanol production, but still till date, only one sweet sorghum hybrid CSH-22SS has been released for commercial cultivation in India. This necessitates the identification of new hybrids with good combining ability to suit under different agro ecological situations for ethanol production. The information on the heterotic patterns and combining ability among sweet sorghum germplasm is essential in maximizing the effectiveness of hybrid development. (Nandeshwar *et al.*, 2020).

Generation mean analysis provides information on the relative importance of average effects of the genes (additive effects), dominance deviations and effects due to nonallelic genetic interactions, yet it is a simple, but useful technique for estimating gene effects for a polygenic trait, its greatest merit lying in the ability to estimate epistatic gene effects such as additive ·additive, dominance ·dominance and additive ·dominance effects. (Ganapati *et al.*, 2020)

Generally, most of the sweet sorghum productivity traits are governed by non-additive gene actions as they are influenced by environment (Pagire *et al.*, 2020). Hence an effort was made to study the stability of hybrids for various traits as there is scarce information available.

Keeping in view of the above huge gap between demand for ethanol and its supply, the present research work is formulated with the following objectives:

OBJECTIVES:

1. To study the nature and magnitude of genetic diversity present in morphological and quality traits in the collected sweet sorghum germplasm through D² analysis.
2. To study the nature and extent of association between ethanol yield and its component traits through correlation studies and direct and indirect effects of various component characters on ethanol yield through path coefficient analysis.
3. To assess the general combining ability of new parental lines and specific combining ability of new combinations using L X T mating design and to assess the heterosis of newly developed hybrids in respect of Stalk and ethanol yield and its attributing characters.
4. To conduct stability analysis in three locations by comparing Eberhart and Russell model and AMMI Analysis.
5. Estimation of Genetic Parameters by Generation mean analysis for morphological and quality traits using 6 parameter model.
6. To identify promising genotypes for ethanol yield and quality traits for their utilization in breeding programmes and further seed multiplication programmes.

CHAPTER-II

REVIEW OF LITEARTURE

2.1 VARAIBILITY STUDIES

Genetic variability has become an obvious feature of considerable importance that renders any crop improvement programme successful. Knowledge on existing variability with respect to yield and yield attributing traits in the existing germplasm of any crop is the basic requirement in order to select the desirable types. Vavilov (1951) for the first time perceived the importance of genetic variability and advocated that the widest range of variability provides a better scope for selecting desired genotypes. According to Allard (1960), heritability is the proportion of observed variability which is due to genetic causes and the remainder being due to the environmental cause. Heritability of a character indicates the extent to which particular character can be transmitted from one generation to another Balouch *et al.* (2003) therefore it becomes a valuable tool for predicting the magnitude of genetic gain that follows selection for a character.

Table 2.1 Review of literature on variability, heritability, Genetic advance as Percent of mean

S. No.	Character	GCV (%)	PCV (%)	H ²	GAM	Reference
1	Days to 50 % flowering (days)	Low	Low	High	Moderate	Chavan <i>et al.</i> (2010)
		Low	Low	High	Moderate	Tomar <i>et al.</i> (2012)
		Low	Low	High	High	Iraddi <i>et al.</i> (2013)
		Low	Low	High	High	Sami <i>et al.</i> (2013)
		Low	Low	High	High	Kalpande <i>et al.</i> (2014)
		-	-	High	High	Nyadanu & Dikera (2014)
		-	-	High	Low	Jain and Patel (2014)
		High	High	High	High	Amare <i>et al.</i> (2015)
		Moderate	Moderate	-	-	Khandelwal <i>et al.</i> (2015)
		High	High	-	-	Muhammed <i>et al.</i> (2015)
		-	-	High	High	Rekha and Biradar, 2015
		-	-	High	Low	Sabiel <i>et al.</i> 2015

S. No.	Character	GCV (%)	PCV (%)	H ²	GAM	Reference
		Moderate	Moderate	High	High	Badigannavar <i>et al.</i> (2017)
		Moderate	Moderate	High	High	Bhagasara <i>et al.</i> (2017)
		Low	Low	Moderate	Moderate	Ranjith <i>et al.</i> (2017)
		Moderate	Moderate	High	High	Swamy <i>et al.</i> (2018a)
		Low	Low	High	Moderate	Gebregergs and Mekbib (2020)
2.	Days to maturity (days)	Low	Low	High	Low	Iraddi <i>et al.</i> (2013)
		Low	Low	High	Low	Kalpande <i>et al.</i> (2014)
		Low	Low	High	Low	Swamy <i>et al.</i> (2018a)
		Low	Low	High	Low	Zinzala <i>et al.</i> (2018)
		Low	Low	Moderate	High	Gebregergs and Mekbib (2020)
3.	Plant height (cm)	High	High	High	High	Vinodhana <i>et al.</i> (2009)
		Moderate	Moderate	High	High	Chavan <i>et al.</i> (2010)
		Moderate	Moderate	High	High	Tomar <i>et al.</i> (2012)
		High	High	High	High	Iraddi <i>et al.</i> (2013)
		-	-	High	High	Seetharam and Ganeshmurthy (2013)
		-	-	High	High	Madhu and Harini (2014)
		High	High	-	-	Santhosh <i>et al.</i> (2014)
		High	High	High	High	Amare <i>et al.</i> (2015)
		Moderate	Moderate	-	-	Khandelwal <i>et al.</i> (2015)
		High	High	High	High	Muhammad <i>et al.</i> (2015)
		-	-	High	-	Sabiel <i>et al.</i> (2015)
		High	High	High	High	Badigannavar <i>et al.</i> (2017)
		-	-	High	-	Bhagasara <i>et al.</i> (2017)
		High	High	High	High	Ranjith <i>et al.</i> (2017)
		-	-	High	High	Hamidou <i>et al.</i> (2018)
		Moderate	Moderate	High	High	Swamy <i>et al.</i> (2018a)
		High	High	High	High	Gebregergs and Mekbib (2020)
4.	Number of nodes per plant	Moderate	Low	Moderate	Moderate	Iraddi <i>et al.</i> (2013)
		Moderate	Moderate	High	High	Sami <i>et al.</i> (2013)
5.	Stem girth (cm)	Moderate	Moderate	High	Moderate	Tomar <i>et al.</i> (2012)
		Low	Low	High	High	Iraddi <i>et al.</i> (2013)

S. No.	Character	GCV (%)	PCV (%)	H ²	GAM	Reference
6.	Panicle weight (g)	Low	High	Low	Low	Sami <i>et al.</i> (2013)
		High	High	High	High	Swamy <i>et al.</i> (2018a)
		-	-	High	High	Hamidou <i>et al.</i> (2018)
		High	High	High	High	Gebregergs and Mekbib (2020)
7.	1000 grain weight (g)	Low	Low	Low	Low	Sami <i>et al.</i> (2013)
		High	High	-	-	Santhosh <i>et al.</i> (2014)
		High	High	-	-	Muhammad <i>et al.</i> (2015)
		-	High	-	-	Bhagasara <i>et al.</i> (2017)
		High	High	-	-	Kassahun <i>et al.</i> (2017)
		High	High	-	-	Mohamad <i>et al.</i> (2017)
		High	High	High	High	Ranjith <i>et al.</i> (2017)
		Moderate	High	Low	Low	Hamidou <i>et al.</i> (2018)
		-	-	High	High	Birhan <i>et al.</i> (2020)
8.	Fresh stalk weight (T ha⁻¹)	High	High	High	High	Tomar <i>et al.</i> (2012)
		Low	Low	High	High	Iraddi <i>et al.</i> (2013)
		Low	High	Moderate	High	Kalpande <i>et al.</i> (2014)
		High	High	High	High	Wadikar <i>et al.</i> (2018)
9.	Juice yield (T ha⁻¹)	High	High	High	High	Tomar <i>et al.</i> (2012)
		High	High	High	High	Iraddi <i>et al.</i> (2013)
		High	High	High	High	Wadikar <i>et al.</i> (2018)
10.	Brix (%)	Moderate	Low	High	Moderate	Tomar <i>et al.</i> (2012)
		Low	Moderate	High	Moderate	Iraddi <i>et al.</i> (2013)
11.	TSS (%)	High	High	High	High	Sami <i>et al.</i> (2013)
		Low	Moderate	High	Moderate	Iraddi <i>et al.</i> (2013)
12.	Ethanol yield (l ha⁻¹)	Low	Moderate	High	Moderate	Iraddi <i>et al.</i> (2013)
13.	Grain yield (T ha⁻¹)	High	High	High	High	Chavan <i>et al.</i> (2010)
		High	High	High	High	Seetharam and Ganeshmurthy (2013)
		High	High	High	High	Iraddi <i>et al.</i> (2013)
		High	High	High	High	Dhutmal <i>et al.</i> (2014)
		High	High	High	High	Kalpande <i>et al.</i> (2014)
		High	High	High	High	Amare <i>et al.</i> (2015)
		High	High	Moderate	High	Bhagasara <i>et al.</i> (2017)
		High	High	Moderate	High	Hamidou <i>et al.</i> (2018)
		High	High	High	High	Swamy <i>et al.</i> (2018a)
		High	High	High	High	Wadikar <i>et al.</i> (2018)

2.2 DIVERSITY STUDIES

Genetic diversity is the underlying cause for several at least two agriculturally important phenomena like heterosis and transgressive segregation. Diverse lines are needed not only for defect correction in commercial varieties but also for the development of novel varieties. Identification of diverse lines (if at all available) and their subsequent utilization becomes the major goal of any crop improvement programme. A technique which reduces the number of comparisons among genotypes by classifying them into different clusters as given by Bhandari *et al.* (2017) is basically developed by Mahalanobis in 1936 and is represented as D^2 which provides a quantitative measure of association between geographic and genetic diversity based on generalized distance.

Rohman *et al.* (2004) studied D^2 in 35 sorghum accessions. Total 5 clusters were formed, maximum number of genotypes were in cluster – I and minimum number in cluster III. Clusters distances were high between clusters, between cluster III and IV highest inter cluster distance was observed and lowest between III and V. Cluster IV possessed highest intra cluster distances and cluster II had the lowest. Out of nine characters studied maximum contribution towards divergence was by days to maturity, number of tiller/plant and 1000 grain weight.

54 genotypes were segregated into 8 clusters by Sameerkumar *et al.* (2010) wherein, 15 genotypes fall in cluster I followed by 10 genotypes in cluster V, 9 genotypes in cluster IV. The three clusters II, VI and VII had 5 genotypes each, cluster III had 4 genotypes each and Cluster VIII is monogenotypic. The following clusters had maximum inter cluster distance between cluster VII and VIII, cluster III and VII and cluster V and VIII. Seed yield had ranked first for contributing maximum to divergence 94.2% followed by plant height and days to 50% flowering.

Based on D^2 statistics 11 clusters were formed for thirteen growth characters in 46 genotypes studied by Shinde *et al.* (2013), for which maximum inter cluster distance (i.e. 34.72) was observed between cluster V and cluster IX and cluster I showed the highest intra cluster value (13.79) followed by cluster II (13.64).

Tomar and Sivakumar (2012a) sorted 52 sweet sorghum genotypes into ten clusters i.e., IV, V, VI, VII, VIII, and X and out of 17 morphological characters presented sucrose per cent, plant height, juice weight, plant height, days to fifty per cent flowering, brix per cent, millable cane weight, stay green trait, fresh cane weight, sucrose yield, stem girth and juice volume accounted maximum contribution to the genetic divergence.

Mahajan and Wadikar (2012) classified the 24 genotypes into eight clusters during the study of genetic divergence. Highest contribution trait to the divergence was Harvest index. Among the clusters formed, clusters VII and VII, II and VIII and cluster II and VI possessed the maximum inter cluster distance.

Fodder yield, days to maturity, plant height and grain yield contributed maximum towards divergence in the study conducted by Sameerkumar *et al.* 2012. The sixty genotypes were grouped into ten clusters Based on D^2 values. 24 genotypes in Cluster I, 12 genotypes in cluster VII, 8 genotypes in cluster IV, 6 genotypes in cluster X with, and with 5 genotypes in cluster VIII and the rest of the Clusters II, III, V, VI and IX consisted solitary genotypes. between cluster III and VI, cluster V and IX and cluster II and IX least D^2 values were recorded extreme inter cluster distance was observed between cluster VIII and X followed by cluster V and VII, cluster VII and X.

Based on D^2 statistics Elangovan *et al.* (2014) assembled 46 genotypes into 11 clusters, out of which highest intra cluster value was in cluster –I (13.79) followed by cluster II (13.64) while cluster V and cluster IX recorded maximum inter cluster distance (*i.e.* 34.72). The diverse pattern indicated that the maximal number of genotypes were included in cluster IV and cluster III with 9 genotypes, cluster VI having 8 genotypes, cluster II having 5 genotypes and cluster I having 3 genotypes respectively. The cluster VII and cluster VIII possessed single genotype.

121 germplasm lines of Rabi sorghum were assessed and congregated into 13 clusters Khadakabhavi *et al.* (2014) where, cluster-I was the largest with 61 genotypes followed by cluster-XIII with 38 genotypes. Whereas, cluster-II, to cluster-XII consisted of 2 genotypes in each clusters. The intra cluster distance was maximum in cluster-XIII and cluster-I followed by cluster-XII and cluster-XI whereas inter cluster distance was maximum between cluster-X and cluster-XI. The genotypes in clusters-VI showed high mean values for most of the characters studied. Maximum contribution to the divergence was by grain yield per plant, 1000 grain weight, ear length, culm height and days to 50 per cent flowering.

Depending on the D^2 values 35 sweet sorghum genotypes of diverse origin were packed in to 6 clusters. Cluster II was the largest and consisted of 10 genotypes and cluster VI was the least with 1 genotype. The intracluster distances were low when compared to the inter-cluster distances. Bahadure *et al.* (2014).

Sujatha & Pushpavalli (2015) studied divergence for 45 rabi sorghum landraces, 13 advanced breeding lines and 4 popular cultivars. The 62 genotypes were grouped 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. The inter cluster distance was maximum between cluster XIII and XIV followed by cluster XIV and XV, cluster XII and XV, cluster XII and XIII and cluster V and XIV. Seed yield contributed maximum to divergence (31.84 %) followed by plant height (20.62 %) and days to 50% flowering (14.38 %).

Sinha and Kumaravadivel (2016) evaluated 40 diverse forms of sorghum like forage sorghum, mutant lines, restorer lines, sweet sorghum, grain sorghum, maintainer lines for genetic diversity using biometric traits. By using hierarchical cluster analysis, 40 accessions were grouped under 6 clusters. Maximum number of accessions were in Cluster I and minimum in cluster VI. The maximum intercluster distance was observed between cluster VI and cluster IV. For 100 seed weight and yield highest mean value was found in Cluster III. Top most character was Ear width to contribute to the divergence while the others are culm girth and leaf breadth.

Doijad *et al.* (2016) formulated the 61 genotypes into 15 clusters, where cluster I comprised maximum of 47 genotypes, while the rest of the clusters had one genotype each. Inter-cluster distance was maximum between the clusters XV and XIV followed by XV and IX. Regarding genetic divergence of the genotypes, relative water content contributed major share followed by grain weight, panicle weight, days to 50% flowering, plant height and fodder weight.

Meena *et al.* (2016) analysed 62 sorghum genotypes for genetic divergence which resulted in 10 clusters, extreme inter-cluster distance between clusters II and IX and least between clusters VI and VIII was observed. Intra-cluster distance was peak in cluster IX and low in cluster VII.

Out of 22 clusters out listed, cluster I comprised maximum of 115 genotypes followed by cluster II with 45 genotypes in the study of 228 sorghum genotypes by Prasad and Biradar (2017a). Inter-cluster distance was maximum between the clusters III and XXI followed by XIII and XXI with 33.50 and 33.26. Primaries per panicle is the next to panicle weight for contribution towards divergence.

60 genotypes of forage sorghum were analysed for D^2 statistics which sorted the genotypes into 5 clusters. Cluster I containing 40 genotypes followed by 16 in cluster II, while cluster III and V were contain 1 genotype and cluster IV had only dyad genotypes. Damor *et al.* (2017).

Ahalawat *et al.* (2018) clustered 30 genotypes into 6 clusters based on D_2 Statistics. The maximum inter-cluster distance was observed between cluster III and VI followed by IV and VI.

In a study of 26 sorghum accessions which were clubbed in to 6 clusters, Cluster I and cluster II are the highest with 11 accessions whereas, remaining 4 clusters had only solitary accession each. The intra and inter cluster distances among the accessions revealed that the high intensity of divergence was observed between the clusters III and IV followed by I and VI, II and IV. More *et al.* (2018)

Swamy *et al.* (2018b) applied mahalanobis D^2 statistics on 122 sorghum genotypes and grouped them 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. Among the 11 biometric characters studied days to 50% flowering contributed high (34.53%) to the total divergence. Maximum intra cluster distance was shown by cluster II (4.46) and maximum inter cluster distance (11.32) was noticed between the clusters V and IX.

The study conducted by Karadi and Kajjidoni (2019) in 25 selected mini core accessions and 16 promising varieties were grouped into 8 and 5 clusters, respectively. Among the selected mini core, cluster I was largest with 12 accessions whereas most of the clusters had one with minimum accessions. Whereas, cluster IV and VI with four accessions each. Among promising varieties, cluster V with 5 accessions, cluster 2 and 5 with minimum two accessions each. Cluster III and I with 4 and 3 accessions, respectively. Among 12 quantitative traits studied, the highest contribution towards the divergence was ear head length (46%) in the selected mini core and plant height (67%) in the promising varieties, respectively.

Khandelwal *et al.* (2019a) conducted an experiment to investigate the genetic diversity among 150 genotypes of sorghum [*Sorghum bicolor* (L.) Moench] and the results revealed that 150 genotypes were clustered into 6 clusters, 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.

2.3 CORRELATION & PATH STUDIES

Yield is a complex quantitative character influenced by several component traits. Knowledge on association among different yield related traits is a prerequisite for developing an appropriate breeding strategy which would bring about the simultaneous improvement in all the desirable traits. The advantage of path analysis is that it permits the portioning of the correlation coefficient into its components – the first component being the path coefficient (or standardized partial regression coefficient) measures the direct effect of a predictor variable up on its response variables, while the second component being the response variable through other predictor variables (Dewey and Lu, 1959). Path coefficient analysis assists plant breeders in identifying traits on which selection pressure should be given for improving yield and the below are the landmarks in this area of study.

2.3.1 Correlation Studies

In a Correlation study with 175 pop sorghums by Mallinath *et al.* (2004) expressed that grain yield per plant was found to be significantly and positively associated with panicle weight, fodder yield per plant.

A significant and highly positive correlation between grain yield and head weight, 1000 grain mass. Similarly, significant but negative correlation exists between panicle count and panicle length was reported by Ezeaku and Mohammed (2006).

In a study involving seven sorghum genotypes Kachapur and Salimath (2009) reported, positive and significant relationship between brix and pol percent but significant and negative relation between brix and ear head weight, brix and grain yield.

The enlisted characters Plant height, Days to 50 per cent flowering, No. Tillers, No. Leaves, Leaf length, Leaf breadth, Leaf stem ratio, Stem thickness, Crude protein, Dry fodder yield had significant positive association with green fodder yield per plant in the study by Iyanar *et al.* (2010).

In an association study of 35 hybrids of sorghum by Prakash *et al.* (2010) green fodder yield per plant was found to be significantly and positively correlated with plant height, number of tillers, leaf length, leaf breadth, stem diameter, hydrocyanic acid and crude fibre. Days to 50 per cent flowering, crude protein, while in vitro dry matter digestibility showed a negative association with green fodder yield per plant.

1000 seed weight showed highly significant association with grain yield per plant at both genotypic and phenotypic level in a study of 64 sorghum genotypes by Warkad *et al.* (2010) and while number of internodes per plant exhibited very strong positive correlation with number of leaves per plant and stem girth while number of leaves showed moderately significant positive association with stem girth.

Ali *et al.* (2011) reported dry shoot weight, fresh shoot weight and Fresh root weight showed significant genotypic correlation with grain yield.

Results of correlation analysis by Din *et al.* (2012) in 25 sorghum restorer lines indicated that number of seeds/head had positive and highly significant correlation with grain yield, whereas, the positive and significant correlation between panicle length and grain yield and on the other hand there are negative and non-significant correlation between panicle width and grain yield/panicle.

In the study of 46 sweet sorghum genotypes for association studied, green stalk yield exhibited highly significant and positive correlations at genotypic and phenotypic levels with plant height, number of internodes, stem girth and juice extraction per cent as revealed by Shinde *et al.* (2012).

In the correlation study by Naim *et al.* (2012) grain yield per hectare had high significant positive correlation with number of grain per panicle and number of panicles per unit area.

In an association study by Tomar and Sivakumar (2012b) in 52 sweet sorghum genotypes sucrose yield showed highly significant positive phenotypic and genotypic correlation with stem girth, millable cane weight, sucrose percentage, juice extraction percentage, cane yield, juice yield.

In the study of 37 sorghum genotypes by Patil *et al.* (2014) grain yield per plant exhibited significant positive association with thousand grain weight, stem girth, leaf length, panicle length, panicle diameter, panicle weight and protein per cent in grain both at genotypic and phenotypic levels.

Correlation coefficients among two F₂ populations of sweet sorghum crosses by Vemana *et al.* (2014) revealed that juice yield was positively associated with fresh stalk yield, total biomass, plant height, grain yield, days 50% flowering, days to maturity, nodes per plant, brix per cent and stem girth.

Arunah *et al.* (2015) conducted association studies between two sorghum varieties for 2 years, where in a positive and highly significant correlation was observed between sorghum yield and plant height, leaf area index, total dry matter, panicle weight and 1000- grain weight.

Evaluation of 224 sorghum genotypes by Khandelwal *et al.* (2015) revealed grain yield per plant was significantly and positively correlated with harvest index, 1000 seed weight, Panicle length, fresh weight per plant and leaf area.

Sowmy *et al.* (2015) correlated days to maturity at genotypic level and days to flowering at both genotypic and phenotypic levels to be highly significant negative correlation with grain yield.

Hundekar *et al.* (2016) studied correlation for five traits where, 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.

Vendruscolo *et al.* (2016) found that there is high genotypic correlation between the traits green mass production and dry matter production in 34 sorghum biomass types.

Correlation study by Phuke *et al.* (2017) in sorghum revealed that iron and zinc associated negatively to grain yield but in low magnitude, whereas 100-seed weight showed significant positive association with both the traits.

Makanda (2017) reported that the dependent variable grain yield, had positive and significant correlation with stem sugar, stem biomass, days to 50% flowering, number of leaves per plant, plant height and stem diameter and significant negative correlation with stem juice score.

Jimmy *et al.* (2017) evaluated 10 sorghum genotypes for association study and reported grain yield was significant and positively associated with days to 50% flowering, number of fertile tillers, panicle width, dry panicle weight and 100 seed mass.

Association studies on 121 germplasm lines of sorghum by Khadakabhavi *et al.* (2017). indicated that at both genotypic and phenotypic levels, panicle width and 1000 grain weight had significantly positive correlation with grain yield per plant.

Chalachew and Rebuma (2018) studied correlation in 15 sweet sorghum genotypes and reported that grain yield had positive and significant correlations with panicle weight and panicle width at both phenotypic and genotypic levels. Further they have also recorded positive and significant correlations between juice, sugar and fresh stalk yields at both genotypic and phenotypic levels with ethanol yield.

In an association study by Deshmukh *et al.* (2018) in rabi sorghum mutants grain yield per plant exhibited positive and significant correlations with total biomass content, 100 seed weight and ear head length.

Mulualet *et al.* (2018) observed that grain yield showed significant and positive phenotypic correlation with number of heads per plot, panicle weight and hundred grain weight. The strongest phenotypic association was observed between days to flowering and days to maturity followed by hundred grain weight and plant height.

Soujanya *et al.* (2018) revealed significant positive association of green fodder yield with early vigour, leaf length, leaf breadth and internodal length during character association studies in 48 forage sorghum hybrids.

In an association study by Swamy *et al.* (2018a) positive and significant correlation was observed between grain yield and days to 50 per cent flowering, days to physiological maturity, plant height, panicle girth, panicle weight, Stover weight and 1000-grain weight in 122 sorghum genotypes.

Correlation studies by Zinzala *et al.* (2018) on 25 genotypes of sorghum indicated that grain yield per plant was found to be significantly and positively associated with panicle length and protein content.

Correlation studies revealed significant trait associations for grain yield with panicle weight, panicle width, stem girth and leaf width. Grain yield revealed a non – significant weak negative correlation with days to 50% flowering. Akatwijuka *et al.* (2019).

2.3.2 Path Coefficient Studies

Partitioning of yield and yield components into direct and indirect effects revealed that head weight had the highest direct effect on grain yield while 1000 grain mass contributed indirectly to grain yield via head weight by Ezeaku and Mohammed (2006).

Kachapur and Salimath (2009) Partitioning of the correlation coefficient through path analysis indicated that the direct effects of brix and juice volume was maximum followed by brix and CCS yield.

In the path analysis of 109 genotypes of multicut forage sorghum by Iyanar *et al.* (2010) plant height contributed maximum direct effect to green fodder yield per plant followed by leaf breadth and leaf stem ratio. Number of tillers and stem thickness also exerted positive direct effect on green fodder yields

In the path analysis of 35 sorghum hybrids by Prakash *et al.* (2010) revealed that plant height contributed high direct effect to green fodder yield per plant followed by leaf breadth and leaf length. Stem diameter and in vitro dry matter digestibility also exerted positive direct effect on green fodder yield.

Warkad *et al.* (2010) studied path analysis in 64 sorghum genotypes, character days to 50% flowering exhibited positive direct effect on grain yield per plant followed by ear head length and 1000 seed weight.

Din *et al.* (2012) conducted path analysis study in 25 sorghum restorer lines and reported that panicle length had low but positive direct effect on grain yield, while number of kernels/head had high positive direct effect on grain yield and positive indirect effect was through days to flowering, plant height, panicle length, panicle width and no of internodes, and its indirect effect was negative through leaf area and 1000-kernel weight.

Tomar and Sivakumar (2012b) studied 52 genotypes of sorghum for path analysis and reported that sucrose yield had maximum positive direct effect on cane yield followed by sucrose percent, juice yield, days to physiological maturity and juice extraction percentage.

Path co-efficient analysis by Patil *et al.* (2014) in 37 sorghum genotypes considering 15 characters showed that the number of leaves per plant had highest positive direct effect on grain yield per plant followed by panicle diameter, leaf length, protein per cent in grain and thousand grain weight.

Vemana *et al.* (2014) revealed the following results in two F₂ populations of sweet sorghum *i.e.*, fresh stalk yield and total biomass in '296 B × URJA' while, plant height and total biomass in '27 B × NSSV 13' exhibited maximum positive direct effect on juice yield.

The highest individual direct effect was made by leaf area index, followed by plant height. Total dry matter, panicle length and weight also contributed positively to the final yield in the path analysis conducted by Arunah *et al.* (2015) in sorghum.

Path coefficient analysis by Khandelwal *et al.* (2015) revealed high or moderate direct effects of harvest index, dry weight per plant and 1000 seed weight on grain yield per plant.

In the Path investigation by Sowmy *et al.* (2015) revealed that, out of six characters, two characters *viz.*, days to flowering and plant height had positive direct effect on grain yield. While the character days to maturity showed high negative direct effect on grain yield and panicle length had non-significant association with grain yield.

Path analysis in 32 sorghum hybrids had positive direct effects on grain yield through test weight, panicle length, days to 50% flowering and days to maturity at both phenotypic and genotypic levels were Hundekar *et al.* (2016).

The path analysis study in 34 biomass sorghum types demonstrated that green mass production and number of leaves can assist in the selection of dry matter production. Vendruscolo *et al.* (2016).

Khadakabhavi *et al.* (2017) studied partitioning of yield and yield components both at phenotypic and genotypic levels in 121 germplasm lines of sorghum and revealed that the characters 1000 grain weight, panicle length, days to maturity had positive direct effects on grain yield at both genotypic and phenotypic level.

Path-coefficient analysis by Makanda (2017) in 100 sorghum genotypes revealed that the number of leaves per plant had high, positive direct effect on grain yield.

Shukla *et al.* (2017) observed from the experiments indicated that high sugar concentration in sweet sorghum is not conditional on the plants being tall, making the development of short, sweet inbred lines feasible.

Earhead length exhibited the highest positive direct effect on grain yield followed by days to maturity, plant height, seed weight, harvest index and number of branches per panicle in a study conducted by Deshmukh, *et al.* (2018) on rabi sorghum mutants.

In the path analysis conducted by Mangena *et al.* (2018) in 190 sweet sorghum genotypes biomass yield had the greatest direct effect on ethanol production while the other characters like days to flowering, plant height, stalk brix and stem diameter exerted the greatest indirect effects on ethanol production through higher biomass production.

Days to maturity, plant height, number of heads per plot, panicle weight and hundred grain weight have exerted positive phenotypic direct effect on grain yield in the path study conducted by Mulualem *et al.* (2018).

Path analysis studied by Soujanya *et al.* (2018) revealed Positive and high direct effect of early vigour, plant height, internodal length, leaf length and leaf breadth.

Zinzala *et al.* (2018) disclosed results of path analysis in 25 sorghum genotypes possessing the highest positive direct effects of days to maturity, dry fodder yield per plant, tannin content, panicle length and 100 seed weight on seed yield per plant.

Akatwijuka *et al.* (2019) studied path analysis in 47 sorghum cultivars and revealed that stem girth, leaf width and panicle width had the highest indirect contributions to grain yield.

2.4 COMBINING ABILITY

Combining ability or productivity in crosses is defined as the ability of cultivars or parents to combine among each other during hybridization process such that desirable genes or characters are transmitted to their progenies. In another definition, combining ability is an estimation of the value of genotypes on the basis of their offspring's performance in some definite mating design. (Allard, 1960). It can seldom be envisaged only based on parental phenotype and thus it is measured by progeny testing. When parental plants produce potent offspring, they are said to have good combining ability.

Two concepts of combining ability, general combining ability (GCA) and specific combining ability (SCA) have had important influence on inbred line evaluation and population development in crop breeding. Sprague and Tatum defined GCA as the average performance of a genotype in a series of hybrid combinations and defined SCA as those cases in which a certain hybrid combinations perform better or poorer than would be expected on the basis of the average performance of the parental inbred lines. Parents showing a high average combining ability in crosses are considered to have good GCA while if their potential to combine well is bounded to a particular cross, they are considered to have good SCA.

From a statistical point of view, the GCA is a main effect while SCA is an interaction effect. Based on Sprague and Tatum (1942) GCA is owing to the activity of genes which are largely additive in their effects as well as additive $\times$ additive interactions (Griffing, 1956). Specific combining ability is regarded as an indication of loci with dominance variance (non-additive effects) and all the three types of epistatic interaction components if epistasis is present. They include additive $\times$ dominance and dominance $\times$ dominance interactions.

Kadam *et al.* (2001) estimated Combining ability in 39 hybrids of sweet sorghum. The magnitude of specific combining ability (*sca*) was higher than the general combining ability (*gca*) for all traits, indicating the predominance of the dominance gene action for these traits. Among the male sterile lines, MMS-35 A was the best general combiner for Green fodder yield (GFY), dry fodder yield (DFY) and number of leaves per plant. Among the testers, RFS-57 was the best general combiner for GFY, DFY and plant height. RFSS-1502 and RFSS-35 were the best general

combiners for number of leaves per plant and leaf length, respectively. The cross MMS-35 A $\times$ RFSS-1966 had significant *sca* effects for all traits and was the best specific cross combination for plant height and leaf length. Four crosses, i.e. MMS-35 A $\times$ RFSS-1966, MMS-53 A $\times$ RFSS-35, MMS-53 A $\times$ RFSS-10 and MMS-104 A $\times$ RFSS-23, had highly significant *sca* effects for GFY and DFY, while MMS-35 A $\times$ RFSS-57 was found to be the best specific cross combination for these traits.

The parental lines and corresponding hybrids were evaluated by Jebril (2004) for biomass production, Brix, juice and sugar yield in 22 sweet sorghum genotypes. All A₃ hybrids were sterile and did not produce seed when heads were covered prior to pollination. CMS were highly significant for Brix%, biomass, juice, and sugar yield. Comparison of parents vs. crosses component was highly significant, indicating marked heterosis effect for the traits. Both general (GCA) and specific (SCA) combining ability effects were also significant for all traits, indicating the role of both additive and dominance genetic effects in the inheritance of the characters studied.

Pataki *et al.* (2005) attempted a study involving four cms lines (S-8 682, P-58 626, SS-1 662, SS-1 664) and two R lines (ES and 42) of sweet sorghum for general combining ability for dry matter content in stem juice and plant height by the line $\times$ tester analysis. Regarding the cms lines, the best combiner for the dry matter content in stem juice was P-58 626 in both years studied. The best combiner for the plant height was SS-1 662, again in both years. Regarding the R lines, the line ES was superior in both characteristics and in both years. The crosses S-8 682 $\times$ ES and S-8 682 $\times$ 42 showed highly significant SCA values for dry matter content in stem juice in the first and second year, respectively. The highest SCA values for plant height in the respective years were shown by the crosses P-58 626 $\times$ ES and SS-1 664 $\times$ 42.

The general combining ability of the 12 parents and specific combining ability of 35 crosses were estimated through combining ability analysis for yield, yield components and juice quality characters in sweet sorghum using a line $\times$ tester mating designed by Indhubala *et al.* (2010). The estimated components of *gca* and *sca* variances showed preponderance of non-additive gene action for all the characters studied. Based on *gca* effects the lines BJ 3A, CK 60A and AKMS 22A and the testers RSSV 9, SSV 84 and ASV 9401 were good combiners for most of the characters. The hybrid combinations AKMS 22A $\times$ RSSV 9, BJ 3A $\times$ VMS 98001, BJ 3A $\times$ RSSV 9, AKMS14A $\times$ RSSV 9 and CK 60 A $\times$ VMS 98001 were recorded as the best specific combiners.

A study was conducted to estimate the combining ability and to determine the type of gene actions involved in the inheritance of yield and yield components traits of 15 F_1 's along with their parents by Mengistu *et al.* (2010). For yield, three parents, 212646, 69543 and 69193 were found to be best general combiners. Based on specific combining ability analysis for grain yield per panicle five hybrids 69543 x 223506, 212646 x 223506, 97MW5122 x 212646, 97MW5122 x 69543 and 212646 x 69193 were the best in the experiment. The estimate of variance components showed that the variance due to SCA was higher in magnitude than GCA in the case of days to maturity, panicle width, panicle weight, kernel number per panicle and grain yield, under the control of non-additive type of gene actions.

A set of 18 crosses produced from parents differing in their *gca* effects for bio-energy traits such as millable cane yield, juice volume and juice sugar content (as indicated by Brix %) were evaluated by Sandeep *et al.* (2010). The study suggested that parents with contrasting *gca* effects produce crosses with higher *sca* and heterotic potential for the bio-energy traits. The use of female parents with higher *gca* effects is important for realizing greater probability of crosses with *sca* effects and heterosis in desirable direction for bio-energy traits.

Sanjanareddy *et al.* (2011) studied association of sugar yield with other agronomic traits studied in 171 hybrids developed by crossing 19 female parents with nine male parents in line $\times$ tester design and evaluated during both rainy and post rainy seasons. The lines (female parents) ICSA 38, ICSA 479, ICSA 702, ICSA 675 and ICSA 474 and the restorers (male parents), SSV 74 and SSV 84 combined well for sugar yield during rainy season and the lines, ICSA 702, ICSA 38 and ICSA 474 and the restorers, ICSV 93046, SPV 1411 and ICSV 700 combined well during post rainy season. The magnitude of SCA variance was higher suggesting the importance of non-additive gene action in inheritance of all the traits though both additive and dominant genes controlled overall sugar yield during both the seasons. Keeping in view mean performance, SCA effects and heterobeltiosis, the hybrids, ICSA 474 $\times$ SSV 84, ICSA 24001 $\times$ ICSV 93046 and ICSA 474 $\times$ SPV 422 were identified promising for rainy season and the hybrids ICSA 24001 $\times$ SPV 1411 and ICSA 511 $\times$ ICSV 93046 were identified for post rainy season.

Combining ability effects and variances were estimated in F_1 's and their parents by Jyoti *et al.* (2012). The results showed that *sca* variance was higher than *gca* variance *i.e.* variance ratio was less than unity, indicating predominance of dominance variance.

Dominance variance was more than additive variance for all the characters studied. The parents SB 7001, CS 3541 and DSV 6 among females and IS 3547 among males were good general combiners for grain yield and its components. Based on the *sca* effects and per se performance the hybrid CS 3541 x IS 8607 was found to be better than commercial hybrids CSH 16 and DSH 3 for grain yield and other traits.

The objective of this study was to assess the GCA & SCA of eight parents and 16 hybrids in a line $\times$ tester mating design by Umakanth *et al.* (2012a). The GCA variance was higher than the SCA variance for fresh stalk yield, juice yield, brix content, total sugar yield and computed bioethanol yields indicating additive gene action. For the characters total biomass, juice extraction and grain yield the variance component estimates of specific combining ability (SCA) were greater than that of general combining ability (GCA) indicating the non-additive control of genetic variation. DMS 13A $\times$ Rio and DMS 23A $\times$ RS 647 were the best hybrids for total biomass, fresh stalk yield, juice yield, juice extraction, total sugar content and computed bioethanol yields.

15 hybrids along with parents, and three inbred checks were evaluated for sugar yield and related traits under two environments by Bunphan *et al.* (2014). General combining ability was observed for most traits. Overall, the hybrids KKA-11 $\times$ BJ248, KKA-11 $\times$ KKAU40, KKA-139 $\times$ BJ248, KKA-14 $\times$ KKAU40, and KKA-53 $\times$ Theis had the greatest SCA for theoretical sugar yield.

Hundekar *et al.* (2014) studied combining ability and the *gca* effect and revealed that parents DSV 6, DNB 4 GMRP 16, 108 and 97 were found to be good general combiners for yield and grain mold resistance traits. The hybrid DNB 4 x GMRP 950-285 had high *sca* effect for grain yield and mold resistance. DSV 6 x GMRP 97, DNB 4 x GMRP 108 and DSV 6 x GMRP 16 had high per se performance and moderate *sca* effect.

In the study conducted by Ahmed *et al.* (2014) five exotic cytoplasmic male sterile lines of forage sorghum were crossed with 11 fertile local inbred lines, as testers, to produce 55 F₁-hybrids. Both parental lines and their F₁-hybrids were field-evaluated for yield and quality traits at four environments. The predominance of additive gene effect was high for forage fresh and dry yields, whereas there was predominance of non-additive gene effect for most of the quality traits. For forage fresh and dry yields,

the testers exhibited higher contribution to the GCA variance than the lines. The best general combiners for forage yield were Aklamoi (sweet sorghum) and Kambal among testers, Atlas and E. Sumac among lines. The highest SCA effect for forage yield was given by the hybrid E. Sumac x Aklamoi.

Combining ability studies with five females, six males and 30 hybrids of sweet sorghum developed through a line x tester mating design. Bahadure *et al.* (2015) revealed that estimates of variance components exhibited presence of additive gene action for total soluble solids and non-additive for fresh stalk yield, juice yield, bio ethanol yield and grain yield. Among female NSS 1016 A was highly efficient and productive line for all characters, best general combiner for these traits. Female NSS 8 A for grain yield and PMS 71 A for fresh stalk yield, total soluble solids and grain yield indicate that the best general combiner for these traits. Tester SSV-74 was potential male parent with high significant GCA effect for all traits and RSSV-138-1 was best general combiner for fresh stalk yield, juice yield and bio ethanol yield.

In a study involving 90 crosses of sorghum by Mohammed *et al.* (2015) the GCA/SCA, and the predictability ratios indicated predominance of additive gene effects for majority of the traits studied. Plant height and grain yield across seasons, days to 50% flowering, inflorescence exertion, and panicle shape in the post rainy season showed greater SCA variance, indicating the predominance of non-additive type of gene action. Additive gene action in the rainy season, and dominance in the post rainy season for days to 50% flowering and plant height suggested G X E interactions for these traits.

Combining ability studies was carried out by Patil and Kute (2015) in 45 hybrids. The estimates of *gca* and *sca* variances indicated the presence of non-additive gene action for most of the characters. The line RMS 2010-24 A and testers RSV 1059, RSV 1145, RSLG 2291, RSV 1009 and RSV 912 were found to be good general combiners for yield and yield contributing traits. The hybrids 185 A x RSV 1145, RMS 2010-10A x RSR 231 and RMS 2010- 24A x RSV 1130 were identified with significant and positive SCA for grain yield.

Knoll & Anderson (2016) crossed three female lines and 19 male lines of sweet sorghum in a factorial mating design experiment and revealed late-flowering lines, including Brandes, M 81E, Mer 76-3, and Top76-6, had good general combining ability

for sugar yields, and hybrids, mostly with N109A as the female parent, had specific combining ability for reduced lodging percentage. Only M 81E had higher juice dissolved solids concentration in its hybrids than in the inbred line. Overall, sugar yields tended to be similar between inbred male lines and their hybrids, but hybrids usually flowered earlier, thus producing similar yields in less time.

An experiment was conducted by Kale and Desai (2016) to estimate the combining ability using three females [Cytoplasmic-Genetic Male Sterile (CGMS) Lines], 18 males (testers) and their 54 hybrids developed through line x tester mating design in three diverse seasons. Combining ability analysis over environments revealed importance of both additive and nonadditive components. Combination having high *per se* performance also had high SCA effects and involved at least one good general combining parent. The female parents 28A and 86A and among male parents, KR 125, KR 191, KR 196, PMSC-43, GJ 38, GSF 5 and CSV 21F were good general combiners for grain yield and its component traits.

Chikuta *et al.* (2017) have evaluated 23 crosses of sorghum at three locations in Uganda during two rainy seasons of 2014 and the results indicated that the gene action for the traits leaf area, leaf-stem ratio, plant height, seed weight, grain yield, and biomass was controlled by both additive and non-additive genetic effects. Significant SCA estimates were prominent in most of the individual parental combinations for all traits studied except leaf area and leaf-stem ratio indicating the role of dominance gene action. Majority of the parental lines had significant GCA estimates for all traits.

Dehinwal *et al.* (2017) conducted combining ability studies in 24 hybrids along with their parents and checks. Among female parents, 9A and 14A was the best combiner for green fodder yield and 14A for dry fodder yield in more than two different environments. Among male parents, HJ 513 and G 46 were found to be the best general combiner for green fodder yield and dry fodder yield. The cross combination of 465A × HJ 513 and 9A × IS 2389 exhibited high and positive sca effects for green fodder yield as well as for dry fodder yield.

An investigation was carried out by Jadhav and Deshmukh (2017) across four environments to assess magnitude of heterosis and combining ability of 30 hybrids developed by crossing three females and ten male lines in line x tester fashion. Non-additive gene action played a major role in the inheritance of most of the traits (viz.,

days to 50 per cent flowering, days to maturity, plant height, number of primaries panicle-1, panicle weight, fodder yield plant-1, grain yield plant-1, leaf area index and harvest index) under study except panicle length, number of grains panicle-1 and 100 seed weight for which additive gene action was found to be important. Based on consistent performance over four environments, AKMS-30A, AKR- 504, Rb-342-2 and AKR-354 were found to be best general combiners for grain yield and yield related traits. Among the hybrids, AKMS-30A X Rb-324-3, AKMS-70A X AKR-354, AKMS-70A X Rb- 342-2 and AKMS-30A X Rb-301-4-1 were found to be good specific combiners with highest standard heterosis and per se performance for grain yield plant⁻¹ over the environments.

The estimates of general combining ability (GCA) and specific combining ability (SCA) variances by Prasad and Biradar (2017b) indicated the presence of higher magnitude of non-additive gene action for most of the characters studied, IS 31651 was good general combiner for days to flowering, maturity and grain yield. The crosses BJV-44 x IS 26025; BJV-44 x IS 31651; 104B x IS 31651 and M35-1 x IS 26025 were identified as promising for improving grain yield while crosses M35-1 x IS 28614 and 104B x IS 26025 have been selected for breeding for earliness.

Soujanya *et al.* (2017) conducted an experiment to exploit heterosis in 48 F₁ hybrids of sweet sorghum (*Sorghum bicolor* L.). The SCA variance was higher in magnitude than GCA variance for most of the traits days to 50 % lowering, plant height, No of leaves/plant, leaf length, breadth, no of nodes/plant, internode length, stem girth, leaf to stem ratio, green fodder yield indicating predominance of non-additive gene action in the genetic control of those traits. Line 185A and testers RSSV138-1, RSSV466 and RSSV404 emerged as good general combiners for single-cut green fodder yield. Based on *sca* effects, 185A x RSSV466, 185A x RSSV138-1, PMS71A x RSSV138-1 and PMS71A x RSSV404 were identified as good specific combiners for green fodder yield and its attributing traits. 185A x RSSV466 recorded maximum single-cut green fodder yield with 12.53 per cent heterosis over the best check CSV30F.

Rocha *et al.* (2018) evaluated five fertility restorer lines, four male-sterile lines, and their hybrids of sweet sorghum in the municipalities of Lavras, MG and Sete Lagoas, MG, Brazil. There was a significant effect of GCA and SCA for most of the traits evaluated, indicating the participation of additive or dominant genes in inheritance. The restorer lines CMSX508, BRS 511, CMSXS643, and CMSXS646 show potential for use as parents in sorghum breeding programs.

Lombardi *et al.* (2018) evaluated 20 genotypes, of which 4 are fertility-restorer lines (R), 3 are male-sterile lines (A), and 12 are experimental hybrids (H) resulting from the partial diallel cross between lines A and R, besides a commercial hybrid CV198 used as a check, in four harvest seasons for traits were plant height, green mass production, juice extraction, total soluble solids content, and megagrams of Brix per hectare. The experiments were carried out in the municipalities of Lavras and Sete Lagoas, in the state of Minas Gerais, Brazil. The male-sterile A₁ and the fertility-restorer R₁ and R₃ lines showed the best potential per se, considering all traits and their accumulation rate and predictability over harvest times.

Ingle *et al.* (2018) assessed the magnitude of heterosis and combining ability of 30 F₁ hybrids of Rabi sorghum (*Sorghum bicolor* (L.) Moench) by crossing three lines and ten testers in line x tester fashion. Among the thirty hybrids, three potential hybrids AKRMS 30A X AKRB 431, AKRMS 30A X AKRB 335-3, AKRMS 30A X AKRB 428 were found to be good specific combiners. AKRMS 30A was identified as the good general combiner. The estimates of general combining ability and specific combining ability revealed the presence of both additive and non-additive genetic components for characters like days to 50 per cent flowering, plant height, number of leaves per plant, panicle length, panicle weight, panicle breadth, number of primary panicles⁻¹, 100 grain weight, number of grains panicle⁻¹ and grain yield plant⁻¹.

Combining ability analysis was carried out by Rani *et al.* (2020) in 30 sweet sorghum hybrids which revealed the predominance of non-additive gene action for days to 50 per cent flowering, days to maturity, plant height, brix per cent, total soluble solids, total sugar index, juice yield, juice extraction per cent and grain yield. Among the parents, RS 1220B, CSV 19SS and SSV 74 were found to be good general combiners, while the cross combinations viz., NSS 1007A × CSV 19SS and NSS 1016A × SSV 84 showed good specific combining ability coupled with high per se performance for ethanol yield.

Nandeshwar *et al.*, (2020) evaluated 45 hybrids for combining ability to identify good general combiners and superior cross combinations for high ethanol yield from sweet sorghum. RSSV-21-2 has been identified as the best general combiner.. ARS-SS-35-1 × NSS-218 and ARS-SS-83 × NSS-221-2 have been identified as the best specific combinations.

He *et al.* (2020) observed that character Plant height was the most GCA-sensitive trait and the most important for biomass production in the combining ability study conducted for dual-purpose sorghum for food and biomass as fuel. Female lines AMP418, AMP431, AMP434, AMP443, AMP495, AMP496 and the male line X097 were selected as being high-GCA effect germplasm.

Dual purpose analysis was carried out by Khan *et al.* (2020) for 100 genotypes including 75 F₁s with 20 parents and 5 checks. For juiciness, 19 crosses exhibited positive significant SCA effects and the cross ICSA 29002 × SU 1571 exhibited the highest value. Likewise, 21 crosses were positive significant for TSS, the highest magnitude being expressed by ICSA 208 × SU 1570.

2.4.1 Heterosis

Prabhakar (2001) in a study of 18 hybrids developed through L × T mating design involving 3 lines and 6 restorers, reported significant heterobeltiosis and useful heterosis for days to 50 per cent flowering ranging from -11.53 to -1.41 per cent and significant heterosis over better parent to the extent of 102.9 per cent for grain yield per plant.

Agarwal & Shrotria (2005) studied the magnitude of heterosis and inbreeding depression of fifty hybrids (F₁'s) and their F₂'s. Variable magnitude of three types of heterosis (better parent, mid-parent and standard) were observed for different cross combinations for all the traits. Based on per se performance and heterotic response for green and dry fodder yield, the best crosses were viz., ICSA 94 x Pant Chari-4, ICSA94 x SDSL92111, ICSA94 x SDSL92113, ICSA94 x SDSL92140, ICSA94 x Selection 984, ICSA95 x ICSV96062 and 296A x SDSL92111. Response of inbreeding depression for these traits was significant in positive direction except T.S.S. %, protein % and shoot fly infestation.

Umakanth *et al.* (2006) evaluated 20 hybrids, their parents and checks in rabi season. Heterosis over standard checks CSH 19R and M35-1 and better parent was studied for grain yield and its component characters. Negative heterosis over the checks for days to flowering and plant height was observed in most of the hybrids indicating their earliness and at par status for plant height. Heterosis for test weight over CSH 19R was higher and significant for all the hybrids. Among landraces, PU 28 and PU 16 proved to be better because of their good combining ability and could be utilized as restorers for commercial exploitation of heterosis.

Among the seven characters studied in 18 hybrids by Sandeep *et al.* (2009) cane height, cane weight, juice volume, stem girth, ethanol yield exhibited significant heterosis over mid parent as well as better parent in most of the crosses highlighting non-additive gene action. Only in two hybrids, standard heterosis was significant in desirable direction in respects of juice P^H and brix per cent, while 5 to 13 hybrids in respect of other five characters exhibited significant standard heterosis. Out of 18 hybrids, 8 exhibited high overall (H) heterotic status across the characters.

Pothisoong and Jaisil (2011) evaluated 20 sweet sorghum F₁'s were for heterosis. The F₁ hybrids showed % heterosis over better male parent for days to flowering, plant height, percent brix, stripped stalk yield, grain yield, and percent cane juice extracted up to -7.83, 8.06, 7.60, 15.47, 66.33 and 34.89%, respectively. The high potential F₁ hybrids were L103/KKU40, L103/Urja, L104/KKU40, L102/Urja, and L106/Urja.

In a L × T analysis involving 72 hybrids produced by crossing 4 CMS lines with 18 testers, Vinaykumar *et al.* (2011) reported significant standard heterosis for ethanol yield and grain yield in six and one hybrids respectively.

Pandey and Shrotria (2012) studied 54 crosses F₁'s for three type of heterosis (*viz*; better parent, mid parent and standard) for all the traits. Based on *per se* performance and heterotic response for green and dry fodder yield, two best crosses identified were ICSA-271 x UTM-523 and ICSA-271 x 700R.

Bunphan *et al.* (2014) evaluated 15 hybrids along with parents, and three inbred checks for sugar yield and related traits under two environments for heterosis. Positive heterosis for juice, dissolved solids was not observed, though five hybrids had negative mid-parent heterosis for this trait. Positive heterosis for biomass yield, theoretical juice yield, and grain yield was observed in some hybrids.

Vyas *et al.* (2014a) reported that heterosis over better parent was maximum for grain yield per plant. Cross SPV 1329 × ICSV 272 had maximum heterobeltiosis in both the environments (95.38% in E₁ and 94.74% in E₂). Crosses SU 248 × ICSV 298, SPV 1329 × ICSV 272 and SU 248 × ICSV 272 had maximum grain yield per plant along with higher biological yield per plant thus indicated suitability for dual purpose hybrids. These crosses had highest the heterobeltiosis effects for grain yield per plant,

number of primaries per panicle, 100 grain weight, and biological yield per plant and harvest index. Most of the high heterotic crosses showed high inbreeding depression for plant height, panicle length, 100 grain weight.

Heterosis for some grain yield and its components were studied among 28 sorghum crosses and their eight parents by Aaref *et al.* (2016) and the results depicted clear differences comparison the better parent, for 1000 grain weight, the best two crosses denoted significant positive heterotic effect relatively over better parent viz., $P_2 \times P_5$ and $P_1 \times P_6$ in Sohag location, $P_1 \times P_5$ and $P_2 \times P_5$ in Assiut. As for grain yield / plant, the best two crosses in Sohag were $P_6 \times P_7$ and $P_7 \times P_8$ and in Assiut were $P_7 \times P_8$ and $P_3 \times P_4$, respectively.

Combining ability for grain yield and its components was studied by Chaudhari *et al.* 2016 using five lines and seven testers. The estimates of general combining ability (gca) and specific combining ability (sca) variances indicated the presence of higher magnitude of non-additive gene action for all the characters except days to 50 per cent flowering and days to maturity. The lines 296A, AKMS-14A and 1005A and testers SR-2872 and SR-2879 were found to be good general combiners for grain yield and its contributing traits. The crosses, 1009A $\times$ SR-2872 (346.536), 1005A $\times$ Pantchari (211.482) and AKMS-14A $\times$ Nizer goti (206.119) were identified with high significant and positive SCA effects for grain yield.

Kumar *et al.* (2016) carried out an investigation for two seasons to study heterosis and inbreeding depression in four crosses of sweet sorghum (*Sorghum bicolor* (L.) Moench) and their F_2 have revealed positive mid-parent and better parent heterosis for majority of the characters. Sugar yield was found to be the most heterotic trait, as all the crosses depicted significant positive heterosis over their mid parent and better parent values in case of all the contributing characters indicating dominance gene action. Further high inbreeding depression for sugar yield reflected high heterosis during the two seasons for all the crosses suggesting the operation of non-additive gene action.

Heterosis for grain yield and biomass over both the mid and better parents was shown by more than half of the crosses studied by Chikuta *et al.* (2017) in 23 crosses of sorghum

Ingle *et al.* (2018) observed that the hybrids AKRMS-30A X AKRB 335-3 and AKRMS-30A X AKRB 428 showed desirable standard heterosis percentage over both the checks (CSH-15R and CSH-19R) for grain yield and other characters like days to 50 per cent flowering, plant height, number of leaves per plant, panicle length, panicle weight, panicle breadth, number of primary panicles⁻¹, 100 grain weight, number of grains panicle⁻¹.

An investigation was taken by Meena *et al.* (2020) for 10 lines and 3 tester, 30 hybrids and three checks viz., CSV 23, CSV 27 and CSH25. cross ICSA 29003 B × SPV 1822 is having high heterosis, good SCA and involving both good general combiner parents, selection may also be exercised for transgressive segregants in segregating generations.

LiMing *et al.* (2020) evaluated sixty-four hybridized combinations for heterosis. Mid-parent heterosis of traits from high to low was: biomass per plant, grain yield per plot, panicle weight, biomass per plot, plant height, panicle length, 1000-grain weight, stem diameter, growth duration, days to flowering, tillers and sugar content. Among which, heterosis of growth duration, days to flowering, tillers and sugar content was negative. The sequence of Mid parent heterosis for all traits was almost the same as that of better parent heterosis. Heterosis of yield related traits was higher, and that of sugar content and tillers was lower among all traits.

2.5 STABILITY & AMMI

Yield stability has always been considered as an important topic in plant breeding but will be more concern by the continued variation in climatic condition. The phenotype of an individual is a mixture of both genotype (G) and environment (E). As a consequence of G × E interaction, crop varieties may not show uniform performance across different environments. The term genotype refers to the genetic makeup of an organism while environment refers to biophysical factors that have an effect on the growth and development of a genotype [Basford and Cooper, 1998]. The G × E study is especially important in countries with various agro-ecologies. Significant G × E interaction is a consequence of variations in the extent of differences among genotypes in diverse environments (called as a qualitative or rank changes) or variations in the comparative ranking of the genotypes (called as a quantitative or absolute differences between genotypes) (Fasahat *et al.* 2015).

Static meaning of stability defined by Becker and Leon (1988), a stable genotype is the one possessing a constant performance irrespective of any changes in environmental conditions.

According to Eberhart and Russell, 1966 model, genotypes are grouped based on their variance of the regression deviation (either equal or not to zero). A genotype with variance in regression deviation equal to zero is highly predictable, whilst a genotype with regression deviation more than zero has less predictable response (Scapim *et al.* 2010) Although, regression model is displayed to be the most useful approach for geneticists Fasahat *et al.* 2015.

The additive main effects and multiplicative interaction (AMMI) method which gives information on main and interaction effects in addition to a biplot. It is specifically efficient for illustrating adaptive responses (Fasahat *et al.* 2014.) and is recently suggested as a replacement to the joint regression analysis for most of the breeding programmes.

Madhusudhana *et al.* (2003) evaluated 22 rabi sorghum hybrids including two standard checks CSH 15R and CSH 19R, and a popular variety M35-1 under 16 locations. Out of the 22 genotypes tested, only one hybrid, CSH 15R was found to be highly stable across all the environments. This hybrid showed unit regression, non-significant deviation from regression and good grain yield. On the other hand, the hybrid CSH 19R, was found to be unstable but highly suitable for favourable locations as displayed by $b_i > 1$ and non-significant S^2_{di} . CSH 15R was found suitable for general cultivation while CSH 19R was found to be an ideal hybrid for favourable locations. The variety M35-1 was however, found to be unstable in its performance across the three production environments (deep soils, shallow soils and irrigated)

Rohmani *et al.* (2006) conducted stability analyses for days to maturity, number of fertile tillers/plant, 100-grainweight, and yield/plant using eight exotic and one local genotypes across three locations. Considering all the stability parameters, genotype BSV16 was found to be more stable as having very low S^2_{di} with near unit regression and high yield. Genotypes BSV34, BSV 45, BSV7b, and Khagrachari local were highly responsive to favourable environment for grain yield. The genotype BSV33 was found to be suitable for unfavourable environment for grain yield.

Based on the AMMI model, genotypes ICSA 22 X M4850 and ICSA 15 X ICSR 14 were reported to be the most stable by Adugna (2007), although genotypes ICSA 21 X ICSR 50 and ICSA 15 X M5568 had satisfactory levels of yield performance as well as stability.

Patil *et al.* (2007) studied nineteen genotypes comprising varieties, hybrids and elite lines under three environments (sowing dates) for 10 quantitative traits including grain yield. Stability parameters revealed that the genotype SPV-1592 possesses average stability for grain yield.

Ezzat *et al.* (2010) evaluated 25 F₁'s and their 10 parents at two locations (Assiut and Qena governorates) Most of hybrids were significantly earlier in duration, taller in plant height, heavier grain weight and higher grain yield compared to their parents and checks. Stability analysis for grain yield demonstrated that most of F₁ hybrids had higher yields than their parents, but the parents were relatively more stable. Four genotypes (three crosses; (A-73 x R-272), (A-604 x R-92010) and (A-613 x R-210) and one parent (R-273)) were formed to be the best stable genotypes.

Genotype x environment interactions in 22 Rabi (winter season) sorghum varieties were studied over 3 environments by Prabhakar *et al.* (2010) for flowering, maturity, grain and fodder yields. Significant differences were observed among environments and varieties for the characters. The varieties, namely 'SLV 15', 'SLV 29', 'SLV 45' and 'CRS 1 ' were found stable for earliness and they can be directly used in breeding for earliness. For improvement of grain yield, the varieties 'SLV 40', 'SLV 43', 'SLV 44', 'SLV 50' and 'SLV 51' were found to be the most stable under rainfed situation. For both grain and fodder yields, the stable varieties identified are 'SLV 40', 'SLV 43', 'SLV 44' and 'SLV 51'.

Rao *et al.* (2011) evaluated 11 improved sweet sorghum hybrids in both seasons for three years. The stable hybrid, based on additive main effects and multiplicative interaction (AMMI) and GGE biplot analysis is the one that performed well across seasons and over the years for grain yield and stalk sugar yield. The genotypes Viz; hybrid ICSSH 28, ICSSH 57 and ICSSH 21 were best adapted for rainy season. The hybrid 'SSV 84' was the best for Brix% in rainy season whereas ICSSH 16 and ICSSH 57 were reported to be the best performing sweet sorghum hybrids for Brix% in post rainy season.

Ghazymona *et al.* (2012) concluded in the experiment that F₁ hybrid No.7 - Hybrid (piper black x male sterile line 2002-41) and 8- Hybrid (piper black x male sterile line 2002-46) were stable for total fresh and dry forage yield. On the other hand, the F₁ hybrid-1 (Giza 1 x male sterile line ICS 399-39) F₁ hybrid-2 (Giza 1 x male sterile line 2002-39). 1 and 2 were the unstable for total dry forage yield.

Umakanth *et al.* (2012b) have evaluated nine newly bred varieties and a hybrid at seven locations. The hybrid 'SPH 1467' had the highest phenotypic index and was found stable for fodder and biomass yields. Among the varieties tested, 'SPV 1750' recorded the highest grain yield while 'SPV 1716' had the highest fodder and biomass yield, but were not stable across locations for these traits. The genotype 'SPV 1616' showed high adaptability for grain yield fodder yield and biomass.

Souza *et al.* (2013) studied the adaptability of 25 sweet sorghum cultivars of Embrapa Maize and Sorghum in five Brazilian environments. Genotypes CMSXS 634, BRS 506, and CMSXS 646 were the most stable and adapted for Fresh biomass yield and total soluble solids concomitantly CMSXS 634 being more adapted to favourable environments and CMSXS646 being more adapted to unfavourable environments.

Filho *et al.* (2014) has conducted an experiment with 25 grain sorghum hybrids, of which 22 were pre-commercial and 3 were cultivars in 7 locations in Brazil. AMMI model indicated the suitability of cultivar 1G 282 for the cities of Guaira, Sete Lagoas, and Vilhena, and hybrids 0307087 and 0307091 for the southeast of Goiás. The associations of the Eberhart and Russell method with AMMI indicated that 0307071, 0307131, 0307511 showed adaptability to favourable environments. Hybrid 0009061 stood out as the most adaptable and stable cultivar.

Shivani and Sreelakshmi (2014) evaluated 60 rabi sorghum genotypes for three years in a single location to examine the existence of genotype x environment (G x E) interaction for grain yield and related traits. PVR 659 and RSV 1161 had unit regression coefficient indicating average response over varying environments. Siddheswar Local (32.0), Barshi Joot (36.7) and Yermala Local (30.8) had non- significant deviation from regression indicating their stability over environments for panicle length. Highest seed yield was recorded with RSV 821 followed by RSV 1037, RSV 744, Chungi Maldandi and RSV 1203.

Vange *et al.* (2014) evaluated six sorghum genotypes for stability analysis in 4 different environments in the Southern Guinea Savanna. The highest yield genotype was SSV2006019 (6.06t/ha) while the least yield was SSV2006043 (4.02t/ha), based on the stability parameters, Genotypes SSV2006019, SSV2006039 and SSV2006040 with ecovalence values of 0.28, 0.003 and 0.14 and b_i values of 0.99, 0.84 and 1.01 respectively appeared to be stable and adapted to the best environments while SSV2006002 and SSV2006006 with yield values of 4.82 and 4.47 T ha⁻¹ respectively appears to be good for poor environments.

In the stability study by Anarase *et al.* (2016) eight male parents, 31 hybrids and check CSH 15R showed average stability over environments for days to 50% flowering, whereas the female parent 104A showed above average stability and suitability to poor environments. Five male parents, 17 hybrids and check CSH 15R showed average stability over environments for days to maturity. As regards to plant height 6 males and 25 hybrids were found stable and four hybrids were found above average stable and suitable for poor environments whereas, one hybrid 9168A x RSV 1006 was found below average stable for this trait. For dry stover yield per plant, ten male parents and 22 hybrids were considered stable for this trait. The hybrid 9168A x RSV 1006 showed below average stability which was suitable for rich environments.

An experiment was conducted by Girish *et al.* (2016) involving 23 advanced breeding lines along with two checks at four locations. The pooled analysis of variance revealed that mean sum of squares due to genotypes was significant for ear head diameter, days to 50 per cent flowering, days to maturity and fodder yield, indicating presence of considerable amount of variability in the genotypes. On the basis of stability parameters a four genotypes viz., GS-6, GS-16, GS-22 and GS-23 were found to be the most stable over Gulbarga, Raichur, Bellary and Malnoor environments of Hyderabad Karnataka region.

Admas and Tesfaye (2017) conducted a multi-environment varietal trial comprised of nine genotypes and one standard check, “yeju”. AMMI analysis based on grain yield data revealed that genotypes ICSV 1112BF, 82 LPYT-2 # 5 x 81ESIP 46, and PGRC/E #222880 were superior to the standard check both in grain yield and stability.

Disasa *et al.* (2017) studied 180 accessions of sweet sorghum in two environments. Collections from northern part of Ethiopia (Wello and Tigray) showed significantly high Brix mean value while collections from the rest of the regions (Hararge, West Shewa, East Wollega and Gojam) expressed lower Brix mean value but higher biomass for stalk sugar yield.

The AMMI analysis of variance carried out by Naggar *et al.* (2018) in 25 sorghum B-lines indicated that the genotype (G), environment (E) and GE interaction had significant influence on sorghum grain yield. BTX TSC-20 (G25) followed by ICSB -1808 (G10) showed both high yielding and stability across the test environments. ICSB-8001 (G11) and BTX-407 (G21), showed maximum stability, but only with moderate grain yield.

Additive main effect and multiplicative interaction (AMMI) analysis of variance carried out by Udoh *et al.* (2018) in 22 genotypes of both ICRISAT and Dutch showed significant effect of G, E and the GEI accessions were identified to be stable across the two locations with respect to different biofuel attributes. Nine, seven, and six genotypes were found to be stable for grain yield, biomass yield and brix value, respectively.

Khandelwal *et al.* (2019b) conducted stability analysis for grain yield and component traits in 150 accessions of sorghum during Kharif, 2013, 2014 and 2015 under rainfed condition. The genotype GPU-4 for grain yield/ plant, earliness, maturity and leaf area and GPU- 8 for grain yield/ plant, fodder weight/ plant and dry weight/ plant exhibited high per se performance, non-significant S_2 di and regression coefficient around unity. EJ-34 showed good performance for grain yield, maturity and peduncle width under unfavourable environment and IS-6953 and GPU-14 was suitable for grain yield, earliness and peduncle width under favourable environment.

To evaluate the yield stability of 16 genotypes experiment was conducted by Khazaei *et al.* (2019) at 4 locations of Iran. The analysis of variance by AMMI method and fitting of principal components to the interaction effects of genotype and environment showed that the two principal components were significant for fresh and dry forage yield. According to the AMMI model and AMMI stability value (ASV), genotypes No. 8 (Siloking) and 12 (FGCSI12) with the high yield and stability were identified as suitable genotypes

Stability analysis was carried out by Rani *et al.* (2020) in 30 sweet sorghum hybrids viz., NSS 8A × SSV 84 and NSS 1007A × CSV 19SS for ethanol yield, juice yield and total biomass which were found to be stable and well adapted to all environments.

An investigation was conducted by Worede *et al.* (2020) to study yield stability and adaptability of 13 sorghum genotypes across six environments. Additive Main-effect and Multiplicative Interaction (AMMI) analyses were computed. The AMMI analysis explained 68.67% of the G × E variance. The AMMI1 biplot depicted that G₁₁ and G₂ were higher-yielding genotypes; genotypes G₅, G₉, G₁, G₄ and *Miskir* had more than average grain yield. Genotype G₃ had grain yield as equal as the grand mean value, while G₆, G₁₀, G₈ and G₇ had below average grain yield. Nevertheless, *Jigurti* was the lowest yielder. Moreover, *Jigurti*, G₈, G₁ and G₅ had high G × E. In contrast, G₇, G₃, G₄, G₆, G₂ and G₁₀ had lower G × E, the rest had moderate G × E.

The present investigation was undertaken by Meena *et al.* (2020) for 10 lines and 3 tester, 30 hybrids and three checks viz., CSV 23, CSV 27 and CSH25. In 22 stable genotypes for plant height line L₄ and crosses L₂ × T₁ and L₄ × T₂ having bi = 1 for rest of the 19 genotypes bi neither deviating from zero nor from unity.

Alvels *et al.* (2021) evaluated sorghum hybrids for stability analysis, in which N43A1001 stood out for obtaining the highest genotypic means for the evaluated traits, besides showing adaptability and stability for the studied sweet sorghum traits like biomass and plant height.

2.6 GENERATION MEAN ANALYSIS

Generation mean analysis (Mather and Jinks, 1982) provides information on the relative importance of average effects of the genes (additive effects), dominance deviations and effects due to nonallelic genetic interactions in determining genotypic values of the individuals and consequently, the mean genotypic values of families and generations. Generation mean analysis is a simple but useful technique for estimating gene effects for a polygenic trait. Its greatest merit lying in the ability to estimate epistatic gene effects such as additive × additive, dominance × dominance and additive × dominance effects. (Said, 2014)

Through six generation analysis of seven crosses involving Sorghum × Sudan grass, Baskheti and Arun Bhatt (2005) reported additive, dominance as well as digenic interactions for days to 50 per cent flowering, plant height, stem girth and number of nodes.

Additive gene action for days to 50 per cent flowering and plant height and non-additive gene action for number of leaves was reported by Rajguru *et al.* (2005) in a study involving 30 sorghum hybrids.

Presence of non-additive gene action in the control of days to flowering, plant height and Brix was reported by Premalatha *et al.* (2006) in a study of 36 sorghum hybrids.

Sandeep (2007) through L × T analysis of 18 hybrids produced by crossing three lines with six testers of sweet sorghum reported predominance of non-additive gene action for days to 50 per cent flowering, plant height, stem girth, nodes per plant, mean internodal length, cane height, cane weight, juice volume, Brix and ethanol yield.

In respect of days to 50 per cent flowering, plant height, stem girth, nodes per plant, mean internodal length, cane height, cane weight, juice volume, juice weight, juice extraction per cent, Brix, total sugars, reducing sugars and ethanol yield predominance of non-additive gene action was observed in a study of 72 hybrids produced by crossing 18 restorers with four male sterile lines of sweet sorghum by Vinaykumar (2009).

Generation mean analysis of two crosses sweet sorghum by Audilakshmi *et al.* (2010) indicated preponderance of both additive [d^*] and dominance [h^*] for plant height, stalk yield, juice yield, Brix and sucrose content. However, additive × additive [i^*] and dominance × dominance [l^*] interactions for plant height, stalk yield and Brix and only additive × additive [i^*] gene interaction for juice yield were noticed in the inheritance of respective characters. While, interaction component was absent for sucrose content.

Sanjanareddy *et al.* (2011) studied the association of sugar yield with other agronomic traits in 171 hybrids of sorghum. The significant differences between the seasons for all the traits suggested that these traits are greatly influenced by the

environment. The magnitude of SCA Variance was higher suggesting the importance of non –additive gene action I the inheritance of all traits though both additive and dominant genes controlled overall sugar yield during both the seasons.

Kumar *et al.* (2011) estimated the nature and magnitude of gene effects for sugar yield and its component traits in sweet sorghum [*Sorghum bicolor* (L.) Moench]. The mean performance of the F₁'s in all the crosses indicated dominant gene effect for all the characters. Simple additive-dominance model indicated presence of epistatic interaction. High positive additive × additive interaction effects were also found in all the crosses. Higher magnitude of dominance and dominance × dominance gene interactions which were found minimized the expression of heterosis and lead to non-exploitation of crosses with duplicate epistasis.

Shivani and Sreelakshmi (2013) conducted genetic analysis for grain and fodder yield in sorghum genotypes using six generation means indicated the major role of additive genetic effects (d) for days to maturity and grain yield in both the crosses viz., EP 82 x CRS 1 and CSV 14R x SPV 1375. Among the epistatic components of genetic variance, the fixable additive x additive component (i) was significant for almost all the traits except, days to 50% flowering in the cross EP 82 x CRS 1 and fodder yield in the cross CSV 14 R x SPV 1375. Grain yield exhibited significant dominance variance in the cross CSV 14R x SPV 1375.

Iraddi *et al.* (2014) carried out generation mean analysis to estimate the nature and magnitude of gene effects for sugar content, green cane yield and its component traits in sweet sorghum. The scaling tests as well as chi square test from joint scaling test were highly significant for all the fourteen quantitative characters, indicating inadequacy of simple additive - dominance model. Both additive and dominance gene effects were highly significant for all the traits barring stem girth, grain yield, total biomass and fresh stalk yield where only dominance component is predominant in first two traits, while additive in later two traits. Among non-allelic interactions, dominance x dominance (l) gene interaction was of greater magnitude than main gene effects for all the characters.

The nature of gene effects was analysed by Vyas *et al.* (2014b) in three crosses. Grain yield per plant, harvest index and biological yield per plant appeared to be influenced by additive and non-additive gene actions. Additive as well as dominance gene actions were prevalent in expression of harvest index, biological yield per plant and grain yield per plant except in both the environments. Epistatic components were

found to be important for all most all the characters. Duplicate type of interaction was predominantly involved in the inheritance of most of the characters. The non-allelic interactions particularly at three gene level were predominant for the trait harvest index.

In a study conducted by Karande and Lad (2015) six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) of the cross RSV1098 x RSV458 in sorghum was carried out for the traits associated with drought resistance. The joint scaling test for almost all the characters was found highly significant in all the crosses, indicating inadequacy of additive-dominance model. The dominance (h) gene effects were found predominant along with dominance x dominance (l) interaction effects in the inheritance of traits viz., relative leaf water content (RWC), chlorophyll stability index (CSI), harvest index and grain yield.

Gaddameedi *et al.* (2018) performed generation mean analysis for four crosses ICSB 52 $\times$ IS 13211, ICSB 52 $\times$ SPV 1359, IS 20843 $\times$ IS 2248 and IS 2248 $\times$ IS 20843. Generation mean studies revealed the presence of both additive and dominant gene interactions in inheritance of agronomic traits. Duplicative epistasis was observed for days to flowering, plant height, grain yield/plant, 100-grain weight, and grain Zn with a predominance of dominant gene action in inheritance of these traits. Panicle length, panicle width, and grain Fe showed both additive and dominance gene effects, with higher magnitude of dominance.

Generation mean analysis involving six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) of four crosses associated with shoot fly resistance was evaluated by Lad *et al.* (2019). The joint scaling test for almost all the characters was found highly significant in all the crosses indicating inadequacy of additive-dominance model and presence of higher order interactions. Dominance and dominance x dominance gene interactions were found in control of number of plant height at maturity, number of leaves per plant and grain yield per plant traits associated with shoot fly resistance. Dominance x dominance (l) interaction was predominantly made significant contribution for plant height at maturity, number of leaves per plant and grain yield per plant.

CHAPTER-III

MATERIAL AND METHODS

The present investigation entitled “Stability analysis in Sorghum [*Sorghum bicolor* (L.) Moench] Genotypes” was undertaken to study the diversity, correlation, path analysis, combining ability, stability and gene action for ethanol yield and yield contributing characters at Agricultural college farm, Bapatla which is located at an altitude of 5.49 m above mean sea level, 15° 55’ N latitude, 80° 28’ E longitude and about 12 Km from the Bay of Bengal. The details of materials used and methodologies adopted during the course of investigation are elucidated under appropriate heads.

3.1 MATERIAL

The experimental material comprised of 110 germplasm lines selected from IIMR, Hyderabad and ICRISAT, Patancheru, Hyderabad based on the brix %. The details of the sorghum genotypes along with their source/pedigree are furnished in Table 3.1

Table 3.1. List of 110 sorghum genotypes (germplasm and advance breeding lines) with their sources available

S. No.	Genotype	Place of Collection/Pedigree			Brix %
		District	State	Country	
1	CJV-07	Dharwad	Karnataka	India	10.67
2	CJV-16	Dharwad	Karnataka	India	6.00
3	CJV-17	Dharwad	Karnataka	India	10.67
4	CJV-18	Dharwad	Karnataka	India	9.67
5	CJV-19	Dharwad	Karnataka	India	9.00
6	CJV-21	Dharwad	Karnataka	India	9.33
7	CJV-24	Dharwad	Karnataka	India	10.00
8	CJV-25	Haveri	Karnataka	India	5.67
9	CJV-26	Haveri	Karnataka	India	6.67
10	DHBM-3	From IIMR, Hyderabad			10.00
11	DHBM-5	From IIMR, Hyderabad			9.00
12	E-40	Banda	Uttar Pradesh	India	6.67
13	E-63	Jhansi	Uttar Pradesh	India	9.00
14	EB-14	Jhabua	Madhya Pradesh	India	9.00
15	EB-15	Jhabua	Madhya Pradesh	India	8.00

S. No.	Genotype	Place of Collection/Pedigree			Brix %
		District	State	Country	
16	EB-19	Jhabua	Madhya Pradesh	India	7.67
17	EB-20	Jhabua	Madhya Pradesh	India	9.33
18	EB-22	Dhar	Madhya Pradesh	India	10.33
19	EC-15	Cuddapah	Andhra Pradesh	India	7.33
20	EC-20	Cuddapah	Andhra Pradesh	India	7.67
21	EC-22	Cuddapah	Andhra Pradesh	India	11.00
22	EC-23	Cuddapah	Andhra Pradesh	India	9.33
23	EC-25	Cuddapah	Andhra Pradesh	India	13.33
24	EG-11	Coimbatore	Tamil Nadu	India	13.33
25	EG-19	Erode	Tamil Nadu	India	7.33
26	EG-21	Karur	Tamil Nadu	India	9.33
27	EG-22	Karur	Tamil Nadu	India	7.67
28	EG-23	Karur	Tamil Nadu	India	7.33
29	EG-24	Karur	Tamil Nadu	India	8.00
30	EG-25	Karur	Tamil Nadu	India	5.00
31	EG-39	Virudhunagar	Tamil Nadu	India	7.33
32	EG-78	Vellore	Tamil Nadu	India	10.33
33	EG-80	Vellore	Tamil Nadu	India	10.67
34	EG-81	Tiruvannamalai	Tamil Nadu	India	4.00
35	EG-82	Tiruvannamalai	Tamil Nadu	India	7.33
36	EG-83	Cuddalore	Tamil Nadu	India	8.00
37	EG-84	Cuddalore	Tamil Nadu	India	10.67
38	EP-29	Gulbarga	Karnataka	India	12.67
39	EP-61	Beed	Maharashtra	India	12.00
40	EP-80	Solapur	Maharashtra	India	8.00
41	EP-84	Solapur	Maharashtra	India	9.33
42	GGUB-13	Shajapur	Madhya Pradesh	India	9.33
43	GGUB-27	Jhabua	Madhya Pradesh	India	9.00
44	GGUB-28	Jhabua	Madhya Pradesh	India	9.00
45	GGUB-29	Jhabua	Madhya Pradesh	India	9.67

S. No.	Genotype	Place of Collection/Pedigree			Brix %
		District	State	Country	
46	GGUB-33	Jhabua	Madhya Pradesh	India	10.67
47	GGUB-43	Jhabua	Madhya Pradesh	India	10.33
48	GGUB-45	Betul	Madhya Pradesh	India	10.00
49	GGUB-50	Betul	Madhya Pradesh	India	9.67
50	GGUB-54	Khargaom	Madhya Pradesh	India	9.67
51	GGUB-61	Vidisha	Madhya Pradesh	India	13.00
52	GGUB-62	Vidisha	Madhya Pradesh	India	10.67
53	GGUB-63	Vidisha	Madhya Pradesh	India	13.00
54	GGUB-64	Guna	Madhya Pradesh	India	13.33
55	GGUB-65	Guna	Madhya Pradesh	India	9.33
56	GGUB-67	Vidisha	Madhya Pradesh	India	10.67
57	GGUB-68	Vidisha	Madhya Pradesh	India	11.00
58	ICSSH-71	From ICRISAT, Hyderabad			12.67
59	ICSV-12012				14.33
60	ICSV-15006				17.33
61	ICSV-25306				9.33
62	ICSV-25308				11.67
63	ICSV-25316				13.67
64	IS-1331			Nigeria	11.00
65	IS-2337	-	Wad Medani	Sudan	6.00
66	IS-27072	-	Masvingo	Zimbabwe	9.00
67	IS-27239	-	Soum	Burkina Faso	9.00
68	IS-2814	-	-	Zimbabwe	10.00
69	IS-2834	-	-	Zimbabwe	15.00
70	IS-29308	-	-	Swaziland	15.00
71	IS-29469	-	Mohale's Hoek	Lesotho	9.33
72	IS-29650	-	-	China	8.00
73	IS-30310	-	-	China	3.67

S. No.	Genotype	Place of Collection/Pedigree			Brix %
		District	State	Country	
74	IS-3515	-	South Kordofan	Sudan	9.33
75	IS-3980	-	-	U.S.A	4
76	IS-4599	-	Maharashtra	India	11.33
77	IS-6910	-	-	Sudan	6.67
78	IS-1474	-	Tamil Nadu	India	11.33
79	NSJB-6577	Khammam	Telangana	India	7.00
80	NSJB-6585	Khammam	Telangana	India	9.00
81	NSJB-6605	Khammam	Telangana	India	9.33
82	NSJB-6629	Khammam	Telangana	India	8.00
83	NSJB-6648	Khammam	Telangana	India	8.00
84	NSJB-6657	Khammam	Telangana	India	8.00
85	NSJB-6662	Khammam	Telangana	India	8.00
86	PHULE VASUNDHARA	185 A X RSSV 260	Rahuri	India	11.00
87	POP-15	From IIMR, Hyderabad			9.00
88	PV-12	Sangli	Maharashtra	India	10.33
89	PV-22	Solapur	Maharashtra	India	9.33
90	RAJ-24	Ajmer	Rajasthan	India	4.67
91	RSSV-138-1	From IIMR, Hyderabad			14.00
92	SCVS-29				10.33
93	SEVS-04	Khammam	Telangana	India	11.00
94	SEVS-08	Khammam	Telangana	India	10.00
95	SEVS-20	Khammam	Telangana	India	8.67
96	SEVS-29	Khammam	Telangana	India	7.67
97	SPV-2196	From IIMR, Hyderabad			11.00
98	SPV-2325	From IIMR, Hyderabad			10.33
99	SPV-2328	From IIMR, Hyderabad			8.00
100	SSS-10	IS - 11496 x IS – 9705			10.00
101	SSS-14	IS - 11496 x IS – 9705			10.67
102	SSS-15	IS - 19626 x IS – 9767			10.67
103	SSS-23	SSV - 84 x IS – 776			9.33
104	SSS-46	IS - 8218 x IS – 6962			11.67
105	SSS-62	IS - 8218 x IS – 6962			12.00
106	SSS-65	IS - 8218 x IS – 6962			11.00
107	SSV-74	Dharwad			15.00
108	SSV-84	Selection from zera sorghum variety IS-23568			12.33
109	CSV-19SS (VC)	RSSV 2 X SPV 462			12.33
110	CSV-24SS (VC)	NSS 1005 A X (SSV-84 X 401 B)			12.33
	CSH-22SS (HC)	ICSA 38 X SSV 84			12.67

Table 3.2 List of ‘A’ and ‘B’ lines with their pedigree and origin

S. No.	A and B lines	Pedigree	Origin
1	ICSA 14029	(IS 8157 x ICSB 73)-1-5-2-1-1-1-1-1	ICRISAT, Patancheru, Hyderabad
	ICSB 14029	(IS 8157 x ICSB 73)-1-5-2-1-1-1-1-1	
2	ICSA 14030	(IS 8157 x ICSB 73)-1-5-2-1-3-1-3-1	
	ICSB 14030	(IS 8157 x ICSB 73)-1-5-2-1-3-1-3-1	
3	ICSA 14033	(IS 8157 x ICSB 73)-1-5-2-1-6-1-2-1	
	ICSB 14033	(IS 8157 x ICSB 73)-1-5-2-1-6-1-2-1	
4	ICSA 14035	ICSB 418-2-1	
	ICSB 14035	ICSB 418-2-1	

3.2 METHODS

Experiment I: During *Kharif*, 2017 the following objectives were studied. Genetic variability, divergence studies, correlation and path studies were performed using the 110 genotypes including two checks. The details of the experiment is given below.

Season	<i>Kharif</i> , 2017
Design	RBD (Folded)
Replications	3
Spacing	45 X 15 cm
Number of rows per entry	5 rows
Length of the row	2m
Gross plot size	4.5 sq.m
Net plot size	2.16 sq.m

The recommended package of practices were followed during the crop season.

Experiment –II: For assessing the general and special combining ability, the parental material selected from the divergence study consisted of four lines (male sterile) and five testers in L X T fashion to generate 20 crosses. In order to achieve synchronization three staggered plantings were adopted. The details of the experiment, are as follows:

Season	<i>Early Kharif, 2018</i>
Lines(4)	1. ICSA 14029
	2. ICSA 14030
	3. ICSA 14033
	4. ICSA 14035
Testers (5)	1. SEVS-08
	2. GGUB 28
	3. ICSV 15006
	4. IS 29308
	5. IS 3980
Spacing	45 x 15 cm
Number of rows per entry	5rows/genotype
Length of the row	2m
Gross plot size	4.5 sq.m
Net plot size	2.16 sq.m

The recommended package of practices were followed during the crop season.

Note: In 4 x 5 series of crosses one set of cross (ICSA 14030 x IS-3980) was not successful in seed setting, the complete series of crosses were eliminated, because statistical evaluation cannot be carried out with incomplete number of crosses. So 4 x 4 series of crosses was considered.

EXPERIMENT –III-A: The 16 crossed seed harvested from experiment –II are used to raise the F₁'s. The details are furnished below.

Season	<i>Early Rabi, 2018-19</i>			
Hybrids/Lines/Testers/Check	16(H)	4(L)	4(T)	1©
No of rows	2 rows/ cross			
Replications	2			
Row length	3m			
Spacing	45 x 15 cm			
Gross plot size	2.7 sq.m			
Net plot size	0.72 sq.m			

S. No.	16 Hybrids
1	ICSA 14029 x SEVS-08
2	ICSA 14029 x GGUB 28
3	ICSA 14029 x ICSV-15006
4	ICSA 14029 x IS 29308
5	ICSA 14030 x SEVS -08
6	ICSA 14030 x GGUB 28
7	ICSA 14030 x ICSV 15006
8	ICSA 14030 x IS 29308
9	ICSA 14033 x SEVS-08
10	ICSA 14033 x GGUB -28
11	ICSA 14033 x ICSV-15006
12	ICSA 14033 x IS-29308
13	ICSA 14035 x SEVS-08
14	ICSA 14035 x GGUB 28
15	ICSA 14035 x ICSV-15006
16	ICSA 14035 x IS-29308

EXPERIMENT –III-B

The sixteen F₁'s were raised at three different locations for testing the stability and combining ability analysis. The details are furnished below

Season	<i>Rabi</i> , 2018-19
Location	a. Agricultural College Farm, Bapatla, A.P
	b. RARS, LAM, Guntur, A.P
	c. ARS, Garikapadu, Krishna Dist, A.P
No of crosses	16 Hybrids+ 4 Female parents + 4 male parents + 1 hybrid check (CSH-22SS)
No of replications	2
No of rows	2
Row length	3m
Spacing	45 x 15 cm
Gross plot size	2.7 sq.m
Net plot size	0.72 sq.m

The recommended package of practices were followed during the crop season.

Note: Simultaneously backcrosses were carried out in this same season for carrying out generation mean analysis.

EXPERIMENT –IV

Out of the 16 crosses, only one cross (ICSB 14029 X ICSV 15006) has been evaluated for generation mean analysis (backcross seed was ample in only one cross). The details of the experiment are as follows.

Season	Summer, 2019		
Design	RBD		
Replications	4		
Length of the row	4m	No of plants	
Number of rows per replication	P ₁ , P ₂ , F ₁	2 each	26 plants/row
	F ₂	10	248
	BC ₁ , BC ₂	2 each	48 plants/row
Spacing	45 X 15 cm		

The recommended package of practices were followed during the crop season.

3.3 RECORD OF OBSERVATIONS

Observations were recorded on five randomly selected plants per treatment per replication for ethanol yield, its attributing traits and grain yield separately and were used for statistical analysis. (As per AICRP Sweet sorghum guidelines)

1. Days to 50 % flowering (days)	7. 1000 grain weight (g)
2. Days to maturity (days)	8. Fresh stalk/yield (T ha ⁻¹)
3. Plant height (cm)	9. Juice yield (l ha ⁻¹)
4. Number of nodes per plant	10. Brix %
5. Stem girth (cm)	11. Ethanol yield (l ha ⁻¹)
6. Panicle wt (g)	12. Total soluble sugars (Sucrose, Fructose, Glucose)
	13. Grain yield (T ha ⁻¹)



Plate 1. General View of Experimental plot (@ Agricultural College, Bapatla).



Plate 2. Hand Refractometer (0-32 % brix).



**Plate 3. Phule Vasundhara
with 540.80 cm**



Plate 4. IS-3980 (early flowering)



Plate 5. Late maturing types



Plate 6. Medium maturing types



Plate 7. F₁ Hybrid ICSA 14029 x ICSV 15006

1. Days to 50 per cent flowering (days)

The number of days taken from the date of sowing to the date when 50 per cent of the plants in a genotypes shows anthesis in the top spikelets is recorded.

2. Days to Maturity (days)

The number of days from sowing date to the 95% of the panicles in a plot reached physiological maturity. The number of days taken from the date of sowing to the day on which 95% of the panicles in a plot are physiologically mature as monitored by the appearance of black glumes.

3. Plant height (cm)

The height of the plant was measured from base of the plant (ground level) to the tip of the panicle at the time of harvest recorded in centimetres.

4. Number of nodes per plant

The number of distinguishable nodes above the ground level was counted at the time of harvest.

5. Stem girth (cm)

This was measured at the middle of the first internode above the ground level with the help of Vernier callipers.

6. Panicle weight (g)

The average gram weight of individual panicle as measured using five representative samples in a plot at harvesting, which is weighed in grams.

7. 1000 grain weight (g)

One thousand seeds collected at random from threshed grains of each dried panicle was counted and weighed in grams.

8. Fresh Stalk Weight (T ha⁻¹)

The fresh weight of each cane (from base of the stem to upper most node) at physiological maturity after removal of leaf and leaf sheath was recorded and converted to tonnes per hectare.

9. Juice yield (l ha⁻¹)

Total quantity of juice obtained by crushing the cane (harvested at physiological maturity stage) using roller crusher was collected in a measuring jar and the volume was recorded and converted to litre per hectare.

10. Brix per cent (Per cent)

This was measured by taking the extracted juice of the cane on to the space provided for the same in Hand refractometer having a capacity to measure 0 to 34 per cent brix.

11. Total Soluble Sugars (Per cent)

It is the total fermentable sugars such as glucose, fructose, and sucrose *etc.* including starch in the juice. For predicting the total soluble sugars by using juice Brix, the following regression equation given by Corleto and Cazzato (1997), as reported by Reddy *et al.* (2005) was used.

$$\text{Total Soluble Sugars (TSS)} = 0.1516 + (\text{Brix \%} \times 0.8746)$$

12. Computed ethanol yield (l ha⁻¹)

Computed ethanol yield (CEY) is measure using the following formula

$$\text{Total sugar yield (t/ha)} = [(\text{TSS \%}) / 100] \times \text{Juice yield (L/ha)} / 1000$$

$$\text{CEY} = \text{Total sugar yield (t/ha)} / 5.68 \times 3.78 \times 1000 \times 0.8$$

(Smith, G.A and Buxton. 1993)

TSS = Total Soluble Sugars

13. Grain yield (T ha⁻¹)

The total cleaned grains obtained after threshing of each panicle was weighed and recorded, converted hectare plant yield to tonnes/hectare.

3.4 STASTICAL ANALYSIS

Statistical analysis

The data collected for the above mentioned characters were subjected to the following statistical analysis with the help of appropriate standard statistical procedures:

3.4.1 Descriptive Statistics

3.4.2 Analysis of variance

3.4.3 Estimation of genetic divergence using Mahalonobis generalized distances (D^2)

3.4.4 Estimation of correlation coefficients

3.4.5 Direct and indirect effects of characters using path coefficient analysis

3.4.6 Line x tester analysis

3.4.7 Stability analysis using Eberhart and Russell & AMMI

3.4.8 Generation mean analysis

3.4.1 Descriptive Statistics: The following descriptive statistics were calculated as per Sharma (2003).

3.4.1.1 Mean :

$$\text{Mean} = \Sigma xi/n$$

Where, xi = i_{th} observation of a trait

n = number of observations

3.4.1.2 Range : Range is the minimum and maximum limits of the observations in a sample.

3.4.1.3 Standard Error:

$$SE = SD/\sqrt{n}$$

Where,

SD = Standard deviation and n = Number of observations

3.4.1.4 Variance :

$$\text{Variance} = \frac{\sum x_i^2 - (\sum x)^2/n}{n - 1}$$

Where,

x_i = i^{th} observation of a population

n = number of observations

3.4.2 Analysis of Variance

To proceed to biometrical genetic analysis we need to check for significant differences in genotypes. Hence the data for different characters were statistically analysed for significance using ANOVA technique described by Panse and Sukhatme (1967). The adopted design was Randomized Block Design (RBD) replicated thrice.

The linear mathematical model:

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

Y_{ij} = Phenotypic observation of i^{th} genotype in j^{th} replication

μ = General mean

g_i = True effect of i^{th} genotype

r_j = True effect of j^{th} replication

e_{ij} = Random error associated with i^{th} genotype and j^{th} replication

Table 3.3. ANNOVA table for Randomized block design

Source	Sum of squares	Degrees of freedom	Mean sum of squares	F-ratio
Replication	P	(r-1)	Mr`	Mr`/Me`
Treatment	Q	(t-1)	Mt`	Mt`/Me`
Error (e)	R	(r-1) (t-1)	Me`	
Total	S	(rt-1)	TMSS	

d.f.: degrees of freedom; SS: Sum of squares; MSS: mean sum of squares

Where,

r = number of replications

t = number of treatments

P = Replication sum of squares

Q = Treatments sum of squares

R = Error sum of squares

S = Total sum of squares

Mr`, Mt`, Me` stands for mean sum of squares due to replications, treatments and error respectively. The significance of mean sum of squares for each character was tested against the error degrees of freedom using 'F' Test (Fisher and Yates, 1967).

3.4.3 Estimation of Genetic Parameters

3.4.3.1 Phenotypic and genotypic variance

This was estimated according to the method given by Lush (1940).

$$\text{Genotypic variance } (\sigma^2g) = \frac{M_t - M_e}{r}$$
$$\text{Phenotypic variance } (\sigma^2p) = \sigma^2g + M_e = \frac{M_t - M_e + M_e}{r}$$

3.4.3.2 Coefficient of Variation

Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton and Devane (1953).

$$\text{GCV} = \frac{\text{Genotypic standard deviation } (\sigma g)}{\text{General mean } (\bar{x})} \times 100$$

$$\text{Phenotypic standard deviation } (\sigma p) = \sqrt{\sigma p^2} = \sqrt{\sigma g^2 + \sigma e^2}$$

$$\text{PCV} = \frac{\text{Phenotypic standard deviation } (\sigma p)}{\text{General mean } (\bar{x})} \times 100$$

As suggested by Subramanian and Menon (1973), GCV and PCV were categorized into

Low	=	Less than 10 %
Moderate	=	10-20 %
High	=	More than 20 %

Heritability in broad sense was estimated as per the formula given by Allard (1960).

$$h^2_{(b)} = \frac{\text{Genotypic variance } (\sigma^2_g)}{\text{Phenotypic variance } (\sigma^2_p)}$$

As suggested by Johnson *et al.* (1955), $h^2_{(b)}$ estimates were categorized

Low	=	0 – 30 %
Medium	=	31-60 %
High	=	61 % and above

3.4.3.3 Genetic advance as per cent of mean (GAM)

Genetic advance was estimated as per the formula proposed by Johnson *et al.* (1955).

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

Where,

K = Selection differential at 5 % selection intensity which accounts to constant value of 2.06

σ_p = phenotypic standard deviation

$h^2_{(b)}$ = heritability in broad sense

$$\text{GAM} = \frac{\text{Genetic advance}}{\text{Grand mean } (\bar{x})} \times 100$$

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al.* (1955).

Low	=	Less than 10 %
Moderate	=	10-20 %
High	=	More than 20 %

3.4.3.4 Heritability

Broad sense heritability was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Hanson *et al.*, 1956).

$$\text{Heritability (h}^2\text{)} = \frac{V_g}{V_p} \times 100$$

Where, V_g = Genotypic variance

V_p = Phenotypic variance

The Heritability percentage was are categorized as low, moderate and high and are given below,

0-30 per cent	- Low
30-60 per cent	- Moderate
>60 per cent	- High

3.4.4 Estimation of genetic divergence by Mahalanobis generalized distance (D^2)

The genetic divergence between forty genotypes was estimated using Mahalanobis (1936) D^2 statistic technique.

D^2 value between i_{th} and j_{th} genotypes for 'p' characters was calculated as:

$$D^2_{ij} = \sum_{t=1}^p (\bar{Y}_{it} - \bar{Y}_{jt})^2$$

Where,

Y_{it} = Uncorrelated mean values of i_{th} genotype for 't' character

Y_{jt} = Uncorrelated mean values of j_{th} genotype for 't' characters and

D^2_{ij} = D^2 between i_{th} and j_{th} genotype

3.4.4.1 Test of significance

After testing the differences between genotypes for each of the characters, a simultaneous test for significance for difference between in the mean values of a number of correlated variations with regard to the pooled effect of characters was carried out by using 'V' statistic which in turn utilizes wilk's 'Λ' criterion. The sum of

squares and sum of product of error genotype were used for this purpose. The estimation of ‘ Λ ’ (wilk’s criterion) was done using the following relationship.

$$\Lambda = \frac{|W|}{|S|}$$

Where,

Λ = Wilk’s criterion

$|W|$ = Determinant of error matrix and

$|S|$ = Determinant of error + variety matrix

The significance of Λ was tested by V (stat.). The value of ‘ V ’ statistic was worked out using Wilk’s lambda criterion.

$$V(\text{stat.}) = -m \log_e \Lambda = -\left(n - \frac{p + q + 1}{2}\right) \log_e \Lambda$$

Where,

$m = n - p + q + 1/2$

p = Number of variables (or) characters

q = Number of genotypes – 1 (or degrees of freedom for population)

n = Degrees of freedom for error + genotypes

$e = 2.7183$

Or $\log_e \Lambda = 2.3026 \log_{10} \Lambda$

V (stat.) is distributed as χ^2 with ‘ pq ’ degrees of freedom. The tabulated value of χ^2 for ‘ pq ’ degrees of freedom at 5% level is used to compare with the above calculated value of χ^2 for testing the significance.

Where degrees of freedom were beyond 100, then the tabulated χ^2 value is calculated by the formula as given by Singh and Chaudhary (1977).

$$Z = \sqrt{2\chi^2} - \sqrt{2n - 1}$$

Where,

Z = tabulated χ^2 value

n = number of degrees of freedom

3.4.4.2 Transformation of correlated variables

In the present model, computation of D^2 values are reduced to simple summation values of the differences in mean values of various characters of the two genotypes i.e., $\sum di^2$. Therefore, transformation of correlated variables to uncorrelated ones was done before working out the D^2 values. Transformation was done by using pivotal condensation method

3.4.4.3 Computation of D^2 values

For a given combination of 'i' and 'j' genotype, the mean deviation viz., $Y_{it} - Y_{jt}$ for $t=1, 2, \dots, p$ variables were computed and the D^2 values were calculated as sum of squares of deviations i.e.,

$$D^2_{ij} = \sum_{t=1}^p (\bar{Y}_{it} - \bar{Y}_{jt})^2$$

Where,

Y_{it} = Uncorrelated mean values of ith genotype for 't' character

Y_{jt} = Uncorrelated mean values of jth genotype for 't' characters and

D^2_{ij} = D^2 between ith and jth genotype

3.4.4.4 Testing the significance of D^2 values

The D^2 values obtained for a pair of genotypes was taken as the calculated value of χ^2 and was tested against the tabulated value of χ^2 for 'p' degrees of freedom, where 'p' was the number of characters considered.

3.4.4.5 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of their contribution towards divergence between two entries ($d_i = Y_{it} - Y_{jt}$). Rank 1 was given to the highest mean difference and rank 'p' to the lowest difference, where 'p' is the total number of characters considered.

% contribution of each character (X) towards genetic divergence was calculated using the formula:

$$\% \text{ contribution of character, } X = \frac{N}{M} * 100$$

Where,

N = Number of genotype contributions where the character was ranked first

M = All possible combinations of genotypes considered

3.4.4.6 Grouping of genotypes into various clusters

Grouping of genotypes into different clusters was done using Tocher's method as described by Rao (1952). The criterion used in clustering by this method is that any two genotypes belonging to the same cluster should show at least on an average smaller D^2 value among themselves than those associated to different clusters.

The first step in grouping the genotypes into different clusters was to arrange the genotypes in the order of their relative distance from each other. For this purpose, D^2 values of all combinations of each genotype were arranged in increasing order of their magnitude in a tabular form as described by Singh and Chaudhary (1977). To start with the two genotypes having the smallest distance from each other were considered first to which a third population having the smallest average D^2 value from the first two genotypes was added. Similarly, next nearest fourth genotype was considered and this procedure was continued. At certain stage where it was felt that after adding a particular genotype, there was abrupt increase in the average D^2 value, that population was not considered for including in that cluster. The group of the first cluster was then omitted and the rest was treated in a similar way. This process was continued till all the genotypes were included into one or other clusters.

3.4.4.7 Average intra cluster distance

For the measurement of intra cluster distance, the formula used was $\Sigma D^2i / n$.

Where,

ΣD^2i = sum of distances between all possible combinations (n) of the Population included in a cluster

n = number of genotypes included in a cluster

3.4.4.8 Average inter –cluster distance

Clusters were taken one by one and their distance from other clusters was calculated. The distance between two clusters was the sum of D^2 values between the members of one cluster to each of the member of other cluster divided by the product of number of genotypes in both the clusters under consideration.

The square root of the average D^2 value gave the genetic distance ‘D’ between the clusters. Based on D values (inter cluster distance) the scale given by Rao (1952) for rating of the distance was adopted and the cluster diagram was prepared.

$$\text{Average intercluster distance} = \frac{D^2}{n_1 \times n_2}$$

Where,

n_1 and n_2 are the number of genotypes in cluster 1 and cluster 2, respectively.

Category	‘D’ values
Closely related	Below 22
Moderately divergent	Between 22 and 30
Highly divergent	Above 30

3.4.5 Estimation of Correlation Coefficients

Character association refers to the association of characters i.e., a change in one character is accompanied by a change in the other character. The data on 13 quantitative characters were utilized for the computation of phenotypic and genotypic correlation co-efficient between ethanol yield and yield contributing traits of 110 germplasm lines in sorghum.

Phenotypic and genotypic correlation co-efficient were calculated for the characters by working out the variance components of each character and the covariance components for each pair of characters using the formulae suggested by AL-Jibouri *et al.* (1958).

$$\text{Genotypic correlation coefficient, (rg)} = \frac{\text{Cov xy (genotypic)}}{\sqrt{(\text{Var x}). (\text{Var y}) (\text{genotypic})}}$$

Where,

$$\text{Genotypic variance} = \frac{\text{Treatment MS} - \text{Error MS}}{\text{Number of replications}}$$

Similarly,

$$\text{Genotypic covariance} = \frac{\text{Treatment Cov} - \text{error Cov}}{\text{Number of replications}}$$

$$\text{Phenotypic Correlation coefficient, (rp)} = \frac{\text{Cov xy (phenotypic)}}{\sqrt{(\text{Var x}) \cdot (\text{Var y (phenotypic)})}}$$

The values of genotypic correlation exceeding unity should be considered as unit only (of same sign). To test the significance of correlation coefficients, the estimated values were compared with the table values of correlation coefficients (Fisher and Yates, 1967) at 5% and 1% level of significance with (n-2) degrees of freedom, where 'n' is the number of pairs of observations used in the experiment.

3.4.6 Path Coefficient Analysis

The use of path coefficient analysis explains cause and effect relationship among the variables. It is a standardized partial regression coefficient and as such measures the direct influence of one variable upon another and permits the separation of the correlation coefficients into components of direct and indirect effects (Dewey and Lu, 1959). This method permits breeder to identify relatively important components of a variable, on the basis of their direct and indirect influences.

The direct and indirect effects both at genotypic and phenotypic level were estimated by taking ethanol yield per plant as dependent variable using path coefficient analysis recommended by Wright (1921) and Dewey and Lu (1959).

The following set of instructions equations were formed and solved for estimating various direct and indirect effects.

$$r_{1y} = p_{1yr11} + p_{2yr12} + p_{3yr13} \dots \dots \dots + p_{nyr1n}$$

$$r_{2y} = p_{1yr21} + p_{2yr22} + p_{3yr23} \dots \dots \dots + p_{nyr2n}$$

$$r_{ny} = p_{1y rn1} + p_{2y rn2} + p_{3y rn3} \dots \dots \dots + p_{ny rn n}$$

Where,

1, 2.....n = independent variable

Y = dependent variable (yield per plant)

r_{1y}, r_{2y}..... r_{ny} = coefficient of correlation between casual factors '1' to 'n' on dependent character 1

p_{1y} p_{2y}.....p_{ny} = Direct effect of characters '1' to 'n' on character Y

The above equations can be written in matrix form as:

$$\begin{pmatrix} A \\ r_{1y} \\ r_{2y} \\ : \\ : \\ r_{ny} \end{pmatrix} \begin{pmatrix} C \\ 1 & r_{12} & r_{13} & \dots & r_{1n} \\ r_{21} & 1 & r_{23} & \dots & r_{2n} \\ : & : & : & & : \\ : & : & : & & : \\ r_{n1} & r_{n2} & r_{n3} & \dots & 1 \end{pmatrix} \begin{pmatrix} B \\ p_{1y} \\ p_{2y} \\ : \\ : \\ p_{ny} \end{pmatrix}$$

A and B vector values are known. Hence, to calculate C vector

$$B=[C]^{-1}A$$

Where,

$$C^{-1} = \begin{pmatrix} C_{11} & c_{12} & c_{13} & \dots & c_{1n} \\ C_{21} & c_{22} & c_{23} & \dots & c_{2n} \\ : & : & : & & : \\ : & : & : & & : \\ C_{n1} & c_{n2} & c_{n3} & \dots & c_{n4} \end{pmatrix}$$

Direct effects were as follows:

$$\begin{aligned} p_{1y} &= \sum_{i=1}^k c_{1i} r_{iy} \\ p_{2y} &= \sum_{i=1}^k c_{2i} r_{iy} \\ p_{ny} &= \sum_{i=1}^k c_{nj} r_{iy} \end{aligned}$$

Residual effect (PR_y), which measures the contribution of characters not considered, in the casual scheme was obtained as:

$$\text{Residual effect (PR}_y) = \sqrt{(1 - r^2)}$$

Where,

$$r^2 = P_{1y} r_{1y} + P_{2y} r_{2y} + \dots \dots \dots P_{ny} r_{ny}$$

P_{ny} = Direct effect of X_n on Y

r_{ny} = Correlation coefficient of X_n on Y

3.4.7 Combining Ability and Heterosis for 13 Characters in Sorghum

3.4.7.1 Combining ability analysis

The mean values computed for each character were subjected to combining ability analysis (Kempthorne, 1957). The structure of ANOVA for combining ability analysis is given below:

Table 3.4. ANOVA structure for combining ability

Source	Df	MSS	Expected MSS
Replication	(r - 1)		
Crosses	(lt - 1)		
Lines	(l - 1)	M _l	$\sigma^2_e + r \sigma^2_{sca} + tr \sigma^2_{gca}$
Testers	(t - 1)	M _t	$\sigma^2_e + r \sigma^2_{sca} + lr \sigma^2_{gca}$
Line x Tester	(l - 1) (t - 1)	M _{lt}	$\sigma^2_e + r \sigma^2_{sca}$
		M _e	σ^2_e

σ^2_{gca} = Co-variance of half sibs

$\sigma^2_{sca} = [\text{Cov (FS)} - 2 \text{Cov (HS)}]$

From the expectations of mean sum of squares, the GCA variance of the lines and testers and SCA variance of hybrids were calculated using the formula,

$$\text{GCA variance for lines} = \frac{M_l - M_{lt}}{tr}$$

$$\text{GCA variance for testers} = \frac{M_t - M_{lt}}{lr}$$

$$\text{SCA variance for hybrids} = \frac{M_{lt} - M_e}{r}$$

Further, the covariance of full sibs and covariance of half sibs were estimated as given below,

$$\text{Co-variance of full sibs} = \frac{M_l + M_t + M_{lt} - 3M_e + 6r [\text{Cov (HS)}] - r (l + t) \text{Cov (HS)}}{3r}$$

$$\text{Co-variance of half sibs (Average)} = \frac{1}{r (2l_t - l - t)} \left[\frac{(l - 1) (M_l) + (t - 1) (M_t)}{(l + t - 2)} - M_{lt} \right]$$

After estimating Cov (HS) and Cov (FS), the additive and dominance variance are computed as given below

$$\sigma^2 \text{GCA} = \text{Cov (HS)} = \frac{1}{4} \text{VA}$$

Hence, $4 \sigma^2 \text{GCA} = \text{VA} = \text{Additive Variance}$

$$\sigma^2 \text{SCA} = \text{Cov (FS)} - 2 \text{Cov (HS)} = \frac{1}{4} \text{VD}$$

Hence, $\text{VD} = 4 \sigma^2 \text{SCA} = \text{Dominance Variance}$

Where,

M_l = Mean sum of squares of lines

M_t = Mean sum of squares of testers

M_{lt} = Mean sum of squares of line x tester

M_e = Mean sum of squares of error.

After estimating the GCA and SCA variances, the ratio of GCA/SCA variance were computed to predict the type of gene action involved.

3.4.7.1.1 Estimation of general combining ability and specific combining ability effects: To estimate general combining ability (gca) and specific combining ability (sca) effects of *ijk* observations the following linear model (Kempthorne, 1957) was used.

$$Y_{ij} = \mu + g_i + g_j + S_{ij} + e_{ijk}$$

Where,

μ = Population mean

g_i = gca effect of i^{th} female parent

g_j = gca effect of j^{th} male parent

S_{ij} = sca effect of ij^{th} combination

e_{ijk} = Environmental effect pertaining to ijk^{th} individuals

i = Number of female parents

j = Number of male parents

k = Number of replications

(i) General combining ability effects:

$$\text{a. Lines: } g_i = \frac{X_{i..}}{tr} - \frac{X_{...}}{ltr}$$

Where,

$x_{i..}$ = Total of all crosses involving i^{th} per cent (replication total of line 'i' with all testers)

$x_{...}$ = Total of all hybrids

g_i = General combining ability effects of i^{th} line

$$\text{b. Testers: } g_j = \frac{X_{.j.}}{lr} - \frac{X_{...}}{ltr}$$

Where,

$x_{...}$ = Total of all hybrids over female and male parents

$x_{.j.}$ = Total of all crosses involving j^{th} male parent

g_j = General combining ability effects of j^{th} tester

(ii) Specific combining ability effects:

$$S_{ij} = \frac{X_{ij.}}{r} - \frac{X_{i..}}{tr} - \frac{X_{.j.}}{lr} + \frac{X_{...}}{ltr}$$

Where,

S_{ij} = Specific combining ability effect of ij_{th} cross combination

$X_{i..}$ = Total of all crosses involving 'i' as one parent

$X_{.j.}$ = Total of all crosses involving 'j' as one parent

$X_{...}$ = Grand total of all crosses

$X_{ij.}$ = Total of particular ij_{th} cross combination over all the replications

The standard errors for testing the significance of gca and sca effects were estimated using the following formulae:

Standard error (SE) of $g_i = (Me/tr)^{1/2}$

Standard error (SE) of $g_j = (Me/lr)^{1/2}$

Standard error (SE) of $s_{ij} = (Me/r)^{1/2}$

The estimates of g_i and s_{ij} were tested for their statistical significance by 't' test.

For testing the significance of difference between gca effects of two lines (or two testers) and sca effects of two hybrids, the standard error is as follows.

Standard error of $(g_i - g_j)$ for lines = $(2Me/tr)^{1/2}$

Standard error of $(g_i - g_j)$ for testers = $(2Me/lr)^{1/2}$

Standard error of $(s_{ij} - s_{kl})$ for crosses = $(2Me/r)^{1/2}$

The critical difference is computed by multiplying SE value with table 't' value at error degrees of freedom.

3.4.7.2 Pooled or combined analysis of variance for line x tester

The experiment was conducted in three locations to provide consistently stable performance of the test genotypes or hybrids. Since the variance arises from single environment may have biased due to genotype x environment interactions.

The model used for the pooled analysis was given as follows:

$$Y_{ijk} = \mu + g_i + g_j + S_{ij} + I_k + gI_{ik} + gI_{jk} + S_{ijk} + e_{ijk}$$

Where,

Y_{ijk} = Value of ijk th observations

μ = General mean

g_i = gca effect of the i th line

g_j = gca effect of the j th tester

S_{ij} = sca effect of the ij th crosses

I_k = Environment effect of K th environment

gI_{ik} = female x environment of I th female in k th environment

gI_{jk} = male x environment interaction of j th male in k th environment

S_{ijk} = Interaction of sca effect of progeny with environment in k th environment

e_{ijk} = Random error effect associated with ijk observations.

Table 3.5. ANOVA of pooled over seasons or environments

The analyses of variance for combining ability over the seasons (environments) were estimated.

Source of variation	d.f.	Sum of squares	Mean sum squares
Season/Environment	(I-1)	M_1	$\sigma_e^2 + r \sigma^2_{fmI} + rm \sigma^2_{fI} + rf \sigma^2_{mI} + rfm \sigma^2_I$
Female	(f-1)	M_2	$\sigma_e^2 + r \sigma^2_{fmI} + fmI + rI \sigma^2_{fm} + rm \sigma^2_{fi} + rfi \sigma^2_f$
Males	(m-1)	M_3	$\sigma_e^2 + r \sigma^2_{fmI} + rI \sigma^2_{fm} + rf \sigma^2_{mI} + rfi \sigma^2_m$
Females x environments/seasons	(f-1) (I-1)	M_4	$\sigma_e^2 + r \sigma^2_{fmI} + rm \sigma^2_{fI}$
Males x seasons	(m-1) (I-1)	M_5	$\sigma_e^2 + r \sigma^2_{fmI} + rf \sigma^2_{fm}$
Females x males	(f-1) (m-1)	M_6	$\sigma_e^2 + r \sigma^2_{fmI} + rI \sigma^2_{mI}$
Females x males x seasons	(f-1) (m-1) (I-1)	M_7	$\sigma_e^2 + r \sigma^2_{Mi}$
Error	I (fm-1) (r-1)	M_8	σ_e^2

The estimates for σ^2_f , σ^2_m , σ^2_{fm} , σ^2_I , σ^2_{fI} , σ^2_{mI} and σ^2_{fmI} were obtained by equating mean squares to their respective expectations and solving the resulting equations.

The estimates are

$$\sigma^2_f = (M_2 - M_4 - M_6 + M_7)/rml$$

$$\sigma^2_m = (M_3 - M_6 - M_5 + M_7)/rfl$$

$$\sigma^2_{fm} = (M_6 - M_7)/rI$$

$$\sigma^2_I = (M_1 - M_4 - M_5 + M_7)/rmf$$

$$\sigma^2_{fI} = (M_4 - M_7)/rm$$

$$\sigma^2_{mI} = (M_5 - M_7)/rf$$

$$\sigma^2_{fmI} = (M_7 - M_8)/r$$

$$\sigma^2_{gca} = \frac{M_2 + M_3 - 2M_6 - M_4 - M_5 + 2M_7}{rI(f + m)}$$

$$\sigma^2_{sca} = \frac{M_6 - M_7}{rI}$$

$$\sigma^2_{gca \times Env.} = \frac{M_4 + M_5 - 2M_7}{r(f + m)}$$

$$\sigma^2_{sca \times Env.} = \frac{M_7 - M_8}{r}$$

3.4.7.3 Test of significance

To test the significance if these various combined variance estimates “F” test was used from Singh and Joshi (1966).

a) σ^2_f , $F = (M_2 + M_7)/M_6 + M_4$, for n_1 and n_2 d.f.

Where,

$$n_1 = \frac{(f-1)(m-1)(I-1)(M_2 + M_7)^2}{(m-1)(I-1)M_6^2 + M_7^2}$$

$$n_2 = \frac{(f-1)(m-1)(I-1)(M_6 + M_4)^2}{(I-1)M_6^2 + (m-1)M_4^2}$$

b) $\sigma^2 m$, $F = (M_3 + M_7) / M_6 + M_5$, for n_1 and n_2 d.f.

Where,

$$n_1 = \frac{(f-1)(m-1)(I-1)(M_3 + M_7)^2}{(m-1)(I-1)M_3^2 + M_7^2}$$

$$n_2 = \frac{(f-1)(m-1)(I-1)(M_6 + M_5)^2}{(I-1)M_6^2 + (m-1)M_5^2}$$

c) $\sigma^2 fm$, $F = M_6 / M_7$ for n_1 and n_2 d.f.

Where, $n_1 = (f-1)(m-1)$

$$n_2 = (f-1)(m-1)(I-1)$$

d) $\sigma^2 I$, $F = (M_1 + M_7) / (M_4 + M_5)$, for n_1 and n_2 d.f.

Where,

$$n_1 = \frac{(f-1)(m-1)(I-1)(M_1 + M_7)^2}{(f-1)(m-1)M_3^2 + M_7^2}$$

$$n_2 = \frac{(f-1)(m-1)(I-1)(M_4 + M_5)^2}{(I-1)M_6^2 + (m-1)M_5^2}$$

e) $\sigma^2 fI$, $F = M_4/M_7$, for n_1 and n_2 d.f.

Where, $n_1 = (f-1)(m-1)$

$$n_2 = (f-1)(m-1)(I-1)$$

f) $\sigma^2 mI$, $F = M_5/M_7$, for n_1 and n_2 d.f.

Where, $n_1 = (f-1)(m-1)$

$$n_2 = (f-1)(m-1)(I-1)$$

g) $\sigma^2 fmI$, $F = M_7/M_8$, for n_1 and n_2 d.f.

Where, $n_1 = (f-1)(m-1)$

$$n_2 = (f-1)(m-1)(I-1)$$

h) σ^2 gca, $F = (M_2 + M_3 - M_4 - M_5 / 2M_6 - M_7)$, for n_1 and n_2 d.f.

$$n_1 = \frac{(f-1)(m-1)(I-1)(M_2 + M_3 - M_4 - M_5)^2}{(I-1)(m-1)M_2^2 + (I-1)(f-1)M_3^2 + (m-1)(f-1)M_4^2 + M_5^2}$$

$$n_2 = \frac{(f-1)(m-1)(I-1)(M_6 - M_7)^2}{(I-1)M_6^2 + M_7^2}$$

i) σ^2 sca $F = M_6 / M_7$ for n_1 and n_2 d.f.

Where, $n_1 = (f-1)(m-1)$

$n_2 = (f-1)(m-1)(I-1)$

j) σ^2 gca X Environment $F = M_6 + M_5 / 2M_7$ for n_1 and n_2 d.f.

$$n_1 = \frac{(f-1)(m-1)(I-1)(M_4 - M_5)^2}{(I-1)(m-1)M_4^2 + (f-1)M_5^2}$$

$n_2 = (f-1)(m-1)(I-1)$

k) σ^2 sca X Environment $F = M_7/M_8$, for n_1 and n_2 d.f.

Where, $n_1 = (f-1)(m-1)(I-1)$

$n_2 = (fm-1)(r-1)I$

Other components such as $\sigma^2 A$, $\sigma^2 D$ both at $F = 0$, $F=1$, $\sigma^2 D / \sigma^2 A$, h_2 were estimated in the same way which were estimated in single season analysis.

3.4.7.4 Pooled estimates of gca and sca effects

For the estimation of gca and sca effects a two way table of females vs male was made of a total of all replications over three locations. Then, gca and sca effects of ijk_{th} observations for pooled over seasons were calculated as in single season analysis with a denominator value of “rfmI” in all the cases.

Similarity, for calculating S.E., same formulae were used as in single environment data except the denominator which was multiplied by a locations/environments *i.e.*, I . Critical differences (C.D.) were also calculated in the same way as in single environment /season analysis at 5% and 1% level of probability.

3.4.7.5 Estimation of Heterosis

The treatment mean values for each trait was used for the estimation of heterosis. Heterosis over mid parent (MP), better parent (BP) and standard check (SC) were computed by the formulas suggested by Turner (1953) and Hayes *et al.* (1955).

$$\text{Heterosis per cent over mid parent (\%)} = \frac{F_1 - MP}{MP} \times 100$$

$$\text{Heterosis per cent over better parent (\%)} = \frac{F_1 - BP}{BP} \times 100$$

$$\text{Heterosis per cent over standard check (\%)} = \frac{F_1 - SC}{SC} \times 100$$

To compute the standard error (SE) of estimates of heterosis, mean squares due to error (Me) was considered.

$$\text{SE for heterosis over mid parent (MP)} = (3 \text{ Me} / 2 r)^{1/2}$$

$$\text{SE for heterosis over better parent (BP)} = (2 \text{ Me} / r)^{1/2}$$

$$\text{SE for heterosis over standard check (SC)} = (2 \text{ Me} / r)^{1/2}$$

Where,

Me = Error MSS in general ANOVA table

r = Number of replications

F₁ = Mean value of hybrid over two replication

MP = Mean value of mid parent over two replication

BP = Mean value of better parent over two replication

SC = Mean value of standard check over two replication

Further 't' value is calculated to test the significance for heterosis

$$\text{'t' value for mid parent heterosis} = \frac{F_1 - MP}{\text{SE (MP)}}$$

$$\text{'t' value for better parent heterosis} = \frac{F_1 - BP}{SE(BP)}$$

$$\text{'t' value for standard heterosis} = \frac{F_1 - SC}{SE(SC)}$$

The calculated 't' value was compared with table 't' value at error degrees of freedom.

3.4.8 Stability analysis using Eberhart and Russell Model, AMMI

The experiment was focused on understanding changes in the relative performance of genotypes across different environments *i.e.*, genotype x environment interactions. The information helps in development of cultivars for specific environments and also to identify genotypes stable across environments.

3.4.8.1 Analysis of variance for stability

Eberhart and Russell (1966) model was adopted for stability analysis. The phenotypic stability is based on regression analysis. The environment and genotype × environment interactions were partitioned into three components viz., environment (linear), genotype x environment (linear) and deviation from regression (pooled deviation over the genotypes).

The structure of ANOVA is given below.

Table 3.6. Pooled analysis of variance for Stability

Source	d.f.	SS	MS	F values
Genotypes (g)	(g-1)	$1/n \sum_i Y_i^2 - CF$	M_1	M_1/M_3
Environment (e) + Interaction (g x s)	(e-1) + (g-1) (e-1) = g (e-1)	$\sum_i \sum_j Y_{ij}^2 - \sum_i Y_i^2/n$		
Environment (linear)	1	$1/g (\sum_i Y_i I_j)^2$		
Genotype x environment (linear)	g-1	$\sum (C \sum_j Y_{ij})^2 \sum_i I_j^2$ (linear) S.S.	M_2	M_2/M_3
Pooled deviation	g (e-2)	$\sum_i \sum_j S_{ij}^2$	M_3	M_3/M_4
Genotype 1	(e-2)	$[(\sum_i Y_{ij}^2 - (Y_i)^2/n) - (\sum_i Y_{ij} I_j)^2 / \sum_i I_j^2]$		
Genotype 2	(e-2)	$[(\sum_i Y_{ij}^2 - (Y_i)^2/n) - (\sum_i Y_{ij} I_j)^2 / \sum_i I_j^2]$ $= \sum_i S_{ji}^2$		
Pooled error	e (r-1) (g-1)	$\sum_i \sum_j Y_{ij}^2 - CF$	M_4	
Total	(eg-1)			

I_j = The environmental index obtained as the deviation of the mean of all the genotypes at the j^{th} environment from the grand mean.

S_{ij} = The deviation from regression of the i^{th} genotype of j^{th} environment

e = Number of environments

g = Number of genotypes

r = Number of replications

CF = Correction factor

3.4.8.2 The stability analysis was done using the linear regression model suggested by Eberhart and Russell (1966) and the model is presented below.

$$Y_{ij} = \mu_i + b_i I_j + d_{ij}$$

Y_{ij} = Mean of i^{th} genotype at j^{th} environment

μ_i = The mean of i^{th} genotype over all the environments

b_i = The regression coefficient of the i^{th} genotype on the environmental index which measures the response of the i^{th} genotype to varying environments.

I_j = The environmental index obtained as the deviation of the mean of all the genotypes at the j^{th} environment from the grand mean

d_{ij} = The deviation from regression of the i^{th} genotype of j^{th} environment

Based on this model, the mean (μ_i), the regression coefficient (b_i) and the mean square deviation from linear regression line ($s^2 d_i$) are the three stability parameters proposed by Eberhart and Russell (1966) in this model. These parameters were computed using the following formula.

$$\mu_i (\text{mean}) = \frac{\sum_j Y_{ij}}{n}$$

$$b_i (\text{regression coefficient}) = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

$$s^2 d_i (\text{deviation from the regression}) = [\sum_j s^2_{ij} / (n-2)] - (s^2 e / r)$$

Where,

n = Number of environments

Y_{ij} = Performance of i^{th} genotype in j^{th} environment

$\sum_i s^2_{ij}$ = Sum of squares of deviation from the regression line

$s^2_{e/r}$ = Estimate of pooled error

I_j = Environmental index (i.e., environmental mean – grand mean)

3.4.8.3 ‘F’ and ‘t’ tests

As illustrated above appropriate ‘F’ and ‘t’ tests were used to find out the significance of various parameters.

- a) ‘F’ test for testing the significance of the difference among the entries means is defined as

$$F = M_1/M_3$$

- b) To test the varieties (entry) do not differ for their regression on the environmental index, the appropriate ‘t’ test was used.

$$t = \frac{1 - b_i}{SE}$$

- c)

$$SE(b_i) = \frac{\sum Y^2 - (\sum Y)^2/n - b^2 \sum (X - \bar{X})^2}{(n-2) \sum (X - \bar{X})^2}$$

Y = Yield

X = Environmental index

n = Number of environments

$\bar{X}$ = Mean of genotypes

- d) Individual deviation from linear regression is tested as follows.

$$F = \left(\frac{\sum_i s^2_{ij}}{(e-2)} \right) / \text{Pooled error mean square}$$

e = Number of environments

3.4.8.4 AMMI Analysis

Additive main effect and multiplicative interaction (AMMI) model in GenStat 12.1 [Payne *et al.* 2009] was used to find out the stability of the genotypes across environments. The AMMI model first detects the additive effects for the genotypes and the growing environments and multiplicative term for interactions.

The AMMI model according to Farshadfar *et al.* [2011] is presented as

$$Y_{ij} = \mu + g_i + e_j + \sum \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij}$$

where Y_{ij} is the yield of the i^{th} genotype in the j^{th} environment, g_i is the mean of the i^{th} genotype minus the grand mean, λ_k is the square root of the eigenvalue of the PCA axis k , and α_{ik} and γ_{jk} are the principal component scores for PCA axis of the i^{th} genotype and the j^{th} environment, respectively, and e_{ij} is the residual. The environment and genotypic PCA scores are expressed as unit vector times the square root of λ_k i.e., environment PCA score = $\lambda_k^{0.5} \gamma_{jk}$; genotype PCA score = $\lambda_k^{0.5} \alpha_{ik}$

AMMI analysis portioned G x E interaction into different principle component analysis (PCA). Biplots are commonly used to explain AMMI results considering one or two Principle component Analysis at a time represented in the form of Figures. The main effects, genotype means and environment means are shown along the abscissa (x axis) and the ordinate (y-axis) represents the first PCA.

The usual interpretation of a bi plot assay is that if a genotype or an environment has a PCA score of nearly '0', it has small interaction effects and when a genotype and an environment have the same sign on the PCA axis, their interaction is positive; if different, their interaction is negative.

These AMMI biplots help in visual interpretation of the GE patterns and identify genotypes or locations that exhibit low, medium or high levels of interaction effects and stability parameter.

3.4.9 Generation Mean Analysis

The details of statistics procedures adopted for analysis of six generation viz., P_1 , P_2 , F_1 , F_2 , BC_1 , BC_2 of selected cross on the mature and magnitude of various types of gene action are presented below.

3.4.9.1 Mather's scaling tests

The three quantities of scaling tests viz., A, B and C were calculated following methods of Mather (1949) to detect the presence of absence of epistasis as detailed below.

$$A = 2 B_1 - P_1 - F_1$$

$$B = 2 B_2 - P_2 - F_2$$

$$C = 4 F_2 - 2F_1 - P_1 - P_2$$

Where,

P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 are the mean values of the respective generations.

Significant deviation of A, B and C values from zero indicates presence of epistasis justifying the use of six parameter model. Variances of means of the corresponding generations (squares of standard errors) were used to compute the variance of A, B and C as shown below.

$$V_A = 4 V (BC_1) + V (P_1) + V (F_1)$$

$$V_B = 4 V (BC_2) + V (P_2) + V (F_1)$$

$$V_C = 16 V (F_2) + 4 V (F_1) + V (P_1) + V (P_2)$$

Where,

V_A , V_B , and V_C are the variances of A, B and C, respectively. VP_1 , VP_2 etc. are the variances of means of the respective generations. The 't' values for each of these three quantities were calculated to test their significant as follows.

$$t (A) = A/SE (A)$$

$$t (B) = B/SE (B)$$

$$t (C) = C/SE (C)$$

Where, standard error (SE) is the square root of respective variance for example

$$SE (A) = (V_A)^{1/2}$$

3.4.9.2 Joint scaling test

In the Cavalli's (1952) joint scaling test, genetic parameters viz., m , (d) and (h) are estimated from the observed means of three or more generations. When more than three generation means are available to estimate the above three parameters a weighed least square analysis is employed which enables precise estimation of (m) , (d) and (h) , such that deviations of observed from expected values are least. In this approach, reciprocals of variance of each of the means is used as a weight. Six equations from six generations viz., P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 would be available for estimation of (m) , (d) and (h) that are obtained by equating the observed family means to their expectations in terms of three genetic parameters as detailed below.

Generation	Weight	Coefficient			Observed generation mean
		(m)	(d)	(h)	
P_1	$1/VP_1$	1	-1	0	P_1
P_2	$1/VP_2$	1	1	0	P_2
F_1	$1/VF_1$	1	0	1	F_1
F_2	$1/VF_2$	1	0	0.5	F_2
BC_1	$1/VB_1$	1	-0.5	0.5	BC_1
BC_2	$1/VB_2$	1	-0.5	0.5	BC_2

The six equation and their weights are combined to get three simultaneous normal equations yielding weighted least squares estimates of the three parameters m , (d) and (h) as follows.

Each of the equation is multiplied through by the coefficient, which if contains and by its weight and the six equations are then summed to get the first normal equation. The two further equations are obtained in the similar way using the coefficients of m , (d) and (h) and the weights as multiplier. The solution to these three simultaneous normal equations is obtained by way of matrix inversion, that is in the form of $M = J^{-1}S$.

Where,

M = Matrix of the estimations of the parameters viz., m , (d) and (h)

J^{-1} = Inverse of the information matrix (J) and is a variance – covariance matrix

S = Column matrix obtained by multiplying respective observed values by coefficients and weight and is matrix of score.

By using the inversion matrix, the values of m, (d) and (h) were computed. The adequacy of the additive-dominance model was next tested by predicting the expected family means from the estimated of the three genetic parameters and comparing with the observed generation means with the help of chi-square test. Significance of calculated chi-square values depicts the inadequacy of additive-dominance model and further analysis using Hayman's approach (1958) is required to cater for the possible non-allelic interaction effects.

3.4.9.3 Estimation of gene effects using six generation means

The generation means were analysed by the method suggested by Hayman (1958) to provide information on the inheritance of various traits. The generation means were used to estimate the six genetic parameters viz., (m), (d), (h), (i) and (1) of digenic interaction model representing F₂ mean, additive gene action, dominance genetic effect, additive x additive gene interaction effect, additive x dominance interaction effect and dominance x dominance gene effects, respectively assuming that no linkage and no higher order gene interaction exists. Considering the generation means as reference values, the above six genetic parameters were calculated following relationship between respective generation mean and genetic effects.

3.4.9.4 Components of generation means

$$P_1 = m + (d) + (i)$$

$$P_2 = m - (d) + (i)$$

$$F_1 = m + (h) + (1)$$

$$F_2 = m + \frac{1}{2} (h) + \frac{1}{4} (1)$$

$$BC_1 = m + \frac{1}{2} (d) + \frac{1}{2} (h) + \frac{1}{4} (i) + \frac{1}{4} (j) + \frac{1}{4} (1)$$

$$BC_2 = m - \frac{1}{2} (d) + \frac{1}{2} (h) + \frac{1}{4} (i) + \frac{1}{4} ((j) + \frac{1}{4} (1)$$

Accordingly, by least squares computation method, the formula for different gene effects are as follows.

3.4.9.5 Formulae for gene effects

$$\text{Mean} = m = F_2$$

$$\text{Additive effect} = (d) = B_1 - B_2$$

$$\text{Dominance effect} = (h) = 2B_1 + 2B_2 + F_1 + 4F_2 - \frac{1}{2}P_1 - \frac{1}{2}P_2$$

$$\text{Additive x additive epistatic effect} = (i) = 2B_1 + 2B_2 - 4F_2$$

$$\text{Additive x dominance epistatic effect} = (j) = B_1 + \frac{1}{2}P_1 - B_2 - \frac{1}{2}P_2$$

$$\text{Dominance x dominance interaction effect} = (l) = P_1 + P_2 + 2F_1 + 4F_2 - 4B_1 - 4B_2$$

The variance of these gene effects involving the variance of means of the generations were calculated as follows.

$$V_m = V F_2$$

$$V_d = V B_1 + V B_2$$

$$V_h = V F_1 + 16 V F_2 + \frac{1}{4} V P_2 + 4V B_1 + 4 V B_2$$

$$V_i = 4 V B_1 + 4 V B_2 + 16 V F_2$$

$$V_j = 4 V B_1 + 4 V B_2 + V P_1 + V P_2$$

$$V_l = V P_1 + V P_2 + 4 V F_1 + 16 V F_2 + 16 V B_1 + 16 V B_2$$

Where,

V_m = Variance of mean effect

V_d = Variance of additive effect

V_h = Variance of dominance effect

V_i = Variance of additive x additive interaction effect

V_j = Variance of additive x dominance interaction effect

V_l = Variance of dominance x dominance interaction effect

Square roots of the variance provided respective standard errors.

B_1 = Back cross 1 and B_2 = Back cross 2.

The standard errors were used to calculate the 't' values for testing significance of the corresponding variances, for example.

$$t(d) = \sqrt{2} \text{ SE } (d),$$

Where, $\text{SE } (d) = [V (d)]^{1/2}$

CHAPTER –IV

RESULTS AND DISCUSSION

The present study entitled “Stability analysis in sorghum [*Sorghum bicolor* (L.) Moench] genotypes” was carried out to estimate variability and diversity in 110 genotypes including indigenous, exotic lines, advance breeding lines and 2 checks. An attempt was made for selecting the diverse lines for crossing with male sterile lines to study the combining ability. This in turn has resulted in the identification of the most stable hybrid combination of sorghum over the three locations followed by identifying the gene action governing the ethanol yield and its attributing traits through generation mean analysis. The results thus obtained during the investigation were presented under the following headings.

- 4.1 Variability studies
- 4.2 Diversity studies
- 4.3 Correlation and Path analysis
- 4.4 Combining ability studies
- 4.5 Stability studies
- 4.6 Generation mean analysis

4.1 STUDIES ON ASSESSMENT OF VARIABILITY

4.1.1 Mean Performance of Genotypes

Using first order robust statistics such as Mean, SEM, SD, CD 5% and CV %, the performance of 110 genotypes in respect of 13 quantitative characters of sorghum was analysed and presented in Table 4.1

4.1.1.1 Days to 50 % flowering (days)

The population mean for days to 50% flowering was 81 days and ranged from 26 days (IS -3980) to 115 days (EG-83). When compared with the best check CSV-24SS (84 days) the following 25 genotypes SSS-46, GGUB-61 (86 days); E-63, PV-12 (89 days); GGUB-50 (92 days); CJV-16 (93 days); SPV-2196 (95 days); CJV-18, SSS-65 (97 days) ; EG-39, GGUB-27 (98 days); CJV-24 (101 days); NSJB-6577 (104 days); NSJB-6662 (108 days); NSJB-6585, NSJB-6648 (110 days); NSJB-6657 (111 days); EC-23, GGUB-63, IS-27072 (112 days); NSJB-6629, PHULE VASHUNDHARA (113 days); EG-80 (114 days); EG-83 (115 days) have recorded significantly more no. of

days to 50% flowering because sweet sorghum genotypes require medium to late flowering for maximizing the ethanol yields (Oyier *et al.*, 2017).

4.1.1.2 Days to maturity (days)

In general the desirable character is early maturing genotypes but for sweet sorghum medium to late maturing types are preferred. The average days to maturity was 116 days and ranged from 53 days (IS -3980) to 159 days (EG-80). The below mentioned 23 genotypes were significantly medium to late maturing types when compared to best check variety CSV-24SS (121.67 days).

CJV-16 (127 days); SSS-10, GGUB-43 (128 days); GGUB-27 (129 days); CJV-18 (132 days); SSS-65 (133 days); E-40, SPV-2196 (135 days); ICSV-25306, ICSV 25308, NSJB-6629 (136 days); CJV-24 (137 days); EG-39 (138 days); EC-23, NSJB-6577 (141 days); NSJB-6662, NSJB-6585 (144 days); EG-83 (145 days); NSJB-6648 (146days); NSJB-6657 (147days); GGUB-63 (152days); PHULE VASHUNDHARA (153 days); EG-80 (159 days) and have recorded significantly more no. of days to maturity. As the maturity delays, conversion of sugars is maximum, when compared to the early matured genotypes.

4.1.1.3 Plant height (cm)

As quoted by Tomar *et al.* (2012) tall and thick stems of sorghum contribute for high biomass and juice yield. In the present study also the mean value recorded for plant height was 371.72 cm, the tallest genotype was Phule vasundhara (540.80 cm) and the dwarf among the test genotypes is IS-30310 (107.67cm).

Twenty four genotypes have marked significant superiority above the best check variety CSV-24SS (357.13 cm) are EG-25 (422.33 cm); ICSV-25308 (422.95 cm); SSS-46(423.60 cm); GGUB-61 (424.50); SSS-10 (427.73 cm); EC-22 (428.67 cm); CJV-07 (431.07 cm); DHBM-3 (434.27 cm); EG-80 (434.55); NSJB-6629 (439.77 cm); SSS-23 (441.20cm); EC-20(441.87 cm); EG-83 (442.28 cm); EG-82 (445.42 cm); EG-81 (447.00 cm); CJV-16 (448.17 cm); IS-27072 (457.67 cm); NSJB-6585 (462.87 cm); NSJB-6657 (470.20 cm); NSJB-6662 (480.73 cm); EG-39 (486.38 cm); GGUB-68 (512.85 cm); SSS-15 (522.10 cm); Phule vasundhara (540.80 cm).

Table 4.1. Mean performance of 110 genotypes for 13 characters in Sorghum [*Sorghum bicolor* (L.) Moench]

S. No.	Genotype	DAF 50%	DM	PH	N.N.S	SG	PW	1000 GW	FSTK YD (T ha ⁻¹)	JY (1 ha ⁻¹)	Brix %	TSS	EY (1 ha ⁻¹)	GY (T ha ⁻¹)
1	CJV-07	74.00	110.33	431.07*	16.00*	1.63	27.80	28.25	53.75	12294.33*	10.67	9.48	640.04*	1.74
2	CJV-16	93.00*	127.33*	448.17*	19.00*	1.60	19.60	25.49	53.46	6182.71	6.00	5.40	177.72	0.98
3	CJV-17	81.67	117.67	306.03	14.33	2.24	24.17	37.18*	81.74*	6883.94	10.67	9.48	348.58	2.03
4	CJV-18	97.00*	132.67*	410.47	13.00	2.03	48.11*	27.38	77.47*	15348.13*	9.67	8.61	701.29*	3.99
5	CJV-19	85.67	107.67	414.92	16.00*	2.08	21.88	20.38	67.65*	16933.32*	9.00	8.02	723.29*	2.08
6	CJV-21	72.00	107.00	390.63	13.00	2.18	26.83	28.59	65.00*	10572.83*	9.33	8.31	487.81	2.48
7	CJV-24	101.33*	137.00*	395.57	18.33*	2.28	35.00	33.66	45.44	14092.33*	10.00	8.90	665.45*	2.93
8	CJV-25	77.33	118.33	224.67	11.00	2.54	45.19*	34.59	65.07*	6261.72	5.67	5.11	163.17	4.05
9	CJV-26	66.00	100.33	360.70	12.67	0.53	27.93	26.21	16.62	6607.40	6.67	5.98	210.85	2.07
10	DHBM-3	66.00	110.00	434.27*	12.67	1.85	51.13*	30.76	61.12*	6246.91	10.00	8.90	294.68	4.07
11	DHBM 5	70.00	115.00	409.07	13.67	2.20	38.20	28.49	34.27	5434.00	9.00	8.02	251.10	3.41
12	E-40	90.00*	135.00*	376.28	12.67	2.35	63.32*	33.11	66.86*	6824.68	6.67	5.98	219.97	4.34
13	E-63	89.00*	115.00	402.14	16.00*	2.57	49.17*	32.48	64.84*	10488.88*	9.00	8.02	452.64	4.82
14	EB-14	69.00	106.00	409.90	14.33	2.18	47.77*	19.05	41.47	5293.82	9.00	8.02	226.12	4.99
15	EB-15	92.00	118.00	414.58	11.33	2.27	43.50	27.95	36.06	8691.35	8.00	7.15	329.62	4.73
16	EB-19	85.67	121.33	391.87	14.33	2.23	42.83	16.03	58.56*	13832.08*	7.67	6.86	507.47	4.41
17	EB-20	75.33	114.33	340.91	11.00	2.57	49.97*	27.08	64.49*	13767.89*	9.33	8.31	609.42*	5.82
18	EB-22	55.00	87.00	415.08	11.00	0.33	46.90*	30.03	13.14	10893.82*	10.33	9.19	534.62	4.18
19	EC-15	77.00	116.67	338.74	14.00	1.62	50.79*	23.19	36.51	6399.67	7.33	6.57	226.00	4.03
20	EC-20	80.33	114.00	441.87*	12.33	0.84	26.13	32.00	21.88	4844.44	7.67	6.86	176.53	2.16
21	EC-22	67.33	106.00	428.67*	14.67	1.79	28.20	31.10	49.41	10242.46*	11.00	9.77	532.69	3.06
22	EC-23	112.67*	141.00*	394.33	14.00	2.63*	17.07	30.64	62.27*	9076.53	9.33	8.31	401.74	0.89
23	EC-25	76.33	110.00	367.50	15.00	2.51	28.90	23.16	67.57*	5698.76	13.33	11.81	358.71	2.08
24	EG-11	71.00	113.00	414.33	12.33	2.23	24.43	26.48	50.03	11249.37*	13.33	11.81	739.59*	2.13
25	EG-19	68.00	97.67	329.27	13.33	2.70*	20.83	28.50	63.65*	5767.90	7.33	6.57	218.76	0.81

Table 4.1 contd..

S. No.	Genotype	DAF 50%	DM	PH	N.N.S	SG	PW	1000 GW	FSTK YD (T ha ⁻¹)	JY (1 ha ⁻¹)	Brix %	TSS	EY (1 ha ⁻¹)	GY (T ha ⁻¹)
26	EG-21	66.00	93.33	322.31	12.00	2.29	32.18	22.81	68.11*	15506.16*	9.33	8.31	685.35*	2.33
27	EG-22	65.67	95.67	300.70	12.33	1.97	32.73	19.75	33.92	1876.54	7.67	6.86	68.98	2.53
28	EG-23	73.67	103.67	402.97	14.00	2.81*	17.08	28.46	77.70*	9644.43	7.33	6.57	340.23	0.75
29	EG-24	71.00	114.00	415.99	13.67	2.67*	37.57	26.95	65.29*	4044.44	8.00	7.15	156.18	3.87
30	EG-25	76.67	108.00	422.33*	14.33	2.42	19.71	28.70	71.97*	7649.38	5.00	4.52	182.42	0.74
31	EG-39	98.67*	138.33*	486.38*	13.33	2.41	18.81	21.38	60.46*	10172.83	7.33	6.57	356.25	0.68
32	EG-78	86.00	118.00	258.92	15.67*	2.74*	47.57*	20.07	84.26*	5841.97	10.33	9.19	285.61	4.22
33	EG-80	114.67*	159.00*	434.55*	16.67*	1.93	32.40	33.12	65.68*	3985.18	10.67	9.48	226.38	2.33
34	EG-81	86.67	116.00	447.00*	12.00	2.32	35.83	23.19	49.00	8807.52	4.00	3.65	182.68	3.28
35	EG-82	83.67	113.00	445.42*	15.33	2.24	44.37	16.97	62.86*	5782.71	7.33	6.57	218.95	3.93
36	EG-83	115.33*	145.33*	442.28*	19.67*	3.22*	64.47*	33.38	91.25*	4938.27	8.00	7.15	185.14	5.23
37	EG-84	82.67	116.00	386.30	13.00	0.74	38.47	25.44	22.23	8148.14	10.67	9.48	411.78	4.27
38	EP-29	74.00	120.00	191.67	13.00	2.27	41.27	23.04	47.51	7535.79	12.67	11.23	449.73	3.25
39	EP-61	73.67	105.00	341.02	16.67*	2.14	32.27	29.87	57.05	11619.74*	12.00	10.65	657.03*	3.34
40	EP-80	85.00	109.00	399.00	15.33	2.36	25.27	30.50	52.44	5032.09	8.00	7.15	191.51	1.62
41	EP-84	76.00	105.33	257.90	9.00	2.50	46.97*	30.29	58.27	12967.89*	9.33	8.31	572.65	5.12
42	GGUB-13	83.33	113.00	414.67	14.67	1.32	43.61	29.11	40.04	9535.79	9.33	8.31	429.14	4.63
43	GGUB-27	98.00*	129.00*	416.92	11.67	2.26	52.40*	23.82	65.28*	9654.31	9.00	8.02	412.90	5.02
44	GGUB-28	60.00	83.00	153.00	17.00*	3.32*	44.74	35.03	72.87*	16730.85*	9.00	8.02	718.07*	3.58
45	GGUB-29	55.00	81.00	315.40	11.00	1.90	37.17	33.14	39.11	8809.87	9.67	8.61	403.00	3.63
46	GGUB-33	88.33	122.33	411.47	14.67	2.28	36.70	14.54	48.96	5456.78	10.67	9.48	300.11	3.22
47	GGUB-43	83.00	128.00*	410.50	15.00	2.10	25.87	24.33	46.64	14567.89*	10.33	9.19	712.78*	2.04
48	GGUB-45	67.00	91.00	336.47	11.67	1.69	39.57	31.60	42.40	15688.87*	10.00	8.90	743.19*	2.48
49	GGUB-50	92.33*	124.33	383.92	14.00	1.84	47.88*	23.09	26.69	6829.62	9.67	8.61	314.28	4.40
50	GGUB-54	68.00	93.67	368.23	12.33	2.02	35.50	26.48	56.83	6074.07	9.67	8.61	278.85	3.68
51	GGUB-61	86.00*	114.00	424.50*	14.00	2.42	42.17	36.12	49.53	12982.70*	13.00	11.52	794.33*	3.81
52	GGUB-62	82.00	117.33	362.43	13.67	2.13	34.63	38.10*	46.79	8360.49	10.67	9.48	425.22	3.34

S. No.	Genotype	DAF 50%	DM	PH	N.N.S	SG	PW	1000 GW	FSTK YD (T ha ⁻¹)	JY (1 ha ⁻¹)	Brix %	TSS	EY (1 ha ⁻¹)	GY (T ha ⁻¹)
53	GGUB-63	112.33*	152.33*	410.81	15.00	2.07	21.60	37.29*	56.13	9654.31	13.00	11.52	592.19*	1.92
54	GGUB-64	86.00	107.33	390.33	14.00	2.20	27.92	27.48	55.07	15619.74*	13.33	11.81	983.47*	2.47
55	GGUB-65	90.33	120.00	415.63	15.33	1.42	27.13	37.95*	31.76	13738.26*	9.33	8.31	607.86*	2.75
56	GGUB-67	96.00	119.00	374.54	13.00	1.93	19.77	19.07	68.15*	12049.37*	10.67	9.48	608.24*	1.43
57	GGUB-68	73.00	106.00	512.85*	17.33*	1.53	36.67	35.23	49.54	10098.76	11.00	9.77	526.07	3.48
58	ICSSH-71	97.00	122.67	373.33	14.33	1.89	58.37*	34.23	45.22	12074.06*	12.67	11.23	721.62*	5.06
59	ICSV-12012	80.67	114.33	327.52	13.00	2.76*	38.38	31.11	83.52*	6246.91	14.33*	12.69*	428.36	3.43
60	ICSV-15006	83.33	118.00	315.93	13.00	3.23*	51.58*	29.36	89.95*	12377.44*	17.33*	15.31*	1018.67*	5.08
61	ICSV-25306	89.67	136.00*	362.83	13.33	1.75	49.73*	28.73	49.42	9362.95	9.33	8.31	419.91	5.09
62	ICSV-25308	97.33	136.00*	422.95*	13.00	2.10	42.57	28.65	49.46	5372.83	11.67	10.36	299.12	4.13
63	ICSV-25316	80.00	121.33	368.57	14.00	2.33	40.30	24.25	64.76*	8612.34	13.67	12.10	554.14	4.23
64	IS-1331	71.33	114.33	263.50	14.00	0.83	36.17	35.69	29.07	5451.85	11.00	9.77	282.77	3.12
65	IS-2337	68.67	109.00	408.00	14.67	1.83	36.77	31.96	35.54	10597.52*	6.00	5.40	304.30	3.59
66	IS-27072	112.00*	123.33	457.67*	20.33*	2.40	38.53	32.34	50.62	9362.95	9.00	8.02	401.47	3.34
67	IS-27239	72.00	104.33	376.50	15.00	1.97	45.50*	32.79	34.59	9985.18	9.00	8.02	446.75	4.19
68	IS-2814	74.67	116.67	241.63	16.33	1.67	71.50*	34.04	32.07	6444.44	10.00	8.90	304.24	5.68*
69	IS-2834	73.67	111.67	335.65	11.67	0.48	62.90*	44.62*	27.12	6162.96	15.00*	13.27*	435.22	4.88
70	IS-29308	76.67	124.00	389.13	13.33	1.73	47.28*	33.08	41.53	16597.51*	15.00*	13.27*	1173.29*	4.26
71	IS-29469	61.67	96.67	234.63	8.67	1.00	39.67	22.68	20.26	10207.40	9.33	8.31	466.68	3.37
72	IS-29650	54.00	87.67	255.80	10.00	1.49	42.77	38.76*	31.91	6681.47	8.00	7.15	240.16	4.01
73	IS-30310	66.00	94.00	107.67	10.33	0.52	45.30*	29.69	19.31	17185.17*	3.67	3.36	316.11	5.20*
74	IS-3515	72.00	105.00	329.27	11.33	1.58	15.07	30.86	33.15	7599.99	9.33	8.31	336.08	0.79
75	IS-3980	26.33	53.00	121.00	7.00	0.55	31.82	23.95	17.14	930.86	4	3.65	91.34	4.20
76	IS-4599	61.67	93.67	395.80	12.00	1.37	35.28	29.47	29.25	9333.32	11.33	10.06	526.86	3.04
77	IS-6910	55.33	86.00	185.90	7.33	1.93	42.30	28.72	32.06	22395.04*	6.67	5.98	713.26*	5.47*
78	IS-1474	68.00	111.00	300.83	13.00	1.77	50.61*	34.45	44.75	10967.89*	11.33	10.06	586.90	4.46
79	NSJB-6577	104.67*	141.33*	418.57	17.67*	2.87*	39.47	21.11	79.43*	8933.32	7.00	6.27	293.03	3.42

S. No.	Genotype	DAF 50%	DM	PH	N.N.S	SG	PW	1000 GW	FSTK YD (T ha ⁻¹)	JY (1 ha ⁻¹)	Brix %	TSS	EY (1 ha ⁻¹)	GY (T ha ⁻¹)
80	NSJB-6585	110.33*	144.33*	462.87*	22.00*	2.38	31.04	25.63	75.18*	10671.59*	9.00	8.02	455.44	2.49
81	NSJB-6605	85.00	122.67	386.37	16.33*	2.71	47.34*	33.33	77.30*	10869.12*	9.33	8.31	487.14	5.14*
82	NSJB-6629	113.33*	136.00*	439.77*	18.00*	2.32	26.18	35.96	68.58*	5209.87	8.00	7.15	199.52	2.20
83	NSJB-6648	110.00*	146.33*	271.00	19.67*	2.48	33.68	16.70	67.65*	6158.02	8.00	7.15	234.77	2.19
84	NSJB-6657	111.67*	147.00*	470.20*	21.67*	2.31	37.75	26.75	66.98*	12716.04*	8.00	7.15	482.79	3.25
85	NSJB-6662	108.33*	144.33*	480.73*	20.67*	2.80*	40.24	27.88	77.49*	9748.14	8.00	7.15	369.75	2.10
86	Phule vasundhara	113.33*	153.67*	540.80*	20.00*	3.06*	28.79	30.64	90.75*	6380.24	11.00	9.77	332.22	1.73
87	POP-15	54.33	89.67	388.00	13.00	0.22	16.79	34.45	16.03	9061.72	9.00	8.02	406.55	2.16
88	PV-12	89.00*	124.00	372.73	13.00	0.28	27.09	30.00	25.62	13283.94*	10.33	9.19	649.64*	1.67
89	PV-22	84.67	125.67	330.87	11.00	0.44	32.09	32.49	39.95	9471.60	9.33	8.31	420.23	4.29
90	RAJ-24	73.00	106.00	321.77	14.33	0.93	41.30	26.18	21.28	10943.20*	4.67	4.23	247.40	5.34*
91	RSSV-1381	83.67	125.33	288.67	12.00	2.07	47.63*	31.44	55.76	5195.06	14.00	12.40	342.12	5.02
92	SCVS 29	76.00	117.00	361.22	12.33	0.18	21.33	28.20	12.15	12338.31*	10.33	9.19	431.27	1.53
93	SEVS-04	75.00	118.00	406.83	13.33	1.91	33.94	28.39	47.15	5140.74	11.00	9.77	269.16	4.74
94	SEVS-08	80.00	133.33	411.67	13.00	1.25	17.31	29.66	45.27	27022.20*	10.00	8.90	1265.10*	1.38
95	SEVS-20	71.00	116.33	259.20	11.67	0.40	18.16	38.20*	40.51	10399.99*	8.67	7.73	428.50	0.46
96	SEVS-29	73.00	111.00	334.03	13.00	1.98	28.68	20.64	58.56*	12419.74*	7.67	6.86	452.55	3.18
97	SPV-2196	95.33*	135.67*	416.43	14.33	2.20	40.18	28.14	66.47*	6622.22	11.00	9.77	342.78	4.37
98	SPV-2325	76.00	117.00	361.22	12.33	0.18	40.48	28.20	12.15	13219.74*	10.33	9.19	644.83*	4.41
99	SPV-2328	71.33	109.00	323.87	11.67	1.43	40.41	28.16	46.94	10701.22*	8.00	7.15	406.23	3.78
100	SSS-10	87.00	128.33*	427.73*	15.00	2.18	43.52	32.74	64.25*	6118.51	10.00	8.90	291.17	4.69
101	SSS-14	83.67	123.67	396.15	15.00	2.14	33.59	29.48	63.62*	10483.94*	10.67	9.48	531.16	4.07
102	SSS-15	72.00	106.00	522.10*	17.67*	1.70	37.72	26.88	49.04	8123.45	10.67	9.48	409.90	4.52
103	SSS-23	88.00	124.67	441.20*	12.00	2.20	36.66	24.16	62.67*	12069.12*	9.33	8.31	489.45	3.29
104	SSS-46	86.67*	123.67	423.60*	16.00*	2.17	36.36	31.15	65.15*	9644.43	11.67	10.36	586.79*	3.69
105	SSS-62	88.33	122.33	336.50	17.00*	2.20	41.97	27.83	67.38*	16202.45*	12.00	10.65	917.21*	5.05

S. No.	Genotype	DAF 50%	DM	PH	N.N.S	SG	PW	1000 GW	FSTK YD (T ha ⁻¹)	JY (l ha ⁻¹)	Brix %	TSS	EY (l ha ⁻¹)	GY (T ha ⁻¹)
106	SSS-65	97.00*	133.33*	311.03	13.67	2.26	34.30	27.88	69.24*	6301.23	11.00	9.77	342.01	2.47
107	SSV-74	70.00	103.00	334.33	15.00	2.38	37.68	29.29	70.49*	14158.01*	15.00*	13.27*	1035.09*	4.82
108	SSV-84	72.00	108.00	372.93	15.00	2.62*	41.80	30.28	72.81*	4468.64	12.33	10.94	260.63	3.58
109	CSV-19SS ©	71.67	105.67	346.07	10.67	2.30	35.44	29.69	47.85	7980.24	12.33	10.94	464.14	3.87
110	CSV-24SS ©	84.00	121.67	357.13	13.67	1.13	36.61	31.43	35.20	5975.30	12.67	11.23	356.91	4.34
Mean		81.31	116.20	371.85	14.06	1.92	37.13	28.82	51.65	9613.78	9.78	8.70	449.35	3.40
Range	Lowest	26.33	53.00	107.67	7.00	0.18	15.07	14.54	12.15	1876.54	3.67	3.10	68.98	0.46
	Highest	115.33	159.00	540.80	22.00	3.32	71.50	44.62	91.25	27022.20	17.33	15.31	1265.10	5.68
SD		2.61	3.35	526.95	0.52	0.01	9.02	3.38	10.75	6147137.0	0.25	0.20	1737.06	0.08
SEM		2.79	3.17	39.75	1.24	0.2	5.2	3.18	5.67	4294.34	0.85	0.76	72.18	0.47
CD 5%		4.50	5.10	63.98	2.00	0.32	8.37	5.12	9.14	2214.92	1.41	1.23	116.17	0.77
CV %		3.44	2.72	10.74	8.89	10.31	14.01	11.04	11.07	14.31	8.94	8.79	16.07	14.32

DAF 50%= Days to 50% flowering (Days), **D.M**= Days to maturity (Days), **PH**= Plant height (cm), **N.N.S**= Number of nodes per plant, **S.G**= Stem girth (cm), **PW**= Panicle weight (g), **1000 GW**= 1000 grain weight (g), **FSTK**= Fresh stalk yield (T ha⁻¹), **JY**= Juice yield (T ha⁻¹), **Brix %**, **TSS** = Total soluble sugars (%), **EY**= Ethanol yield (T ha⁻¹), **GY** = Grain yield (T ha⁻¹).

Note: * Significant over superior check

4.1.1.4 Number of nodes per plant

The number of nodes ranged from 7.00 (IS-3980) to 22.00 (NSJB-6585) with a mean of 14.06 nodes per plant.

The number of nodes per plant represents the no of leaves and also contributes to the character plant height directly through internodal length and through the amount of Photosynthates produced indirectly. The following 23 genotypes viz., EG-78 (15.67 nodes); CJV-07, CJV-19, E-63, SSS-46 (16 nodes); NSJB-6605 (16.33 Nodes); EP-61, EG-80 (16.67 Nodes); SSS-62, GGUB-28 (17 Nodes); GGUB-68 (17.33 nodes); SSS-15, NSJB-6577 (17.67 Nodes); NSJB-6629 (18 nodes); CJV-24 (18.33 Nodes); CJV-16 (19 nodes); NSJB- 6648, EG-83 (19.67Nodes); Phule vasundhara (20 nodes), IS-27072 (20.33 nodes); NSJB-6662 (20.67nodes); NSJB-6657 (21.67 nodes); NSJB-6585 (22 nodes) have recorded significantly superior number of nodes per plant when compared to best check CSV-24SS (13.67 nodes).

4.1.1.5 Stem Girth (cm)

Thick stem accompanied by tall genotypes are the most suitable for high biomass production. The average stem girth ranged from 0.18 cm (SPV-2325) to 3.32cm (GGUB-28) with a mean value of 1.92cm.

Among the test entries 13 genotypes viz., SSV-84 (2.62 cm); EC -23 (2.63 cm); EG-24 (2.67 cm); EG-19 (2.70 cm); EG-78 (2.74 cm); ICSV-12012 (2.76 cm); NSJB-6662 (2.80cm); EG-23 (2.81 cm); NSJB – 6577 (2.87 cm); Phule vasundhara (3.06 cm); EG-83 (3.22 cm); ICSV-15006 (3.23cm); GGUB-28 (3.32 cm) have recorded significant superiority over the best check CSV-19SS (1.30 cm) in respect of stem girth.

4.1.1.6 Panicle weight (g)

Panicle weight ranged from 15.07 g (IS-3515) to 71.50 g (IS-2814) with a general mean of 37.13 g.

The following 25 test entries out of 110 genotypes viz., CJV-25 (45.19 g); IS-30310 (45.30 g); IS-27239 (45.50 g); EP-84 (46.97 g); EB-22 (46.90 g); IS-29308 (47.28 g); NSJB-6605 (47.34 g); EG-78 (47.57 g); RSSV-1381 (47.63 g); EB-14 (47.77 g); GGUB-50 (47.88 g); CJV-18 (48.11 g); E-63 (49.17 g); ICSV -25306 (49.73 g); EB-20(49.97 g); IS-1474 (50.61 g); EC-15 (50.79 g); DHBM-3 (51.13 g); ICSV-15006

(51.58 g); GGUB-27 (52.40 g); ICSSH-71 (58.37 g); IS- 2834 (62.90 g); E-40 (63.32 g); EG-83 (64.47 g); IS- 2814 (71.50 g); have witnessed superiority over superior check CSV-24SS (36.61g).

4.1.1.7 1000 grain weight (g)

The general mean for 1000 grain weight recorded was 28.82g, while the range varied from (14.54g) for the GGUB-33 genotype to (44.62g) for the genotype IS-2834, while higher 1000 grain weight is directly influencing grain yield and is desirable.

When compared with the best check CSV-24SS (31.43g) following seven genotypes were found to be significantly superior CJV-17 (37.18g); GGUB-63 (37.29g); GGUB-65 (37.95g); GGUB-62 (38.10g); SEVS-20 (38.20g); IS-29650 (38.76g) and IS-2834 (44.62g).

4.1.1.8 Fresh stalk yield (T ha⁻¹)

The character fresh stalk yield directly contributes to the higher biomass in any crop harvested for raw use of stem either for feeding the animals as green fodder or for extraction of juice for further processing. In this crop high biomass lines are desirable accompanied with high juice output and brix. The mean values of fresh stalk yield ranged from 12.15 T ha⁻¹ to 91.25 T ha⁻¹ with a general mean of 51.65 T ha⁻¹. The genotype EG-83 has recorded the highest (91.25 T ha⁻¹) fresh stalk yield while the genotype SPV-2326 has recorded the lowest (12.15T ha⁻¹).

The below mentioned 46 genotypes viz., SEVS-29 (58.56 T ha⁻¹); EB-19 (58.56 T ha⁻¹); EG-39 (60.46 T ha⁻¹); DHBM-3 (61.12 T ha⁻¹); EC-23 (62.27 T ha⁻¹); SSS-23 (62.67 T ha⁻¹); EG-82 (62.86 T ha⁻¹); SSS-14 (63.62 T ha⁻¹); EG-19 (63.65 T ha⁻¹); SSS-10 (64.25 T ha⁻¹); EB- 20 (64.69 T ha⁻¹); ICSV-25316 (64.76 T ha⁻¹); E-63 (64.84 T ha⁻¹); CJV-21 (65.00 T ha⁻¹); CJV-25 (65.07 T ha⁻¹); SSS-46 (65.15T ha⁻¹); GGUB-27 (65.28 T ha⁻¹); EG-24 (65.29 T ha⁻¹); EG-80 (65.68 T ha⁻¹); SPV-2196 (66.47 T ha⁻¹); E-40 (66.86 T ha⁻¹); NSJB- 6657 (66.98 T ha⁻¹); SSS-62 (67.38 T ha⁻¹); EC-25 (67.57 T ha⁻¹); CJV-19 (67.65 T ha⁻¹); NSJB- 6648 (67.65 T ha⁻¹); EG-21 (68.11 T ha⁻¹); GGUB-67(68.15 T ha⁻¹); NSJB- 6629 (68.58 T ha⁻¹); SSS-65 (69.24 T ha⁻¹); SSV-74 (70.49 T ha⁻¹); EG-25 (71.97 T ha⁻¹); SSV-84 (72.81 T ha⁻¹); GGUB-28 (72.87 T ha⁻¹); NSJB-6585 (75.18 T ha⁻¹); NSJB- 6605 (77.30 T ha⁻¹); CJV- 18 (77.47 T ha⁻¹); NSJB- 6662 (77.49 T ha⁻¹); EG-23 (77.70 T ha⁻¹); NSJB-6577 (79.43 T ha⁻¹) ; CJV-17 (81.74

T ha⁻¹); ICSV-12012 (83.52 T ha⁻¹); EG-78 (84.26 T ha⁻¹); ICSV-15006 (89.95 T ha⁻¹); Phule vasundhara (90.75 T ha⁻¹); EG-83 (91.25 T ha⁻¹); have recorded significantly higher stalk yields over the best check variety CSV-19SS (47.85T ha⁻¹)

4.1.1.9 Juice yield (l ha⁻¹)

Juice yield ranged from 1876 l ha⁻¹(EG-22) to 27022 l ha⁻¹ (SEVS-08) with a general mean of 9613.78 ha⁻¹. Juice yield being a metric measurement and quantitative trait and it effects the ethanol yield, combined with brix value. Hence high yielding genotypes for juice yield are desirable.

The subsequent 44 genotypes IS-29469 (10207.40 l ha⁻¹);EC-22 (10242.46 l ha⁻¹); SEVS-20 (10399.99 l ha⁻¹); SSS-14 (10483.94 l ha⁻¹); E-63 (10488.88 l ha⁻¹); CJV-21(10572.83l ha⁻¹); IS-2337 (10597.52 l ha⁻¹);NSJB-6585 (10671.59l ha⁻¹);SPV-2328 (10701.22 l ha⁻¹); NSJB-6605 (10869.12 l ha⁻¹);EB-22 (10893.82 l ha⁻¹);RAJ-24 (10943.20 l ha⁻¹); IS-1474 (10967.89 l ha⁻¹); EG-11 (11249.37 l ha⁻¹); EP-61 (11619.74 l ha⁻¹); GGUB-67 (12049.37 l ha⁻¹); SSS-23 (12069.12 l ha⁻¹); ICSSH-71 (12074.36 l ha⁻¹); CJV-07 (12294.33 l ha⁻¹); SCVS-29 (12338.31 l ha⁻¹); ICSV-15006 (12377.44 l ha⁻¹); SEVS-29 (12419.74 l ha⁻¹); NSJB-6657(12716.04 l ha⁻¹); EP-84 (12967.89l ha⁻¹); GGUB-61 (12982.70 l ha⁻¹);SPV-2325; (13219.74 l ha⁻¹); PV-12 (13283.94 l ha⁻¹); GGUB-65(13738.26 l ha⁻¹); EB-20 (13767.89 l ha⁻¹); EB-19 (13832.08 l ha⁻¹) ; CJV-24 (14092.33 l ha⁻¹);SSV-74 (14518.01 l ha⁻¹); GGUB-43 (14567.89 l ha⁻¹);CJV-18 (15348.13 l ha⁻¹); EG-21 (15506.16 l ha⁻¹); GGUB-64 (15619.74 l ha⁻¹); GGUB-45(15688.87 l ha⁻¹);SSS-62 (16202.45 l ha⁻¹); IS-29308 (16597.51 l ha⁻¹); GGUB-28 (16730.85 l ha⁻¹); CJV-19 (16933.32l ha⁻¹); IS-30310 (17185.17 l ha⁻¹); IS-6910 (22395.04 l ha⁻¹); SEVS-08 (27022.20 l ha⁻¹) which are ranking higher in performance when compared to the best check CSV -19SS (7980.24 l ha⁻¹).

4.1.1.10 Brix %

High brix is essential for maximizing the amount of sucrose and ethanol produced per unit area cultivated. The mean values for brix content ranged from 3.67 % (IS-30310) to 17.33 % (ICSV-15006) with a general mean of 9.78%.

There are few genotypes ICSV-12012 (14.33%); IS-2834 (15%); IS 29308 (15 %); SSV-74 (15 %) and ICSV-15006 (17.33%) which were found to contain superior level of brix % over and above the best check CSV-24SS (12.67%)

4.1.1.11 Total soluble sugars (%)

The average total sugars recorded was 8.70 % with a range of 3.10 to 15.31 for the similar genotypes as recorded in Brix values because it is derivative factor from brix. ICSV-12012 (12.69 %); IS-2834 (13.27 %); IS-29308 (13.27 %); SSV-74 (13.27 %) and ICSV-15006 (15.31 %) the above mentioned five genotypes were significantly superior to the best check variety CSV-24SS (11.23 %).

4.1.1.12 Ethanol yield (l ha⁻¹)

The average ethanol yield ranged from 69 l ha⁻¹ (EG-22) to 1265 l ha⁻¹ (SEVS-08), with a general mean of 449.35 l ha⁻¹. This calculation is based on the computed ethanol yield formulae which is dependent on brix and juice yield. The genotypes which showed best in the both traits contributed to the maximum ethanol yield as mentioned below

The following 26 genotypes SSS-46 (586.79 l ha⁻¹); GGUB -63 (592.19 l ha⁻¹); GGUB -65 (607.86 l ha⁻¹); GGUB -67 (608.24 l ha⁻¹); SPV-2325 (644.83 l ha⁻¹); IS-6910 (713.26 l ha⁻¹); ICSSH-71 (721.62 l ha⁻¹); EB-20 (609.42 l ha⁻¹); CJV-07 (640.04 l ha⁻¹); EP-61 (657.03 l ha⁻¹); CJV-24 (665.45 l ha⁻¹); EG-21 (685.35 l ha⁻¹); CJV-18 (701.29 l ha⁻¹); GGUB-43 (712.78 l ha⁻¹); GGUB-28 (718.07 l ha⁻¹); CJV-19 (723.29 l ha⁻¹); EG-11 (739.59 l ha⁻¹); GGUB -45 (743.19 l ha⁻¹); GGUB -61 (794.33 l ha⁻¹); ICSV-15006 (1018.67 l ha⁻¹); IS-29308 (1173.29 l ha⁻¹); SEVS-08 (1265.10 l ha⁻¹); PV-12 (649.64 l ha⁻¹); SSS-62 (917.21 l ha⁻¹); GGUB -64 (983.47 l ha⁻¹); (SSV-74 (1035.09 l ha⁻¹)) were found were significantly superior over the best check CSV-24SS (464.14 l ha⁻¹).

4.1.1.13 Grain yield (T ha⁻¹)

Bello *et al.* (2007) reported that the heritability of grain yield is due to the direct or indirect multiplicative effects of several yield components on grain yield. Grain yield ranged from 0.46 T ha⁻¹ to 5.68 T ha⁻¹ with a general mean of 3.40 T ha⁻¹. The genotype IS-2814 has recorded the highest grain yield while SEVS-20 recorded lowest grain yield.

NSJB-6605 (5.14 T ha⁻¹); IS-30310 (5.20 T ha⁻¹); IS-2814 (5.68 T ha⁻¹); RAJ-24 (5.34 T ha⁻¹) and IS-6910 (5.47 T ha⁻¹). The above mentioned genotypes have surpassed the best check variety CSV-24SS (4.34 T ha⁻¹).

4.1.2 Second Order Statistics of variability

4.1.2.1 Analysis of variance

Analysis of variance has revealed highly significant differences among the tested 110 genotypes in respect of all the traits (Table 4.2). The genotypes have also showed a wide range of variation in respect of 13 characters studied which provides ample scope for selection of superior and desirable genotypes for further genetic improvement as detailed in the succeeding paragraphs.

4.1.2.2 Genetic variability, Heritability and Genetic advance as per cent of mean

Progress in plant breeding depends on the extent of genetic variability present in a population. Therefore, the first step in any plant breeding program is the study of genetic variability, which cannot be easily measured. The phenotypic variability in a given environment can be measured easily, but it reflects both non genetic as well as the genetic influence on the phenotypic expression. Genetic facts are inferred from phenotypic observations, which are the results of interactions of a genotype in a given environment. GCV and PCV is only an evidence of the presence of high degree of genetic variation; however, the amount of heritable portion of variation can only be determined with the help of estimates of heritability and genetic advance.

In the current study the estimates of phenotypic coefficients of variation were slightly higher than genotypic coefficient of variation for all characters studied. This indicated that variability for these characters was due to genetic factors and there was less influence of environmental factor in expression of these characters. High values of PCV and GCV indicates that variation in the traits are contributed markedly to the total variability (Biradar *et al.*, 1996). The estimates of variability parameters for 13 characters in sorghum are presented in table 4.3.

4.1.2.2.1 Days to 50 % flowering (days)

Moderate estimate of GCV (19.22 %) and PCV (19.52 %) were observed for this character. These results are in accordance with Khandelwal *et al.* (2015); Bhagasara *et al.* (2017); Badigannavar *et al.* (2017) for GCV and PCV. Narrow difference observed between PCV and GCV indicate less influence of environment on this character. High heritability (97 %) coupled with high Genetic advance as per cent mean (38.97 %) were also observed for this trait. Similar results were reported by Kalpande *et al.* (2014); Nyadanu and Dikera (2014); Amare *et al.* (2015) and Swamy *et al.* (2018a) for heritability and genetic advance.

Table 4.2. Analysis of variance for 110 genotypes for 13 characters in Sorghum [*Sorghum bicolor* (L.) Moench]

S. No.	Source	Df	DAF 50% (Days)	DM (Days)	PH (cm)	N.N.S	SG (cm)	PW (g)	1000 GW (g)	FSTK T ha⁻¹	JY (l ha⁻¹)	Brix (%)	T.S.S (%)	EY (l ha⁻¹)	GY T ha⁻¹
1	Replications	2	11.05	21.45	2523.65	0.42	0.05	1.28	14.14	64.97	184718148.00	0.69	0.44	12862.06	0.03
2	Treatments	109	740.30*	857.65*	17258.28*	22.97*	1.60*	372.47*	85.68*	1151.41*	48380157.60*	17.12*	13.24*	148019.57*	5.16*
3	Error	218	7.82	10.05	1580.85	1.55	0.04	27.06	10.13	32.25	18441411.00	0.76	0.59	5211.17	0.23

NOTE: * and ** Significant at 5 and 1 per cent level respectively

4.1.2.2.2 Days to maturity (days)

The estimates of GCV and PCV for days to maturity were moderate (14.46 % & 14.72 %) respectively. Narrow range of values between GCV and PCV designate that the environment influence was less for this character. The heritability and genetic advance as percent mean were also high 97 % and 29.27 % respectively which may be useful to the plant breeders for making effective selection based on phenotype basis because of governance by additive genes. The results observed for GCV, PCV and GA are deviating from the results quoted by Iraddi *et al.* (2013) and Wadikar *et al.* (2018) while heritability results observed in the present study are similar with Iraddi *et al.* (2013) and Swamy *et al.* (2018a).

4.1.2.2.3 Plant height (cm)

The values of GCV (19.52 %) and PCV (22.28%) recorded for plant height was moderate and high respectively. High heritability (77%) coupled with high genetic advance as per cent of mean (33.93 %) as observed for this trait, is indicating that phenotypic selection may be effective due to presence of additive gene action. Similar findings were also observed by Muhammad *et al.* (2015); Amare *et al.* (2015); Badigannavar *et al.* (2017) and Ranjith *et al.* (2017) for high PCV, heritability and genetic advance.

4.1.2.2.4 Number of nodes per plant

The GCV (19.01 %), PCV (21.00 %) recorded for the number of nodes per plant were moderate and high respectively. High PCV indicates that this character is less influenced by the non-heritable forces such as environment. High heritability (82%) coupled with high genetic advance as per cent of mean (35.41%) as observed designate the predominant role of additive gene action in its genetic control and similar results were reported by sami *et al.* (2013) for moderate PCV and Iraddi *et al.* (2013) for high heritability and genetic advance.

4.1.2.2.5 Stem Girth (cm)

The observed GCV and PCV values were high (37.61 %), (38.99%) respectively with narrow range of difference. High heritability (93 %) coupled with high genetic advance as per cent of mean (73.95 %) are indicating the predominant role of additive gene action and the results are not in accordance with results reported by Tomar *et al.* (2012) and Irradi *et al.* (2013) for GCV and PCV and Heritability.

4.1.2.2.6 Panicle weight (g)

The estimates of GCV (28.90 %) and PCV (32.12 %) for Panicle weight were high (and the difference among these is moderate). High heritability (81 %) accompanied with high genetic advance as percent of mean (53.02 %) obtained for this trait is indicating the additive gene effects. A similar result was reported by Hamidou *et al.* (2018) and Swamy *et al.* (2018a) for heritability and genetic advance and Swamy *et al.* (2018a) for PCV and GCV.

4.1.2.2.7 1000 grain weight (g)

The character test weight has showed higher magnitude of difference between GCV & PCV values. However the moderate value of GCV (17.41%) and high estimates of PCV (20.62 %) were recorded for this character reveals that as a component of grain yield this trait has exhibited high heritability (71%) accompanied with high genetic advance as percent of mean (30.25%) indicating that variations are attributed to high level of additive gene effects. Similar results were already reported by Santosh *et al.* (2014); Mohamad *et al.* (2017) and Ranjith *et al.* (2017).

4.1.2.2.8 Fresh stalk yield (T ha⁻¹)

This character showed high GCV (37.50 %) and PCV (39.09%) with slight difference between these two duly indicating the lower portion of non-heritable forces. Contrary to this the high heritability (92%) accompanied with high genetic advance as percent of mean (73.73 %) obtained for this trait is indicating the maximum contribution of additive genes and thereby rendering selection for this trait is more effective. Tomar *et al.* (2012), Wadikar *et al.* (2018) for high GCV, PCV, Heritability and Genetic advance. Irradi *et al.* (2013), Kalpande *et al.* (2014) too outlined the replica of these results for High Genetic advance and heritability.

4.1.2.2.9 Juice yield (l ha⁻¹)

Very high GCV (40.95 %) and PCV (43.38%) with a higher magnitude of difference between the two was noted for this character. High heritability (89%) accompanied with High genetic advance as percent of mean (79.63 %) has highlighted that variation observed for this character is due to additive gene effects and hence offers a scope for improving this trait. Similar results were quoted by Tomar *et al.* (2012), Irradi *et al.* (2013) and Wadikar *et al.* (2018).

Table 4.3. Estimation of Variability, Heritability and Genetic advance per cent of mean for 13 characters in Sorghum [*Sorghum bicolor* (L.) Moench]

S. No.	Character	GCV (%)	PCV (%)	h ² (%)	GA	GA as% of mean (5 %)
1.	Days to 50 % Flowering (days)	19.22	19.52	97	31.69	38.97
2.	Days to maturity (days)	14.46	14.72	97	34.02	29.27
3.	Plant height (cm)	19.52	22.28	77	130.48	33.93
4.	Number of nodes per plant	19.01	21.00	82	4.97	35.41
5.	Stem girth (cm)	37.61	38.99	93	1.43	73.95
6.	Panicle weight (g)	28.90	32.12	81	19.89	53.02
7.	1000 grain weight (g)	17.41	20.62	71	8.73	30.25
8.	Fresh stalk yield (T ha ⁻¹)	37.50	39.09	92	38.17	73.73
9.	Juice yield (l ha ⁻¹)	40.95	43.38	89	7654.56	79.63
10.	Brix %	23.87	25.49	88	4.50	46.01
11.	Total soluble sugars	23.62	25.20	88	3.97	45.51
12.	Ethanol yield (l ha ⁻¹)	48.58	51.17	90	426.70	93.23
13.	Grain yield (T ha ⁻¹)	37.91	40.52	88	2.47	73.07

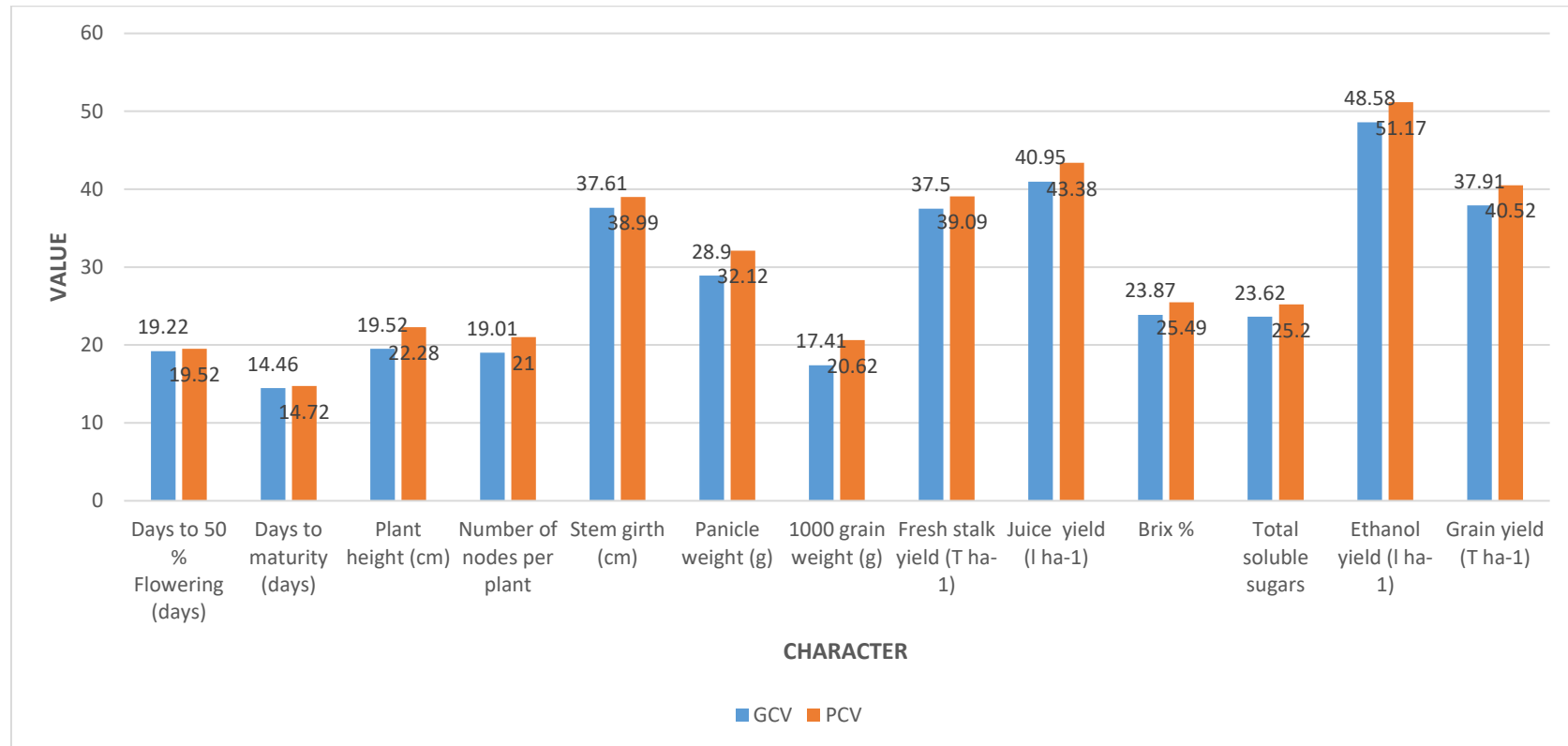


Fig. 4.1.1. Graph depicting the Genotypic and Phenotypic coefficient Values for thirteen characters.

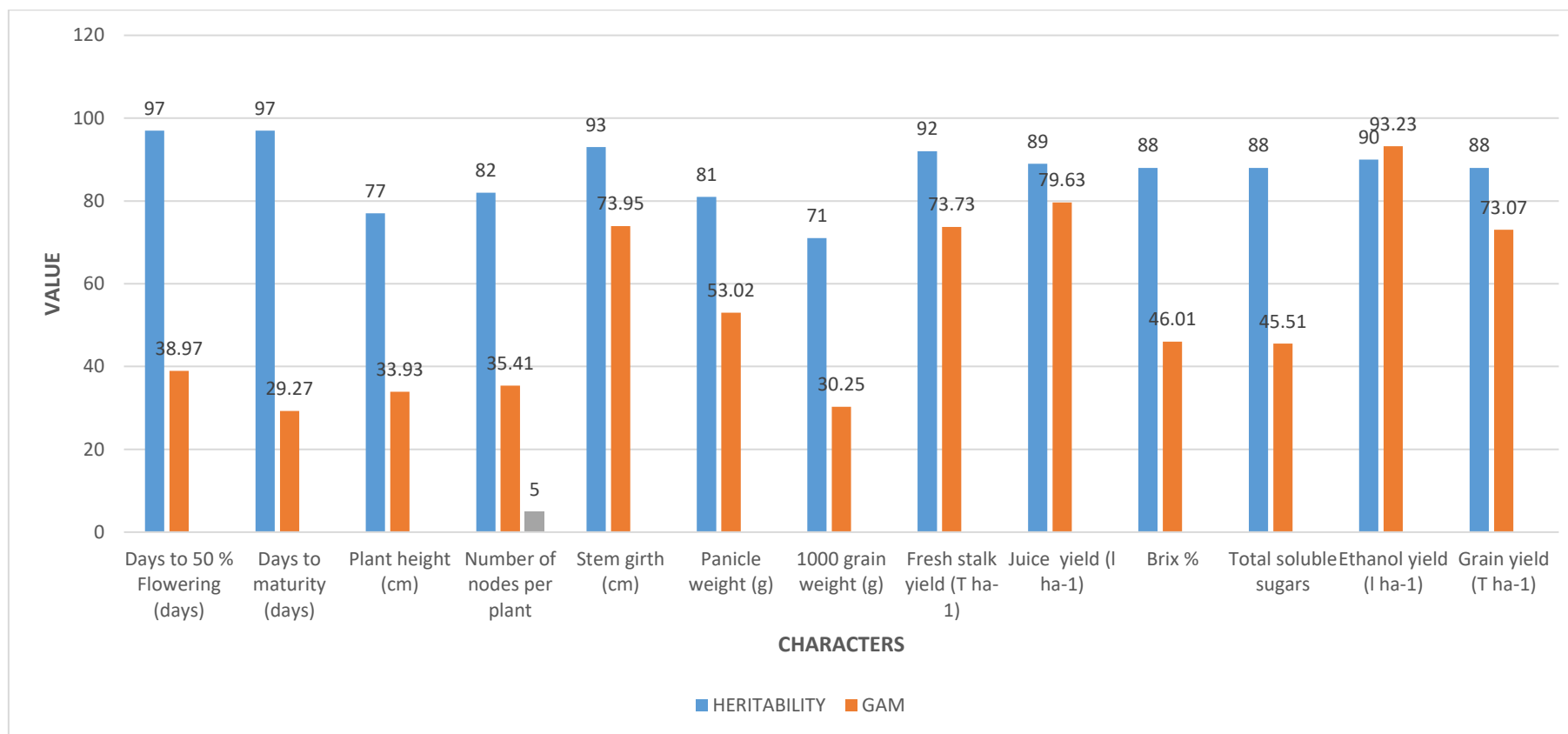


Fig. 4.1.2. Graph depicting the Heritability and Genetic Advance per mean for thirteen characters.

4.1.2.2.10 Brix %

The estimated GCV (23.87 %) and PCV (25.49 %) were high revealing that the genotypes have a broad based genetic background as well as good potential that will respond positively to selection for sucrose yield. High heritability (88 %) accompanied with high genetic advance as percent of mean (46.01%) as observed for this trait is rendering phenotypic selection effective as reported earlier by Tomar *et al.* (2012) and Irradi *et al.* (2013) for high heritability only.

4.1.2.2.11 Total Soluble Sugars (%)

The estimates of GCV (23.62%) and PCV (25.20%) for this character were high with only a moderate difference between the values. High heritability (88 %) accompanied with high genetic advance as percent of mean (45.51%) was obtained for this trait indicating the governance by additive genes making selection more effective. Sami *et al.* (2018) also reported similar results

4.1.2.2.12 Ethanol yield (l ha⁻¹)

The values recorded for both GCV (48.58 %) and PCV (51.17 %) are high and maximum difference between them is only indicating the presence of high environmental influence. High heritability (90 %) accompanied with high genetic advance as percent of mean (93.23 %) observed for this trait is making breeding methods operative due to additive gene action. These results are in accordance with Irradi *et al.* (2013) for high heritability only.

4.1.2.2.13 Grain yield (T ha⁻¹)

The recorded GCV (37.91 %) and PCV (40.52 %) values with a higher magnitude of difference is only indicating the role of environmental influences. High heritability (88 %) accompanied with high genetic advance as percent of mean (73.07 %) observed for this trait is making phenotypic selection more effective due to the additive gene action. Dhutmal *et al.* (2014), Amare *et al.* (2015), Kalpande *et al.* (2014), Rekha and Biradar (2015), (2015) and Swamy *et al.* (2018a) too experienced the similar results for this trait.

Conclusion: Estimates of PCV were narrowly higher than the corresponding GCV values for the characters days to 50 % flowering, days to maturity and Stem girth (cm). Bhagasara *et al.* (2017), Badigannavar *et al.* (2017) observed similar results. The number of nodes per plant, grain yield (T ha^{-1}), fresh stalk yield (T ha^{-1}), brix %, T.S.S (%), juice yield (l ha^{-1}) and ethanol yield (l ha^{-1}) have moderate differences between PCV and GCV values while rest of the characters viz., plant height (cm), 1000 grain weight (g), panicle weight (g) have shown a higher magnitude of difference between GCV and PCV. Narrow and moderate difference between PCV and GCV duly indicated lower environment influence on these characters. Therefore, phenotypic selection alone is effective for the improvement of these traits and selection based on phenotypic performance could be worth in achieving desired results.

The results of heritability act as a predictive tool in expressing the real potential of phenotypic value. Therefore, high heritability helps in predictive selection for a desirable character. Heritability in broad sense is the ratio of genotypic variance to the phenotypic variance and is expressed in percentage. In this current study, all 13 quantitative characters studied have shown high heritability which is clearly indicating, the scope for genetic improvement of these characters through phenotypic selection. If the value of heritability in broad sense is high, it indicates that though the character is least operative by the environmental effects, the selection for enhancement of such character at times may not be useful, because broad sense heritability is based on total genetic variance which includes both fixable (additive) and non- fixable (dominance and epistasis) variances.

On the other hand, if the estimates of genetic advance are high, it shows that the character is dominated by additive genes and hence selection shall be fruitful for the improvement of such trait. So high heritability guided with high genetic advance, indicates most likely the heritability is due to additive gene effect and selection may be rewarding.

In the present investigation, high heritability coupled with high genetic advance as percent of mean was observed for all the 13 characters studied Thus, these traits are predominantly under the control of additive gene action and hence these characters can be improved by selection. Tomar *et al.* (2012), Irradi *et al.* (2013), Kalpande *et al.* (2014), Sami *et al.* (2018) and Wadikar *et al.* (2018) have also reported results which are in accordance with above mentioned results.

4.2 DIVERSITY STUDIES

In any crop improvement plan of action, the prior condition for hybridization programme is the availability of genetic diversity for the desired character. The involvement of genetically diverse lines as parents would result in the creation of superior recombinants (Shinde *et al.* 2013). An effort has been made in the present investigation to study the genetic diversity amongst the randomly acquired 110 genotypes of sorghum [*Sorghum bicolor* (L.) Moench] for thirteen characters. The results of the study thus obtained are presented and discussed below under the following heads.

4.2.1 Wilk's 'V' criterion test

Wilk's 'V' (Statistical) criterion was used to test the significant differences between the groups based on the pooled effects for all the characters. The significance of 'V' (Statistical) value was tested by % at 1417 degrees of freedom. The 'V' statistic value was highly significant indicating that the genotypes differed significantly when all the characters were considered simultaneously.

The analysis of variance for dispersion had clearly indicated the significant pooled effect of all the characters between 110 studied genotypes. Hence, further studies were initiated to estimate D² analysis.

4.2.2 Mahalanobis Generalized Distance D² values

The correlated unstandardized means for 13 quantitative characters studied have been transformed into standardized uncorrelated set of variables by using pivotal condensation method. The statistical distance (Mahalanobis D² values) between a pair of genotypes was obtained as sum of squares of differences between pairs of corresponding uncorrelated values of any two genotypes. These values were considered one at a time and were used in the final grouping of genotypes.

4.2.3 Grouping of Genotypes into Various Clusters (D² analysis)

The studied 110 genotypes were grouped into eight clusters indicating the presence of a wide range of genetic diversity. Cluster- I, among the 8 clusters was possessing the highest number of genotypes (*i.e.*, 78) indicating the genetic similarity

among them and is followed by Cluster-III with 15 genotypes, Cluster - II with 12 genotypes, Cluster-IV, V, VI, VII, VIII are monogenotypic indicating the uniqueness of the genotypes included in those clusters when compared to other genotypes included in the study (Table: 4.4 and Fig: 4.1). The results obtained are collinear with the results of Mahajan and Wadikar (2012); Khadakabhavi *et al.* (2014); Sinha and Kumaravadivel (2016).

Clustering pattern has also revealed that the genotype EC-23 (from A.P), EG-83 (from Tamil Nadu), PHULE VASUNDHARA (from MPKV, Rahuri), GGUB-62 (from Madhya Pradesh), IS-27072 (from Zimbabwe) are originating from different Agro climatic sources and yet were grouped into a single cluster (*i.e.* cluster -II). While genotypes of GGUB series (16 genotypes) are from one single source (*i.e.* M.P, India) were grouped into different clusters *viz.*, (cluster -I, II, III, VI). It denotes that cluster may accommodate the genotypes from different origins or genotypes from different origins may be grouped into single cluster. It confirms that geographic diversity is not fully reflected in genetic diversity. This also indicates there is a wide variability present among the genotypes though collected from a single source and the reason for variability could be introgression of alleles between the contrasting populations present in the same region. Harlan (1975). Murty and Arunachalam (1966) have stated that genetic drift and selection in different environments could cause greater genetic diversity than geographical distance. Such unparallelism between geographic and genetic diversity was also reported by Kadam *et al.* (2001); Meena *et al.* (2016); Damor *et al.* (2017); More *et al.* (2018); Swamy *et al.* (2018b).

Contrary to the above quoted statement, 9 out of 10 entries of CJV series from same source were confined to cluster- I and the remaining one in cluster- II, NSJB series comprising total 6 genotypes from a single source (Khammam, India) and yet confined to cluster-II only, without any distribution. The possibility could be either attributed to the common ancestor of these genotypes having same pedigree or due to unidirectional selection pressure that could have been imposed on the genotypes. Further, the free exchange of seed material among different regions might have consequently caused character constellations because of human interference and material may lose its individuality. Such un-distribution of genotypes was also reported by Swamy *et al.* (2018b).

Table 4.4. Grouping of 110 Sorghum [*Sorghum bicolor* (L.) Moench] genotypes into 8 clusters

Cluster	No of genotypes	Name ` of genotypes
1	78	CJV-07,CJV-16, CJV-17, CJV-18,CJV-19,CJV-21,CJV-24,CJV-25; DHBM-3; DHBM-5; E-40, E-63; EB-14, EB-15, EB-19, EB-20, EC-15, EC-20, EC-22, EC-25; EG-11, EG-19, EG-21, EG-22, EG-23, EG-24, EG-25, EG-39, EG-78, EG-81, EG-82, EG-84; EP-29, EP-61, EP-80, EP-84; GGUB-13, GGUB-27, GGUB-33, GGUB-43, GGUB-45, GGUB-50, GGUB-54, GGUB-61, GGUB-63, GGUB-64,GGUB-65, GGUB-67, GGUB-68; ICSSH-71; ICSV-12012, ICSV-25306, ICSV-25308, ICSV-25316; IS-1331, IS-2337, IS-27239, IS-2814, IS-3515, IS-1474; NSJB-6605; PV-22; RSSV-1381; SEVS-29, SEVS-04, SEVS-20, SEVS-29; SPV-2196, SPV-2328; SSS-10,SSS-14, SSS-15,SSS-23, SSS-46, SSS-62, SSS-65, SSV-74, SSV-84.
2	12	NSJB-6585, 6662,6657,6577,6648, 6629, EC-23, EG-83, EG-80,Phule Vasundhra, GGUB-62, IS-27072
3	15	EB-22,POP-15,CJV-26,IS-4599, IS-29469, IS-29650, RAJ-24, CSV-19SS,SPV-2325, GGUB-29, IS-2834, CSV-24SS, PV-12, IS-30310, IS-6910
4	1	IS-29308
5	1	ICSV-15006
6	1	GGUB-28
7	1	SEVS-08
8	1	IS-3980

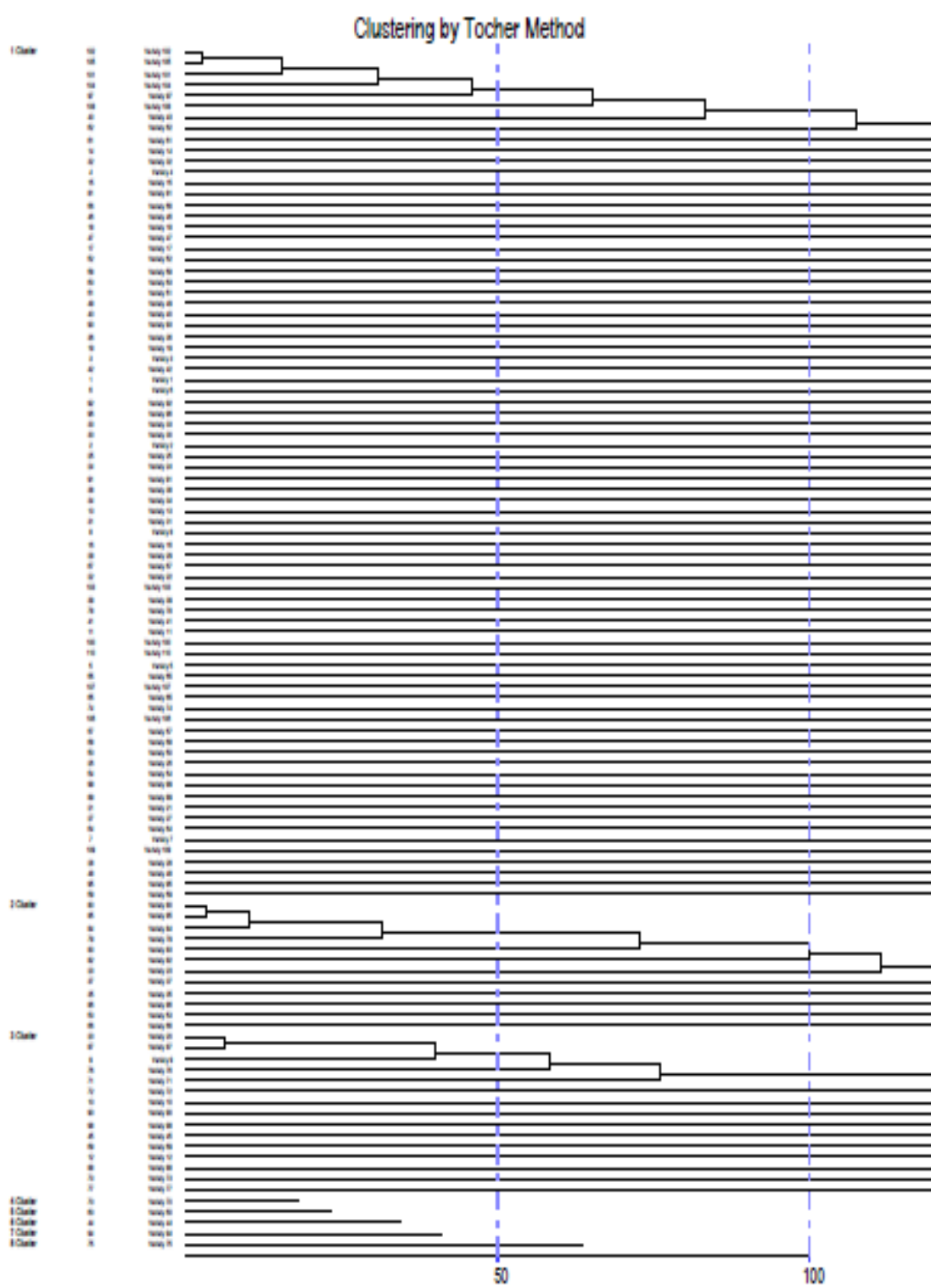


Fig. 4.2. Grouping of 110 Sorghum genotypes into 8 clusters by Tocher's method

4.2.4 Average intra and inter cluster distances

The average intra and inter-cluster values among the eight clusters are presented in Table 4.5. The intra-cluster distances were lower than the inter-cluster distances. Rohman *et al.* (2004); Sameerkumar *et al.* (2010) obtained the same results as mentioned above. Thus the genotypes included within a cluster had less diversity among themselves. The maximum intra-cluster distance (54.16) was observed in cluster III followed by cluster I (39.49), cluster II (26.98) and Cluster IV, V, VI, VII, VIII (0.00). Similar results are in accordance with Shinde *et al.* (2013). It indicated that these accessions were closely related in their evolutionary process and passed through similar evolutionary factors. The genotypes placed within the cluster were less divergent. This might be due to unidirectional selection practised in past that has resulted in uniformity and less divergence between these genotypes.

The highest inter-cluster distance (596.33) was observed between cluster II having the genotypes NSJB-6585, NSJB-6629 (Table 4.3) possessing more plant height, number of nodes, juice yield, fresh stalk yield, ethanol yield over the best check significantly and cluster VIII having IS-3980 which is early maturing (53 days) among the 110 genotypes studied. Therefore crossing between NSJB-6585, NSJB- 6629 with IS-3980 could yield an early maturing, high biomass types with high juice extraction and ethanol yield. This is closely followed by cluster V having a single genotype ICSV-15006 with high stem girth, panicle weight, Fresh stalk yield, brix, juice and ethanol yield and cluster-VIII (406.92) possessing IS-3980 an early maturing genotype, if a crossing programme is attempted between these two genotypes that could result in an early maturing, high biomass and brix, ethanol yielding segregants.

The cluster VII is again a monogenotypic cluster constituting the genotype SEVS-08 with high juice yield and ethanol yield and cluster VIII (406.31) possessing IS-3980 an early maturing genotype, Crossing between these two genotypes could reward an early maturing, ethanol yielding segregants, while the lowest inter cluster distance (50.54) was observed between cluster IV and cluster VII. The genotypes belonging to these clusters were separated by high statistical distance and the genotypes having high *per se* performance should be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, genotypes from cluster V, VI, VII, VIII should be selected as parents in hybridization programme for yield improvement. These findings are in conformity with the findings of Bahadure *et al.* (2014), Elangovan *et al.* (2014), Doijad *et al.* (2016), Prasad and Biradar (2017a).

Table 4.5. Intra and inter cluster distances in 110 Sorghum [*Sorghum bicolor* (L.) Moench] genotypes tested

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	39.49	103.13	93.09	66.15	80.15	108.14	101.85	273.98
Cluster 2		26.98	255.74	115.67	98.58	248.44	134.60	596.33
Cluster 3			54.16	123.11	205.14	144.94	149.37	146.92
Cluster 4				0.00	87.44	141.91	50.54	326.11
Cluster 5					0.00	122.17	171.93	406.92
Cluster 6						0.00	192.45	193.69
Cluster 7							0.00	406.31
Cluster 8								0.00

The genotypes grouped into same cluster have displayed the lowest degree of divergence from one another, and in case crosses are made between genotypes belonging to the same cluster, no transgressive segregant is expected from such combinations. Therefore, hybridization programmes should always be formulated in such a way that the parents belonging to different clusters with maximum divergence could be utilized to get desirable transgressive segregants. The genotypes for hybridization may be chosen from widely separated clusters, as it is observed that there are single genotypes included in the crossing programme from widely separated clusters. Intercrossing of divergent groups would lead to wide genetic base in the base population and greater opportunities for crossing over to occur, which in turn may release the hidden variability by breaking close linkage. Results are collinear with results of Tomar and Sivakumar (2012a) and Sameerkumar *et al.* (2010).

The nearest and the farthest clusters were presented in Table 4.6. As mentioned in the Table: 4.7, the cluster I was lined up with a huge heterogeneous populations. So, attempting crossing between genotypes of cluster I with cluster VIII genotype IS-3980 may result in early maturing, high biomass, ethanol yielding types, apart from the ethanol yielding, forage type sorghum varieties can also be developed. IS-3980 where flowering duration is 23 days can result in the development of extra early sorghum variety. The genotype in cluster IV *i.e.*, IS-29308 had high brix content and high panicle weight could be used for the development of a dual purpose sorghum grain and ethanol.

Cluster II was very close to cluster V, while far from Cluster VIII having the genotype IS-3980 and Cluster –II genotypes are high biomass types and late maturing type, could be improved for this trait when crossed with IS-3980. When cluster II genotypes were crossed with cluster V genotype (ICSV-15006) there is less scope for transgressive segregants.

Table 4.6. The nearest and farthest clusters from each cluster based on D² values in 110 Sorghum [*Sorghum bicolor* (L.) Moench] genotypes

S. No.	Cluster	Nearer Cluster	Farthest Cluster
1	I	IV (66.15)	VIII (273.98)
2	II	V (98.58)	VIII (596.33)
3	III	I (93.09)	II (255.74)
4	IV	VII (50.54)	VIII (326.11)
5	V	IV (87.44)	VIII (406.92)
6	VI	I (108.14)	II (248.44)
7	VII	IV (50.54)	VIII (406.31)
8	VIII	III (146.92)	V (406.92)

Table 4.7. Cluster-I holding the genotypes which are significant for certain characters

S. No.	Significant characters	Genotype
1	DAF 50 %, DM, P.W, FSTK	DHBM-3
2	DAF, DM, FSTK, JY, EY	EG-21
3	DAF, DM, PW, JY, EY	GGUB-45
4	PW,JY,EY	CJV-18
5	N.N.S, FSTK, JY,EY	CJV-19
6	PH, FSTK	EG-39
7	PH, PW, FSTK	EG-82
8	PH, N.N.S	GGUB-68
9	N.N.S, P.W, GY, JY	NSJB-6605
10	PH, N.N.S	SSS-10
11	PH,N.N.S	SSS-15
12	N.N.S, P.W, FSTK, GY	E-63
13	N.N.S, EY	CJV-24
14	FSTK, GY,EY	SSS-62
15	PW, GY, BRIX, TSS, JY,EY	SSV-84
16	PW,GY	SCVS-29
17	GY, BRIX, TSS	RSSV-1381

S. No.	Significant characters	Genotype
18	PW,GY,FSTK	IS-7474
19	PW,GY,JY	RAJ-24
20	PW,GY	IS-4599
21	DM,SG, FSTK	EG-19
22	PH,JY,EY	CJV-07
23	S.G, FSTK	EG-23
24	S.G,P.W,FSTK	EG-78
25	S.G,FSTK,BRIX, TSS	ICSV-12012
26	P.W,GY,JY	EB-14
27	P.W,GY,JY,EY	EB-20
28	FSTK, J.Y	SEVS-29
29	JY,GY	EP-84
30	JY,EY	EG-11;EG-21;EP-61;GGUB-43;GGUB-45;GGUB-61;GGUB-64;GGUB-65;GGUB-67;ICSSH-71; PV-12; SSV-84,SSV-74

Cluster III was nearer to cluster I, crossing among these could be less divergent resulting in segregating off spring, with little scope for improvement, while crossing with cluster II would yield intermediate types to both the parents.

The nearest cluster for cluster IV (genotype IS-29308) was VII (SEVS-08), farthest cluster was VIII (IS-3980) and crossing with this cluster could yield early maturing. Cluster V was farer to cluster VIII (IS-3980) was nearer to cluster – IV (IS-29308). Cluster VI was nearer to cluster –I and farer to cluster II crossing with genotypes of farer cluster would result in transgressive segregants. Cluster VII was nearer to cluster IV (IS-29308), farer to Cluster VIII (IS-3980), cluster VIII was nearer to cluster III, While farer to cluster V. These results were not in accordance with results of reported by Bahadure *et al.* (2014), Damor *et al* (2017) and More *et al.* (2018).

4.2.5 Cluster means of characters

The cluster means for different characters are presented in Table-4.8. The lowest means for days to 50 % flowering and days to maturity are observed in cluster VIII (26.33, 53.00) respectively for a solitary genotypes IS-3980 an early maturing one but significantly poorer in performance in other 11 characters studied. Cluster VI (57.00, 83.00) possessing the genotypes GGUB-28 having significant values for high biomass, early maturing and ethanol yield traits and Cluster III (66.40, 100.00) respectively.

Cluster means for number of nodes was highest in cluster II (18.78), followed by cluster VII (17.00) and lowest in cluster VIII (12.00).

The cluster II has recorded the highest mean for plant height (435.30) while the lowest in cluster VI (153.00).

Fresh stalk yield recorded highest in cluster V (89.95) followed by cluster- II (72.87), cluster-III (71.00), cluster-I (54.28) and lowest in cluster-III (22.30).

Cluster means for character stem girth was highest in cluster- VI (3.32) followed by cluster-V (3.23).

Grain yield recorded maximum in cluster- II (3.33) followed by cluster- III (3.10), cluster IV- (2.97), cluster V and VII (2.53).

1000 Grain weight recorded highest means in cluster- VI (35.03) followed by cluster- IV (33.08) while the lowest in cluster- I (28.33).

The highest means for panicle weight was recorded in cluster- IV (44.17), V (39.20), II (35.45, while the lowest in VI (25.77).

Cluster V (17.33) recorded the highest value for brix % and total sugars estimation followed by cluster- IV (15.00), VIII (11.33), VII (10.00).

Juice yield recorded the highest means in cluster – VII (27022.20) followed by cluster- VI (16730.85) whereas the lowest in Cluster – II (8069.54).

Table 4.8. Cluster means for 13 characters studied in 110 Sorghum [*Sorghum bicolor* (L.) Moench] genotypes

	DAF 50 %	D.M	PH	N.N.S	SG	PW	1000 GW	FSTK	JY	BRIX	TSS	EY	GY	SCORE	RANK
Cluster 1	80.78 (5)	115.84 (4)	373.83 (5)	13.86 (3)	2.03 (4)	33.86 (5)	28.33 (8)	54.28 (4)	9079.93 (6)	9.81 (5)	8.73 (5)	427.43 (6)	2.97 (3)	63	5
Cluster 2	111.56 (1)	114.50 (5)	435.30 (1)	18.78 (1)	2.54 (3)	35.45 (3)	29.29 (7)	71.00 (3)	8069.54 (8)	9.08 (7)	8.10 (7)	347.87 (8)	3.33 (1)	55	4
Cluster 3	66.40 (6)	100.00 (6)	317.14 (6)	11.29 (7)	0.80 (7)	32.17 (6)	30.84 (3)	22.30 (8)	10310.77 (4)	9.40 (6)	8.37 (6)	427.30 (7)	3.10 (2)	74	8
Cluster 4	95.00 (2)	116.33 (3)	389.13 (3)	13.33 (4)	1.73 (5)	44.17 (1)	33.08 (2)	41.53 (6)	16597.51 (3)	15.00 (2)	13.27 (2)	1173.29 (2)	2.60 (5)	40	1
Cluster 5	87.33 (4)	118.00 (2)	315.93 (7)	13.00 (5)	3.23 (2)	39.20 (2)	29.36 (6)	89.95 (1)	8548.14 (7)	17.33 (1)	15.31 (1)	695.53 (4)	2.53 (6)	48	2
Cluster 6	57.00 (7)	83.00 (7)	153.00 (8)	17.00 (2)	3.32 (1)	25.77 (8)	35.03 (1)	72.87 (2)	16730.85 (2)	9.00 (8)	8.02 (8)	718.07 (3)	2.03 (7)	64	6
Cluster 7	93.67 (3)	133.33 (1)	411.67 (2)	13.00 (5)	1.25 (6)	30.64 (7)	29.66 (4)	45.27 (5)	27022.20 (1)	10.00 (4)	8.90 (4)	1265.11 (1)	2.53 (6)	54	3
Cluster 8	26.33 (8)	53.00 (8)	387.67 (4)	12.00 (6)	0.73 (8)	35.15 (4)	29.47 (5)	29.25 (7)	9333.32 (5)	11.33 (3)	10.06 (3)	526.87 (5)	2.87 (4)	70	7

DAF 50%= Days to 50% flowering (Days), **D.M**= Days to maturity (Days), **PH**= Plant height (cm), **N.N.S**= Number of nodes per plant, **SG**= Stem girth (cm), **PW**= Panicle weight (g), **1000 GW**= 1000 grain weight (g), **FSTK**= Fresh stalk yield (T ha⁻¹), **JY**= Juice yield (l ha⁻¹), **Brix %**, **TSS** = Total soluble sugars (%), **EY**= Ethanol yield (l ha⁻¹), **GY** = Grain yield (T ha⁻¹).

The character ethanol yield has recorded the highest value in cluster VII (1265.11) followed by cluster IV (1173.29) and cluster VI (718.07) and cluster V (695.53) whereas the lowest is recorded in cluster –II (347.87). All 110 genotypes were spread over 8 clusters and means were scored across the clusters for all the 13 characters, and this is given in Table 4.8. The highest cluster mean was given the first rank and next cluster is possessing next best means were given 2nd, 3rd and so on up to 8th rank for all the traits. Finally, the clusters are ranked based on the overall score obtained from 13 characters. The lowest scoring cluster was given the first rank, and next cluster is possessing the score above the previous ones were given 2nd, 3rd and so on up to 8th rank. Figures in the parenthesis, indicate the ranks/grade based on cluster mean. The grade given the largest to the smallest.

The cluster IV ranked first with a score of 40 having one genotype IS-29308 showing significant superiority in aspect of brix and high biomass type and cluster V, ranked second with a score of 48 each possessing the genotype ICSV-15006 which is having desirable characteristics like high biomass, brix, juice and ethanol yield. This genotype can be tested across years and locations and if found stable and high yielding can be released as new variety. Cluster VII in third position with genotype SEVS-08 has significant juice and ethanol yield can be ameliorated for other characters like, brix content.

The next best cluster was Cluster-II holding the genotypes NSJB-6585, NSJB-6662, NSJB-6657, NSJB-6577, NSJB-6648, NSJB-6629, EC-23, EG-83, EG-80, Phule Vasundhara, GGUB-62, IS-27072 which were promising to be high biomass types. Cluster–I was heterogeneous with a mixed combination of characters which are significant over the best check. (Table 4.7). Cluster VI at next position with genotype GGUB-28 with high biomass, juice and ethanol yield but can be facelifted for brix content.

Cluster –III had multifarious genotypes like POP-15, CJV-26, IS-29469, IS-29650, GGUB-29 which fall into early maturing group While SPV-2326, PV-12, RAJ-24 for high juice content, EB-22 for juice yield, early maturing and IS-6910 early maturing, High panicle weight, grain yield, juice yield; IS-30310 outraged for grain yield, juice yield; IS-2834 for exorbitant panicle weight, 1000 grain weight, juice yield, brix, grain yield, ethanol yield.

The clusters IV, V, VI, VII and VIII have recorded high mean performance for various characters. Hence the genotypes selected from these clusters can be used as parents in hybridization. Based on cluster means a wide range of variation was observed for ethanol yield and other traits in sweet sorghum. Therefore, it is suggested that lines from most diverse clusters may be used as parents in hybridization programme to develop high yielding hybrids or varieties. It has been well established that the more genetically diverse parents used in hybridization programme, the greater will be the chances of obtaining high heterotic hybrids and broad spectrum of variability in segregating generations. It has also been observed that the most productive hybrids may come from high yielding parents with high genetic diversity. Similar type of results were given by Tomar and Sivakumar (2012a) and Swamy *et al.* (2018b).

4.2.6 Percent contribution of character towards divergence in 110 Sorghum genotypes

The contribution of each character towards total genetic diversity is presented in Table 4.9. Out of 13 characters studied, stem girth has contributed maximum (22.49 %) to the genetic divergence followed by days to maturity (22.2 %), days to 50 % flowering (19.58 %), juice yield (10.39%), brix % (9.89%) followed by fresh stalk weight (7.02%), number of nodes (2.42%), 1000 grain weight (2.22%), plant height (1.48%), ethanol yield (1.32%), grain yield (0.82%), panicle weight (0.17%) whereas total soluble sugars (0%) didn't contribute to the divergence. Similar results are reported by Rohman *et al.* (2004); Tomar and Sivakumar (2012a) and Elangovan *et al.* (2014). In the current study, these above mentioned characters were liable for genetic divergence in the ranking order. Selection of parents for hybridization programme on the basis of these characters stem girth, days to maturity, days to 50 % flowering, juice yield, brix %, panicle weight, grain yield, ethanol yield, plant height. 1000 grain weight, number of nodes, stalk weight could yield better segregants.

Conclusion: Though widely diverse clusters are desirable for hybridization, the selection of parents for crossing programme was done based on cluster means because male sterile lines have been used in the present hybridization programme. The cluster means for brix %, juice yield, ethanol yield were considered as criteria for crossing diverse parents *i.e.*, genotypes from these following clusters cluster IV, cluster V, cluster VI, cluster VII and cluster VIII were selected for hybridization programme. All the above mentioned clusters are solitary.

Table 4.9. Contribution of 13 quantitative characters to divergence studies in Sorghum [*Sorghum bicolor* (L.) Moench] genotypes

S.No.	Source	Contribution	% times ranked first
1	DAF	19.58%	1174
2	DM	22.2%	1331
3	PH	1.48%	89
4	N.N.S	2.42%	145
5	SG	22.49%	1348
6	PW	0.17%	10
7	1000 GW	2.22%	133
8	FSTK	7.02%	421
9	JY	10.39%	623
10	BRIX	9.89%	593
11	TSS	0.00%	--
12	EY	1.32%	79
13	GY	0.82%	49

DAF 50%= Days to 50% flowering (Days), **D.M**= Days to maturity (Days), **PH**= Plant height (cm), **N.N.S**= Number of nodes per plant, **SG**= Stem girth (cm), **PW**= Panicle weight (g), **1000 GW**= 1000 grain weight (g), **FSTK**= Fresh stalk yield (T ha⁻¹), **JY**= Juice yield (l ha⁻¹), **Brix %**, **TSS** = Total soluble sugars (%), **EY**= Ethanol yield (l ha⁻¹), **GY** = Grain yield (T ha⁻¹).

4.3 CORRELATION STUDIES

In a crop species there is every need for developing new varieties with high yield potential and suitable for the prevailing location specific Agro-ecological conditions where the crop is under cultivation. This in turn demands a need for identifying a suitable strategy required for obtaining high yield potential. In addition, the mutual interactions of each character over the other character plays an important role, because characters showing association in a determining fashion play a vital role in the selection of varieties. Correlation coefficients are used to determine the degree and direction of a number of characters/ variables association or relationships among to be examined while path analyses is utilized to determine in detail the direct and indirect contribution of several independent characters on a dependent trait. Correlation analysis in plant breeding is expected to offer precise information pertaining to various yield components and there by facilitate breeders to select superior genotypes from diverse genetic populations.

In the present study Phenotypic and genotypic correlations were worked out on ethanol yield and 12 other yield contributing characters in 110 diverse sorghum genotypes. Results of the study revealed that most of genotypic correlations were found to be higher than phenotypic correlations, which indicate that though there is strong inherent association between characters studied, its expression is minimized due to influence of environment. The insignificant values of studied characters at both phenotypic and genotypic levels clearly indicates the independent nature of the character. The results are furnished in Table: 4.10.

4.3.1 Days to 50 % Flowering (days)

Days to 50 % flowering recorded a positive significant correlation with Days to maturity (0.9384G, 0.9046 P), Number of nodes (0.6217G, 0.5479P), Plant height (0.4632 G, 0.3952 P), Fresh stalk yield (0.4735 G, 0.4439 P), Stem girth (0.3883 G, 3578 P), Grain yield (0.1510 G, 0.1221 P) and Panicle weight (0.2215 G, 0.1551 P). A non-significant association with brix per cent (0.0100 G, 0.0083 P) and total soluble sugars (0.0099 G, 0.0085P). Negative non-significant correlation with 1000 grain weight (-0.0721 G, -0.0628 P), juice yield (-0.0627 G, -0.0577 P) and ethanol yield (-0.0266 G, -0.0242 P). Based on the above presented results, it can be inferred that selection of early maturing types could bring improvement in the grain yield only as it has positive association but not in the juice and ethanol content as the association is negative which means conversion of sucrose requires time so medium to late flowering types are preferred for ethanol purpose.

Based on the mean values (Table:4.3), the genotype CJV-24 (101.33 days); SEVS-08 (93.67 days) and IS-29308 (95 days) is desirable for medium to late flowering with high juice yield and brix signifying the selection for high ethanol yield would be possible in medium to late duration genotypes. These results are in accordance with Jimmy *et al.* (2017) and Swamy *et al.* (2018a).

Table 4.10. Genotypic and phenotypic correlations for 13 characters in 110 sorghum [*Sorghum bicolor* (L.) Moench] genotypes

		DAF 50 %	D.M	N.N.S	PH	FSTK	S.G	GY	1000 GW	PW	BRIX	TSS	JY	EY
DAF 50 %	G	1.0000	0.9384**	0.6217**	0.4632**	0.4735**	0.3883**	0.1510**	-0.0721	0.2215**	0.0100	0.0099	-0.0627	-0.0266
	P	1.0000	0.9046**	0.5479**	0.3952**	0.4439**	0.3578**	0.1221*	-0.0628	0.1551**	0.0083	0.0085	-0.0577	-0.0242
D.M	G		1.0000	0.5595**	0.4145**	0.4390**	0.3119**	0.1101*	-0.0531	0.1425**	0.0376	0.0374	-0.1293*	-0.0819
	P		1.0000	0.4946**	0.3525**	0.4134**	0.2921**	0.0895	-0.0339	0.0910	0.0345	0.0348	-0.1206*	-0.0770
N.N.S	G			1.0000	0.5326**	0.4760**	0.3779**	0.0553	-0.0565	0.1429**	-0.0020	-0.0027	-0.1410**	-0.0666
	P			1.0000	0.4280**	0.3975**	0.3342**	0.0525	-0.0313	0.0551	-0.0020	-0.0007	-0.1364*	-0.0721
P.H	G				1.0000	0.2264**	0.1581**	0.0386	-0.1225*	0.2768**	0.0036	0.0034	-0.1426**	-0.0469
	P				1.0000	0.1856**	0.1363*	0.0318	-0.0801	0.1329*	0.0089	0.0093	-0.1146*	-0.0327
FSTK	G					1.0000	0.8719**	0.1083*	-0.1543**	0.2450**	0.0920	0.0918	-0.0464	0.0169
	P					1.0000	0.7990**	0.0948	-0.1337*	0.1558**	0.0823	0.0828	-0.0394	0.0181
S.G	G						1.0000	0.1302*	-0.2263**	0.2476**	0.0107	0.0109	-0.0763	-0.0404
	P						1.0000	0.0919	-0.1908**	0.1488**	0.0055	0.0049	-0.0622	-0.0349
GY	G							1.0000	-0.0453	0.7853**	-0.1273*	-0.1309*	-0.0843	-0.1820**
	P							1.0000	-0.0260	0.4850**	-0.0932	-0.0882	-0.0803	-0.1589**
1000 GW	G								1.0000	-0.0240	0.2345**	0.2345**	-0.0209	0.0848
	P								1.0000	-0.0407	0.1836**	0.1838**	0.0198	0.0622
PW	G									1.0000	0.0530	0.0538	-0.0391	-0.0102
	P									1.0000	0.0512	0.0501	-0.0220	0.0068
BRIX	G										1.0000	1.0003	-0.0245	0.4781**
	P										1.0000	0.9995**	-0.0213	0.4825**
TSS	G											1.0000	-0.0237	0.4788**
	P											1.0000	-0.0226	0.4812**
JY	G												1.0000	0.8383**
	P												1.0000	0.8284**
EY	G													1.0000
	P													1.0000

DAF 50%= Days to 50% flowering (Days), D.M= Days to maturity (Days), PH= Plant height (cm), N.N.S= Number of nodes per plant, SG= Stem girth (cm), PW= Panicle weight (g), 1000 GW= 1000 grain weight (g), FSTK= Fresh stalk yield (T ha⁻¹), JY= Juice yield (l ha⁻¹), Brix %, TSS = Total soluble sugars (%), EY= Ethanol yield (l ha⁻¹), GY = Grain yield (T ha⁻¹).

NOTE:* and ** Significant at 5 and 1 per cent level respectively

4.3.2 Days to maturity (days)

Results of the study revealed a significant positive association of days to maturity with number of nodes (0.5595G, 0.4946P), Plant height (0.4145 G, 0.3525 P), fresh stalk yield (0.4390 G, 0.4134P), Stem girth (0.3119 G, 0.2921P) at both phenotypic and genotypic levels facilitates simultaneous improvement of both the characters. Non-significant correlation was observed with brix (0.0376 G, 0.0345 P), Total soluble sugars (0.0374 G, 0.0348P) at both levels. The negative significant association with Juice yield (-0.1293 G, -0.1206 P) and negative non-significant association with 1000 grain weight (-0.0531G, -0.0339 P), ethanol yield (-0.0819 G, -0.0770P) was observed which clearly spells out that some economic compromise is a must.

This result signifies that selection for early maturity may result in high grain yield which is advantageous to drought prone areas at the cost of compromising for juice and ethanol yield. Swamy *et al.* (2018a) and Hundekar *et al.* (2016) reported similar results for grain yield. Therefore, selection for medium to late maturing types possessing high brix and juice yield which is desirable. The genotypes GGUB-65 (120.00 days), EB-19 (121.33 days), SEVS-08 (133.33 days), CJV -24 (137 days) has the desirable characters as mentioned. Vemana *et al.* (2014) had quoted negative association with juice yield which is deviating from the current result.

4.3.3 Plant height (cm)

This character exhibited positive significant correlation with Fresh stalk yield (0.2264 G, 0.1856 P), stem girth (0.1581 G, 0.1363 P), and panicle weight (0.2768 G, 0.1329 P) at both genotypic and phenotypic levels are expected to bring simultaneous improvement in these characters. Grain yield (0.0386 G, 0.0318 P), brix per cent (0.0036 G, 0.0089 P), Total soluble sugars (0.0034 P, 0.0093 G) had nonsignificant contribution. Negative significant correlation was recorded for juice yield (-0.1426 G, -0.1146P) at both phenotypic and genotypic levels, may hinder simultaneous expression of both these characters, while nonsignificant correlation was recorded for ethanol yield (-0.0469 P, -0.0327 G) and 1000 grain weight at phenotypic level (-0.0801 P).

The desirable trait is more plant height and high biomass producing types. Since the association of plant height with brix and ethanol yield is significantly negative, which means tall genotypes have recorded low brix and ethanol yield. E.g. CJV-16

(448.17cm) had brix of 6 % with ethanol yield (177.72 l ha^{-1}). The results recorded by Hundekar *et al.* (2016) and Makanda (2017) are deviating from the above quoted results. However, by making a little bit compromise for medium tall, plant type with more stem girth and biomass yield such as mentioned below are desirable. Eg- EB-20 (Plant height of 340.91 cm with stem girth (2.57 cm) and fresh stalk weight of (64.49 T ha^{-1}), EG-21 (Plant height of 322.31 cm with stem girth (2.29 cm) and fresh stalk weight of (68.11 T ha^{-1}),

4.3.4 Number of nodes per plant

The trait number of nodes per plant has recorded significant positive correlation with plant height (0.5326G, 0.4280P), Fresh stalk yield (0.4760 G, 0.3975 P), Stem girth (0.3779G, 0.3342P) at dual levels of phenotypic and genotypic while panicle weight (0.1429 G) only at genotypic level. A non-Significant positive correlation was observed with panicle weight (0.0551 P) at phenotypic level, grain yield (0.0553 G, 0.0525 P) at both phenotypic and genotypic levels. Negative significant association with Juice yield (-0.1410 G, -0.1364 P) and negative non-significant association was recorded for 1000 grain weight (-0.0565 G, -0.0313 P), brix % (-0.0020 G, -0.0020 P), total soluble sugars (-0.0027 G, -0.0007 P) and ethanol yield (-0.0666G, -0.0721P).

When the desired selection criteria is for a high biomass type then, plant height can be considered as advantageous because genotypes with maximum number of nodes and stem girth could yield high biomass types but again compromising for juice and ethanol yield. The genotypes GGUB-68, IS-27072, NSJB-6577, SSS-10, SSS-15 PHULE VASUNDHARA, NSJB-6662 (Means table: 4.1) are possessing significant plant height and number of nodes, direct selection from these genotypes could be made desirable if the criteria is for high biomass type. But with ethanol and juice yield the association being negative which indicates tall types are not preferable.

The below mentioned genotypes were few examples for medium plant height with high juice and ethanol yields. EG-21 (Plant height of 322.31cm with 12 nodes per plant , $15506.16 \text{ l ha}^{-1}$ juice yield and 685.35 l ha^{-1} ethanol yield), Vemana *et al.* (2014) observed a quite different result showing positive association with juice and brix content

4.3.5 Stem girth (cm)

Stem girth has recorded positive significant correlation with panicle weight (0.2476 G, 0.1488 P) at both phenotypic and genotypic levels and grain yield (0.1302 G) at genotypic level only. While non-significant correlation was recorded with brix % (0.0107 G, 0.0055 P), Total soluble sugars (0.0109 G, 0.0049 P). A negative significant correlation was reported with 1000 grain weight (-0.2263 G, -0.1908 P). Further a Negative non-significant correlation of stem girth was recorded with juice yield (-0.0763 G, -0.0622 P), Ethanol yield (-0.0404 G, -0.0349 P) at both levels.

Though this character has contributed to the divergence maximum, but juice and ethanol yield had negative association with this trait while brix content has positive correlation with stem girth. The genotypes ICSV-12012, EG-23 and EG-19 have significant stem girth and Fresh stalk yield with high brix and low juice and ethanol yield. (Means table: 4.3). The results are in accordance with Tomar and Sivakumar (2012b).

4.3.6 Panicle Weight (cm)

Positive non-significant correlation was observed with brix per cent (0.0530 G, 0.0512 P), total soluble sugars (0.0538 G, 0.0501 P) at both levels and with ethanol yield (0.0068 P) at phenotypic level only. Character juice yield (-0.0391 G, -0.0220 P) and ethanol yield (-0.0102 G) displayed negative non-significant correlation.

This character contributes to the grain yield per plant with high brix but poor juice and ethanol yield. RSSV-1381 has similar combination of characters. Chalachew and Rebuma (2018); Mulualem *et al.* (2018) and Swamy *et al.* (2018 a) had shown similar results with grain yield per plant.

4.3.7 1000 Grain weight (g)

This character has recorded significant positive correlation with brix % (0.2345 G, 0.1836 P), Total soluble sugars (0.2345 G, 0.1838 P) and nonsignificant correlation with ethanol yield (0.0848 G, 0.0622 P) at both levels while juice yield at phenotypic level (0.0198 P) only. Negative non-significant correlation with panicle weight (-0.0240G, -0.0407 P), juice yield (-0.0209 G) at genotypic level respectively.

This character has contributed negative correlation with grain yield and positive correlation with brix and juice and ethanol yield. Khakabhavi *et al.* (2017) and Deshmukh *et al.* (2018) recorded deviating results from the above quoted results.

4.3.8 Fresh stalk yield (T ha⁻¹)

This character has shown positive non-significant association with brix (0.0920 G, 0.0823 P), Total soluble sugars (0.0918 G, 0.0828 P), ethanol yield (0.0169 G, 0.0181 P) and positive significant association with stem girth (0.8719 G, 0.7990 P), Panicle weight (0.2450 G, 0.1558 P). Negative significant association was recorded for 1000 grain weight (-0.1543 G, -0.1337 P), Negative non-significant correlation was recorded for juice yield (-0.0464 G, -0.0394 P).

Juice yield had shown negative contribution with this trait, positive association with brix and ethanol content. ICSV-12012 was a high biomass type with high brix and ethanol yield. (Means table: 4.3). Results quoted here are deviating from the results given by Vemana *et al.* (2014).

4.3.9 Juice yield (l ha⁻¹)

Juice yield has recorded positive significant contribution with ethanol yield (0.8383 G, 0.8284 P) at both the levels.

This character directly contributes to the ethanol yield and simultaneous improvement could be possible because of positive association. EG-11, EG-21, EP-61, GGUB-43, GGUB-45, GGUB-61, GGUB-64, GGUB-65, GGUB-67, ICSSSH-71, PV-12, SSV-74 (means table 4.3) has significant juice and ethanol yields. Similar results are reported by Chalachew and Rebuma (2018), for ethanol yield while contradictory result to brix content.

4.3.10 Brix %

This character has shown significant positive correlation with ethanol yield (-0.4781 G, 0.4825 P), total soluble sugars (0.9995 P) at phenotypic level while positive non-significant (1.0003 G) at genotypic level. Negative non-significant correlation was observed with juice yield (-0.0245 G, -0.0213 P) at both the levels.

Simultaneous improvement of the genotype for ethanol yield is possible by increasing the brix and total soluble sugars. The results displayed are not in tune with findings of Vemana *et al.* (2014).

4.3.11 Total soluble sugars (%)

This character also recorded positive significant correlation with ethanol yield (0.4788 G, 0.4812 P) and negative non-significant association was observed for juice yield (-0.0237 G, -0.0226 P) at both levels. The results are in accordance with the results of brix content as it is a derived factor from Brix directly. Shukla *et al.* (2017) reported that total soluble sugars had negative association with ethanol yield.

4.3.12 Ethanol yield (l ha⁻¹)

The dependant variable ethanol yield has recorded positive significant correlation with Brix per cent, (0.4781 G, 0.4825 P); Total soluble sugars (0.4788 G, 0.4812 P) and Juice yield (0.8383 G, 0.8284 P) while negative significant association was with grain yield (-0.1820 G, -0.1589P) and non -significant positive association with Fresh stalk yield (0.0169 G, 0.0181 P), 1000 grain weight (0.0848 G, 0.0622 P) at both levels and Panicle weight (0.0068 P) at phenotypic level only. Negative non-significant association with days to 50 % flowering (-0.0266 G, -0.0242 P), days to maturity (-0.0819 G, -0.0770 P), plant height (-0.0469 G, -0.0327 P), number of nodes (-0.0666 G, -0.0721 P), Stem girth (-0.0404 G, -0.0349 P) at both levels and panicle weight (-0.0102 G) at genotypic level.

These results are in accordance with findings of Vemana *et al.* (2014), Chalachew and Rebuma (2018).

4.3.13 Grain yield (T ha⁻¹)

Recorded positive significant contribution with panicle weight (0.7853 G, 0.4850 P) at both phenotypic and genotypic levels, no character was found for positive non-significant. Negative significant correlation was observed for ethanol yield at both levels (-0.1820 G, -0.1589P) while for brix (-0.1273 G) and total soluble sugars (-0.1309 P) only at genotypic level. Negative non-significant for 1000 grain weight (-0.0453 G, -0.0260 P), juice yield (-0.0843 G, -0.0803 P) at both levels, brix (-0.0932 P), Total soluble sugars (-0.0882 P) at phenotypic level only.

It clearly indicate that simultaneous improvement of grain yield and ethanol yield couldn't be possible because they have a negative association with brix, juice and ethanol yield. E-63, EG-83, IS-7474, SCVS-29 had similar combination of characters. The results given are in accordance with Makanda *et al.* (2017).

Conclusion: Simultaneous improvement of the traits like brix, juice yield and ethanol yield is possible as they are showing positive correlation. Since most of the studied genotypes have possessed only one or two characters in combination such as brix and ethanol with poor juice content or juice and ethanol with low brix. Plant height had shown negative correlation with ethanol yield hence intermediate types could be preferred. High biomass types are preferred for ethanol content, but they are poor juice yielders with high brix content. Grain yield had positive correlation with brix but not with juice and ethanol content. Simultaneous improvement of these traits could be hampered.

The possible reason for these type of combinations like high brix with high grain yield might have maximum conversion of sugars to the grain sink compromising on the juice yield. High biomass types with high plant heights would have maximum utilization of the plant energy for vegetative growth where nothing is left for conversion of sugars which results in low brix content. Hence based on these results, the below mentioned genotypes have been selected along with divergence results for attempting the crossing programme. GGUB-28 had intermediate plant height with high juice content, ICSV-15006 had high brix & juice yield with intermediate plant height, contributing to the ethanol content. SEVS-08 had high juice yield with high plant height. IS-29308 having high brix with intermediate juice and ethanol content.

4.4 PATH COEFFICIENT ANALYSIS

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. Whereas the correlation studies offer relation between two variables only. Since the analysis offer the estimation of direct effects of various characters on yield in addition to the indirect effects via other component traits. This objective was incorporated in the present study to aid in indirect selection *i.e.*, selection of components for bringing in yield improvement and there by select superior genotypes from diverse breeding populations.

The data collected from replicated trials on thirteen polygenic traits in 110 sorghum genotypes was subjected to statistical analysis described by Dewey and Lu, 1959 has revealed the

- (i) Direct effect (effect of an independent character on dependent character)
- (ii) Indirect effect (effect from independent character on dependent character via other independent characters and
- (iii) Residual effect (effect of other possible independent variables not included in the study on dependent variables)

A path diagram is constructed using simple correlation coefficients among the characters included in the study to depict the cause and effect situation in a simple yet attractive presentation of results and association between different traits and helps in understanding the direct and indirect contribution of different independent variables against a dependent variable *i.e.*, ethanol yield in addition to the estimation of direct effects through simultaneous equations.

Based on the importance of phenotypic effects, the present results of phenotypic and genotypic path coefficient ethanol yield and yield contributing characters are presented in the Table 4.11 and depicted in fig: 4.2, 4.3 and discussed here under character wise.

4.4.1 Days to 50 % flowering (days)

Days to 50 % flowering had negative direct effect on ethanol yield (-0.0266 G, -0.0242 P) at both phenotypic and genotypic levels, while correlation studies of this character has shown the similar results. This could be possibly due to the indirect negative effect of days to maturity (-0.0465 G, -0.0515 P); Fresh stalk yield (-0.0272 G, -0.0063 P); Juice yield (-0.0536 G, -0.0485 P) at both genotypic and phenotypic levels while brix % (-0.0012 G) at genotypic level only. Therefore indirect selection through such traits as mentioned above will lead to yield improvement.

Further, early flowering types have low ethanol yield due to the low biomass, juice yield and brix content. Based on the means table (4.3), the genotypes ICSV-15006 (83.33 days), SSS-62 (88.333 days), SSS-14 (83.67 days), PV-12 (89 days), SEVS-08 (93.67 days), IS-29308 (95 days), CJV-18 (97 days), CJV-24 (101.33 days), GGUB-67

(96 days) are desirable for medium to late flowering and high juice yield and brix content and there by signifying the selection for high ethanol yield would be possible only in medium to late flowering genotypes. These results are in accordance with Jimmy *et al.* (2017), Swamy *et al.* (2018b).

4.4.2 Days to maturity (days)

Days to maturity also exhibited negative direct effect on ethanol yield (-0.0819 G, -0.0770 P), whereas association of this character to ethanol yield was non-significant negative. This could be due to the negative indirect effect of days to maturity (-0.0496 G, -0.0570 P); Fresh stalk yield (-0.0252 G, -0.0058 P); grain yield (-0.0090 G, -0.0053 P); Juice yield (-0.1105 G, -0.1014 P) at both genotypic and phenotypic levels while brix content at genotypic level (-0.0045 G) only.

Table 4.11. Phenotypic (P) and Genotypic (G) Path coefficient analysis indicating direct (bold and diagonal) and indirect effects of Characters on ethanol yield in 110 sorghum [*Sorghum bicolor* (L.) Moench] genotypes

		DAF 50 %	D.M	N.N.S	PH	FSTK	S.G	GY	1000 GW	P.W	BRIX	TSS	JY	EY
DAF 50 %	G	0.0268	-0.0465	0.0282	0.0248	-0.0272	0.0186	-0.0124	0.0004	0.0095	-0.0012	0.0061	-0.0536	-0.0266
	P	0.0406	-0.0515	0.0171	0.0195	-0.0063	0.0043	-0.0072	0.0005	0.0030	0.0018	0.0024	-0.0485	-0.0242
D.M	G	0.0252	-0.0496	0.0254	0.0222	-0.0252	0.0149	-0.0090	0.0003	0.0061	-0.0045	0.0229	-0.1105	-0.0819
	P	0.0368	-0.0570	0.0155	0.0174	-0.0058	0.0035	-0.0053	0.0003	0.0018	0.0076	0.0097	-0.1014	-0.0770
N.N.S	G	0.0167	-0.0277	0.0453	0.0285	-0.0274	0.0181	-0.0045	0.0003	0.0061	0.0002	-0.0017	-0.1205	-0.0666
	P	0.0223	-0.0282	0.0313	0.0212	-0.0056	0.0040	-0.0031	0.0002	0.0011	-0.0004	-0.0002	-0.1146	-0.0721
PH	G	0.0124	-0.0205	0.0242	0.0535	-0.0130	0.0076	-0.0032	0.0007	0.0118	-0.0004	0.0021	-0.1219	-0.0469
	P	0.0161	-0.0201	0.0134	0.0494	-0.0026	0.0017	-0.0019	0.0006	0.0026	0.0020	0.0026	-0.0964	-0.0327
FSTK	G	0.0127	-0.0218	0.0216	0.0121	-0.0575	0.0417	-0.0089	0.0008	0.0105	-0.0111	0.0563	-0.0396	0.0169
	P	0.0180	-0.0235	0.0124	0.0092	-0.0141	0.0097	-0.0056	0.0010	0.0030	0.0181	0.0230	-0.0331	0.0181
S.G	G	0.0104	-0.0155	0.0171	0.0085	-0.0501	0.0479	0.0062	-0.0118	0.0118	0.0005	0.0005	-0.0037	-0.0404
	P	0.0145	-0.0166	0.0105	0.0067	-0.0113	0.0121	0.0011	-0.0023	0.0018	0.0001	0.0001	-0.0008	-0.0349
GY	G	0.0041	-0.0055	0.0025	0.0021	-0.0089	0.0062	-0.0818	0.0002	0.0336	0.0153	-0.0803	-0.0721	-0.1820
	P	0.0050	-0.0051	0.0016	0.0016	-0.0056	0.0011	-0.0588	0.0002	0.0093	-0.0205	-0.0246	-0.0675	-0.1589
1000 GW	G	-0.0019	0.0026	-0.0026	-0.0066	0.0089	-0.0118	0.0037	-0.0054	-0.0010	-0.0282	0.1439	-0.0179	0.0848
	P	-0.0026	0.0019	-0.0010	-0.0040	0.0119	-0.0023	0.0015	-0.0074	-0.0008	0.0403	0.0511	-0.0166	0.0622
P.W	G	0.0059	-0.0071	0.0065	0.0148	-0.0141	0.0118	-0.0642	0.0001	0.0427	-0.0064	0.0330	-0.0334	-0.0102
	P	0.0063	-0.0052	0.0017	0.0066	-0.0022	0.0018	-0.0285	0.0003	0.0193	0.0112	0.0139	-0.0185	0.0068
BRIX	G	0.0003	-0.0019	-0.0001	0.0002	-0.0053	0.0005	0.0104	-0.0013	0.0023	-0.1202	0.6140	-0.0209	0.4781
	P	0.0003	-0.0020	-0.0001	0.0004	-0.0012	0.0001	0.0055	-0.0014	0.0010	0.2195	0.2782	-0.0179	0.4825
TSS	G	0.0003	-0.0019	-0.0001	0.0002	-0.0053	0.0005	0.0107	-0.0013	0.0023	-0.1202	0.6139	-0.0203	0.4788
	P	0.0003	-0.0020	0.0000	0.0005	-0.0012	0.0001	0.0052	-0.0014	0.0010	0.2194	0.2783	-0.0190	0.4812
JY	G	-0.0017	0.0064	-0.0064	-0.0076	0.0027	-0.0037	0.0069	0.0001	-0.0017	0.0029	-0.0146	0.8549	0.8383
	P	-0.0023	0.0069	-0.0043	-0.0057	0.0006	-0.0008	0.0047	0.0001	-0.0004	-0.0047	-0.0063	0.8405	0.8284

DAF 50%= Days to 50% flowering (Days), D.M= Days to maturity (Days), PH= Plant height (cm), N.N.S= Number of nodes per plant, SG= Stem girth (cm), PW= Panicle weight (g), 1000 GW= 1000 grain weight (g), FSTK= Fresh stalk yield (T ha⁻¹), JY= Juice yield (l ha⁻¹), Brix %, TSS = Total soluble sugars (%), EY= Ethanol yield (l ha⁻¹), GY = Grain yield (T ha⁻¹).
Residual factor was 0.23P, 0.19G.

As the ethanol contributing characters like juice yield and brix content have negative indirect effect might have led early maturing types as poor ethanol yielders. Therefore, Intermediate to late maturing types are preferred like the genotypes ICSV 15006 (118.00 days), IS-29308 (124 days) have the desirable characters as mentioned. Vemana *et al.* (2014) had similar results in his study while Sowmy *et al* (2015) recorded negative results.

4.4.3 Number of nodes per plant

This character has shown negative direct effect on ethanol yield (-0.0666 G, -0.0721 P) at both phenotypic and genotypic levels, while correlation for this character was negative significant which could be due to the indirect effect of days to maturity (-0.0277G, 0.0282 P); Fresh stalk yield (-0.0274 G, -0.0056 P); grain yield (-0.0045 G, -0.0031 P); Juice yield (-0.1205 G, -0.1146 P) and total sugars estimation (-0.0017 G, 0.0002 P) at both genotypic and phenotypic levels while brix % content at phenotypic level (-0.0004 P) only.

The number of nodes had negative direct effect on ethanol content. If selection based on this trait is considered, plant height will be improved but tall genotypes have shown low brix values and high juice content nullifying the effect of juice yield on ethanol content. Vemana *et al.* (2014) observed a quite different result showing positive direct effect with juice and brix content.

Correlation for number of nodes per plant with plant height was positive, where significant number of nodes contributed to tall plant types like GGUB-68 (512.68 cm with 17.33 nodes); Phule vasundhara (540.80 cm with 20 nodes); SSS-15 (522.10 cm with 17.67 nodes). But there are few cases as mentioned below where number of nodes per plant was low but the plant height recorded was high which is due to high internodal length.eg; EG-11(414.33 cm with 12.33 nodes), EG-81 (447 cm with 12 nodes), Internodal length is the deciding factor in determining plant height and also for maximum juice extraction.

Phenotypal Path Diagram for ETHANOL YLD

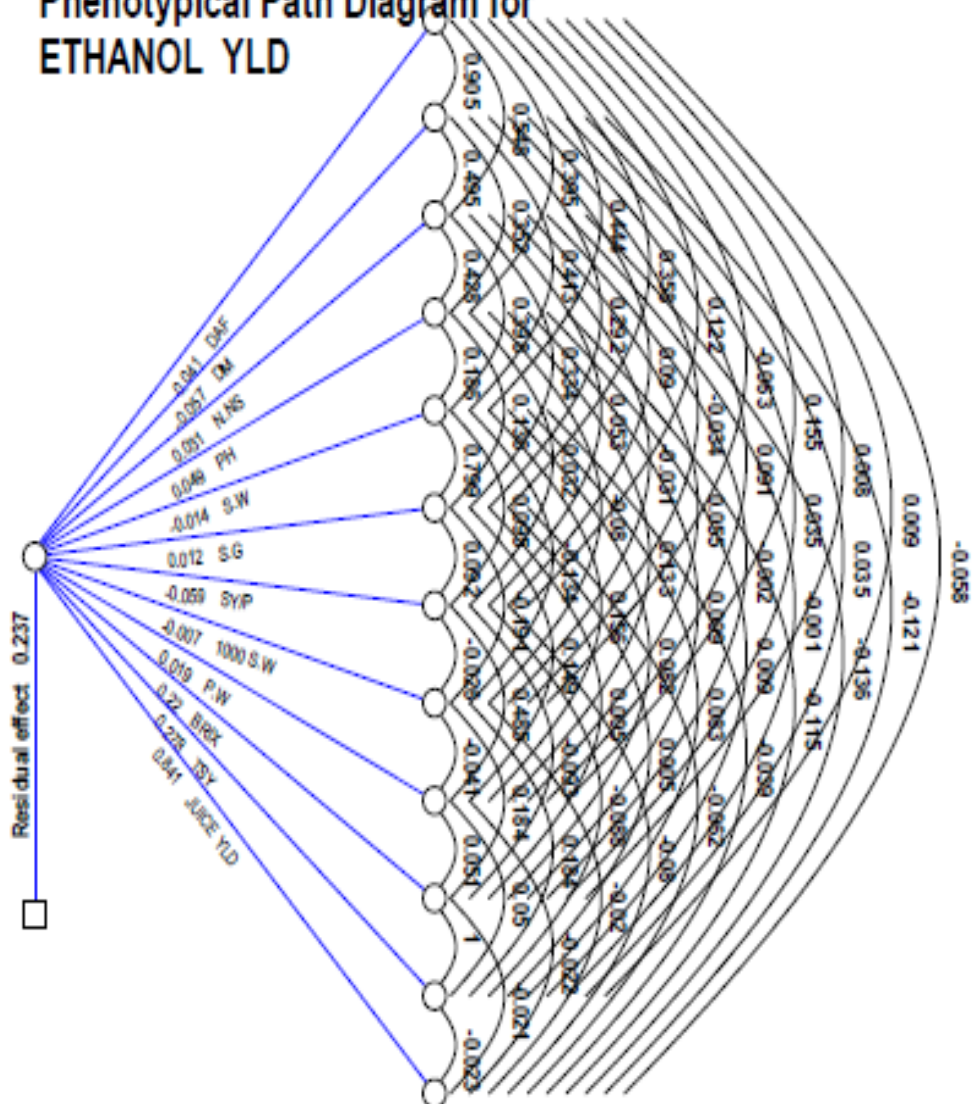


Fig. 4.3.2 Phenotypal Path Diagram for 110 sorghum genotypes.

4.4.4 Plant height (cm)

Plant height has shown negative direct effect on ethanol yield (-0.0469 G, 0.0327 P) at both phenotypic and genotypic levels, while negative nonsignificant correlation was recorded for ethanol yield which is due to the indirect effects of days to maturity (-0.0205 G, -0.0201 P); Fresh stalk yield (-0.0130 G, -0.0026 P); grain yield (-0.0032 G, -0.0019 P) and Juice yield (-0.1219 G, -0.0964 P) at both genotypic and phenotypic levels and brix % at (-0.0004 G) at genotypic level only.

The tall genotypes have recorded high juice yield with low brix values, which is nullifying the ethanol content eg: EC-22 (428.67 cm plant height, 11 % brix with juice yield 10242.46 l ha⁻¹ and ethanol yield 455.44 l ha⁻¹). Hence for selection intermediate genotypes are preferred. The results recorded by Hundekar *et al.* (2016) and Makanda (2017) are deviating from the above quoted results for direct and indirect effects.

4.4.5 Fresh stalk yield (T ha⁻¹)

This character has shown positive direct effect on ethanol yield (0.0169 G, 0.0181 P), while this character has shown positive non-significant association with ethanol yield which could be due to the positive indirect effects of days to 50% flowering (0.0127 G, 0.180 P); number of nodes (0.0216 G, 0.0124 P); plant height (0.0121 G, 0.0092 P); stem girth (0.0417 G, 0.0097 P); 1000 grain weight (0.0008 G, 0.0010 P); Panicle weight (0.0105 G, 0.0030 P) and Total soluble sugars (0.0563 G, 0.0230 P) at both phenotypic and genotypic levels.

Though this character has shown positive direct effect on ethanol yield, because tall genotypes are indirectly contributing to high biomass, but as seen in correlation studies, juice yield had shown negative contribution with this trait, which means high biomass type are low yielders for juice but, positive association with brix and ethanol content. The genotype ICSV-12012 was a high biomass type with high brix and ethanol yield. (Means table: 4.3) and in this case direct selection if practiced facilitates reduction of undesirable indirect effects. Results quoted here are deviating from the results given by Vemana *et al.* (2014).

4.4.6 Stem girth (cm)

Stem girth has shown negative direct effect with ethanol yield (-0.0404 G, -0.0349P) while correlation studies revealed negative non-significant association with Ethanol yield. This could be due to the negative indirect effect of days to maturity (-0.0155 G, -0.0166 P); Fresh stalk yield (-0.0501 G, -0.0113 P); 1000 grain weight (-0.0118 G, -0.0023 P) and Juice yield (-0.0037 G, -0.0008 P) at both genotypic and phenotypic levels.

Selection for high stem girth combined with tall genotypes could result in high biomass types, but not in juice and ethanol yield as this character had negative association with this trait. Brix content has positive correlation with stem girth. The genotypes ICSV-12012, EG-23 and EG-19 have significant stem girth and Fresh stalk yield with high brix and low juice and ultimately high ethanol yield. (Means table: 4.3). The results are in accordance with the findings of Tomar and Sivakumar (2012).

4.4.7 Grain yield (T ha⁻¹)

Grain yield has recorded negative direct effect with ethanol yield (-0.1820 G, -0.1589 P) while Negative significant correlation was observed for ethanol yield at both levels which may be due to the negative indirect effects of days to maturity (-0.0055 G, -0.0051 P); Fresh stalk yield (-0.0089 G, -0.0056P); Juice yield (-0.0721G, -0.0675 P) and total soluble sugars (-0.0803 G, -0.0246 P) at both genotypic and phenotypic levels and brix per cent(-0.0205 G) at phenotypic level only.

Selection of high grain yielders could result in poor ethanol yielders because they have a negative indirect effect through brix, juice and ethanol yield. The genotypes E-63, EG-83, IS-7474, SCVS-29 had similar combination of characters. The results given are in accordance with findings of Makanda *et al.* (2017) and Mulualet *et al.* (2018).

4.4.8 1000 Grain weight (g)

1000 grain weight has recorded positive direct effect with ethanol yield (0.0848 G, 0.0622 P) while this character has recorded positive nonsignificant correlation with ethanol yield at both levels which is due to the positive indirect effect of days to maturity (0.0026 G, 0.0019 P); Fresh stalk yield (0.0089 G, 0.0019 P); grain yield (0.0037 G, 0.0015 P) and total soluble sugars (0.1439 G, 0.0511 P) at both levels while brix content (0.0403 P) at phenotypic level only.

This character has exhibited positive direct effect which could be useful for selection and even the association of this character with brix content, juice yield and ethanol yield are positive, this could be due to the indirect effects of total soluble sugars and brix. The direct effect reveals a true relationship between these characters hence direct selection for this trait facilitates yield improvement. Khakabhavi *et al.* (2017), Deshmukh *et al.* (2018) recorded deviating results from the above quoted results.

4.4.9 Panicle Weight (g)

Panicle weight has recorded positive direct effect on ethanol yield (0.0068 P) at phenotypic level only while negative direct effect at (-0.0102 G) genotypic level only. The character ethanol yield has displayed negative non-significant correlation which is due to the negative indirect effect of days to maturity (-0.0071G, -0.0052 P); Fresh stalk yield (-0.0141 G, -0.0022 P) and grain yield (-0.0642 G, -0.0285 P) at both levels while brix content (0.0064 G) at genotypic level only.

The selection of this character could result in improvement of grain yield per plant with high brix but poor juice and ethanol yielder. RSSV-1381 has similar combination of characters. Chalachew and Rebuma (2018), Mulualet *et al.* (2018), Swamy *et al.* (2018b) had shown similar results with indirect effects for brix content.

4.4.10 Brix %

This character has shown positive direct effect on ethanol yield (0.4781 G, 0.4825 P) and has shown significant positive correlation with ethanol yield which is due to the positive direct contribution of days to 50 % flowering (0.0003 G, 0.0003 P); plant height (0.0002 G, 0.0004 P); stem girth (0.0005 G, 0.0001 P); grain yield (0.0104 G, 0.0055 P); panicle weight (0.0023 G, 0.0010 P); total soluble sugars (0.6140 G, 0.2782 P) at both the levels.

Simultaneous improvement of the genotype for ethanol yield is possible by imparting the selection criteria with increasing the brix and total soluble sugars. ICSV-12012 is the genotype possessing with brix and total sugar content without significant levels of juice and ethanol content. The results displayed are not intune with Vemana *et al.* (2014) for indirect effects.

4.4.11 Total soluble sugars (%)

This character has shown positive direct effect on ethanol yield (0.4788 G, 0.4812 P) and has shown significant positive correlation with ethanol yield which is due to the positive direct contribution of days to 50 % flowering (0.0003 G, 0.0003 P); plant height (0.0002 G, 0.0004 P); stem girth (0.0005 G, 0.0001 P); grain yield (0.0107 G, 0.0052 P); panicle weight (0.0023 G, 0.0010 P) at both the genotypic and phenotypic levels.

This character also recorded positive direct effect with ethanol yield. The results are in accordance with the results of brix content as it is a derived factor from Brix directly. Shukla *et al.* (2017) reported that total sugar yield had negative direct effect with ethanol yield

4.4.12 Juice yield (l ha⁻¹)

Juice yield has recorded positive direct effect on ethanol yield (0.8383 G, 0.8284 P) while correlation studies recorded positive significant contribution with ethanol yield at both the levels which is due to the positive direct effect of days to maturity (0.0064 G, 0.0069P); Fresh stalk yield (0.0027 G, 0.0006 P); grain yield (0.0069 G, 0.0047P); 1000 grain weight (0.0001 G, 0.0001 P) at both levels; brix % (0.0029 G) only at genotypic level.

Selection for this character directly contributes to the ethanol yield, simultaneous improvement is possible because of positive association with brix and ethanol content. The genotypes EG-11, EG-21, EP-61, GGUB-43, GGUB-45, GGUB-61, GGUB-64, GGUB-65, GGUB-67, ICSSSH-71, PV-12, SSV-84, SSV-74 (means table 4.3) have significant juice and ethanol yields. Similar results are reported by Chalachew and Rebuma (2018), for ethanol yield while deviating from the result of brix content.

The association of different component characters among themselves and with yield is quite important for devising an efficient selection criterion for yield. The total correlation between yield and component characters may be sometimes misleading, as it might be an over-estimate or under estimate because of its association with other characters. Hence, indirect selection by correlated response may not be sometimes

fruitful. When many characters are affecting a given character, splitting the total correlation into direct and indirect effects of cause as devised by wright (1921) would give more meaningful interpretation to the cause of association between the dependent variable like yield and independent variables like yield components. This kind of information will be helpful in formulating the selection criteria.

The residual effect determines how best the causal factors account for the variability of the dependent factor. If the residual effect is high, some other factors which have not been considered here need to be included in this analysis to account fully for the variation in yield. In this case, residual factor was 0.23P, 0.19G.

Path coefficient analysis revealed that juice yield exerted the highest positive direct effect on ethanol yield followed by brix %, total soluble sugars along with positive correlation for all the above mentioned characters.

Fresh stalk yield had exhibited the positive indirect effect through days to 50% flowering; number of nodes per plant; plant height; stem girth; 1000 grain weight; Panicle weight; Total soluble sugars, 1000 grain weight exhibited positive indirect effect through days to maturity; Fresh stalk yield; grain yield; total soluble sugars and brix % content. While the rest of the characters like days to 50% flowering, days to maturity, number of nodes per plant, plant height, stem girth, grain yield. 1000 grain weight, panicle weight, brix, total soluble sugars, juice yield had similar correlation and path results. These results are in accordance with Shukla *et al.* (2017), Makanda *et al.* (2017) and Mulualet *et al.* (2018)

In the present investigation from path analysis study it can be concluded that juice yield, total soluble sugars content, brix%, Fresh stalk yield and 1000 grain weight would play an important role in selection criteria for improving the character ethanol content.

4.5 COMBINING ABILITY

Genetically divergent parents are expected to yield heterotic hybrids with a high frequency, in addition to generating a broad spectrum of variability in segregating generations (Chavan *et al.* (2010). In theoretical terms general combining ability (GCA) is defined as the average performance of a line in hybrid combinations and additive portion of genetic variance is responsible (Sprague and Tatum, 1942) whereas, specific

combining ability (SCA) is the deviation from expectation on the basis of average performance which is due to dominance and epistasis or nonadditive genetic variance. Additive variance (σ^2A) is due to the average effects of alleles (additive effects, same locus) and dominance variance (σ^2D) is due to interaction of average effects of alleles (dominance effects, same locus) Halluer *et al.* (2010).

In order to study the combining ability variances and effects, L X T analysis was carried out with 16 hybrids evolved from crossing 4 lines with 4 testers which were evaluated at three locations viz: Bapatla, Guntur and Garikapadu. The results thus obtained are outlined here. Pooled analysis of variance for combining ability was carried out using mean value across three locations (Kempthorne, 1957) to test the significance of differences among the genotypes including crosses and parents. (Snedecor and Cochran, 1967), (Panse and Sukhatme, 1964).

4.5.1 Analysis of variance

The pooled analysis of variance for 13 characters measured over three locations in the present investigation revealed significant differences among environments, lines, testers, crosses, environment x line x tester for all the characters studied except panicle weight. Characters like plant height, fresh stalk yield, panicle weight, brix content and grain yield have been found to be significant in replications too. (Table: 4.12). The paramount share of variance is through testers for all the characters studied. Similar results were quoted by Indhubala *et al.* (2010) and Umakanth *et al.* (2012a), Bahadure *et al.* (2015) and Ahmed *et al.* (2014) in earlier studies of sorghum.

4.5.2 Per se performance

The mean performance and range of lines, testers and hybrids are presented in table: 4.13 and 4.14, Appendix: 2, 3, 4 and briefed under following headings:

4.5.2.1 Days to 50 % flowering (days): Among the lines, L-3(ICSA- 14033) with 72.50 days was Late to flower, followed by L-4 (ICSA 14035) with 71.50 days and L-1 (ICSA- 14029) and L-2 (ICSA-14030) are the earliest to flower with a mean of 70 days

Table 4.12. Pooled analysis of variance for combining ability (Line x Tester) for ethanol yield and other traits in Sorghum [*Sorghum bicolor* (L.) Moench]

Source of variation	Degrees of freedom	Days to 50% flowering (Days)	Days to maturity (Days)	Number of nodes	Plant height (cm)	Fresh Stalk yield (T ha ⁻¹)	Stem girth (cm)	1000 grain weight (g)	Panicle weight (g)	Brix %	Total soluble sugars (%)	Juice yield (l ha ⁻¹)	Ethanol yield (l ha ⁻¹)	Grain yield (T ha ⁻¹)
Replications	1	14.69	9.50	12.25	580.81**	30.68**	0.03	604.46	239.94**	1.56*	1.48*	38532.62	4529.62	1.33*
Environments	2	53.52**	37.02**	3.93**	36752.57**	276.53**	3.37**	419.55**	1101.02**	34.17**	25.72**	29092637.07**	18152.66**	3.90**
Parents (line)	3	90.59**	160.48**	14.66**	24260.18**	108.28**	0.64**	153.95**	212.47**	48.55**	42.60**	76247364.84**	201027.46**	1.41**
Parents (testers)	3	4.55**	56.22**	0.26	9077.26**	15.03**	0.12**	27.42**	159.00	1.11*	1.52**	3899348.03**	13786.70*	3.08**
Crosses	15	458.53**	355.55**	9.97**	10204.63**	565.59**	0.99**	51.39**	176.24	21.48**	16.43**	74958299.40**	462077.25**	1.56**
Line * tester effect	9	62.18**	109.64**	8.5**	1358.24**	362.13**	0.59**	63.99**	154.30	12.26**	9.38**	35475264.82**	204317.24**	0.98**
Env *Line effect	6	126.57	85.61	7.70	6322.70	162.63	1.38	43.14	224.13	11.50	8.79	83668964.39*	385546.04	2.78
Env * tester effect	6	108.35	157.78	8.06	8226.78	718.62*	1.50	69.86	148.15	21.04	16.08	40194526.24**	284742.65	5.09
Env * L * T effect	18	89.01**	127.74**	4.68**	3835.91**	203.55**	0.60**	77.34**	152.27	10.09**	7.72**	28797361.51**	14933.95**	2.65**
Error	69	0.73	2.00	0.55	37.01	1.38	0.00	2.86	8.87	0.37	0.37	933387.97	4292.32	0.27

NOTE: * and ** Significant at 5 and 1 per cent level respectively

Table 4.13. Mean performance of 4 lines, 4 testers and 16 hybrids along with 1 hybrid check for 13 characters in Sorghum [*Sorghum bicolor* (L.) Moench]

	Lines/Testers/ Hybrids	Days to 50% flowering (Days)	Days to maturity (Days)	Plant height (cm)	Number of nodes per plant	Stem girth (cm)	Panicle weight (g)	1000 Grain weight (g)	Fresh Stalk yield (T ha ⁻¹)	Juice yield (l ha ⁻¹)	Brix %	Total soluble sugars (%)	Ethanol yield (l ha ⁻¹)	Grain yield (T ha ⁻¹)
L -1	ICSA 14029	70.67	110.00	198.13	9.83	3.08	49.00	26.14	51.20	9639.50	15.67	13.52	691.41	4.59
L-2	ICSA 14030	70.67	117.33	161.62	9.83	3.07	50.50	29.07	40.79	9706.53	16.33	13.98	706.05	5.67
L-3	ICSA 14033	72.50	115.00	171.63	10.17	3.35	53.52	31.09	45.95	8212.34	16.67	14.73	646.31	5.35
L-4	ICSA 14035	71.50	114.33	175.40	9.67	3.03	60.59	30.10	46.87	8123.45	16.00	13.95	599.97	5.81
GM		69.38	114.17	176.70	9.88	3.13	53.40	29.10	46.20	8862.95	16.17	14.04	660.94	5.35
T-1	SEVS-08	79.17	120.33	329.56	14.17	2.43	36.18	31.10	57.20	18911.09	9.83	8.75	869.74	3.51
T-2	GGUB-28	62.17	109.83	203.51	11.17	2.83	36.0	36.06	54.55	14197.52	10.83	9.63	717.82	2.94
T-3	ICSV-15006	81.67	124.17	319.24	14.17	2.8	47.41	26.38	57.98	10550.62	16.01	14.15	783.25	4.04
T-4	IS-29308	78.50	119.17	339.87	11.83	2.28	45.97	24.84	53.43	16548.13	14.00	13.30	1134.59	3.86
GM		75.38	118.38	287.58	12.83	2.58	41.56	29.59	55.79	15051.84	12.67	11.46	876.35	3.59
H-1	ICSA 14029 x SEVS-08	80.33	125.00	123.30	10.17	2.07	42.01	31.86	43.32	14281.47	11.33	10.06	764.88	4.03
H-2	ICSA 14029 x GGUB 28	65.50	109.17	178.52	9.67	2.28	52.95	36.60	46.12	17180.23	14.00	12.40	1130.31	4.73
H-3	ICSA 14029 x ICSV-15006	78.83	123.00	289.14	12.17	2.58	51.32	31.46	62.15	18066.65	15.67	13.86	1345.87	5.07
H-4	ICSA 14029 x IS 29308	91.33	124.50	261.30	10.67	2.33	46.37	33.63	45.02	7817.28	13.83	12.25	506.11	4.57

	Lines/Testers/Hybrids	Days to 50% flowering (Days)	Days to maturity (Days)	Plant height (cm)	Number of nodes per plant	Stem girth (cm)	Panicle weight (g)	1000 Grain weight (g)	Fresh Stalk yield (T ha ⁻¹)	Juice yield (l ha ⁻¹)	Brix %	Total soluble sugars (%)	Ethanol yield (l ha ⁻¹)	Grain yield (T ha ⁻¹)
H-5	ICSA 14030 x SEVS -08	82.67	122.33	264.30	11.33	1.73	59.74	34.09	35.65	10227.15	11.67	10.36	535.27	5.34
H-6	ICSA 14030 x GGUB 28	62.67	104.17	172.09	9.00	2.62	48.38	36.78	46.47	15933.32	10.33	9.19	815.38	4.45
H-7	ICSA 14030 x ICSV 15006	80.00	123.33	301.01	12.83	2.95	52.39	34.86	61.53	18348.13	14.67	12.98	1259.71	4.55
H-8	ICSA 14030 x IS 29308	82.50	125.33	258.58	9.17	1.56	53.65	37.13	27.80	11316.04	15.67	13.86	802.38	4.81
H-9	ICSA 14033 x SEVS-08	81.83	119.67	255.31	12.66	1.83	48.63	40.51	35.97	13397.52	12.83	11.38	777.07	4.77
H-10	ICSA 14033 x GGUB -28	66.67	115.00	178.42	12.17	2.55	46.72	29.95	41.19	17876.53	12.00	10.65	1004.05	4.82
H-11	ICSA 14033 x ICSV-15006	79.17	121.83	271.68	10.83	2.96	48.61	32.38	59.14	14234.55	16.00	14.14	1078.60	4.78
H-12	ICSA 14033 x IS-29308	83.50	118.50	248.48	12.50	2.17	50.22	32.93	43.40	8720.98	12.00	10.65	493.32	5.17
H-13	ICSA 14035 x SEVS-08	83.17	126.16	274.0	11.50	2.58	46.21	34.07	46.26	12812.33	11.33	10.06	695.96	3.89
H-14	ICSA 14035 x GGUB 28	59.83	101.16	171.65	9.33	2.25	48.51	38.91	36.22	10251.84	11.33	10.06	533.13	4.24
H-15	ICSA 14035 x ICSV-15006	79.67	124.00	247.63	11.17	2.67	46.58	31.78	38.18	16286.40	14.33	12.69	1150.25	4.04
H-16	ICSA 14035 x IS-29308	78.17	117.83	276.52	12.67	2.15	34.96	32.44	38.36	9775.30	15.50	13.71	740.07	3.41
GM		77.24	118.81	207.88	11.07	2.33	48.58	34.34	44.17	13532.86	13.28	11.77	852.02	4.54
CHK	CSH-22SS ©	88.83	126.17	333.77	14.67	2.15	51.03	40.87	43.92	9725.92	13.00	11.52	597.52	3.59

Table 4.14. Range of characters for lines, testers and hybrids for 13 characters in Sorghum [*Sorghum bicolor* (L.) Moench]

S. No.	Character	Lines range	Testers range	Hybrids range
1	Days to 50% flowering (Days)	70.67 – 72.50	62.17– 81.67	59.83 - 91.33
2	Days to maturity (Days)	110.00 - 117.83	109.83 – 124.17	101.16 – 126.16
3	Plant height (cm)	161.32 - 198.13	203.51 – 339.87	123.35 – 301.01
4	Number of nodes per plant	9.67 - 10.17	11.17 – 14.17	9.0 – 12.83
5	Stem girth (cm)	3.03 - 3.35	2.28 – 2.83	1.56 – 2.96
6	Panicle weight (g)	49 - 60.59	36 – 47.41	34.96 – 59.74
7	1000 grain weight (g)	26.14 - 31.09	24.84 – 36.06	29.95 – 40.51
8	Fresh Stalk yield (T ha ⁻¹)	40.79 – 51.20	53.43 – 57.98	27.80 – 62.15
9	Juice yield (l ha ⁻¹)	8123.45 - 9706.53	10550.62 -18911.09	7817.27 – 18348.13
10	Brix %	15.67 - 16.67	9.83 – 16.01	10.33 – 16.00
11	Total soluble sugars (%)	13.52 - 14.73	8.75 – 14.15	9.19 – 14.14
12	Ethanol yield (l ha ⁻¹)	599.97 -706.05	717.82 – 1134.59	493.32 – 1345. 87
13	Grain yield (T ha ⁻¹)	4.59 – 5.81	2.94 – 4.04	3.40 – 5.34

In the testers, T-1(SEVS-08) with mean of 79.17 days and T-3(ICSV-15006) is late flowering with 81.67 days to flower. T-2 was earliest to flower (GGUB 28) 62.17 days followed by T-4 (IS-29308) with a mean of 78.50 days; The range of lines varied from 70.67 – 72.50 days and testers from 62.17 – 81.67 days

Among the hybrids, all the 16 hybrids were found to be early flowering when compared with check CSH-22SS (88.33 days) except H-4 which is late flowering type. H-12 (83.50 days), H-13 (83.17 days), H-5 (82.67 days) were the late to flower and rest of the hybrids were intermediate in between 65.50 to 82.50 days. The range of hybrids varied from 59.83 - 91.33days.

4.5.2.2 Days to maturity (days)

In female parents, L-2 (ICSA-14030) was late maturing with 117.33 days to mature. L-1 (ICSA-14029) was early to mature with a mean of 110 days followed by L-4 (ICSA-14035), L-3 (ICSA-14033) taking 114.33 and 115 days respectively. The male parents T-3 (ICSV 15006) with a mean of 124.17days was found to be late maturing followed by T-1 (SEVS-08) with 120.33 days, T-4 (IS-29308) with 119.17 days and T-2 (GGUB-28) were found to be early maturing with a mean of 109.83days.

H-13 recorded the highest for days to maturity (126.06) followed by H-15 (124 days) and H-2 (109.17 days) and H-13 (126.16 days) and check CSH-22SS are on par with 126.17 days and the rest of the hybrids were found to be early maturing when compared with check. The range of lines, testers and hybrids ranged from 110.00 - 117.83 days, 109.83 – 124.17 days and 101.16 – 126.16 days respectively.

4.5.2.3 Plant height (cm)

The range of female parents for plant height varied from 161.62 - 198.13cm, L-2 (ICSA-14030) recorded the lowest value and L-1(ICSA-14029) recorded the highest. The range for plant height in male parents varied from 203.51 – 339.87 cm. T-4 (IS-29308) has recorded the highest value and T-2 (GGUB-28) recorded the lowest value.

Among the hybrids, the range varied from 123.30 – 301.01 cm the tallest hybrid was H-7 and the dwarf is H-1. All the hybrids recorded low values when compared to check CSH-22SS (333.77 cm).

4.5.2.4 Number of nodes per plant

The average number of nodes per plant among females is 9.67 for L-4 (ICSA-14035) followed by L-1 (ICSA -14029), L-2 (ICSA-14030) possessing 9.83 nodes and L-3 (ICSA-14033) having 10.17 nodes. Among males T-1 (IS-29308) and T-3 (ICSV-15006) recorded 14.17 nodes each, followed by T-4(SEVS-08) and T-2(GGUB-28) 11.83 and 11.17 nodes each respectively. Testers are possessing more number of nodes per plant when compared to females.

Among hybrids, the number of nodes per plant varied from 9.0–12.83 nodes in H-6 to H-9. All hybrids recorded low values when compared to check CSH-22SS (14.67) nodes.

4.5.2.5 Stem girth (cm)

The stem girth for Lines ranged from 3.03 - 3.35cm, the lowest recorded is for L-4 (ICSA-14035) the highest is for L-3 (ICSA-14033). Range of testers varied from 2.28 – 2.83cm, T-1 recorded lowest Value (2.23cm) and T-2 (ICSA-14030) recorded the highest value (2.83cm). When compared to male parents female parents are slightly higher than male parents.

Stem girth for hybrids ranged from 1.56 – 2.96cm. H-8 recorded the lowest value and H-11 recorded the highest followed by H-7 (2.95cm), H-15 (2.67cm), H-6(2.62cm), H-3 and 13(2.58cm), H-10 (2.55cm) have recorded the respective values above the check CSH-22SS (2.15cm).

4.5.2.6 Panicle weight (g)

Among the female parents L-4(ICSA-14035) has recorded the highest value 60.59g followed by L-3 (ICSA-14033) with 53.52 g. Among male parents T-4 (SEVS-08) recorded the highest mean value 45.97 g followed by T-3 (ICSV-15006) with a mean of 47.41 g.

Panicle weight ranged from 34.96 – 59.74g among the hybrids, H-5 has the highest mean value and the lowest by H-16. H-2 (52.95g), H-3 (51.32g), H-8 (53.65 g) has recorded the superior mean values when compared with the check CSH-22SS (51.03g).

4.5.2.7 1000 grain weight (g)

L-3 (ICSA-14033) has recorded 31.09g, followed by L-4 (ICSA-14035) with a mean of 30.10g and L-2 (ICSA-14030) and L-1 (ICSA-14029) with means of 29.07 and 26.14g respectively. In testers, T-2 (GGUB-28,) has recorded highest value of 36.06g, followed by T-1 (SEVS-08), T-3 (ICSV-15006) and T-4 (IS-29308) with general means of 31.10, 26.38 and 24.84 g respectively. No much variation has been observed for stem thickness in both male and female parental lines.

The hybrids ranged from 29.95 – 40.51g, H-9 is the highest and H-10 is the lowest. H-8 (37.13g), H-14 (38.91g), H-6 (36.78g) have recorded the mean values which were low when compared to check CSH-22SS (40.87g).

4.5.2.8 Fresh stalk yield (T ha⁻¹)

L-1 (ICSA-14029) and L-4 (ICSA-14035) have recorded the mean values of 51.20 T ha⁻¹ and 46.87 T ha⁻¹ respectively and L-1 (ICSA-14030) recorded the highest mean value 51.20 T ha⁻¹ and the lowest by L-2 (ICSA-14030). In testers T-3 (ICSV-15006) recorded the highest mean value of (57.98 T ha⁻¹) and lowest mean value (40.79 T ha⁻¹) by T-4 (IS-29308).

Among the hybrids, the range varied from 27.80 – 62.15 T ha⁻¹, the highest mean value recorded for H-3 (62.15 T ha⁻¹), followed by H-7 (61.53 T ha⁻¹), H-11 (59.14 T ha⁻¹) over the check CSH-22SS (43.92 T ha⁻¹). The lowest mean value recorded for fresh stalk yield is H-8 (27.80 T ha⁻¹).

4.5.2.9 Juice yield (l ha⁻¹)

Among the female parents, L-2 (ICSA-14030) has recorded the highest means (9706.53 l ha⁻¹), followed by L-1 (ICSA-14029) 9639.50 l ha⁻¹. L-3 (ICSA-14030) and L-4 (ICSA-14035) recorded 8212.34 l ha⁻¹ and 8123.45 l ha⁻¹ respectively. Among male parents, T-1 (SEVS-08) recorded the highest value 18911.09 l ha⁻¹, followed by T-4 (IS-29308) with 16548.13 l ha⁻¹, T-2 (GGUB-28) with 14197.52 l ha⁻¹ and T-3 (ICSV-15006) with 10550.62 l ha⁻¹. Male parents were found to be good juice yielders when compared to female parents. Bahadure *et al.* (2015) observed similar results.

When compared to check CSH-22SS (9725.92 l ha⁻¹) H-7 (18348.13l ha⁻¹), H-3 (18066.65 l ha⁻¹), H-10 (17876.53 l ha⁻¹), H-2 (17180.23 l ha⁻¹), H-15 (16286.40 l ha⁻¹) and H-6 (15933.32 l ha⁻¹) have recorded the respective high means.

4.5.2.10 Brix%

The brix per cent ranged from 15.67 - 16.67 % in lines and 9.83 – 16.01 % in testers and in hybrids the range was 10.33 %– 16.00 %.

Among lines L-3(ICSA-14033) recorded the highest value (16.67%), followed by L-2 (ICSA- 14030), L-4 (ICSA-14035) and L-1(ICSA-14029). Among testers, T-3 (ICSV-15006) has recorded the highest 16.00 % followed by T-4 (IS-29308) with 14.00%. Lowest mean recorded by T-1(SEVS-08) with 9.83%. Not much variation was reported between female and male parents while female parents have shown slightly higher brix per cent when compared to male parents.

Among hybrids, H-11 (16.00%) H-3 and H-8 (15.67%), H-16 (15.50%), H-7(14.67%), H-15 (14.33%), H-2 (14.00%) have recorded the values which are above the check value CSH-22SS (13.00%).

4.5.2.11 Total soluble sugars (%)

Among the lines it ranged from 13.52 - 14.73, testers from 8.75 – 14.15, hybrids from 9.19 – 14.14 %.

Among lines L-3 (ICSA-14033) recorded the highest value (14.73 %), followed by L-2 (ICSA- 14030), L-4 (ICSA-14035) and L-1 (ICSA-14029). Among testers, T-3 (ICSV-15006) has recorded the highest 14.15% followed by T-4 (IS-29308) with 13.30 %. Lowest mean recorded by T-1(SEVS-08) with 8.75%.

Among hybrids, H-11 (14.14%) H-3 and H-8 (13.86%), H-16 (13.71%), H-7(12.98%), H-15 (12.69%), H-2 (12.40%) have recorded the values which are above the check value CSH-22SS (11.52%).

4.5.2.12 Ethanol yield (l ha⁻¹)

Among the lines L-2 (ICSA-14030) was highest with a mean of 706 l ha⁻¹ followed by L-1 (ICSA- 14029) with 691 l ha⁻¹, L-3 (ICSA- 14033) with 646.31 l ha⁻¹ and (ICSA 14035) with 599.97 l ha⁻¹

In the testers, T-4 was highest (IS-29308) with 1134.59 l ha⁻¹ followed by T-1(SEVS-08) with a mean of 869.74 l ha⁻¹, T-3 (ICSV-15006) with 783.25 l ha⁻¹ and T-2 (GGUB-28) with 717.82 l ha⁻¹ respectively. The range of lines varied from 599.97 -706.05l ha⁻¹ and testers from 717.82 – 1134.59l ha⁻¹. In the current study testers were high ethanol yielders which is of prime importance. Earlier similar results were reported by Bahadure *et al.* (2015).

The range of hybrids varied from 493.32 – 1345. 87 l ha⁻¹. When compared to check CSH-22SS (597.52 l ha⁻¹) H-3 (1345.87 l ha⁻¹) has recorded highest mean value followed by H-7 (1259.71 l ha⁻¹), H-2 (1130.31 l ha⁻¹), H-15 (1150.25 l ha⁻¹), H-11 (1078.60 l ha⁻¹), H-10 (1004.05 l ha⁻¹) has recorded the respective high means. Lowest means was recorded for H-12(493.32 l ha⁻¹).

4.5.2.13 Grain yield (T ha⁻¹)

The range of female parents varied from 4.59 – 5.81 T ha⁻¹. L-1 (ICSB-14029) recorded the lowest value and L-4 (ICSB-14035) recorded the highest. The range for male parents varied from 2.94– 4.04T ha⁻¹. T-3 (ICSV-15006) has recorded the highest value and T-2 (GGUB-28) recorded the lowest value. Among 4 lines, L-4 has also recorded high 1000 grain weight and panicle weight which are contributing to the highest grain yield and similar case with male parent ICSV 15006 possessing high panicle weight only.

Among the hybrids, the range varied from 3.40 – 5.34 T ha⁻¹the highest mean value recorded for hybrid H-5 and the lowest is H-16. H-3 (5.07 T ha⁻¹), H-12 (5.17 T ha⁻¹) has recorded high values when compared to check CSH-22SS (5.02 T ha⁻¹).

The range of expression for parents and hybrids for most of the traits are intermediate like 1000 grain weight, juice yield, brix per cent, total soluble sugars and grain yield. While hybrids has shown better performance than their parents in characters like days to 50 % flowering, days to maturity, fresh stalk weight, ethanol yield.

4.5.3 GCA Effects

Estimate of *gca* effects and status for 13 different traits, 4 lines and 4 testers are presented in Table 4.15 and 4.15.1. The identification of new hybrids and parents with good combining ability for different traits of interest was one of the important objective of the present study.

Female line 1 (ICSA-14029) was found to be a promising general combiner for fresh stalk yield (4.978), brix% (0.427), total soluble sugars (0.374), Juice yield (803.549), and ethanol yield (84.772) with higher positive significant GCA effects. while line 2 (ICSA-14030) was good general combiner for panicle weight (4.961), Juice yield (423.302) and grain yield (0.245) significantly and line 3 (ICSA-14033) for days to 50% flowering (0.552), number of nodes per plant (0.969), fresh stalk yield (0.749), stem girth (0.048) and grain yield (0.343) and negative non-significant for brix per cent (-0.073), total soluble sugars (-0.064), ethanol yield (-13.763) while line 4 (ICSA-14035) was negatively significant for the characters studied like days to 50 % flowering (-2.031) and days to maturity (-1.521) which is suitable for developing short duration types except and positive for number of nodes per plant (0.094), stem girth (0.081) and plant height (1.599) indicating that this line was poor combiner for all the characters.

Among the testers which are used as male parents, tester 3 (ICSV 15006) has shown positive significant *gca* for all the traits like no.of nodes (0.510), plant height (28.811), Fresh stalk yield (11.079), stem girth (0.460), panicle weight (1.146), brix per cent (1.885), total soluble sugars (1.649), juice yield (3201.077) and ethanol yield (356.587) except grain yield (0.068) which has non-significant *gca* and negative significant *gca* for character 1000 grain weight (-1.715) followed by tester 2 (GGUB 28) possessing positive *gca* for juice yield (1777.623) and ethanol yield (18.694) and negative *gca* for rest of the traits. Tester 4 (IS 29308) had positive significant *gca* for brix % (0.969), total soluble sugars (0.848). Tester 1 (SEVS-08) has recorded positive significant *gca* for characters days to 50% flowering (4.760), days to maturity (4.479), number of nodes per plant (0.344), plant height (16.877), 1000 grain weight (0.796) and negative significant association for brix, total soluble sugars, juice yield, ethanol yield and grain yield. Bahadure *et al.* (2015) and Ingle *et al.* (2018) observed similar results for *gca* effects for plant height, panicle weight and grain yield.

4.5.4 SCA Effects

Sca effects pertaining to 16 hybrids are presented in table 4.16. Among the hybrids, hybrid 3 has excelled with high *sca* effects in respect of brix% (1.406), total soluble sugars (1.229), juice yield (1619.287), and ethanol yield (176.772).

Table 4.15. GCA effects for 13 characters in Sorghum [*Sorghum bicolor* (L.) Moench]

Parents	Days to 50 % flowering (Days)	Days to maturity (Days)	Plant height (cm)	No. of nodes per plant	Stem girth (cm)	Panicle weight (g)	1000 grain weight (g)	Fresh stalk yield (T ha ⁻¹)	Juice yield (l ha ⁻¹)	Brix %	Total soluble sugars (%)	Ethanol yield (l ha ⁻¹)	Grain Yield (T ha ⁻¹)
ICSA 14029	1.760**	1.604**	0.538	-0.406*	-0.015	-0.415	-0.948*	4.978**	803.549**	0.427**	0.374**	84.772**	0.058
ICSA 14030	-0.281	-0.021	0.444	-0.656**	-0.115**	4.961**	1.379**	-1.310**	423.302**	-0.198	-0.173	1.162	0.245*
ICSA 14033	0.552**	-0.063	-2.580	0.969**	0.048*	-0.033	-0.393	0.749**	24.537	-0.073	-0.064	-13.763	0.343**
ICSA 14035	-2.031**	-1.521**	1.599	0.094	0.081**	-4.513**	-0.039	-4.416**	-1251.387**	-0.156	-0.136	-72.171**	-0.646**
SEVS-08	4.760**	4.479**	16.877**	0.344*	-0.277**	0.572	0.796*	-3.874**	-853.241**	-1.490**	-1.303**	-158.727**	-0.033
GGUB-28	-13.573**	-11.438**	-65.857**	-1.031**	0.094**	0.560	1.224*	-1.676**	1777.623**	-1.365**	-1.193**	18.694	0.020
ICSV-15006	2.177**	4.229**	28.811**	0.510**	0.460**	1.146*	-1.715**	11.079**	3201.077**	1.885**	1.649**	356.587**	0.068
IS-29308	6.635**	2.729**	20.169**	0.177 l	-0.277**	-2.278**	-0.306	-5.529**	-4125.458**	0.969**	0.848**	-216.554**	-0.005
CD @ 95%	0.384	0.669	2.654	0.309 l	0.038	1.027	0.726	0.518	330.621	0.250	0.219	26.095	0.227

NOTE: * and ** Significant at 5 and 1 per cent level respectively

Table 4.15.1. Status of GCA in 13 characters in Sorghum [*Sorghum bicolor* (L.) Moench]

Parents	Days to 50 % flowering (Days)	Days to maturity (Days)	Plant height (cm)	No. of nodes per plant	Stem girth (cm)	Panicle weight (g)	1000 grain weight (g)	Fresh stalk weight (T ha ⁻¹)	Juice yield (l ha ⁻¹)	Brix %	Total soluble sugars (%)	Ethanol yield (l ha ⁻¹)	Grain Yield (T ha ⁻¹)
ICSA 14029	+ H	+ H	+ L	-H	- L	-L	-H	+H	+H	+H	+H	+H	+L
ICSA 14030	- L	- L	+ L	-H	- H	+H	+H	-H	+H	-L	-L	+L	+H
ICSA 14033	+H	- L	- L	+H	+ H	-L	-L	+H	+L	-L	-L	-L	+H
ICSA 14035	-H	-H	+ L	+L	+ H	-H	-L	-H	-H	-L	-L	-H	-H
SEVS-08	+ H	+ H	+ H	+H	-H	+L	+H	-H	-H	-H	-H	-H	-L
GGUB-28	- H	-H	-L	-H	+ H	+ L	+H	-H	+H	-H	-H	+L	+L
ICSV-15006	+ H	+ H	+H	+H	+ H	+ H	-H	+H	+H	+H	+H	+H	+L
IS-29308	+ H	+ H	+H	+L	-H	- H	-L	-H	-H	+H	+H	-H	-L

+H= Positive High

+L= Positive Low

-H= Negative High

-L= Negative Low

Significant positive *sca* effects for number of nodes per plant(1.323), plant height (13.072), fresh stalk yield (4.314), positive non-significant for stem girth (0.015), negative significant for panicle weight(-6.821) followed by hybrid 2 having high *sca* effects for brix % (1.656), total soluble sugars (1.449), juice yield (1066.203) and ethanol yield (174.823), 1000 grain weight(1.989), panicle weight (4.228) and non-significant positive association for days to 50% flowering (0.073), days to maturity (0.188), number of nodes per plant (0.031), plant height (2.887) and negative significant for fresh stalk yield (-1.357),

Hybrid 8 showing high *sca* effects for brix per cent (1.615), total soluble sugars (1.412), juice yield (1485.338), ethanol yield (165.746), days to maturity (3.813), 1000 grain weight (1.720), panicle weight (2.387) and negative significant for number of nodes per plant (-1.427), days to 50 % flowering (-1.094), fresh stalk yield (-9.534), stem girth (-0.373)

Hybrid 9 possessing high *sca* effects for brix percent (1.115), total soluble sugars (0.976), juice yield (693.36) and ethanol yield (97.539), 1000 grain weight (5.775), days to 50% flowering (0.719) and number of nodes per plant (0.281) and negative for days to maturity (-3.563), fresh stalk yield (-5082), stem girth (-0.269)

Hybrid 10 showing positive significant *sca* effects for days to 50% flowering (2.448), days to maturity (7.688), number of nodes per plant (1.156), plant height (5.805), stem girth (0.077), positive non-significant *sca* effects for brix % (0.156), total soluble sugars (0.136) and significant *sca* effects for juice yield (2541.510) and ethanol yield (147.09).

Hybrid 13 has shown significant *sca* effects for juice and ethanol yield (1384.105), (74.833) respectively.

High significant *sca* effects for grain yield (0.027) and non-significant positive *sca* effects for hybrid 2, 4,8, 12, 13,14,15, 16 was observed . However, the grain yield is a secondary source of income in sweet sorghum and hence priority is for biofuel production. Reddy *et al.* (2005), Umakanth *et al.* (2012).

Hybrid 1 has shown positive significant *sca* effects for juice yield (798.301) only and positive non-significant *sca* effects for days to maturity (0.104), stem girth (0.027). Negative significant *sca* effects for days to 50% flowering (-3.427), number of nodes per plant (-0.844), plant height (-21.165), fresh stalk yield (-1.958), 1000 grain weight (-2.326), panicle weight (-6.724), brix % (-0.885), total soluble sugars (-0.775) and grain yield (-0.533) and non-significant *sca* effects for ethanol yield (-13.185).

Hybrid 16 has shown highly significant *sca* effects for number of nodes per plant (0.990), plant height (18.741), fresh stalk yield (1.920), ethanol yield (52.49) positive non-significant *sca* effects for panicle weight (2.011), brix% (0.073), total soluble sugars (0.063), juice yield (529.166), while negative significant *sca* effects for days to 50% flowering(-2.344), days to maturity(-1.646) stem girth(-0.194) and negative non-significant for 1000 grain weight (-0.212).

Hybrid 4 has shown positive significant *sca* effects for days to 50% flowering (5.698), plant height (-0.462), panicle weight (0.484), negative significant *sca* effects for brix % (-0.844), total soluble sugars (-0.737) ethanol yield (-214.13).

Hybrid 5 has shown positive significant *sca* effects for days to 50 % flowering (0.948), plant height (5.392), panicle weight (5.633), and number of nodes per plant (0.573) has shown non-significant *sca* effects, days to maturity (-50.938), fresh stalk yield (-3.339), stem girth (-0.206), 1000 grain weight (-2.420), juice yield (-2875.769), ethanol yield (-159.18) has shown negative significant *sca* effects and negative non-significant *sca* effects for days to maturity (-50.938).

Hybrid 6 has shown positive *Sca* effects for fresh stalk yield (5.279), stem girth (0.306), and non-significant for juice yield (199.37).

Hybrid 7 has shown positive significant effects for days to 50% flowering (0.865), number of nodes per plant (1.240), fresh stalk yield (7.593), stem girth (0.273), juice yield (1190.894), positive non-significant for days to maturity (0.313), plant height (0.701), 1000 grain weight (0.859), and ethanol yield (49.942).

Hybrid 11 has positive *sca* effects for fresh stalk yield (3.139), stem girth (0.127), brix% (0.906), total soluble sugars (0.791) and non-significant *sca* effects for plant height (4.39), 1000 grain weight (0.153) negative significant effects for days to 50% flowering (-0.802), number of nodes per plant (-1.719), juice yield (-2523.918), non-significant for panicle weight (-1.081).

Hybrid 12 showing positive *sca* effects for the characters fresh stalk yield (4.004), and panicle weight (3.949). Non-significant positive *Sca* effect for number of nodes per plant (0.281), stem girth (0.065). Negative significant *Sca* effects for days to 50 % flowering (-0.927), days to maturity (-2.979), plant height (-10.158) non-significant *Sca* effects for 1000 grain weight (-0.711).

Table 4.16. SCA effects for 13 characters in Sorghum [*Sorghum bicolor* (L.) Moench] hybrids

	HYBRIDS	Days to 50 % flowering (Days)	Days to maturity (Days)	Plant height (cm)	Number of nodes per plant	Stem girth (cm)	Panicle weight (g)	1000 grain Weight (g)	Fresh stalk yield (T ha ⁻¹)	Juice yield (1 ha ⁻¹)	Brix %	Total soluble sugars (%)	Ethanol yield (1 ha ⁻¹)	Grain Yield (T ha ⁻¹)
H-1	ICSA 14029 x SEVS-08	-3.427**	0.104	-21.165**	-0.844**	0.027	-6.724**	-2.326**	-1.958**	798.301*	-0.885**	-0.775**	-13.185	-0.533*
H-2	ICSA 14029 x GGUB 28	0.073	0.188	2.887	0.031	-0.127**	4.228**	1.989**	-1.357*	1066.203**	1.656**	1.449**	174.823**	0.112
H-3	ICSA 14029 x ICSV-15006	-3.677**	-2.188**	13.072**	1.323**	0.015	-6.821**	-1.558	4.314**	1619.287**	1.406**	1.229**	176.772**	-0.433
H-4	ICSA 14029 x IS 29308	5.698**	1.354*	-0.462	-0.177	0.294**	0.484	0.549	1.395**	-2393.670**	-0.844**	-0.737**	-214.13**	0.023
H-5	ICSA 14030 x SEVS -08	0.948*	-50.938	5.932*	0.573	-0.206**	5.633**	-2.420**	-3.339**	-2875.769**	0.073	0.063	-159.18**	0.586*
H-6	ICSA 14030 x GGUB 28	-0.719	-3.188**	-3.551	-0.385	0.306**	-5.725**	-0.159	5.279**	199.37	-1.385**	-1.212**	-56.500*	-0.355
H-7	ICSA 14030 x ICSV 15006	0.865*	0.313	0.701	1.240**	0.273**	-2.294*	0.859	7.593**	1190.894**	-0.302	-0.264	49.942	-0.305
H-8	ICSA 14030 x IS 29308	-1.094**	3.813**	-3.082	-1.427**	-0.373**	2.387*	1.720*	-9.534**	1485.338**	1.615**	1.412**	165.746**	0.073
H-9	ICSA 14033 x SEVS-08	0.719	-3.563**	-0.041	0.281	-0.269**	-0.484	5.775**	-5.082**	693.36*	1.115**	0.976**	97.539**	-0.080
H-10	ICSA 14033 x GGUB -28	2.448**	7.688**	5.805*	1.156**	0.077*	-2.385*	-5.217**	-2.061**	2541.510**	0.156	0.136	147.09**	-0.083
H-11	ICSA 14033 x ICSV-15006	-0.802*	-1.146	4.394	-1.719**	0.127**	-1.081	0.153	3.139**	-2523.918**	0.906**	0.791**	-116.24**	-0.174
H-12	ICSA 14033 x IS-29308	-0.927*	-2.979**	10.158**	0.281	0.065	3.949**	-0.711	4.004**	-710.956*	-2.177**	-1.904**	-128.38**	0.337
H-13	ICSA 14035 x SEVS-08	3.198**	4.396**	15.275**	-0.010	0.448**	1.575	-1.029	10.379**	1384.105**	-0.302	-0.265	74.833**	0.027
H-14	ICSA 14035 x GGUB 28	-1.802**	-4.688**	-5.141	-0.802*	-0.256**	3.882**	3.387**	-1.861**	-3807.250**	-0.427	-0.373	-265.41**	0.326
H-15	ICSA 14035 x ICSV-15006	2.281**	2.479**	-23.836**	-0.510	-0.206**	1.364	-0.801	-12.652**	803.858*	-0.677**	-0.591**	13.81	0.081
H-16	ICSA 14035 x IS-29308	-2.344**	-1.646*	18.741**	0.990**	-0.194**	2.011	-0.212	1.920**	529.166	0.073	0.064	52.49*	0.398
	CD @95%	0.769	1.337	5.308	0.618	0.076	2.054	1.451	1.035	661.242	0.500	0.438	52.190	0.455

NOTE: * and ** significant at 5 and 1 per cent respectively

Days to 50 % flowering (3.198), days to maturity (4.396), plant height (15.275), fresh stalk yield (10.379), stem girth (0.448) have shown positive significant *sca* effects in hybrid 13. Non-significant for character panicle weight (1.575) and negative non-significant *sca* effects for number of nodes per plant (-0.010), 1000 grain weight (-1.029), brix % (-0.302), total soluble sugars (-0.265).

Hybrid 14 has shown *sca* effects for 1000 grain weight (3.387), panicle weight (3.882) and negative significant *sca* effects for days to 50% flowering (-1.802), days to maturity (-4.688), number of nodes per plant (-0.802), fresh stalk yield (-1.861), stem girth (0.256) juice yield (-3807.250), ethanol yield (-265.41) and negative non-significant *sca* effects for plant height (-5.141), brix % (-0.427), total soluble sugars (-0.373).

Hybrid 15 has shown positive *sca* effects for days to 50 % flowering (2.281), days to maturity (2.479), juice yield (803.858) and non-significant for panicle weight (1.364), ethanol yield (13.81) and negative significant *Sca* effects for plant height (-23.836), fresh stalk yield (-12.652), stem girth(-0.206), brix % (-0.677), total soluble sugars (-0.591) and non-significant *Sca* effects for number of nodes per plant (-0.510), 1000 grain weight (0.801).

4.5.5 *Gca* and *Sca* variance

The *sca* variance component estimates were greater than that of *gca* for the characters (Table 4.17) no of nodes (1.33 > 0.47), fresh stalk yield (60.09 > 36.21), stem girth (0.09 > 0.06), 1000 grain weight (10.14 > 1.22), panicle weight (24.67 > 8.45), brix% (1.98 > 1.45), total soluble sugars (1.51 > 1.11), juice yield (5804759.00 > 5564006.00) and grain yield (0.11 > 0.08) indicating the non-additive control of genetic variation in these traits. Similar results were reported by Sanjanareddy *et al.* (2011) and Indhubala *et al.* (2010) have reported non additive gene action for all the characters studied. Mengistu *et al.* (2010) for panicle weight and grain yield. Bhadure *et al.* (2015) for fresh stalk yield, juice yield, grain yield. Mohammed *et al.* (2015) for plant height and grain yield. Rani *et al.* (2020) for plant height, brix per cent, total soluble solids, juice yield and grain yield. On the contrary, the *gca* variance was higher than the *Sca* variance for days to 50% flowering (43.84 > 10.21), days to maturity (30.07 > 17.83), plant height (976.35 > 219.42), ethanol yield (35195.36 > 33381.42) indicating the presence of additive gene action. Umakanth *et al.* (2012a) reported similar results

Table 4.17. GCA and SCA variance for 13 characters in Sorghum [*Sorghum bicolor* (L.) Moench]

Source of variation	Days to 50 % flowering (days)	Days to maturity (days)	Plant height (cm)	No. of nodes per plant	Stem girth (cm)	Panicle weight (g)	1000 grain weight (g)	Fresh stalk yield (T ha ⁻¹)	Juice yield (l ha ⁻¹)	Brix %	Total soluble sugars (%)	Ethanol yield (l ha ⁻¹)	Grain yield (T ha ⁻¹)
σ^2 Gca	43.84	30.07	976.35	0.47	0.06	8.45	1.22	36.21	5564006.00	1.45	1.11	35195.36	0.08
σ^2 Sca	10.21	17.83	219.42	1.33	0.09	24.67	10.14	60.09	5804759.00	1.98	1.51	33381.42	0.11
Gca/Sca	4.29	1.68	4.44	0.35	0.66	0.34	0.12	0.60	0.95	0.73	0.73	1.05	0.77
σ^2 A(F=1)	87.68	60.14	1952.71	0.95	0.13	16.91	2.44	72.43	11128010.00	2.91	2.22	70390.71	0.17
σ^2 D(F=1)	10.21	17.83	219.42	1.33	0.09	24.67	10.14	60.09	5804759.00	1.98	1.51	33381.42	0.11
σ^2 D/ σ^2 A	8.58	3.37	8.89	0.71	1.33	0.68	0.24	1.20	1.91	1.46	1.46	2.10	1.55
(D.O.D)1/2	0.34	0.54	0.33	1.18	0.86	1.20	2.03	0.91	0.72	0.2	0.2	0.68	0.80
σ^2 A(F=0)	175.36	120.29	3905.42	1.91	0.26	33.82	4.89	144.86	22256020.00	5.82	4.45	140781.40	0.35
σ^2 D(F=0)	40.87	71.33	877.71	5.34	0.39	98.70	40.58	240.36	23219040.00	7.93	6.06	133525.70	0.45
σ^2 A/ σ^2 D	4.29	1.68	4.45	0.35	0.66	0.34	0.12	0.603	0.95	0.73	0.73	1.05	0.77
(D.O.D)1/2	0.48	0.77	0.47	1.67	1.22	1.70	2.87	1.28	1.02	1.16	1.16	0.97	1.13

Note: Highlighted text is for Gca/Sca variance.

for ethanol yield. Further these results are also confirmed by the ratios of $\sigma^2_{gca} / \sigma^2_{sca}$. Characters having ratio $\sigma^2_{gca} / \sigma^2_{sca} > 1$ indicate additive gene action and < 1 depicting the non-additive gene action. General combining ability arises due to additive gene action, while specific combining ability is due to non-additive gene action i.e. dominance and epistasis. This implies that improvement for these traits can be achieved through both selection and hybridization.

Conclusion:

Among the lines and testers the following Female parent line 1 (ICSA-14029) was found to be promising general combiner for brix content, total soluble sugars, juice yield, and ethanol yield with higher positive significant GCA effects and this line showed significant positive gca effects for days to 50 % flowering and days to maturity which can result in late flowering and late maturing types and is quite desirable for sweet sorghum which requires medium to late maturing types for maximum sugar accumulation and juice extraction (Table: 4.16). The other promising lines were line 2 (ICSA-14030) for juice yield and line 3 (ICSA-14033) for juice yield, on the other hand the line 4 (ICSA-14035) was found to be a poor combiner for all the characters.

Among the male parents, tester 3 (ICSV 15006) can be considered as a good combiner for brix %, total soluble sugars, juice yield, ethanol yield except 1000 grain weight followed by tester 2 (GGUB 28) possessing positive gca for juice yield and ethanol yield and negative gca for rest of the traits studied like days to 50 % flowering and maturity which yields early maturing hybrids possibly for usage in fodder sorghum and tester 4 (IS 29308) had positive significant gca for brix %, total soluble sugars. Tester 1 (SEVS-08) was poor combiner for ethanol yield related traits. Similar results were reported by Bahadure *et al.* (2015) for male and female parents.

Among the 16 hybrids studied, hybrid 3 with $H^+ gca \times H^+ gca$ combination (Table 4.17) has outperformed with high significant sca effects for brix%, total soluble sugars, juice yield, and ethanol yield followed by hybrid 2 with $H^+ gca \times H^- gca$ combination for brix %, total soluble sugars, juice yield ($H^+ gca \times H^+ gca$) and ethanol yield ($H^+ gca \times L^+ gca$), 1000 grain weight ($H^- gca \times H^+ gca$), panicle weight ($L^- gca \times L^+ gca$); hybrid 8 showing high sca effects for brix per cent, total soluble sugars with $L^- gca \times H^+ gca$ combination, Juice yield with $H^+ gca \times H^- gca$, ethanol yield with $L^+ gca \times H^- gca$ combination; hybrid 9 possessing high sca effects for brix, total soluble

sugars, ethanol yield with $L^- gca \times H^- gca$ combination and juice yield with $L^+ gca \times H^- gca$ combination; hybrid 10 showing positive non-significant *sca* effects for brix per cent with, total soluble sugars with $L^- gca \times H^- gca$ combination and significant *sca* effects for juice yield with $L^+ gca \times H^+ gca$ and ethanol yield with $L^- gca \times L^+ gca$ combination and hybrid 13 showing significant *sca* effects for juice and ethanol yield with $H^- gca \times H^- gca$ combination.

The best performing hybrids for 13 different characters were presented in table 4.22. Among the Hybrids H-3, H-2, H-8 and H-10 were found to be superior for juice, brix percent and ethanol content. Umakanth *et al.* (2012), while Bahadure *et al.* (2015) has observed high *sca* effects for all the crosses studied, Bhunpan *et al.* (2014) observed five cross combinations for sugar yield. Soujanya *et al.* (2017) for four cross combinations for single cut forage sorghum. Jadav and Desmukh (2017) found four cross combinations for grain yield. Ingle *et al.* (2018) for three hybrids for grain yield, Rani *et al.* (2020) for two hybrid combinations for ethanol yield.

The above presented results indicated that the crosses with high *sca* effects for desirable characters are possible from the parental combinations of ($H^+ \times H^+$); ($H^+ \times H^-$); ($L^+ \times H^+$); ($L^+ \times H^-$); ($L^- \times L^+$) and ($L^- \times H^+$). The cross between two high *gca* revealed additive and additive x additive genetic components. The cross between high x high *gca* resulted in exclusive cross combination which might be due to duplicate action raised out of both additive and non-additive genetic components. The superiority of the crosses having low *gca* parent may be due to high nicking ability of the parents.

High significant *sca* effects for grain yield in H-5 (0.586) and non-significant positive *Sca* effects for hybrid 2, 4, 8, 12, 13, 14, 15 and 16 was observed.

4.5.6 Heterosis

Since the expression of heterosis is under the influence of genetic diversity of parents all the 16 hybrids generated in L x T mating design needs to be evaluated for identification of desirable heterotic combinations as the heterosis phenomenon is confined only to F_1 generation and mostly governed either by nuclear genes alone or in combination and interaction with cytoplasm demands precise estimation in different mean ways available such that the same can be exploited for bringing improvement. The data collected is analysed for estimating three types of heterosis and the results thus obtained in respect of 13 different quantitative characters for both parents and hybrids are presented in Table 4.18.1 to 4.18.5 and 4.19.

4.5.6.1 Days to 50 per cent flowering (days)

The Mid parent heterosis ranged from -19.78 (ICSA 14035 x GGUB 28) to 21.24 per cent (ICSA 14029 x IS 29308). With respect to standard heterosis cross (ICSA 14029 x IS 29308) has shown high positive heterosis (1.67) while cross (ICSA 14035 x GGUB 28) has shown high negative heterosis (-33.40). In case of better parent heterosis same crosses have reported similar results. The F₁ hybrid of (ICSA 14029 x IS 29308), is desirable because of positive standard heterosis which can result in late flowering type which is suitable for sweet sorghum. (ICSA 14029 x ICSV 15006) for medium maturing type. Prabhakar (2001), Umakanth *et al.* (2006) had reported similar results for this trait.

4.5.6.2 Days to maturity (days)

The cross (ICSA 14035 x GGUB 28) has reported high negative heterosis (-12.91) (-13.78) and (-19.82) in case of mid parent, better parent and standard parent heterosis respectively, which indicates for early maturing types useful for fodder purpose. While high positive heterosis was reported in cross (ICSA 14035 x SEVS -08) for mid parent (12.15) and in cross (ICSA 14030 x SEVS-08) for better parent (11.04) and cross ICSA 14030 x IS 29308(-0.66) for standard parent. Prabhakar (2001), Umakanth *et al.* (2006) had reported similar results for this trait.

Hybrids of crosses ICSA 14030 x IS 29308 (-0.66) were found to be late maturing when compared to standard check variety.

4.5.6.3 Plant height (cm)

Hybrid ICSA 14030 x ICSV 15006 has recorded positive heterosis for mid parent (44.49), (33.17) and better parent respectively. When compared to standard check, none of the hybrids have quoted high positive heterosis, while the results are deviating from the results of Ingle *et al.* (2018) where positive heterosis was observed for the studied F₁ hybrids.

High negative heterosis was outlined in the cross ICSA 14035 x GGUB 28 (-31.54), (-49.49), (-48.57) for mid parent, better parent and standard heterosis respectively which means this hybrid is dwarf among the hybrids studied, which is desirable when combined with the output of high ethanol yield.

4.5.6.4 Number of nodes per plant

Positive significant mid parent heterosis was resulted in the hybrid of cross ICSA 14035 x IS-29308 (17.83) and in case of better parent heterosis cross ICSA 14030 x ICSV 15006 has resulted in positive significant heterosis (8.96) and in case of standard heterosis none of the crosses have resulted in positive heterosis. Pandey and Shrotria (2012) had reported positive result in case of standard heterosis.

For mid parent heterosis hybrid of cross ICSA 14029 x GGUB 28 (-19.44) was found negative significant and for better parent and standard heterosis ICSA 14035 x GGUB 28(-34.12) (-36.36) was found to be negative significant respectively.

4.5.6.5 Stem girth (cm)

Mid parent negative heterosis value of (-41.41) has been reported in cross ICSA 14030 x SEVS -08, better parent value of (- 40.54) was reported in cross ICSA 14033 x SEVS-08 and in cross ICSA 14030 x IS 29308 has reported negative significant heterosis value (-27.13).

Stem girth combined with plant height contribute for fresh stalk yield so high stem girth is desirable. In this study positive significant better parent heterosis was observed for ICSA 14030 x IS 29308 (48.35) and for standard parent heterosis cross ICSA 14033 x ICSV-15006 has shown highest value (37.98). Most of the hybrids have shown positive significant values over the better parent like ICSA 14030 x ICSV 15006 (37.21), ICSA 14035 x ICSV-15006 (24.03), ICSA 14030 x GGUB 28 (21.71), ICSA 14029 x ICSV-15006 and ICSA 14035 x SEVS-08 (20.16). Kumar *et al.* (2016) quoted similar positive heterobeltiosis results.

4.5.6.6 Panicle weight (g)

Cross ICSA 14030 x SEVS -08 has reported (39.43) highest positive significant heterosis, while cross ICSA 14029 x GGUB 28 (4.85) for better parent and ICSA 14030 x SEVS-08 (17.08) for standard parent. Most of the crosses have reported negative heterosis except ICSA 14029 x GGUB 28 (3.77), ICSA 14029 x ICSV-15006(0.57), ICSA 14030 x ICSV 15006 (2.67), ICSA 14030 x IS 29308 (5.13) which reported positive standard heterosis.

Table 4.18.1. Mean performance and heterosis (%) over mid parent (MP), better parent (BP) and standard heterosis (STD) for days to 50% flowering, days to maturity in 16 Sorghum [*Sorghum bicolor* (L.) Moench] hybrids

			1. Days to 50% flowering				2. Days to maturity		
S.No	HYBRIDS	Mean	MP Heterosis	BP Heterosis	STD Heterosis	Mean	MP Heterosis	BP Heterosis	STD Heterosis
H-1	ICSA 14029 x SEVS-08	80.33	7.23**	1.47*	-10.58**	125.00	8.54**	3.88**	-0.92
H-2	ICSA 14029 x GGUB 28	65.50	-12.57**	-17.26**	-27.09**	109.17	-8.13**	-9.28**	-13.47**
H-3	ICSA 14029 x ICSV-15006	78.83	3.96**	-0.42	-12.24**	123.00	4.53**	2.22**	-2.51**
H-4	ICSA 14029 x IS 29308	91.33	21.24**	15.37**	1.67**	124.50	6.11**	3.46**	-1.32
H-5	ICSA 14030 x SEVS -08	82.67	15.48**	4.42**	-7.98**	122.33	11.13**	11.04**	-3.04**
H-6	ICSA 14030 x GGUB 28	62.67	-12.46**	-20.84**	-30.24**	104.17	-8.42**	-11.22**	-17.44**
H-7	ICSA 14030 x ICSV 15006	80.00	10.34**	1.05	-10.95**	123.33	9.55**	7.25**	-2.25**
H-8	ICSA 14030 x IS 29308	82.50	14.58**	4.21**	-8.16**	125.33	11.66**	9.62**	-0.66
H-9	ICSA 14033 x SEVS-08	81.83	7.44**	3.37**	-8.91**	119.67	3.46**	-1.37	-5.15**
H-10	ICSA 14033 x GGUB -28	66.67	-12.47**	-15.79**	-25.9**	115.00	-3.63**	-5.22**	-8.85**
H-11	ICSA 14033 x ICSV-15006	79.17	2.70**	0.00	-11.87**	121.83	3.10**	0.41	-3.43**
H-12	ICSA 14033 x IS-29308	83.50	9.03**	5.47**	-7.05**	118.50	0.57	-2.34**	-6.08**
H-13	ICSA 14035 x SEVS-08	83.17	11.51**	5.05**	-7.42**	126.17	12.15 **	9.71**	0.00
H-14	ICSA 14035 x GGUB 28	59.83	-19.78**	-24.42**	-33.40**	101.17	-12.91**	-13.78**	-19.82**
H-15	ICSA 14035 x ICSV-15006	79.67	5.52**	0.63	-11.32**	124.00	7.83**	7.83**	-1.2*
H-16	ICSA 14035 x IS-29308	78.17	4.22**	-1.26	-12.99**	117.83	2.76**	2.46**	-6.61**
	S.E		0.46	0.53	1.25		0.81	0.93	0.93
	CD @ 5%		0.94	1.08	1.45		1.63	1.89	1.89
	CD @ 1%		0.53	1.08	1.45		2.18	2.52	2.52

NOTE: * and ** Significant at 5 and 1 per cent level respectively

MP = Mid parent; BP = Better parent; STD = Standard heterosis

Contd...

Table 4.18.2. Mean performance and heterosis (%) over mid parent (MP), better parent (BP) and standard heterosis (STD) for plant height, number of nodes per plant in 16 Sorghum [*Sorghum bicolor* (L.) Moench] hybrids

		3. Plant height (cm)				4. Number of nodes per plant			
S.No	HYBRIDS	Mean	MP Heterosis	BP Heterosis	STD Heterosis	Mean	MP Heterosis	BP Heterosis	STD Heterosis
H-1	ICSA 14029 x SEVS-08	123.30	-17.61**	-27.99**	-28.90**	10.17	-15.28**	-28.24**	-30.68**
H-2	ICSA 14029 x GGUB 28	178.52	-27.27**	-45.80**	-46.48**	9.67	-19.44 **	-31.76**	-34.09**
H-3	ICSA 14029 x ICSV-15006	289.14	15.38**	12.26**	-13.37**	12.17	0.00	-14.12**	-17.05**
H-4	ICSA 14029 x IS 29308	261.30	3.49**	-20.71**	-21.71**	10.67	-10.49**	-24.71**	-27.27**
H-5	ICSA 14030 x SEVS -08	264.30	17.48**	7.24**	-20.81**	11.33	7.94*	1.49	-22.73**
H-6	ICSA 14030 x GGUB 28	172.09	-5.74**	-15.44**	-48.44**	9.00	-14.29**	-19.40**	-38.64**
H-7	ICSA 14030 x ICSV 15006	271.01	44.49**	33.17**	-18.80**	12.17	14.06**	8.96*	-17.05**
H-8	ICSA 14030 x IS 29308	258.58	36.49**	27.07**	-22.53**	9.17	-12.00**	-17.91**	-37.50**
H-9	ICSA 14033 x SEVS-08	255.31	-9.74**	-20.03**	-23.51**	12.67	5.56	-10.59**	-13.64**
H-10	ICSA 14033 x GGUB -28	178.42	-25.79**	-44.11**	-46.54**	12.17	1.39	-14.12**	-17.05**
H-11	ICSA 14033 x ICSV-15006	271.68	10.69**	-14.90**	-18.60**	10.83	-10.96**	-23.53**	-26.4**
H-12	ICSA 14033 x IS-29308	248.48	0.47	-22.16**	-25.55**	12.50	4.90	-11.76**	-14.77**
H-13	ICSA 14035 x SEVS-08	274.0	-6.26**	-19.14**	-17.67**	11.50	6.15	-18.82**	-21.59**
H-14	ICSA 14035 x GGUB 28	171.65	-31.54**	-49.49**	-48.57**	9.33	-13.85**	-34.12**	-36.36**
H-15	ICSA 14035 x ICSV-15006	247.63	-3.18*	-27.14**	-25.81**	11.17	1.52	-21.18**	-23.86**
H-16	ICSA 14035 x IS-29308	276.52	7.33**	-18.64**	-17.15**	12.67	17.83**	-10.59**	-13.64**
	S.E		3.22	3.72	8.68		0.37	0.43	0.43
	CD @ 5%		6.50	7.50	10.02		0.75	0.87	0.87
	CD @ 1%		8.68	7.50	10.02		1.01	1.16	1.16

NOTE: * and ** Significant at 5 and 1 per cent level respectively

MP = Mid parent; BP = Better parent; STD = Standard heterosis

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4.5.6.7 1000 grain weight (g)

Positive heterosis was observed in all the hybrids with respect to mid parent and better parent heterosis except in ICSA 14033 x GGUB -28 (-3.70). Positive heterosis is desirable for this trait, yet no positive standard heterosis was observed in any one of the hybrids. Vyas *et al.* (2014a) observed similar results for mid and better parent heterosis.

All the hybrids have shown negative standard heterosis for 1000 grain weight. The cross ICSA 14029 x ICSV-15006 has recorded the lowest positive significant heterosis (1.19). The cross ICSA 14033 x GGUB -28 has shown negative significant better parent heterosis (-3.70).

4.5.6.8 Fresh stalk yield (T ha⁻¹)

Mid parent heterosis among the hybrids for Fresh stalk yield ranged from significantly negative -40.99 (ICSA 14030 x IS 29308) to 25.58 (ICSA 14030 x ICSV 15006). Whereas, the better parent heterosis too varied significantly and ranged from -47.97 per cent (ICSA 14030 x IS 29308) to 34.59 per cent (ICSA 14033 x SEVS-08). The standard heterosis was found to be significantly positive. In the hybrid viz., (ICSA 14029 x ICSV-15006 with 41.50 per cent followed by ICSA 14030 x ICSV 15006 with 40.10 per cent. Kumar *et al.* (2016) and Chikuta *et al.* (2017) has observed similar results.

4.5.6.9 Juice yield (l ha⁻¹)

The hybrids ICSA 14033 x GGUB-28 followed by ICSA 14030 x ICSV 15006 and ICSA 14033 x ICSV 15006 have recorded significantly superior mid parent heterosis in positive direction, whereas the hybrid ICSA 14029 x IS 29308 recorded negatively significant heterosis of 42.17 %. The hybrid ICSA 14033 x GGUB-28 has recorded significantly positive better parent heterosis of 69.44 % followed by ICSA 14033 x ICSV 15006 with 34.92 %. The hybrid ICSA 14029 x IS 29308 followed by ICSA 14035 x IS-29308 and ICSA 14035 x GGUB-28 have recorded significantly negative better parent heterosis of -58.66, -40.93 and -38.05 respectively. 11 out of 16 hybrids have recorded significantly positive standard heterosis. Of the remaining five hybrids ICSA 14029 x IS 29308 and ICSA 14033 x IS -29308 have recorded significantly negative standard heterosis.

Table 4.18.3. Mean performance and heterosis (%) over mid parent (MP), better parent (BP) and standard (STD) for stem girth (g), panicle weight (g) in 16 Sorghum [*Sorghum bicolor* (L.) Moench] hybrids.

S.No	HYBRIDS	5. Stem girth (cm)				6. Panicle weight (g)			
		Mean	MP Heterosis	BP Heterosis	STD Heterosis	Mean	MP Heterosis	BP Heterosis	STD Heterosis
H-1	ICSA 14029 x SEVS-08	2.07	-22.26**	-32.97**	-3.88	42.01	-1.36	-14.26**	-17.67**
H-2	ICSA 14029 x GGUB 28	2.28	-13.84**	-25.54**	6.20*	52.95	22.18**	4.85	3.77
H-3	ICSA 14029 x ICSV-15006	2.58	-7.46**	-22.89**	20.16**	51.32	14.43**	-4.10	0.57
H-4	ICSA 14029 x IS 29308	2.33	-11.39**	-23.08**	8.53**	46.37	-4.16	-23.47**	-9.13**
H-5	ICSA 14030 x SEVS -08	1.73	-41.41**	43.78**	-19.38**	59.74	39.43**	21.92**	17.08**
H-6	ICSA 14030 x GGUB 28	2.62	-11.30**	-14.67**	21.71**	48.38	10.95**	-4.21	-5.20
H-7	ICSA 14030 x ICSV 15006	2.95	-4.58**	-11.94**	37.21**	52.39	16.15**	-2.11	2.67
H-8	ICSA 14030 x IS 29308	1.57	-46.59**	48.35**	-27.13**	53.65	10.29**	-11.46**	5.13
H-9	ICSA 14033 x SEVS-08	1.83	-37.85**	-40.54**	-14.73**	48.63	0.89	-0.75	-4.69
H-10	ICSA 14033 x GGUB -28	2.55	-13.31**	-16.85**	18.60**	46.72	-4.56	-7.48*	-8.44**
H-11	ICSA 14033 x ICSV-15006	2.97	-3.78**	-11.44**	37.98**	48.61	-3.67	-9.17*	-4.74
H-12	ICSA 14033 x IS-29308	2.17	-25.93**	-28.57**	0.78	50.22	-7.01**	-17.12**	-1.59
H-13	ICSA 14035 x SEVS-08	2.58	-3.73*	-16.22**	20.16**	46.21	-2.68	-5.69	-9.44**
H-14	ICSA 14035 x GGUB 28	2.25	-15.89**	26.63**	4.65	48.51	0.57	-3.95	-4.94
H-15	ICSA 14035 x ICSV-15006	2.67	-5.33**	-20.40**	24.03**	46.58	-6.37*	-12.97**	-8.73**
H-16	ICSA 14035 x IS-29308	2.15	-19.12**	-29.12**	0.00	34.97	-34.37**	-42.29**	-31.47**
	S.E		0.04	0.05	0.12		1.24	1.44	1.44
	CD @ 5%		0.09	0.10	0.14		2.51	2.90	2.90
	CD @ 1%		0.12	0.14	0.14		3.36	3.87	3.87

NOTE: * and ** Significant at 5 and 1 per cent level respectively

MP = Mid parent; BP = Better parent; STD = Standard heterosis

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Table: 4.18 Contd...

Table 4.18.4. Mean performance and heterosis (%) over mid parent (MP), better parent (BP) and standard heterosis (STD) for 1000 grain weight, fresh stalk yield (T ha⁻¹) in 16 Sorghum [*Sorghum bicolor* (L.) Moench] hybrids.

S.No	HYBRIDS	7. 1000 grain weight (g)				8. Fresh stalk yield (T ha ⁻¹)			
		Mean	MP Heterosis	BP Heterosis	STD Heterosis	Mean	MP Heterosis	BP Heterosis	STD Heterosis
H-1	ICSA 14029 x SEVS-08	31.86	11.32**	2.44	-22.04**	43.32	-14.09**	-21.21**	-1.38
H-2	ICSA 14029 x GGUB 28	36.60	21.66**	17.69**	-10.44**	46.12	-8.15**	15.46**	5.00**
H-3	ICSA 14029 x ICSV-15006	31.46	1.19	1.16	-23.01**	62.15	20.59**	8.64**	41.50**
H-4	ICSA 14029 x IS 29308	33.63	9.91**	8.14*	-17.70**	45.02	-9.34**	-15.75**	2.49
H-5	ICSA 14030 x SEVS -08	34.09	9.63**	9.62**	-16.58**	35.65	-25.55**	-35.16**	-18.84**
H-6	ICSA 14030 x GGUB 28	36.78	12.95**	18.26**	-10.00**	46.47	-2.53	-14.82**	5.79**
H-7	ICSA 14030 x ICSV 15006	34.86	3.85	12.09**	-14.70**	61.53	25.58**	7.57**	40.10**
H-8	ICSA 14030 x IS 29308	37.13	12.25**	19.39**	-9.14**	27.80	-40.99**	-47.97**	-36.71**
H-9	ICSA 14033 x SEVS-08	40.52	54.29**	30.27**	-0.86	35.97	-32.26**	34.59**	-18.12**
H-10	ICSA 14033 x GGUB -28	29.95	8.02*	-3.70	-26.71**	41.19	-22.11**	-24.51**	-6.23**
H-11	ICSA 14033 x ICSV-15006	32.38	12.70**	4.12	-20.76**	59.14	9.11**	3.38*	34.64**
H-12	ICSA 14033 x IS-29308	32.93	16.59**	5.87	-19.43**	43.40	-17.05**	-18.78**	-1.20
H-13	ICSA 14035 x SEVS-08	34.07	33.66**	9.53**	-16.64**	46.26	-8.33**	-15.86**	5.32**
H-14	ICSA 14035 x GGUB 28	38.91	44.36**	25.11**	-4.79	36.22	-27.92**	-33.61**	-17.54**
H-15	ICSA 14035 x ICSV-15006	31.78	13.67**	2.19	-22.23**	38.18	-25.97**	-33.25**	-13.07**
H-16	ICSA 14035 x IS-29308	32.44	18.08**	4.29	-20.64**	38.36	-22.80**	-28.21**	-12.66**
	S.E		0.88	1.01	1.01		0.62	0.72	0.72
	CD @ 5%		1.77	2.05	2.05		1.26	1.46	1.46
	CD @ 1%		2.37	2.74	2.74		1.69	1.95	1.95

NOTE: * and ** Significant at 5 and 1 per cent level respectively
MP = Mid parent; BP = Better parent; STD = Standard heterosis

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4.5.6.10 Brix %

The cross ICSA 14033 x GGUB-28 has revealed high mid parent heterosis in negative direction (-25.77 per cent) while the heterosis in positive direction was 23.93 per cent as recorded by the cross combination of ICSA 14030 x GGUB 28. The magnitude of better parent heterosis ranged from -30.61 (ICSA 14035 x GGUB 28) to -2.08 (ICSA 14030 x IS 29308). Over standard check, the hybrid ICSA 14030 x GGUB 28 displayed highest negative heterosis of -20.51 per cent, while the hybrid ICSA 14033 x ICSV-15006 with 23.08 per cent standard heterosis in positive direction was on the other extreme.

Other hybrids which excelled than standard parent are ICSA 14029 x ICSV-15006 (20.51); ICSA 14030 x IS 29308 (20.51); ICSA 14035 x IS-29308 (19.23); ICSA 14029 x SEVS-08; ICSA 14030 x ICSV 15006 (12.82). The results presented here are in accordance with Sandeep *et al.* (2009) and Pothisoong and Jaisil (2011).

4.5.6.11 Total soluble sugars (%)

The magnitude of mid parent heterosis ranged from -26.13 (ICSA 14035 x GGUB-28) to 17.99 per cent in (ICSA 14029 x ICSV-15006). The better parent heterosis also varied from -27.87 (ICSA 14035 x GGUB 28) - to -0.86 per cent (ICSA 14030 x IS 29308). Heterosis of -12.66 per cent over the standard check was observed in the cross ICSA 14035 x SEVS-08 while the heterosis was positive and highest (22.75 per cent) in ICSA 14033 x ICSV-15006.

4.5.6.12 Ethanol yield (l ha⁻¹)

Mid parent heterosis among the hybrids for ethanol yield ranged from -42.07 (ICSA 14035 x GGUB 28 to 84.69 (ICSA 14030 x ICSV 15006) and the better parent heterosis varied from -41.81 per cent (ICSA 14029 x IS 29308) to 54.74 per cent (ICSA 14029 x ICSV-15006). The standard heterosis was found highest in the hybrid (ICSA 14029 x ICSV-15006) with 125.54 per cent in positive direction while hybrid (ICSA 14033 x IS-29308) was towards other extreme but in negative direction *i.e.*, -17.44 per cent. Vinaykumar *et al.* (2011) and Kumar *et al.* (2016) has observed similar results.

4.5.6.13 Grain yield (T ha⁻¹)

Heterosis over the mid parent, better parent and standard check were found to be respectively significant with -34.01, -47.28, -32.08 as recorded by the hybrid ICSA 14035 x IS-29308. While significantly highest heterosis in the positive direction was 39.03, 12.62, 6.1 per cent (ICSA 14030 x SEVS -08) for mid parent, better parent and standard heterosis respectively.

Table 4.18 Contd...

Table 4.18.5: Mean performance and heterosis (%) over mid parent (MP), better parent (BP) and standard check (STD) for Juice yield (l ha⁻¹), brix% in 16 Sorghum [*Sorghum bicolor* (L.) Moench] hybrids

S.No.	HYBRIDS	9. Juice yield (l ha ⁻¹)				10.Brix %			
		Mean	MP Heterosis	BP Heterosis	STD Heterosis	Mean	MP Heterosis	BP Heterosis	STD Heterosis
H-1	ICSA 14029 x SEVS-08	14281.47	0.04	-24.48**	46.84**	11.33	-11.11**	-27.66**	12.82**
H-2	ICSA 14029 x GGUB 28	17180.23	21.04**	-9.15**	76.64**	14.00	7.01**	-14.29**	7.69**
H-3	ICSA 14029 x ICSV-15006	18066.65	33.22**	-4.47	85.76**	15.67	18.24**	-6.00**	20.51**
H-4	ICSA 14029 x IS 29308	7817.28	-42.17**	-58.66**	-19.62**	13.83	7.10**	-13.54**	6.41*
H-5	ICSA 14030 x SEVS -08	10227.15	-14.19**	-27.97**	5.15	11.67	-11.95**	-25.53**	-10.26**
H-6	ICSA 14030 x GGUB 28	15933.32	34.61**	12.23**	63.82**	10.33	23.93**	-36.73**	-20.51**
H-7	ICSA 14030 x ICSV 15006	18348.13	63.75**	29.23**	88.65**	14.67	6.67**	-12.00**	12.82**
H-8	ICSA 14030 x IS 29308	11316.04	1.39	-20.30**	16.35**	15.67	16.77**	-2.08	20.51**
H-9	ICSA 14033 x SEVS-08	13397.52	32.71**	26.98**	37.75**	12.83	-18.95**	-19.79**	-1.28
H-10	ICSA 14033 x GGUB -28	17876.53	78.52**	69.44**	83.80**	12.00	-25.77**	-26.53**	-7.69**
H-11	ICSA 14033 x ICSV-15006	14234.55	51.73**	34.92**	46.36**	16.00	-2.04	-4.00	23.08**
H-12	ICSA 14033 x IS-29308	8720.98	-6.60	-17.34**	-10.33*	12.00	-25.00**	-25.00**	-7.69**
H-13	ICSA 14035 x SEVS-08	12812.33	-2.15	-22.58**	31.73**	11.33	-23.60**	-27.66**	-12.82**
H-14	ICSA 14035 x GGUB 28	10251.84	-21.21**	-38.05**	5.41	11.33	-25.27**	-30.61**	-12.82**
H-15	ICSA 14035 x ICSV-15006	16286.40	31.55**	-1.58	67.75**	14.33	-6.52**	-14.00**	10.26**
H-16	ICSA 14035 x IS-29308	9775.30	-20.76**	-40.93**	0.51	15.50	3.33	-3.13	19.23**
	S.E		402.09	464.29	464.29		0.30	0.35	0.35
	CD @ 5%		809.85	935.13	935.13		0.61	0.70	0.70
	CD @ 1%		1081.46	1248.76	1248.76		0.81	0.94	0.94

NOTE: * and ** Significant at 5 and 1 per cent level respectively

MP = Mid parent; BP = Better parent; STD = Standard heterosis

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In all the 16 hybrids studied most of the crosses had negative standard heterosis as well as better parent heterosis. While positive mid parent heterosis was reported for crosses ICSA 14029 x GGUB 28 (3.16), ICSA 14029 x ICSV 15006 (14.39), ICSA 14030 x GGUB 28 (3.47), ICSA 14030 x ICSV 15006 (9.77), ICSA 14030 x IS 29308 (2.18), ICSA 14033 x SEVS-08 (8.67), ICSA 14035 x ICSV-15006 (1.77). The results obtained here are deviating from the results presented by Vinaykumar *et al.* (2011), Vyas *et al.* (2014a), Kumar *et al.* (2016), Ingle *et al.* (2018) for standard heterosis and Chikuta *et al.* (2017), meera *et al.* (2020), Liming *et al.* (2020) reported similar result for mid parent heterosis.

Conclusion: The range of heterosis over mid parent, better parent and commercial check indicated that it was high with respect to ethanol productivity related traits particularly juice yield and brix per cent. However, it was deviating for days to 50 per cent flowering, days to maturity, number of nodes per plant, plant height, and 1000 grain weight which has shown negative heterosis. As far as ethanol and juice yields are concerned medium flowering and intermediate plant height are desirable. As observed in the correlation studies grain yield and ethanol yield are found to be contrary traits. In hybrids, there is an improvement in the juice, brix per cent and ethanol yield, but heterosis is limited for 1000 grain weight and ultimately grain yield.

Considering standard heterosis as reference point and based upon the magnitude of standard heterosis in respect of juice yield, brix and ethanol yield, following six hybrids have performed well ICSA 14029 x ICSV-15006; ICSA 14030 x ICSV 15006; ICSA 14035 x ICSV-15006; ICSA 14029 x GGUB 28; ICSA 14030 x GGUB 28 and ICSA 14033 x ICSV-15006. These six hybrid combinations may thus be considered as the combinations which can be used as dual types for both ethanol and grain. Thus they can be exploited for both the economic end products either through hybrids. This situation support draws from the argument of Arunachalam (1976) who suggested that additive, additive $\times$ additive based gene interactions can also result in heterosis.

The parents acting as best and poor combiners for different characters and hybrids with high SCA effects, Top ranking hybrids for specific combining ability with their *per se* performance, Standard heterosis were presented in Tables: 4.20-4.22.

Table 4.18.6. Mean performance and heterosis (%) over mid parent (MP), better parent (BP) and standard check (STD) for Total soluble sugars (%), Ethanol yield (l ha⁻¹) in 16 Sorghum [*Sorghum bicolor* (L.) Moench] hybrids

S. No.	HYBRIDS	11. Total soluble sugars (%)				12. Ethanol yield (l ha ⁻¹)			
		Mean	MP Heterosis	BP Heterosis	STD Heterosis	Mean	MP Heterosis	BP Heterosis	STD Heterosis
H-1	ICSA 14029 x SEVS-08	10.06	-9.62**	-25.56**	-12.66**	764.88	-2.01	-12.06**	28.01**
H-2	ICSA 14029 x GGUB 28	12.40	9.20**	-11.16**	7.59**	1130.31	43.46**	29.96**	89.17**
H-3	ICSA 14029 x ICSV-15006	13.85	17.99**	-5.95**	20.24**	1345.87	77.55**	54.74**	125.24**
H-4	ICSA 14029 x IS 29308	12.25	7.82**	-12.33**	6.34*	506.11	-31.13**	-41.81**	-15.30*
H-5	ICSA 14030 x SEVS -08	10.36	-10.52**	-23.40**	-10.13**	535.27	-24.03**	-38.46**	-10.42
H-6	ICSA 14030 x GGUB 28	9.19	-22.05**	-34.14**	-20.24**	815.38	14.53**	-6.25	36.46**
H-7	ICSA 14030 x ICSV 15006	12.98	6.58**	-11.88**	12.66**	1259.71	84.69**	44.84**	110.82**
H-8	ICSA 14030 x IS 29308	13.86	17.41**	-0.86	20.25**	802.38	21.77**	-7.75	34.28**
H-9	ICSA 14033 x SEVS-08	11.38	-17.76**	-15.84**	-1.26	777.07	5.39	-10.65*	30.05**
H-10	ICSA 14033 x GGUB -28	10.65	-24.23**	-23.70**	-7.59**	1004.05	34.84**	15.44**	68.03**
H-11	ICSA 14033 x ICSV-15006	14.14	-2.05	-3.98	22.75**	1078.60	50.90**	24.01**	80.51**
H-12	ICSA 14033 x IS-29308	10.65	-24.29**	-23.82**	-7.59**	493.32	-28.67**	-43.28**	-17.44**
H-13	ICSA 14035 x SEVS-08	10.06	-24.95**	-25.56**	-12.66**	695.96	-23.77**	-19.98**	16.47*
H-14	ICSA 14035 x GGUB 28	10.06	-26.13**	-27.87**	-12.64**	533.13	-42.07**	-38.70**	-10.78
H-15	ICSA 14035 x ICSV-15006	12.69	-9.46**	-13.86**	10.13**	1150.25	29.18**	32.25**	92.50**
H-16	ICSA 14035 x IS-29308	13.71	0.53	-1.91	18.98**	740.07	-14.67**	-14.91**	23.86**
	S.E		0.26	0.30	0.30		31.73	36.45	36.64
	CD @ 5%		0.53	0.61	0.61		63.91	73.80	73.80
	CD @ 1%		0.71	0.61	0.82		85.35	98.56	98.56

NOTE: * and ** Significant at 5 and 1 per cent level respectively

MP = Mid parent; BP = Better parent; STD = Standard heterosis

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Table 4.18.7. Mean performance and heterosis (%) over mid parent (MP), better parent (BP) and standard check (STD) for grain yield in 16 Sorghum [*Sorghum bicolor* (L.) Moench] hybrids

S. No.	HYBRIDS	13.Grain yield (T ha ⁻¹)			
		Mean	MP Heterosis	BP Heterosis	STD Heterosis
H-1	ICSA 14029 x SEVS-08	4.03	-2.18	-14.90*	-19.59**
H-2	ICSA 14029 x GGUB 28	4.73	3.16	-16.48*	-5.71
H-3	ICSA 14029 x ICSV-15006	5.07	14.39*	-5.30	0.96
H-4	ICSA 14029 x IS 29308	4.57	-8.39	-29.34**	-8.97
H-5	ICSA 14030 x SEVS -08	5.34	39.03*	12.62	6.1
H-6	ICSA 14030 x GGUB 28	4.45	3.47	-21.42**	-11.29
H-7	ICSA 14030 x ICSV 15006	4.55	9.77	-14.95*	-9.33
H-8	ICSA 14030 x IS 29308	4.81	2.18	-25.68**	-4.25
H-9	ICSA 14033 x SEVS-08	4.77	8.67	0.63	-4.2
H-10	ICSA 14033 x GGUB -28	4.82	-0.64	-14.89*	-3.92
H-11	ICSA 14033 x ICSV-15006	4.78	1.77	-10.69	-4.78
H-12	ICSA 14033 x IS-29308	5.17	-1.63	-20.08**	2.96
H-13	ICSA 14035 x SEVS-08	3.89	-9.60	-17.96*	-22.48**
H-14	ICSA 14035 x GGUB 28	4.24	-10.98	-25.13**	-15.48*
H-15	ICSA 14035 x ICSV-15006	4.04	-12.21*	-24.39**	-19.40**
H-16	ICSA 14035 x IS-29308	3.41	-34.01**	-47.28**	-32.08**
	S.E		0.27	0.31	0.31
	CD @ 5%		0.31	0.64	0.64
	CD @ 1%		0.31	0.85	0.85

NOTE: * and ** Significant at 5 and 1 per cent level respectively

MP = Mid parent; BP = Better parent; STD = Standard heterosis

Table 4.19. Range of heterosis % in 13 characters of 16 sorghum [*Sorghum bicolor* (L.) Moench] hybrids

S. No.	Character	Mid parent	Better parent	Standard parent
1	DAF 50%	-19.58 to 21.24	-24.42 to 15.37	-33.40 to 1.67
2	DM	-12.91 to 12.15	-13.78 to 11.04	-19.82 to -0.66
3	PH	-31.54 to 44.49	-49.49 to 33.17	-48.57 to -13.37
4	N.N.S	-19.44 to 17.83	-34.12 to 8.96	-36.36 to -13.64
5	SG	-41.41 to -3.73	-40.54 to 48.35	-27.13 to 37.98
6	PW	-34.37 to 39.43	-42.29 to 4.85	-31.47 to 17.08
7	1000 GW	1.19 to 54.29	-3.70 to 30.27	-26.71 to -0.86
8	FSTK	-40.99 to 25.58	-47.97 to 34.59	-36.71 to 41.50
9	JY	-42.17 to 78.52	-58.66 to 69.44	-19.62 to 88.65
10	BRIX %	-25.77 to 23.93	-30.61 to -2.08	-20.51 to 23.08
11	TSS	-26.13 to 17.99	-27.87 to -0.86	-12.66 to 22.75
12	EY	-42.07 to 84.69	-41.81 to 54.74	-17.44 to 125.24
13	GY	-34.01 to 39.03	-47.28 to 12.62	-32.08 to 6.1

DAF 50%= Days to 50% flowering (Days), **D.M**= Days to maturity (Days), **PH**= Plant height (cm), **N.N.S**= Number of nodes per plant, **SG**= Stem girth (cm), **PW**= Panicle weight (g), **1000 GW**= 1000 grain weight (g), **FSTK**= Fresh stalk yield (T ha⁻¹), **JY**= Juice yield (l ha⁻¹), **Brix %**, **TSS** = Total soluble sugars (%), **EY**= Ethanol yield (l ha⁻¹), **GY** = Grain yield (T ha⁻¹).

Table 4.20. Parents acting as best and poor combiners for different characters

S. No.	Parents (4 lines and 4 testers)	Best combiner for characters	Poor combiner for characters
1	ICSA 14029	Days to 50% flowering, Fresh stalk yield, Total soluble sugars, brix, Juice yield and Ethanol yield	No. of nodes per plant, Stem girth, 1000 seed weight, Panicle weight
2	ICSA 14030	Panicle weight, Juice yield and Grain yield	Days to 50% flowering, Days to maturity, No. of nodes per plant, Fresh stalk yield, Stem girth, Brix %, Total soluble sugars
3	ICSA 14033	Days to 50% flowering, No. of nodes per plant, Fresh stalk yield, Stem girth and Grain yield	Days to maturity, Plant height, 1000 grain weight, Panicle weight, Brix%, Total soluble sugars, Juice and Ethanol yield
4	ICSA 14035	Stem girth, No.of nodes per plant, Plant height	Poor combiner for remaining 10 traits
5	SEVS-08	Days to 50% flowering, Days to maturity, No. of nodes per plant, Plant height, 1000 Grain weight	Brix, Total soluble sugars, Juice yield, Ethanol yield and Grain yield.
6	GGUB 28	Juice yield and Ethanol yield	Days to 50% flowering, Days to maturity, No.of nodes per plant, Plant height, Fresh stalk weight,Brix %, Total soluble sugars
7	ICSV 15006	Days to 50% flowering, Days to maturity, No.of nodes per plant, plant height, Fresh stalk weight, Stem girth, Panicle weight, Brix %, Total soluble sugars, Juice yield, Ethanol yield, grain yield	1000 Grain weight
8	IS 29308	Days to 50% flowering, Days to maturity, No.of nodes per plant, Plant height, Brix, Total soluble sugars.	Fresh stalk weight,1000 Grain weight, Panicle weight, Panicle weight, Juice yield, Ethanol yield, Grain yield

Table 4.21. Hybrids with high SCA effects in different characters

S. No.	Hybrids	Characters with high SCA effect	Desirable/undesirable
1	ICSA 14029 x SEVS-08	Juice yield, Stem girth	Desirable
2	ICSA 14029 x GGUB 28	Brix %, Total soluble sugars, Juice and Ethanol yield	Desirable
3	ICSA 14029 x ICSV-15006	Brix %, Total soluble sugars, Juice and Ethanol yield	Desirable
4	ICSA 14029 x IS 29308	Days to 50% flowering, Days to maturity, Fresh stalk weight, Stem girth,	Desirable for rest of the traits Undesirable for days to 50% flowering and days to maturity
5	ICSA 14030 x SEVS -08	Plant height, Panicle weight, Grain yield	Desirable
6	ICSA 14030 x GGUB 28	Fresh stalk weight, Stem girth, Juice yield	Desirable
7	ICSA 14030 x ICSV 15006	Days to 50% flowering, Fresh stalk yield, Stem girth, Juice yield	Desirable for rest of the traits Undesirable for days to 50% flowering and days to maturity
8	ICSA 14030 x IS 29308	Days to maturity, 1000 Grain weight, Panicle weight, Brix %, Total soluble sugars, Juice and Ethanol yield	Desirable for rest of the traits Undesirable for days to maturity
9	ICSA 14033 x SEVS-08	1000 Grain weight, Brix %, Total soluble sugars, Juice and Ethanol yield	Desirable for all traits
10	ICSA 14033 x GGUB -28	Days to 50% flowering, Days to maturity, No. of nodes per plant, Plant height, Stem girth, Juice and Ethanol yield	Desirable for rest of the traits Undesirable for days to 50% flowering and days to maturity
11	ICSA 14033 x ICSV-15006	Fresh stalk yield, Stem girth, Brix %, Total soluble sugars	Desirable
12	ICSA 14033 x IS-29308	Fresh stalk yield, Panicle weight	Desirable
13	ICSA 14305 x SEVS-08	Days to 50% flowering, Days to maturity, Plant height, Fresh stalk yield, Stem girth, Juice yield, Ethanol yield	Desirable for rest of the traits Undesirable for days to 50% flowering and days to maturity
14	ICSA 14305 x GGUB 28	1000 Grain weight, Panicle weight	Desirable
15	ICSA 14305 x ICSV-15006	Days to maturity, Juice yield	Desirable for rest of the traits Undesirable for days to 50% flowering and days to maturity
16	ICSA 14305 x IS-29308	No. of nodes per plant, Plant height, Fresh stalk yield, Ethanol yield	Desirable

Table 4.22. Top ranking hybrids for specific combining ability with their *per se* performance, standard heterosis

S.No.	Character	Predominant gene action Gca/Sca variance	Crosses	GCA status of parents	Value of SCA effect	Per se performance	Standard Heterosis
1	Days to 50% flowering (Days)	4.29 Additive	H-14 H-8 H-12 H-11	-H x -H -L x +H +H x +H +H x +H	-1.802 -1.094 -0.927 -0.802	59.83 82.50 83.50 79.17	-33.40 -8.16 -7.05 - 11.87
2	Days to maturity (Days)	1.68 Additive	H-16 H-3 H-12	- H x +H + H x +H - L x +H	-1.646 -2.188 -2.979	117.83 123.00 118.50	-6.61 -2.51 -6.08
3	Plant height (cm)	4.44 Additive	H-16 H-13 H-3 H-5	+ L x +H + L x +H +L x +H +L x +H	18.741 15.275 13.072 5.932	276.52 274.00 289.14 264.30	-17.15 -17.67 -13.37 -20.81
4	Number of nodes per plant	0.35 Non-additive	H-16 H-10 H-7 H-3	+L x +L +H x -H -H x +H -H x +H	0.990 1.156 1.240 1.323	12.67 12.17 12.17 12.17	-13.64 -17.05 -17.05 -17.05
5	Stem girth (cm)	0.66 Non-additive	H-13 H-6 H-4 H-7	+H x -H -H x +H - L x -H -H x +H	0.448 0.306 0.294 0.273	2.58 2.62 2.33 2.95	20.16 21.71 8.53 37.21
6	Panicle weight (g)	0.34 Non-additive	H-5 H-2 H-12 H-14	+H x +L - L x +L -L x -H -H x +L	5.633 4.228 3.949 3.882	59.74 52.95 50.22 48.51	17.08 3.77 -1.59 -4.94

S.No.	Character	Predominant gene action Gca/Sca variance	Crosses	GCA status of parents	Value of SCA effect	Per se performance	Standard Heterosis
7	1000 grain weight (g)	0.12 Non-additive	H-9 H-14 H-2 H-8	- L x +H - L x +H -H x +H +H x - L	5.775 3.387 1.989 1.720	40.52 38.91 36.60 37.13	-0.86 -4.79 -10.44 -9.14
8	Fresh Stalk yield (T ha ⁻¹)	0.60 Non-additive	H-13 H-7 H-6 H-3	-H x -H -H x +H -H x -H +H x +H	10.379 7.593 5.279 4.314	46.26 61.53 46.47 62.15	5.32 40.10 5.79 41.50
9	Juice yield (l ha ⁻¹)	0.95 Non-additive	H-10 H-3 H-8 H-13	+ H x +H +H x +H +H x -H -H x -H	2541.510 1619.203 1485.338 1384.105	17876.53 18066.65 11316.04 12812.33	83.80 85.76 16.35 31.73
10	Brix %	0.73 Non-additive	H-2 H-8 H-3 H-9	-L x -H +H x +H +H x +H - L x -H	1.656 1.615 1.406 1.115	14.00 15.67 15.67 12.83	7.69 20.51 20.51 -1.28
11	Total soluble sugars (%)	0.73 Non-additive	H-2 H-8 H-3 H-9	+H x -H -L x +H +H x +H - L x -H	1.449 1.412 1.229 0.976	12.40 13.86 13.85 11.38	7.59 20.25 20.24 -1.26
12	Ethanol yield (l ha ⁻¹)	1.05 Additive	H-3 H-2 H-8 H-10	+H x +H +H x + L +L x -H -L x +L	176.772 174.823 165.746 147.09	1345.27 1130.31 802.38 1004.05	125.24 89.17 34.28 68.03
13	Grain yield (T ha ⁻¹)	0.77 Non-additive	H-5	+H x -L	0.586	5.34	6.1

4.6 EBERHART AND RUSSELL'S (1966) STABILITY MODEL

The results of the present investigation on stability analysis among the 16 hybrids developed in L x T fashion from 4 Lines and 4 testers for identification of stable hybrids in sorghum are presented below:

4.6.1 Pooled Analysis of Variance

Pooled ANOVA over three locations for stability of different characters (Eberhart and Russell, 1966) are given in Table 4.23. Out of the 13 characters studied, the mean sum of squares due to genotypes were significant for six characters studied except number of nodes per plant, fresh stalk yield, stem girth, panicle weight, brix %, total soluble sugars and grain yield indicating the presence of substantial amount of variation in the material used for carrying out the present investigation. The mean sum of squares due to environments was non-significant for most of the characters studied except plant height, stem girth, 1000 grain weight, panicle weight and total soluble sugars. The non-significant mean squares due to genotypes $\times$ environment (G $\times$ E) interactions observed in most of the characters except plant height and 1000 grain weight were indicating the lesser influence of environment on the hybrids evaluated. Khandelwal *et al.* (2005) and Prabhakar *et al.* (2010) and Umakanth *et al.* (2012b) observed similar results.

The significant environment (linear) component observed for traits such as plant height, fresh stalk yield, stem girth, 1000 grain weight, panicle weight, total soluble sugars indicated the existence of major environmental differences at all three locations studied for these characters. Whereas genotype $\times$ environment (Linear) interaction was non-significant for all the traits except plant height and 1000 grain weight. However, the magnitude of mean squares for environment (linear) was higher compared to genotypes $\times$ environments (linear) which indicated that, linear response of environment has accounted for the major part of total variation for all the characters studied and which may be responsible for higher adaptation. Iyanar and Ravikesavan (2005) reported similar result. As regard the mean squares due to pooled deviation (non-linear portion of variance), which is unpredictable portion of genotype $\times$ environment interaction was significant for most of the traits except brix %. These results suggested that both linear and non-linear components have played a vital role in building up of total G $\times$ E interaction for various yield and yield attributing traits.

Table 4.23. Pooled Annova for stability analysis for 13 characters in 16 Sorghum [*Sorghum bicolor* (L.) Moench] hybrids

	df	DAF 50%	D.M	PH	N.N.S	SG	PW	1000 GW	FSTK	JY	BRIX %	TSS	EY	GY
Varieties	16	242.92**	176.21* *	6300.34**	6.95	0.472	83.67	31.61*	265.13	37694260.00*	10.08	7.71	228028.60*	0.77
Environment	2	60.15	19.32	23376.42**	0.65	2.118*	468.55**	283.12**	312.36	7486505.00	23.04*	17.61*	155932.70	0.25
Var*env	32	47.62	61.52	2453.62*	2.79	0.447	89.42	33.24**	145.71	19868140.00	6.03	4.62	106711.20	1.91
Environments (linear)	1	120.30	38.65	46752.83**	1.30	4.236**	937.11**	566.24**	624.72	14973010.00	46.08**	35.23**	311865.30	0.50
Var*env(linear)	16	35.54	52.11	3852.17**	1.82	0.412	98.16	55.59**	130.37	26225910.00	6.54	5.00	123469.00	2.20
Pooled deviation	17	56.18**	66.76**	992.99**	3.55**	0.454**	75.93**	10.25**	151.58**	12715650.00**	5.21**	3.98 **	84661.91**	1.53**
Pooled error	48	0.43	1.28	21.38	0.30	0.05	3.44	1.49	0.78	304677.30	0.17	0.13	1900.99	0.15

NOTE: * and ** Significant at 5 and 1 per cent level respectively

DAF 50%= Days to 50% flowering (Days), **D.M**= Days to maturity (Days), **PH**= Plant height (cm), **N.N.S**= Number of nodes per plant, **SG**= Stem girth (cm), **PW**= Panicle weight (g), **1000 GW**= 1000 grain weight (g), **FSTK**= Fresh stalk yield (T ha⁻¹), **JY**= Juice yield (l ha⁻¹), **Brix %**, **TSS** = Total soluble sugars (%), **EY**= Ethanol yield (l ha⁻¹), **GY** = Grain yield (T ha⁻¹).

4.6.2 Mean performance, range and environmental index values in different environments

The data recorded on 13 quantitative characters of sorghum in three locations analysed E₁- Bapatla, E₂- Guntur, E₃- Garikapadu and the mean, range and environmental indices are presented trait-wise in Table 4.24.

4.6.2.1 Days to 50% flowering (days)

The average values for this trait indicate that days to 50 per cent flowering differed from environment to environment as indicated by varying environmental indices (-1.05 to 2.19). The environmental index (2.19) and environmental mean (80.12 days) were maximum at E₃ and minimum at E₂ (-1.14 and 76.09 days). The range for days to 50 per cent flowering was observed at E₂ environment (53 to 97.50 days) while range of (61 to 90.50 days) for E₁ and (60.50 – 91.50 days) for E₃. Across the environments, H-4 was the last to flower (89.00 days) while the H-10 was the earliest (61.00 days) in Bapatla location, H-6 (53.50 days) was earliest to flower and H-4 (97.50 days) was late flowering in Guntur location and in Garikapadu location H-14 (60.50 days) earliest to flower and hybrid check CSH-22SS (91.50 days) late to flower. The results are indicating that the hybrids possessing advantage because of their earliness.

4.6.2.2 Days to maturity (days)

Environmental indices and environmental mean for this character varied from -0.25 to 0.96 and from 118.53 days to 120.47 days, respectively. Among the environments, the range for days to maturity was maximum in E₂ (91.50 to 137.50 days). Among the entries, in Bapatla location H-6 (104.50 days) was early maturing, H-11 (127.50 days) was late maturing followed by Guntur location H-14 (91.50 days) found to be early maturing and H-13 (137.50 days) found to be late maturing, while in Garikapadu location H-14 (98.50 days) found to be early maturing and H-16 (133.50 days) found to be late maturing .

4.6.2.3 Plant height (cm)

It is evident from the table that environmental indices and environment mean for this trait ranged from -32.77 to 39.83 and 208.28 to 281.58 cm respectively. The E₃ environment has recorded the highest mean (281.58 cm) for this trait while E₂ showed the least (208.28cm). Across the 2 locations i.e., Bapatla and Guntur, none of the hybrids recorded the high values when compared to check variety CSH-22SS (311.30 cm and 306.50 cm) respectively, while dwarf types were H-14 (103.05 cm) and H-10 (127.60 cm), in respective environments and in Garikapadu H-13 recorded highest plant height (403.96 cm) and H-6 (185.87 cm) recorded the lowest.

Table 4.24. Summary of mean, range and environment index values in respect of 13 traits across environments in 16 Sorghum [*Sorghum bicolor* (L.) Moench] hybrids

S. No.	Character	Mean			Range			Environmental index		
		Env 1	Env 2	Env 3	Env 1	Env 2	Env 3	Env 1	Env 2	Env 3
1	DAF 50%	76.76	77.03	80.12	61.00 -90.50	53.00-97.50	60.50 – 91.50	-1.05	-1.14	2.19
2	DM	118.53	118.74	120.47	91.50 – 127.50	91.50 – 137.50	98.50 – 133.50	-0.25	-0.71	0.96
3	PH	238.58	208.28	281.58	103.05 – 311.30	127.60 – 306.50	185.87 – 403.96	-7.06	-32.77	39.83
4	N.N.S	11.12	11.50	11.24	7.50 – 15.50	9.50 – 15.00	7.00 – 15.50	-0.16	0.20	-0.04
5	S.G	2.42	1.90	2.56	1.30 - 3.75	0.70 - 3.05	1.60-3.60	0.13	-0.41	0.28
6	P.W	45.84	45.48	55.16	31.13 – 54.75	24.56 – 70.47	36.14 – 70.04	-2.65	-4.03	6.68
7	1000 GW	32.76	32.34	39.41	28.78 - 38.52	26.61 – 41.92	29.33 – 61.37	-1.74	-3.13	4.88
8	FSTK	44.78	39.55	48.00	30.23- 68.76	15.70 – 68.82	30.47 – 73.20	0.73	-5.17	4.44
9	JY	13574.44	13798.03	12489.31	6844.44 – 22742.57	5444.44 – 25029.60	5792.59 – 21955.53	363.8	507.40	-871.29
10	BRIX %	14.38	13.24	12.12	9.50 – 18.50	7.50 – 18.50	8.00 – 18.50	1.18	0.12	-1.31
11	TSS	12.71	11.83	10.72	8.46– 16.33	6.71 – 16.33	7.15 – 15.45	1.038	0.109	-1.148
12	EY	921.12	852.67	734.43	530.83 – 1874.27	372.66 – 1651.84	314.72 – 1249.52	95.19	19.21	-114.41
13	GY	4.70	4.18	4.55	2.31– 6.74	1.96 – 6.51	2.21 – 6.95	0.238	-0.296	0.058

DAF 50%= Days to 50% flowering (Days), **D.M**= Days to maturity (Days), **PH**= Plant height (cm), **N.N.S**= Number of nodes per plant, **SG**= Stem girth (cm), **PW**= Panicle weight (g), **1000 GW**= 1000 grain weight (g), **FSTK**= Fresh stalk yield (T ha⁻¹), **JY**= Juice yield (l ha⁻¹), **Brix %**, **TSS** = Total soluble sugars (%), **EY**= Ethanol yield (l ha⁻¹), **GY** = Grain yield (T ha⁻¹).

Env 1-Bapatla, A.P

Env 2- Guntur, A.P

Env 3- Garikapadu, A.P

4.6.2.4. Number of nodes per plant

Environmental index values for this character ranged from -0.04 to 0.20. The environmental means ranged 11.12 to 11.50 nodes per plant. More number of nodes per plant were registered in E₂ (11.50) and lowest in E₁ (11.12). The range for number of nodes per plant varied from 7 -15.50 nodes per plant in E₃, 7.5 -15.50 nodes per plant in E₁, 9.50 -15.00 nodes per plant in E-2. In Bapatla location check has recorded 14.50 nodes per plant and H-14 recorded 7.50 nodes per plant. In Guntur location also check has recorded 15.00 nodes per plant while hybrids H-6 and H-13 has recorded the lowest number of nodes per plant (9.50). In Garikapadu location H-13 recorded highest number of nodes *i.e.*, 15.50 nodes per plant and lowest in H-6 with 7.00 nodes per plant.

4.6.2.5. Stem girth (cm)

Variation for environmental indices was from -0.41 to 0.28 and for environmental mean it was between 1.90 to 2.56 cm. Maximum stem girth was recorded by E₃ environment (2.56 cm) followed by E₁ (2.42cm), E₂ (1.90 cm). Among the Hybrids in three locations H-12 (1.30 cm) recorded the lowest stem girth and highest stem girth by H-7 (3.75 cm) in Bapatla location, H-14 (3.05 cm) recorded the highest stem girth and lowest stem girth by H-8 (0.70 cm) in Guntur location and in Garikapadu location H-2 (1.6 cm) has recorded lowest stem girth and H-13 (3.6 cm) recorded the highest stem girth.

4.6.2.6. Panicle weight (g)

It is clear From the Table: 4.24 that E₃ environment showed the maximum environmental mean (55.16 g), followed by E₁ (45.84g), E₂ (45.48g) environments. Environment index varied from -4.03 to 6.68. Among the hybrids, maximum panicle weight was recorded by the hybrid H-6 (70.04 g) and lowest panicle weight by the H-15 (36.14 g) in Garikapadu location, H-5 (70.47 g) recorded the highest panicle weight and lowest by H-16 (23.56 g) in Guntur location and highest panicle weight is for H-14 (54.75 g) and H-9 (31.13 g) in Bapatla location.

4.6.2.7. 1000 grain weight (g)

Environmental index for 1000 grain weight varied from -3.13 to 4.88 and means varied from 32.34 to 39.41 g, respectively. The range of 1000 grain weight within the environments was E₁ (28.78 to 38.52 g), E₂ (26.61 to 41.92 g), E₃ (29.33 to 61.37 g). In

Bapatla and Guntur location no hybrid has exceeded the check CSH-22SS (38.52 and 41.92 g) and lowest by H-7 (28.78 g) and H-15 (26.61 g) respectively while in Garikapadu location highest 1000 grain weight by H-9 (61.37 g) and lowest in H-11 (29.33g)

4.6.2.8 Fresh stalk yield (T ha⁻¹)

Among the environments, higher mean value for fresh stalk weight was recorded in E₃ environment (48.00 T ha⁻¹), followed by E₁ (44.787 T ha⁻¹) environmental indices ranged from -5.17 to 4.44. Among the hybrids, the highest value was recorded by H-3 (68.76 T ha⁻¹) and H-5 recorded minimum value (30.23 T ha⁻¹) in Bapatla location and in Guntur location highest value was recorded by H-11 (68.82 T ha⁻¹) and lowest in H-8 (15.70 T ha⁻¹). Garikapadu location H-13 (73.20 T ha⁻¹) recorded the highest value while lowest in H-14 (30.47 T ha⁻¹)

4.6.2.9 Juice yield (l ha⁻¹)

High variation was observed for juice yield between environments as evident from range of environmental indices (-871.29 to 507.40) and environmental means (12489.31 l ha⁻¹ to 13798.03 l ha⁻¹). However, maximum range was observed in E₂ environment (5444.44 l ha⁻¹ to 25029.30 l ha⁻¹). Among the hybrids in Bapatla, Guntur and Garikapadu locations following hybrids has recorded highest values H-3 (22742.57 l ha⁻¹), H-15 (25029.60 l ha⁻¹) H-7 (21955.53 l ha⁻¹) and lowest in H-16 (6844.44 l ha⁻¹), H-4 (5444.44 l ha⁻¹), H-15 (5792.59 l ha⁻¹) in respective locations.

4.6.2.10 Brix%

Environmental indices and environment mean for this trait ranged from -1.31 to 1.18 in E₃ & 12.12 to 14.38 per cent in E₁, respectively. Maximum amount of variability for this character was expressed in environment-1 (14.38 per cent) while E₃ showed the least (10.72 per cent). Across the environments, Bapatla location H-8 (18.50 per cent) has recorded the highest and lowest in H-14 (9.50 per cent), in Guntur location H-11 (18.50 per cent) recorded highest brix percent and H-10 (9.50 per cent) has registered lowest brix per cent. In Garikapadu location, highest brix percent was recorded by H-9 (16.50 per cent) and lowest brix percent by H-6 (8.00 per cent).

4.6.2.11 Total soluble sugars (%)

Environmental indices and environmental mean for this character varied from -1.148 to 1.038 and 10.72 to 12.71 per cent respectively. The maximum range within the environment was in E₂ (6.71 to 16.33). Across the environments, Bapatla location H-7 (16.33 per cent) has recorded the highest and lowest in H-14 (8.46 per cent), in Guntur location H-7 (16.33 per cent) recorded highest brix percent and H-10 (6.71 per cent) has registered lowest brix per cent. In Garikapadu location, highest brix percent was recorded by H-9 (15.45 per cent) and lowest brix percent by H-6 (7.15 per cent).

4.6.2.12 Ethanol yield (l ha⁻¹)

Variation in ethanol yield is noticed across the environments as indicated by varying environmental indices (-114.41 to 95.19) and environmental means too varied from 734.43 to 921.12 l ha⁻¹. The range for this character varied from 372.66 to 1651.84 l ha⁻¹ in E₂ followed by 530.83 to 1874.27 l ha⁻¹ in E₁ and 314.72 to 1249.52 l ha⁻¹ in E₃ environment, when compared to check performance in 3 locations CSH-22SS (553.42 l ha⁻¹, 555.57 l ha⁻¹, 683.59 l ha⁻¹) the following hybrids has recorded the highest values H-3 (1874.27 l ha⁻¹), H-7 (1597.93 l ha⁻¹) in Bapatla location, H-15 (1651.84 l ha⁻¹), H-2 (1342.03 l ha⁻¹) in Guntur location, H-9 (1249.52 l ha⁻¹) and H-8 (1249.52 l ha⁻¹) in Garikapadu location respectively.

4.6.2.13 Grain yield (T ha⁻¹)

The maximum environmental index and environmental mean were recorded at E₁ (0.23 and 4.70 respectively) while these were low at E₂ (-0.29 and 4.18). The overall mean performance of hybrids among three locations are as follows, H-3 (6.74 T ha⁻¹) recorded high grain yield in Bapatla location, H-15 (6.51T ha⁻¹) recorded the highest grain yield in Guntur location and in Garikapadu location H-9 (6.95 T ha⁻¹) recorded the highest when compared to check entry CSH-22SS (3.39 T ha⁻¹, 3.14 T ha⁻¹ and 3.82 T ha⁻¹) at three respective locations.

4.6.3 Environmental Index (%)

Environmental index revealed the suitability of an environment. Based on the positive values of environmental index, for 16 hybrids (Table 4.24) Bapatla location was found to be the most favourable location for brix % (1.18), total soluble sugars (1.038), ethanol yield (95.19) and grain yield (0.238) whereas the environment -2 at

Guntur was the most favourable location for number of nodes per plant (0.20) and juice yield (507.40). However environment-3 *i.e.*, Garikapadu was found to be favourable for days to fifty percent flowering (2.19), days to maturity (0.96), plant height (39.83), fresh stalk yield (4.44), stem girth (0.28), 1000 grain weight (4.88) and panicle weight (6.68). Diasa *et al.* (2017) reported similar results for Brix per cent.

4.6.4 Stability Parameters

The three stability parameters *viz.*, mean, regression co-efficient (b_i) and deviation from linear regression line (S^2d_i) were estimated for all 13 traits and the results obtained are presented in Tables 4.25.1 to 4.25.7.

The genotypes with higher mean values than general mean value, regression coefficient value of unity ($b_i = 1$) and non-significant deviation from linear regression ($S^2d_i = 0$) were considered as stable, and adapted to varied environmental conditions. However, genotypes with a higher mean value than general mean value and value of regression coefficient more than unity ($b_i > 1$) with non-significant deviation from linear regression were considered to be below average stable, and hence suitable for favourable environmental condition. Further, genotypes with higher mean values than general mean value and regression coefficient less than unity ($b_i < 1$) and non-significant deviations from linear regression were considered as above average stable, and hence are suitable for poor environmental condition. Accordingly, the test hybrids were classified as suitable for varied environmental conditions and presented in table 4.25.

4.6.4.1 Days to 50 % flowering (days)

The stability parameters for days to 50% flowering are given in table 4.25.1. Out of 16 hybrids and one hybrid check tested, H-4 required maximum number of days to 50% flowering (91.33) while, H-14 required minimum number of days to 50% flowering (59.83). Whereas mean over three locations was 77.24 days. None of the hybrids have differed significantly from unity for regression coefficient. Only three hybrids H-2, H-3 and H-5 were found to have non-significant deviation from regression, while rest of the 13 hybrids have differed significantly from unity for regression coefficient. None of the hybrids were found to have higher mean than grand mean with regression coefficient around unity ($b_i=1$) and non-significant deviation from regression.

Among the genotypes tested , H-4 is highly desirable for ethanol yield as it has recorded more no of days to 50 % flowering.

4.6.4.2 Days to maturity (days)

The stability parameters for days to maturity are given in table 4.25.1. Out of 16 hybrids together with the hybrid check evaluated, H-13 has required maximum number of days to maturity (126.16) while, H-14 required minimum number of days to maturity (101.16) and mean over three environments was 118.8 days. Only one hybrid differed significantly from unity for regression coefficient. The deviation from regression value was significant for most of the hybrids except H-3 and H-5.

The hybrids which are medium to late to maturing types are more desirable for this character. None of the hybrids were found to have higher mean than grand mean with regression coefficient around unity ($b_i=1$) and non-significant deviation from regression.

4.6.4.3 Plant Height (cm)

The stability parameters for plant height are given in table 4.25.2. Out of 16 hybrid test entries, H-3 recorded maximum plant height of 289.14 cm while, H-14 has recorded minimum plant height of 171.65 cm and mean over three environments was 241.1 cm. The hybrids H-4, H-8 and H-13 differed significantly from unity for regression coefficient. The deviation from regression value was significant for nine hybrids viz., H-1, H-3, H-5, H-6, H-7, H-9, H-12, H-14 and H-15. The hybrids like H-2 ($b_i=1.1$) and H-10 ($b_i=1.44$) have registered lower mean value than grand mean with regression coefficient around unity ($b_i=1$) and non-significant deviation from regression. Hence, these genotypes were considered to possess the average stability for higher plant height at different locations.

Table 4.25.1. Stability parameters in respect of Days to 50% flowering, Days to maturity traits in 16 F₁ hybrids of Sorghum [*Sorghum bicolor* (L.) Moench]

S.No.	Cross	1. Days to 50% flowering (days)			2. Days to maturity (days)		
		μ	bi	$\sigma^2 di$	μ	bi	$\sigma^2 di$
H-1	ICSA 14029 x SEVS-08	80.33	1.94	19.8**	125.00	0.34	7.92*
H-2	ICSA 14029 x GGUB 28	65.50	0.92	1.34	109.16	-3.33	4.8*
H-3	ICSA 14029 x ICSV-15006	78.83	-1.07	-0.09	123.00	-0.71	-0.67
H-4	ICSA 14029 x IS 29308	91.33	-1.80	34.23**	124.50	-3.95	12.87**
H-5	ICSA 14030 x SEVS -08	82.66	3.55	1.19	122.33	5.33**	-1.41
H-6	ICSA 14030 x GGUB 28	62.66	4.08	41.10**	104.16	10.48	12.54**
H-7	ICSA 14030 x ICSV 15006	80.00	0.25	5.55**	123.33	-1.12	-0.15*
H-8	ICSA 14030 x IS 29308	82.50	2.3	123.37**	125.33	4.19	15.11**
H-9	ICSA 14033 x SEVS-08	81.83	-2.50	68.76**	119.66	-7.77	14.06**
H-10	ICSA 14033 x GGUB -28	66.66	0.77	45.35**	115.00	-7.35	53.08**
H-11	ICSA 14033 x ICSV-15006	79.16	-3.47	5.04**	121.83	-4.18	32.74**
H-12	ICSA 14033 x IS-29308	83.50	3.32	213.65**	118.50	12.97	135.19**
H-13	ICSA 14035 x SEVS-08	83.16	0.45	288.70**	126.16	-4.84	187.72**
H-14	ICSA 14035 x GGUB 28	59.83	0.34	11.86**	101.16	0.84	250.18**
H-15	ICSA 14035 x ICSV-15006	79.66	1.72	6.21**	124.00	-0.37	13.89*
H-16	ICSA 14035 x IS-29308	78.16	4.67	14.30**	117.83	15.46	8.33*
CHK	CSH 22SS	89.83	0.87	22.16**	126.2	4.80	103.2**
	Population mean over 3 locations	77.24 days			118.8 days		

bi: Regression coefficient

S²di: Mean square deviation from regression coefficient

* and ** : Significant at 5 and 1 per cent level respectively

Table 4.25.2. Stability parameters in respect of plant height (cm), Number of nodes per plant traits in 16 F₁ hybrids of Sorghum [*Sorghum bicolor* (L.) Moench].

S.No.	Cross	3. Plant height (cm)			4. Number of nodes per plant		
		μ	Bi	$\sigma^2 di$	μ	bi	$\sigma^2 di$
H-1	ICSA 14029 x SEVS-08	237.30	0.57	105.51*	10.16	-1.14	2.18*
H-2	ICSA 14029 x GGUB 28	178.62	1.1	-16.84	9.66	1.43	-0.37
H-3	ICSA 14029 x ICSV-15006	289.14	0.46	113.41*	12.67	-1.1	4.18**
H-4	ICSA 14029 x IS 29308	261.29	1.75*	-22.11	10.66	5.71	5.40**
H-5	ICSA 14030 x SEVS -08	264.30	0.90	3791.51**	11.33	6.29	-0.10
H-6	ICSA 14030 x GGUB 28	172.08	0.19	460.00**	9.00	-0.86	6.06**
H-7	ICSA 14030 x ICSV 15006	271.00	0.22	627.23**	12.16	7.43	0.25
H-8	ICSA 14030 x IS 29308	258.58	-0.07**	-26.07	9.16	6.57	2.63**
H-9	ICSA 14033 x SEVS-08	255.30	3.03	1774.89**	12.66	-9.71	-0.10
H-10	ICSA 14033 x GGUB -28	178.42	1.44	1712	12.16	0.57	0.75
H-11	ICSA 14033 x ICSV-15006	271.67	0.53	18.25	10.83	-2.29	-0.10
H-12	ICSA 14033 x IS-29308	248.48	2.24	3148.29**	12.50	-.86	4.18**
H-13	ICSA 14035 x SEVS-08	274.80	3.31*	56.2	11.50	-3.43	22.75**
H-14	ICSA 14035 x GGUB 28	171.65	1.74	4867.23**	9.33	7.14	1.06
H-15	ICSA 14035 x ICSV-15006	247.62	-1.27	1026.71**	11.16	3.14	6.06**
H-16	ICSA 14035 x IS-29308	276.52	-0.44	42.86	12.66	3.14	0.06
CHK	CSH 22SS	333.80	1.11	3721.6	14.66	1.40	0.16
	Population mean over 3 locations	241.1 cm			11.07		

bi: Regression coefficient

S²di: Mean square deviation from regression coefficient

* and ** : Significant at 5 and 1 per cent level respectively

4.6.4.4 Number of nodes per plant

The stability parameters for number of nodes per plant are given in table 4.25.2. Out of 16 hybrids, H-3 recorded maximum number of nodes per plant (12.67) while, H-6 has recorded minimum number of nodes per plant (9.00) and mean over three environments was (11.07).

Not even a single hybrid has differed significantly from unity for regression coefficient. The deviation from regression value was significant for eight genotypes viz., H-1, H-3, H-4, H-6, H-8, H-12, H-13 and H-15. The hybrids which record more number of nodes per plant are more desirable for this character. Only one hybrid H-10 ($b_i=0.57$) had high mean than grand mean with regression coefficient less than one ($b_i < 1$) and non-significant deviation from regression. This hybrid would perform better in unfavourable environments. The hybrids H-5($b_i=6.29$), H-7($b_i=7.43$) and H-16 ($b_i=3.14$) had high mean than grand mean with regression coefficient more than one ($b_i > 1$) and non-significant deviation from regression. These hybrids would perform better in favourable environments.

4.6.4.5 Stem girth (cm)

The stability parameters in respect of stem girth are given in table 4.25.3. Out of the 16 entries and hybrid check tested over three locations the hybrid H-11 (2.96 cm) recorded maximum stem girth and H-8 (1.56 cm) recorded minimum stem girth and the average over three locations was 2.33 cm. Regression value was non-significant for the all the hybrids. Deviation from regression was significant for all the hybrids except H-1. None of the hybrids have recorded high mean than grand mean with regression coefficient around unity ($b_i=1$) and non-significant deviation from regression.

4.6.4.6 Panicle weight (g)

The stability parameters for panicle weight in F_1 sorghum hybrids are presented in table 4.25.3. Among 16 hybrids and one check tested, the hybrid H-5 has recorded maximum panicle weight of 59.74 g followed by H-8(53.65 g). H-16 has recorded minimum panicle weight of 34.96 g and the mean over three environments was 48.58g. Two hybrids viz., H-6 and H-11 had the significant regression coefficient values. Deviation from regression was significant for ten hybrids viz., H-1, H-4, H-6, H-8, H-11 and only one hybrid H-12 ($b_i=1.09$) exhibited mean (50.21 g) greater than grand

Table 4.25.3. Stability parameters in respect of Stem girth, Panicle weight traits in 16 F₁ hybrids of sorghum [*Sorghum bicolor* (L.) Moench].

S.No.	Cross	5. Stem girth (cm)			6. Panicle weight (g)		
		μ	bi	$\sigma^2 di$	μ	bi	$\sigma^2 di$
H-1	ICSA 14029 x SEVS-08	2.06	0.00	0.01	42.01	1.66	4.85
H-2	ICSA 14029 x GGUB 28	2.28	0.33	1.41**	52.95	1.09	79.75**
H-3	ICSA 14029 x ICSV-15006	2.58	-0.54	0.90**	51.32	0.98	25.23*
H-4	ICSA 14029 x IS 29308	2.33	1.52	0.39**	46.37	1.63	13.83
H-5	ICSA 14030 x SEVS -08	1.73	1.82	0.02*	59.74	0.43	357.22**
H-6	ICSA 14030 x GGUB 28	2.61	2.48	0.59**	48.37	2.50*	-4.64
H-7	ICSA 14030 x ICSV 15006	2.95	2.38	0.38**	52.39	2.38	48.43**
H-8	ICSA 14030 x IS 29308	1.56	2.02	0.03*	53.65	2.05	3.68
H-9	ICSA 14033 x SEVS-08	1.83	0.19	0.07*	48.63	2.58	197.14**
H-10	ICSA 14033 x GGUB -28	2.55	2.95	0.15*	46.72	0.18	114.72**
H-11	ICSA 14033 x ICSV-15006	2.96	-0.19	0.07*	48.61	0.21*	-5.01
H-12	ICSA 14033 x IS-29308	2.16	0.77	1.56**	50.21	1.09	-4.20
H-13	ICSA 14035 x SEVS-08	2.58	1.86	0.77**	46.21	-0.34	54.25**
H-14	ICSA 14035 x GGUB 28	2.25	-1.61	0.56**	48.50	-0.19	43.51**
H-15	ICSA 14035 x ICSV-15006	2.66	1.03	0.25**	46.57	-1.66	45.01**
H-16	ICSA 14035 x IS-29308	2.15	0.99	0.47**	34.96	1.43	26.31**
CHK	CSH-22SS	2.15	0.21	0.02	51.03	-0.65	224.47**
	Population mean over 3 locations	2.33 cm			48.58 g		

bi: Regression coefficient

S²di: Mean square deviation from regression coefficient

* and ** : Significant at 5 and 1 per cent level respectively

mean (48.58 g) with regression coefficient around unity ($b_i=1$) and non-significant deviation from regression. This hybrid was stable for panicle weight which would be expected to perform uniformly well over variable environments. Hybrid H-8 ($b_i=2.05$) exhibited mean value (53.65 g) greater than grand mean with regression coefficient more than unity ($b_i>1$) and non-significant deviation from regression (3.65) and hence is suitable for favourable environments.

4.6.4.7 1000 grain weight (g)

The stability parameters in respect of 1000 grain weight are given in table 4.25.4. Out of the 16 hybrids tested over three locations H-9 (40.51g) recorded maximum pooled 1000 grain weight while the hybrid H-10 (29.95g) has recorded minimum pooled 1000 grain weight and the average over three locations was 34.34 g. Regression value was significant for the hybrids H-9 and H-11. Deviation from regression was non-significant for all the genotypes except H-5 and H-8.

Regression coefficient less than one ($b_i<1$) with higher mean value than general mean and non-significant deviation from regression was observed in H-14 ($b_i=0.60$). This hybrid would perform better in unfavourable environments. Whereas, hybrids H-2 ($b_i=1.44$), H-7 ($b_i=1.52$) having b_i values nearer to one with higher mean value than grand mean and non-significant deviation from regression were considered to be stable over variable locations. The hybrid H-6 ($b_i=2.85$), having b_i value more than one with higher mean value than grand mean and non-significant deviation from regression can be considered to be stable over favourable environments.

4.6.4.8 Fresh stalk yield (T ha⁻¹)

The stability parameters in respect of fresh stalk yield are given in table 4.25.4. Out of the 16 hybrids tested over three locations, the hybrid H-3 has recorded maximum fresh stalk yield (62.15 T ha⁻¹) and H-5 has recorded minimum fresh stalk yield (35.65 T ha⁻¹) and the average over three environments was 44.17 T ha⁻¹. Regression value was significant and more than unity for hybrid, H-14. Deviation from regression was significant for 14 hybrids and rest two hybrids viz., H-9 and H-14 registered non-significant for deviation from regression.

None of the hybrids have recorded higher mean value than grand mean with regression coefficient around unity ($b_i=1$) and non-significant deviation from regression.

4.6.4.9 Juice yield (l ha⁻¹)

The stability parameters for juice yield are given in table 4.25.5. Out of 16 hybrids tested, H-7 has recorded juice yield (18348.13 l ha⁻¹) while, H-12 has recorded the lowest juice yield (8720.98 l ha⁻¹) and mean over three environments was 13532.9 l ha⁻¹.

The hybrid H-8 has differed significantly from unity for regression coefficient. The deviation from regression value was non-significant for H-8, H-11 and H-12.

Regression coefficient less than one ($b_i < 1$) with higher mean value than general mean and non-significant deviation from regression were observed in H-1 ($b_i=0.49$) and H-11 ($b_i=0.68$). These hybrids would perform better in unfavourable environments.

4.6.4.10 Brix %

The stability parameters in respect of Brix per cent are given in table 4.25.5. Out of the 16 hybrids tested over three locations H-11 has recorded Brix (16 %) and H-6 recorded minimum Brix per cent (10.33 %) and the average over three locations was 13.28. Regression value was significant for hybrids, H-1, H-6 and H-13. Deviation from regression was significant for nine hybrids.

Hybrids H-3 ($b_i=1.84$) and H-4 ($b_i=1.63$) have exhibited means greater than grand mean with regression coefficient around unity ($b_i=1$) and non-significant deviation from regression. These hybrids were stable over variable locations. Regression coefficient less than one ($b_i < 1$) with high mean than general mean and non-significant deviation from regression were observed in H-2 ($b_i=-0.63$). This hybrid would perform better in unfavourable environments. Whereas hybrid-15 ($b_i=2.36$) having b_i value greater than one with higher mean value than grand mean and non-significant deviation from regression was considered to perform well in favourable conditions.

Table 4.25.4. Stability parameters in respect of 1000 grain weight, Fresh stalk yield traits in 16 F₁ hybrids of Sorghum [*Sorghum bicolor* (L.) Moench]

S.No.	Cross	7. 1000 grain weight (g)			8. Fresh stalk yield (T ha ⁻¹)		
		μ	bi	$\sigma^2 di$	μ	bi	$\sigma^2 di$
H-1	ICSA 14029 x SEVS-08	31.86	-0.06	8.23	43.31	-0.93	129.56**
H-2	ICSA 14029 x GGUB 28	36.60	1.44	4.01	46.11	0.48	318.35**
H-3	ICSA 14029 x ICSV-15006	31.46	1.10	-5.72	62.15	-0.87	79.19**
H-4	ICSA 14029 x IS 29308	33.63	0.5	-5.36	45.01	2.78	308.15**
H-5	ICSA 14030 x SEVS -08	34.09	1.16	20.70*	35.65	1.97	60.63**
H-6	ICSA 14030 x GGUB 28	36.78	2.85	4.31	46.46	1.81	349.71**
H-7	ICSA 14030 x ICSV 15006	34.86	1.52	14.36	61.53	1.96	17.41**
H-8	ICSA 14030 x IS 29308	37.13	0.07	19.69*	27.80	1.99	32.95**
H-9	ICSA 14033 x SEVS-08	40.51	4.24*	-4.19	35.96	0.17	0.62
H-10	ICSA 14033 x GGUB -28	29.95	1.71	7.40	41.18	2.28	142.40**
H-11	ICSA 14033 x ICSV-15006	32.38	-0.62*	-5.61	59.14	-2.18	44.45**
H-12	ICSA 14033 x IS-29308	32.92	0.02	12.11	43.39	2.43	303.42**
H-13	ICSA 14035 x SEVS-08	34.06	0.06	2.24	46.26	3.71	440.16**
H-14	ICSA 14035 x GGUB 28	38.91	0.60	-2.32	36.22	-1.28*	-0.31
H-15	ICSA 14035 x ICSV-15006	31.78	1.64	10.41	38.18	0.21	132.97**
H-16	ICSA 14035 x IS-29308	32.43	-0.18	-3.27	38.36	1.47	122.11**
CHK	CSH-22SS	40.86	0.21	8.33	43.92	-1.08	43.92
	Population mean over 3 locations	34.34 g			44.17 T ha ⁻¹		

bi: Regression coefficient

S²di: Mean square deviation from regression coefficient

* and ** : Significant at 5 and 1 per cent level respectively

Table 4.25.5. Stability parameters in respect of Juice yield (l ha⁻¹), Brix % traits in 16 F₁ hybrids of Sorghum [*Sorghum bicolor* (L.) Moench]

S.No.	Cross	9. Juice yield (l ha ⁻¹)			10. Brix %		
		μ	bi	$\sigma^2 di$	μ	bi	$\sigma^2 di$
H-1	ICSA 14029 x SEVS-08	14281.46	0.49	563089.98**	11.33	-1.61*	-.18
H-2	ICSA 14029 x GGUB 28	17180.23	2.61	14180199.59**	14.00	-0.63	0.07
H-3	ICSA 14029 x ICSV-15006	18066.65	0.85	35017950.00**	15.66	1.84	0.35
H-4	ICSA 14029 x IS 29308	7817.27	-1.79	4536533.90**	13.83	1.63	0.12
H-5	ICSA 14030 x SEVS -08	10227.15	-4.76	5214430.22**	11.66	1.50	3.89**
H-6	ICSA 14030 x GGUB 28	15933.32	5.48	19894493.41**	10.33	1.80*	-0.20
H-7	ICSA 14030 x ICSV 15006	18348.13	-4.33	4506607.06**	14.66	2.51	3.11**
H-8	ICSA 14030 x IS 29308	11316.04	-8.76*	-250801.85	15.66	0.70	4.40**
H-9	ICSA 14033 x SEVS-08	13397.52	-0.94	36639452.58**	12.83	-1.11	40.57**
H-10	ICSA 14033 x GGUB -28	17876.53	2.55	6433357.84**	12.00	-1.14	8.19**
H-11	ICSA 14033 x ICSV-15006	14234.55	0.68	-103774.08	16.00	2.73	6.84**
H-12	ICSA 14033 x IS-29308	8720.98	-0.75	-109926.48	12.00	2.55	0.81*
H-13	ICSA 14035 x SEVS-08	12812.33	5.28	18702849.45**	11.33	1.40*	-0.20
H-14	ICSA 14035 x GGUB 28	10251.84	3.10	22118445.22**	11.33	-0.24	10.78**
H-15	ICSA 14035 x ICSV-15006	16286.41	12.37	13423530.648**	14.33	2.36	0.39
H-16	ICSA 14035 x IS-29308	9775.29	3.90	34062724.514**	15.50	1.71	4.62**
CHK	CSH-22SS	9725.9	-1.26	1602309.3	13.00	-0.23	0.50
	Population mean over 3 locations	13522.9 l ha ⁻¹			13.28 %		

bi: Regression coefficient

* and ** : Significant at 5 and 1 per cent level respectively

S2di: Mean square deviation from regression coefficient

4.6.4.11 Total soluble sugars (%)

The stability parameters for total soluble sugars are given in table 4.25.6. Out of 16 hybrids, H-11 has recorded the highest total soluble sugars (14.14 %) while, H-6 has recorded the lowest total soluble sugars (9.19 %) and mean over three locations was 11.77 %. The three hybrids, H-1, H-6 and H-13 have differed significantly from unity for regression coefficient. The deviation from regression value was significant for nine hybrids viz., H-5, H-7, H-8, H-9, H-10, H-11, H-12, H-14 and H-16. The genotypes which have recorded the highest total soluble sugars are more desirable for this character.

Hybrids H-3($b_i=1.84$) and H-4($b_i=1.63$) had higher mean than grand mean with regression coefficient around unity ($b_i=1$) and non-significant deviation from regression. Hence, these hybrids were considered to possess the average stability for total soluble sugars at different locations. Regression coefficient less than one ($b_i<1$) with higher mean than general mean and non-significant deviation from regression were observed in H-2($b_i=-0.62$). This hybrid would perform better in unfavourable environments. Regression coefficient more than one ($b_i>1$) with higher mean value than general mean and non-significant deviation from regression was observed in H-15 ($b_i=2.36$) which is expected to perform well in favourable environments.

4.6.4.12 Ethanol yield (l ha⁻¹)

The stability parameters in respect of ethanol yield are given in table 4.25.6. Out of the 16 hybrids tested over three locations, H-3 recorded maximum ethanol yield (1345.9 l ha⁻¹) and H-12 recorded minimum ethanol yield (493.3 l ha⁻¹) and the average over three environments was 852.0 l ha⁻¹. Regression value was non-significant for all the hybrids. None of the hybrids have recorded higher mean than grand mean with regression coefficient around unity ($b_i=1$) and non-significant deviation from regression.

Table 4.25.6. Stability parameters in respect of Total soluble sugars, Ethanol yield traits in 16 F₁ hybrids of Sorghum [*Sorghum bicolor* (L.) Moench]

S.No.	Cross	11. Total soluble sugars (%)			12. Ethanol yield (l ha ⁻¹)		
		μ	bi	$\sigma^2 di$	μ	bi	$\sigma^2 di$
H-1	ICSA 14029 x SEVS-08	10.06	-1.61*	-0.14	764.9	-1.20	1444.40
H-2	ICSA 14029 x GGUB 28	12.39	-0.62	0.05	1130.3	-0.18	69402.73**
H-3	ICSA 14029 x ICSV-15006	13.85	1.84	0.27	1345.9	3.63	124268.34**
H-4	ICSA 14029 x IS 29308	12.25	1.63	0.09	506.1	0.49	29515.59**
H-5	ICSA 14030 x SEVS -08	10.35	1.50	2.98**	535.3	-0.19	25747.38**
H-6	ICSA 14030 x GGUB 28	9.19	1.80*	-0.15	815.4	3.87	16440.40**
H-7	ICSA 14030 x ICSV 15006	12.98	2.51	2.38**	1259.7	1.23	182897.10**
H-8	ICSA 14030 x IS 29308	13.85	0.70	3.35**	802.4	-3.32	50814.87**
H-9	ICSA 14033 x SEVS-08	11.37	-1.11	31.06**	777.1	-.80	18871.40**
H-10	ICSA 14033 x GGUB -28	10.64	-1.14	6.27**	1004.0	0.25	73165.23**
H-11	ICSA 14033 x ICSV-15006	14.14	2.73	5.23**	1078.6	2.39	43124.86**
H-12	ICSA 14033 x IS-29308	10.64	2.55	0.62*	493.3	1.06	6707.91*
H-13	ICSA 14035 x SEVS-08	10.06	1.40**	-0.16	696	1.87	107023.03**
H-14	ICSA 14035 x GGUB 28	10.06	-0.24	8.27**	533.1	1.51	-1751.93
H-15	ICSA 14035 x ICSV-15006	12.68	2.36	0.30	1150.3	6.08	225655.84**
H-16	ICSA 14035 x IS-29308	13.70	3.90	3.52**	740.1	1.30	417676.90**
CHK	CSH-22SS	11.52	-0.24	0.38	597.5	-0.72	11113.1
	Population mean over 3 locations	11.77 %			852.00 l ha ⁻¹		

bi: Regression coefficient

* and ** : Significant at 5 and 1 per cent level respectively

S2di: Mean square deviation from regression coefficient

4.6.4.13 Grain yield (T ha⁻¹)

The stability parameters in respect of grain yield are given in table 4.25.7. Out of the 16 hybrids tested over three locations H-5 has recorded maximum grain yield (5.34 T ha⁻¹) and H-16 has (3.40 T ha⁻¹) recorded minimum grain yield and the average over three locations was 4.54 T ha⁻¹. None of the hybrids were significant for regression coefficient. Deviation from regression was significant for nine hybrids viz. H-1, H-2, H-4, H-6, H-7, H-9, H-10, H-14 and H-15.

Regression coefficient less than one ($b_i < 1$) with high mean than general mean and non-significant deviation from regression were observed in H-5 ($b_i = -3.71$), H-11 ($b_i = -0.16$) and H-12 ($b_i = 0.42$). These genotypes would perform better in unfavourable environments. Whereas, hybrid H-8 ($b_i = 3.00$) having b_i value greater than one with higher mean value than grand mean and non-significant deviation from regression was considered to perform well in favourable conditions.

All the 16 hybrids were broadly classified into 3 groups and presented in table 4.25.8 based on their stability for various quantitative characters.

The hybrid H-11 is found to be suitable for unfavourable environments in respect of Plant height, grain yield and juice yield. The hybrids H-3 and H-4 were found to be more stable in respect of both Brix per cent and TSS per cent. The above quoted results are in accordance with Rao *et al.* (2011), Udoh *et al.* (2018) for brix Per cent, Rohmani *et al.* (2006), Umakanth *et al.* (2012b), Vange *et al.* (2014), Anarse *et al.* (2016), Khandelwal *et al.* (2019) for grain yield whereas the results for biomass by the above authors are deviating from the current results. It is clear from the table that in respect of days to maturity, stem girth, fresh stalk yield and ethanol yield none of the hybrids are suitable to any environment.

4.6.5 AMMI analysis

AMMI analysis is carried out to promote further partitioning of the sum of squares due to G x E interaction into two portions, known as pattern and noise. The noise portion deals with an unpredictable and non-interpretable responses while the pattern portion is obtained after tossing out the noise in addition to the experimental errors, which allows a more in-depth focus of the G x E interaction and the prediction ability of phenotypic responses of the genotypes under study, once they exposed to certain environments in a systematic, significant and interpretable way.

Table 4.25.7. Stability parameters in respect of Grain yield traits in 16 F₁ hybrids of Sorghum [*Sorghum bicolor* (L.) Moench].

S.No.	Cross	13. Grain yield (T ha ⁻¹)		
		μ	Bi	$\sigma^2 di$
H-1	ICSA 14029 x SEVS-08	4.03	0.98	1.43**
H-2	ICSA 14029 x GGUB 28	4.73	-0.54	0.48*
H-3	ICSA 14029 x ICSV-15006	5.06	5.99	0.08
H-4	ICSA 14029 x IS 29308	4.56	6.45	1.28**
H-5	ICSA 14030 x SEVS -08	5.34	-3.71	-0.08
H-6	ICSA 14030 x GGUB 28	4.45	0.32	1.45**
H-7	ICSA 14030 x ICSV 15006	4.55	4.63	1.94**
H-8	ICSA 14030 x IS 29308	4.80	3.00	-0.10
H-9	ICSA 14033 x SEVS-08	4.77	-3.68	8.74**
H-10	ICSA 14033 x GGUB -28	4.82	0.23	0.5*
H-11	ICSA 14033 x ICSV-15006	4.77	-0.16	-0.11
H-12	ICSA 14033 x IS-29308	5.16	0.42	-0.15
H-13	ICSA 14035 x SEVS-08	3.89	1.25	0.30
H-14	ICSA 14035 x GGUB 28	4.24	1.50	0.45*
H-15	ICSA 14035 x ICSV-15006	4.04	-5.15	3.54**
H-16	ICSA 14035 x IS-29308	3.40	4.46	0.08
CHK	CSH-22SS	5.01	-17.22	12.03
	Population mean over 3 locations	4.54 T ha ⁻¹		

bi: Regression coefficient

S2di: Mean square deviation from regression coefficient

* and ** : Significant at 5 and 1 per cent level respectively

Table 4.25.8. Grouping of F₁ hybrids for different characters based on their stability

S.No.	Character	Genotypes suitable for all environments	Genotypes suitable for unfavourable Environments	Genotypes suitable for favourable environments
1.	Days to 50% flowering	H-2	-	-
2.	Days to maturity	-	-	-
3.	Plant height (cm)	H-2 and H-10	H-11, H-16	-
4.	Number of nodes per plant	-	H-10	H-5, H-7 and H-16
5.	Stem girth (cm)	-	-	-
6.	Panicle weight (g)	H-12	-	H-8
7.	1000 grain weight (g)	H-2 , H-7	H-14	H6
8.	Fresh stalk yield (T ha ⁻¹)	-	-	-
9.	Juice yield(T ha ⁻¹)	-	H-11	-
10.	Brix %	H-3 and H-4	H-2	H-15
11.	T.S.S (%)	H-3 and H-4	H-2	H-15
12.	Ethanol yield (T ha ⁻¹)	-	-	-
13.	Grain yield(T ha ⁻¹)	-	H-11,H-5 and H-12	H-3 and H-8

According to Oliveira *et al.* (2003), one of the premises of AMMI analysis is that most of the pattern portion is concentrated on the first axis, increasing the number of axes and the risk of the noise portion. A greater pattern portion was concentrated on the first AMMI axes; as the number of axes increased, the pattern portion decreased and the noise portion increased. Thus, even if only one axis (IPCA1) is selected to explain a small portion of the original sum of squares (G x E). AMMI model stratifies the genotypes and environments into four groups i.e., right up (high yielder stable), right down (high yielder unstable), left up (low yielder stable) and left down (low yielder unstable). The genotypes having a high IPCA score indicated their specific adoption to a given environment while genotypes having IPCA score close to zero are considered stable only in the sampled environment.

The IPCA score of a genotype indicates the stability of a genotype over environments. The combined analysis of variance (ANOVA) of 16 hybrids over 3 locations pertaining to AMMI model for 13 characters are presented in tables 4.26.1 to 4.26.5 and the results are discussed character wise here under.

4.6.5.1 Days to 50% flowering (days)

The ANOVA for days to 50% flowering (Table 4.26.1) showed that genotypes and residual component were significant and accounted for 69.94 *per cent*, 2.16 *per cent* and 27.42 *per cent* of the total variation, respectively by genotypes, environment and G x E interaction. The G x E interaction was partitioned into only one IPCA, which capable of explaining 70.52 *per cent* of the total G x E interaction sum of squares.

To state theoretical concept of AMMI, entries with high mean and IPCA score zero is considered as more stable. In this particular study none of the hybrids were identified as stable. However based on AMMI 1 biplot (Fig. 4.4.1), H-1 showing IPCA scores nearer to zero but with respect to mean value it is higher than the grand mean value which is undesirable, in some other cases like fodder sorghum and grain sorghum early flowering types are desirable whereas in sweet sorghum intermediate flowering types are desirable. The AMMI 2 biplot (Fig. 4.4.2), the H-2 was nearer to IPCA origin and hence this hybrid was considered to be stable over locations. The hybrids which have high IPCA scores are hybrid 8 and 12 which indicate their specific adoption.

H-12 & H-8 are having more days to 50 % flowering and stable, while H-1, H-5, H-7, H-15, H-3, H-11, H-4, H-9, H-13 and check entry are having more days to 50 % flowering and unstable. H-6 with less days to 50 % flowering and yet stable while H-14, H-2 & H-16 are with less days to 50 % flowering and unstable. Location 1 and 3 are having similar main effects and hence they are clustered into single group despite above average mean and negative IPCA scores.

4.6.5.2 Days to maturity (days)

ANOVA for days to maturity (Table 4.26.1) has showed that the genotypes and residual component were significant. The genotypes, environments and genotype x environment interaction were accounting for 57.57 *per cent*, 0.78 *per cent* and 40.20 *per cent* of the total variation, respectively. The ANOVA also indicated that G x E interaction was partitioned into only one IPCA, which was significant and explained 70.11 *per cent* of the total G x E interaction sum of squares.

Based on the AMMI 1 biplot for days to maturity (Fig. 4.4.3), none of the hybrids were identified as stable. H-7 and H-11 which had higher mean and IPCA scores near to zero. The AMMI 2 biplot (Fig. 4.4.4) for days to maturity has revealed that the H-3 and H-5 were nearer to IPCA origin, hence these hybrids could be considered as stable over locations. While the hybrids H-6 and H-14 possessing high IPCA scores adapted to a specific environment only.

The hybrids H-12, H-16, H-5 & H-8 are possessing more days to maturity and stable, while H- 9, H-13, H- 4, H-15, H-1, H-3, H-7, H-11 are possessing more days to maturity and unstable. H-6 & H-14 are having less days to maturity and stable while H-2 is having less days to maturity and unstable. Location 1 and 3 have similar main effects and they are clustered into single group had above average mean and negative IPCA scores.

4.6.5.3 Plant height (cm)

ANOVA for Plant Height (Table 4.26.1) revealed that genotype, environment components and residual were significant. The genotype, environment and genotype x environment interaction respectively accounted for 44.31 *per cent*, 20.55 *per cent* and 34.51 *per cent* of the total variation, respectively. The ANOVA also indicated that G x E interaction was partitioned into single IPCA, which was significant and explained 79.06 *per cent* of the total G x E interaction sum of squares.

However, the AMMI 1 biplot for plant height (Fig. 4.4.5) has revealed that none of the hybrids were identified as stable. H-5 and H-11 were identified as stable genotypes which had higher mean and IPCA scores near to zero. In AMMI 2 biplot (Fig. 4.4.6), H-10 and H-2 were nearer to IPCA origin, hence these hybrids were stable over locations. Intermediate plant types are preferred for high biomass types hence hybrids H-13, H-9, H-12 have high IPCA scores\ with specific adaptation.

H- 4,12,9,13 are having high plant height and stable, while H- 5, H-11, H-7, H-3, H-16, H-8 & H-15 are having high yielders and unstable. H-14, H-10 & H-1 are having low plant height and stable while H-6, is having low plant height and unstable. Location 1 and 2 have similar main effects and they are clustered into single group had below average mean and negative IPCA scores.

4.6.5.4 Number of nodes per plant

ANOVA for number of nodes per plant (Table 4.26.2) showed that genotype and residuals components were significant. The genotypes, environments and genotype x environment interaction were accounting for 50.04 *per cent*, 0.58 *per cent* and 40.25 *per cent* of the total variation, respectively. The ANOVA also indicated that G x E interaction was partitioned into only one IPCA which was significant and explained 73.56 *per cent* of the total G x E interaction sum of squares percentage.

The AMMI 1 biplot (Fig. 4.4.7) has identified H-7 and H-5 as stable hybrids which had higher mean and IPCA scores nearer to zero. In AMMI 2 biplot (Fig. 4.4.8), H-2 and H-16 were nearer to IPCA origin, hence these two hybrids were stable over locations. Hybrids H-13 and H-12 are showing specific adaptation with high IPCA scores among the hybrids studied.

Table 4.26.1. ANNOVA of AMMI model for characters Days to 50% flowering, Days to maturity, Plant height in 16 F₁ hybrids of Sorghum [*Sorghum bicolor* (L.) Moench].

Source	D.F	1. Days to 50% flowering (days)		2. Days to maturity (days)		3. Plant height (cm)	
		MS	Explained %	MS	Explained %	MS	Explained %
Trials	50	110.61*		96.53		4521.48*	
Genotype	16	242.92**	69.94 %	176.20**	57.57 %	6300.34*	44.31%
Environment	2	60.15	2.16%	19.32	0.78%	23376.41**	20.55%
G * E Interaction	32	47.62	27.42%	61.52	40.20%	2453.61	34.51%
IPCA 1	17	63.21	70.52 %	81.18	70.11%	3651.53	79.06%
Residual	15	29.94**	29.48 %	39.23**	29.89%	1095.98**	20.94%
Pooled residual	32	47.62		61.52		1095.98	
Error	51	0.50		1.36		27.19	
Total	101	55.01		48.47		2252.09	

*Significant at 0.05 level

** Significant at 0.01 level

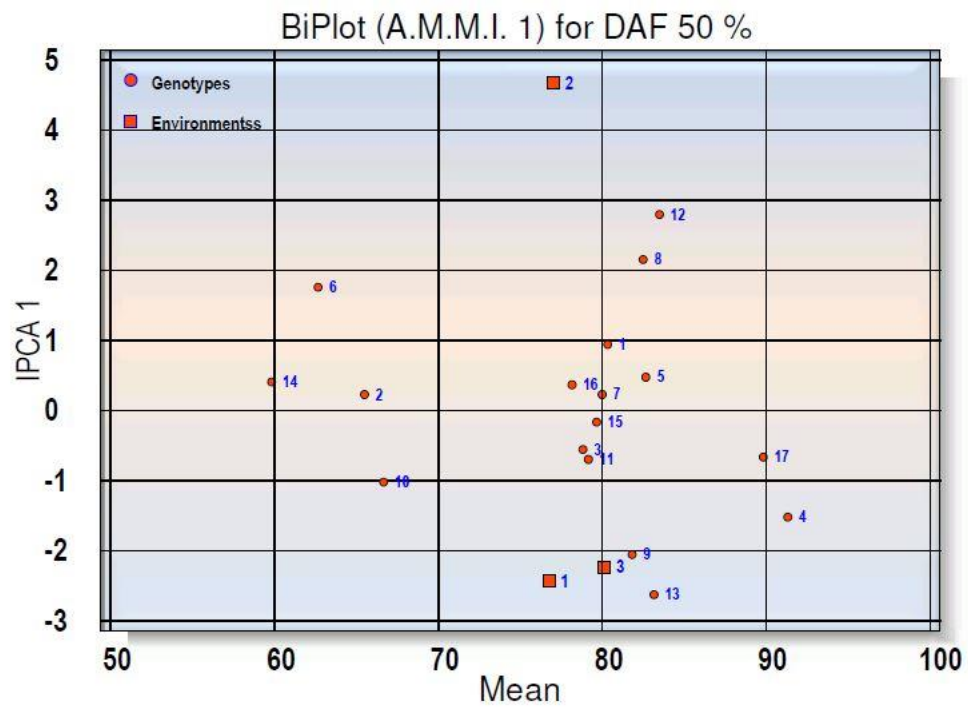


Fig. 4.4.1. Biplot (AMMI 1) for Days to 50% flowering.

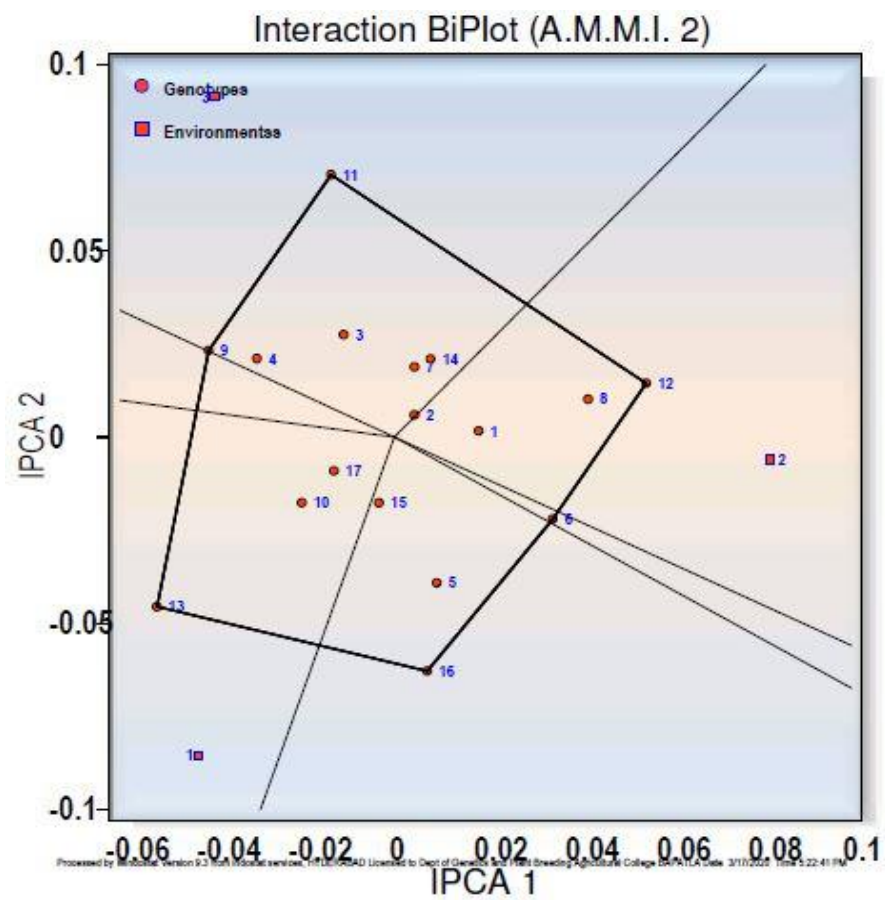


Fig. 4.4.2. Interaction biplot (AMMI 2) for Days to 50% flowering

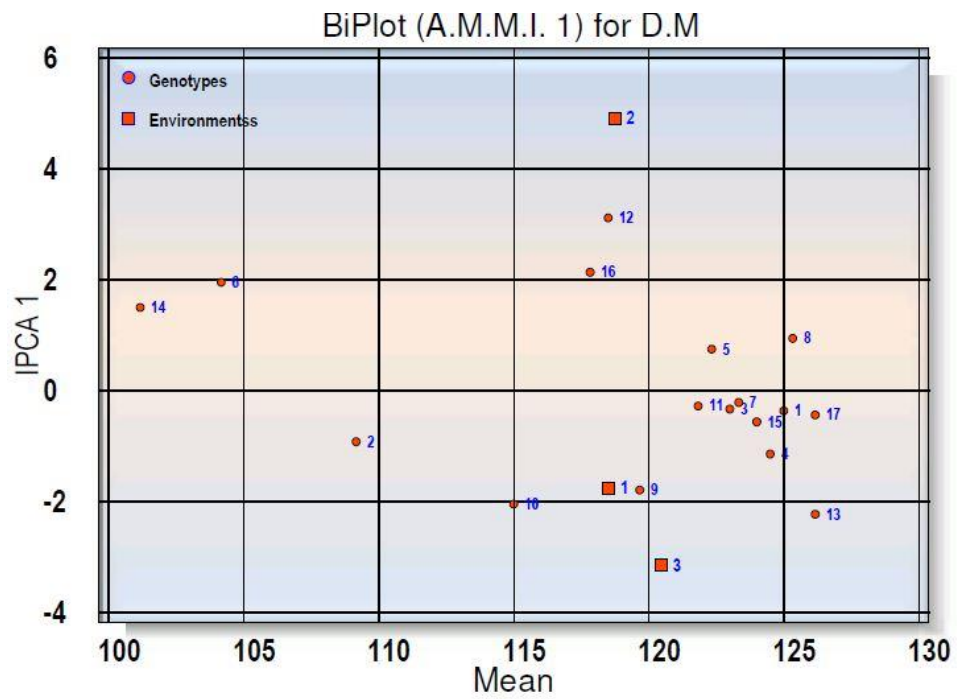


Fig. 4.4.3. Biplot (AMMI 1) for Days to maturity.

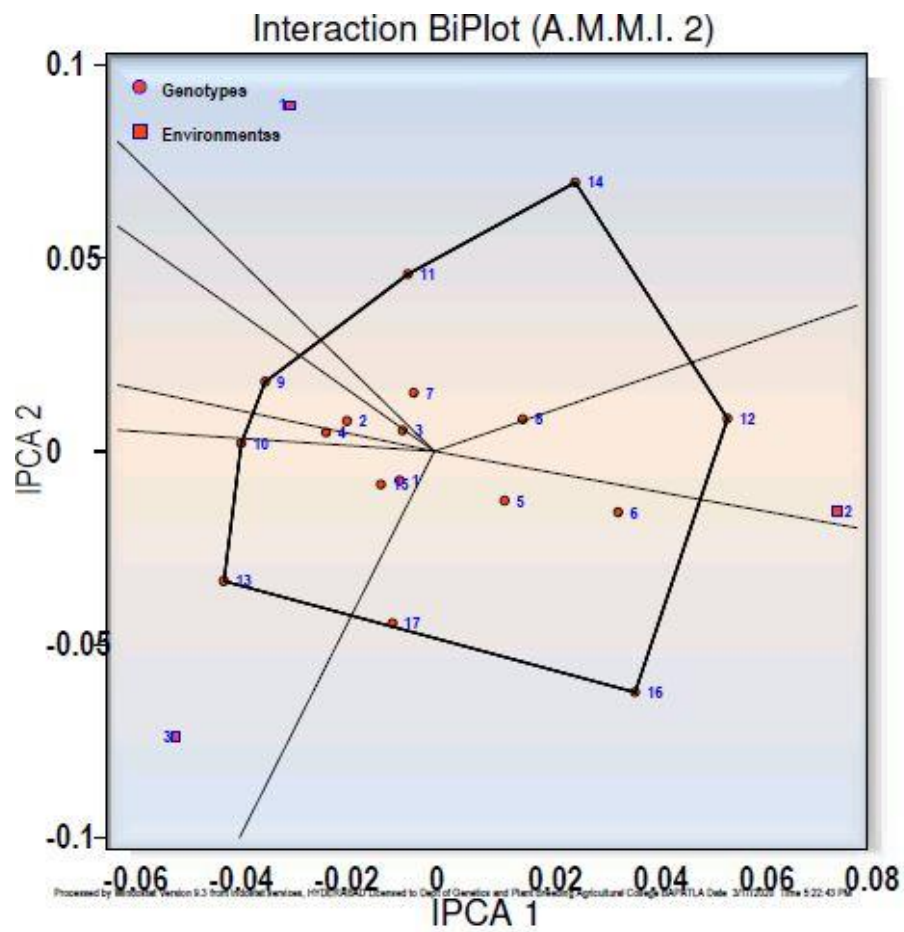


Fig. 4.4.4. Interaction biplot (AMMI 2) for Days to maturity.

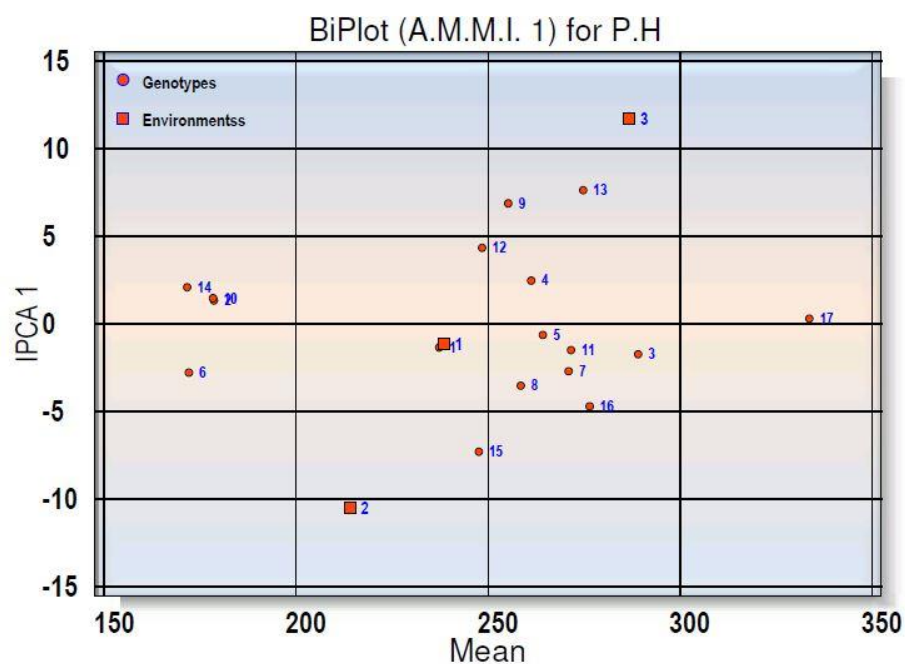


Fig. 4.4.5 Biplot (AMMI 1) for Plant height.

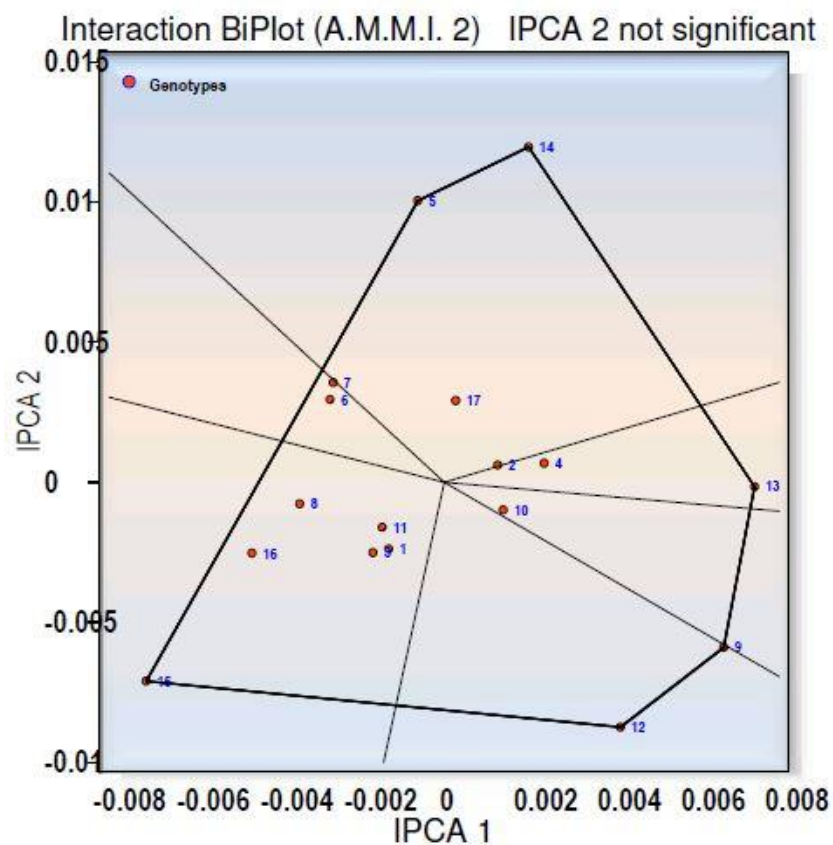


Fig. 4.4.6. Interaction biplot (AMMI 2) for Plant height.

H-12, H-9, H-10, H-7 and hybrid check are having high yield and stable, while H-3, H-16, H-3 are though high yielders are unstable. H-1, H-13 & H -14 low yielders and stable while H-2, H-4, H-5, H-8, H-11 and H-15 are low yielders and unstable.

4.6.5.5 Stem girth (cm)

ANOVA for stem girth (Table 4.26.2) revealed that environment and residual component was significant. The genotypes, environments and genotype x environment interaction were accounting for 28.63 *per cent*, 16.06 *per cent* and 54.31 *per cent* of the total variation, respectively. The ANOVA also indicated that G x E interaction was partitioned into a single IPCA. The IPCA was significant and explained 56.67 *per cent* of the total G x E interaction sum of squares.

The AMMI 1 biplot (Fig. 4.4.9) has revealed that none of the hybrids were identified as stable except H-15 which had higher mean and IPCA scores nearer to zero. In AMMI 2 biplot (Fig. 4.4.10), the H-12 and H-11 were nearer to IPCA origin, hence the hybrids were found to be stable over locations. Stem girth contributes to the high biomass type hence hybrids with high stem girth are preferred.

H-4, H-11, H-13 and H-14 are having high stem girth and stable, while H-2, H-3, H-6, H-7, H-10 & H-15 are having high stem girth and unstable, H-1, H-9, H-12, H-16 and hybrid check are having low stem girth and stable, H-5, H-8 are having low stem girth and unstable.

4.6.5.6 Panicle weight (g)

ANOVA for panicle weight (Table 4.26.2) showed that environment and residual component were significant. The genotypes, environments and genotype x environment interaction were accounting for 24.80 *per cent*, 17.36 *per cent* and 53.02 *per cent* of the total variation, respectively and further indicated that G x E interaction was partitioned into single IPCA, which were significant and explained 58.21 *per cent* of the total G x E interaction sum of squares.

The AMMI 1 biplot (Fig. 4.4.11) has revealed that none of the hybrids were identified as stable except H-2 which had higher mean and IPCA scores nearer to zero. In AMMI 2 biplot (Fig. 4.4.12) H-12 nearer to IPCA origin, hence the hybrids were found to be stable over locations.

H-2, H-5, H-10, H-11, H-13, H-14, H-15 and hybrid check are having high panicle weight and stable, while H-3, H-4, H-6, H-7, H-8, H-9 and H-12 are having high panicle weight and unstable, H-1, H-16 are having low panicle weight and unstable.

Table 4.26.2. ANNOVA of AMMI model for Number of nodes per plant, Stem girth, Panicle weight characters in 16 F₁ hybrids of Sorghum [*Sorghum bicolor* (L.) Moench].

Source	D.F	4. Number of nodes per plant		5. Stem girth (cm)		6. Panicle weight (g)	
		MS	EXPLAINED %	MS	EXPLAINED %	MS	EXPLAINED %
Trials	50	4.04		0.52		102.75	
Genotype	16	6.95*	50.04%	0.47	28.63%	83.67	24.80%
Environment	2	0.65	0.58%	2.11*	16.06%	468.55*	17.36%
G * E Interaction	32	2.79	40.25%	0.44	54.31%	89.42	53.02%
IPCA 1	17	3.87	73.56%	0.46	56.67%	97.98	58.21%
Residual	15	1.57**	26.44%	0.42**	44.33%	79.72**	41.79%
Pooled residual	15	1.57		0.44		89.42	
Error	51	0.39		0.004		5.07	
Total	101	2.20		0.26		53.43	

*Significant at 0.05 level

** Significant at 0.01 level

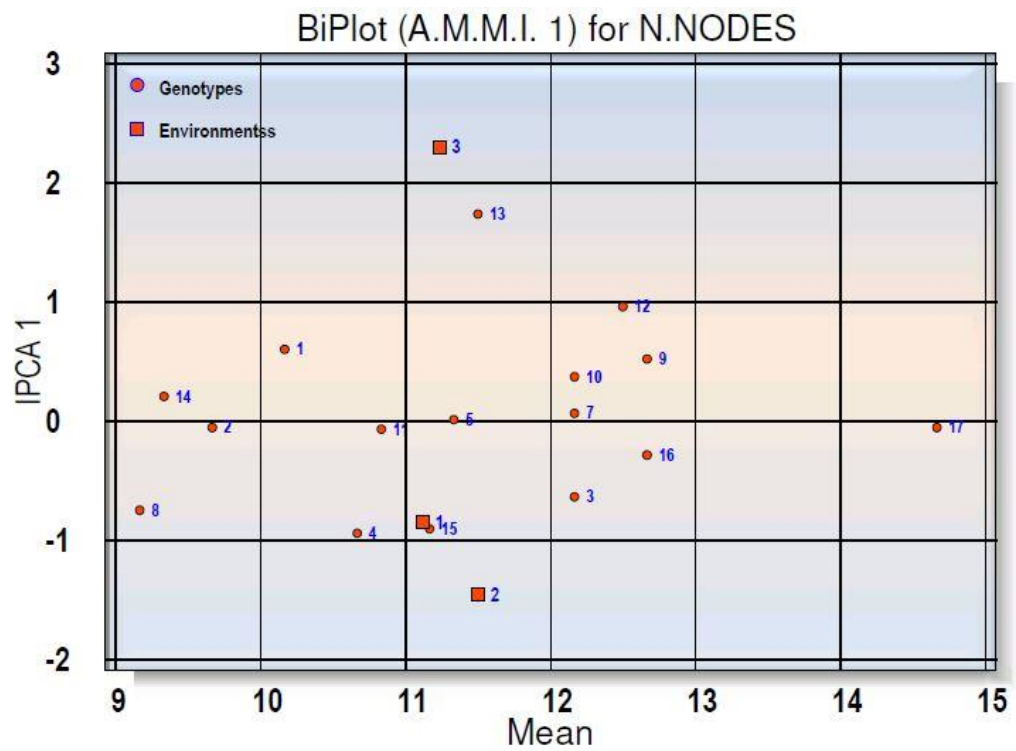


Fig. 4.4.7. Biplot (AMMI 1) for Number of nodes per plant.

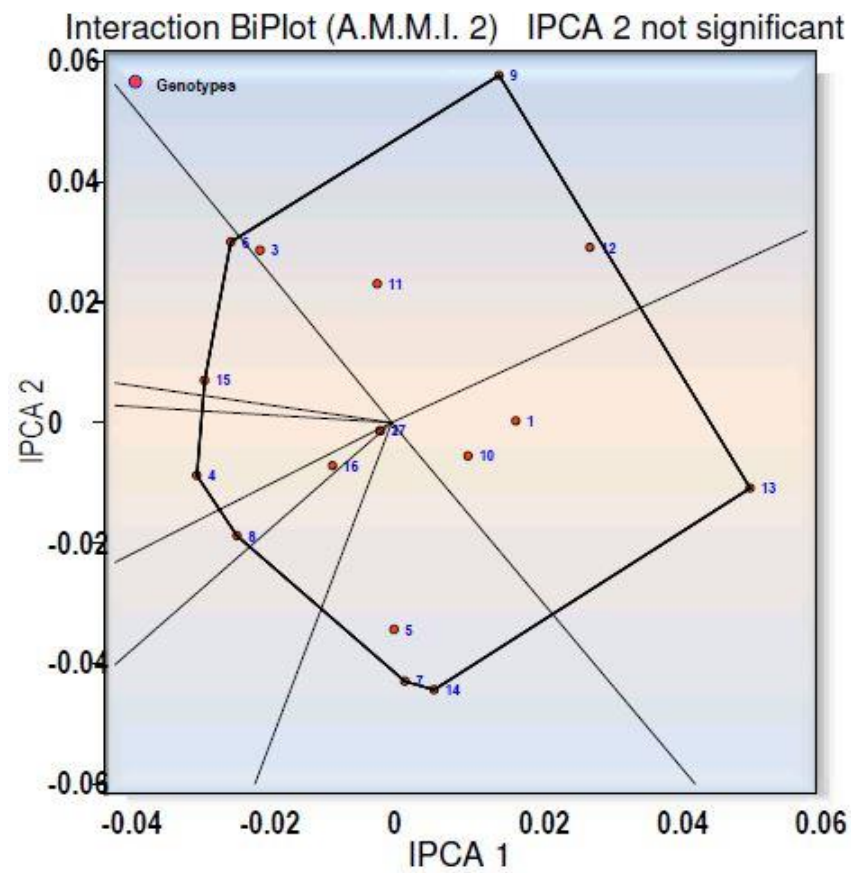


Fig. 4.4.8. Interaction biplot (AMMI 2) for Number of nodes per plant.

4.6.5.7 1000 grain weight (g)

ANOVA for 1000 grain weight (Table 4.26.3) showed that environment and residuals were significant. The genotype, environment and genotype x environment interaction were accounting for 20.77 *per cent*, 23.24 *per cent* and 43.68 *per cent* of the total variation, respectively. The ANOVA also indicated that G x E interaction was partitioned into one IPCA. The IPCA was significant and explained 83.65 *per cent* of the total G x E interaction sum of squares.

In this study sorghum with dual purpose of grain and ethanol are preferred hence hybrids with high 1000 grain weight are prioritized. The AMMI 1 biplot (Fig. 4.4.13), H-7 was identified as stable hybrid which had higher mean and IPCA scores near to zero. In AMMI 2 biplot (Fig. 4.4.14) H-3 and H-4 were nearer to IPCA origin, hence these hybrids were stable over locations. Hybrid 9 had high mean and high IPCA score which indicates specific environment.

H-6, H-9 are having high 1000 grain weight and stable, while H-2, H-8, H-14 and hybrid check though having high 1000 grain weight yet unstable. All the remaining 11 hybrids viz., H-7, H-5, H-13, H-4, H-12, H-16, H-1, H-3, H-15, H-10 and H-11 are low 1000 grain weight and unstable. Location 1 and 2 have similar main effects and they are clustered into single group had below average mean and negative IPCA scores.

4.6.5.8 Fresh stalk yield (T ha⁻¹)

ANOVA for fresh stalk yield (Table 4.26.3) showed that only residual component was significant. The genotypes, environments and genotype x environment interaction were accounting for 44.27 *per cent*, 6.52 *per cent* and 48.66 *per cent* of the total variation, respectively. The ANOVA also indicated that G x E interaction was partitioned into only single IPCA. The IPCA was significant and explained 68.98 *per cent*, of the total G x E interaction sum of squares.

The AMMI 1 biplot (Fig. 4.4.15), H-7 which has identified as stable hybrid for this character as well as for number of nodes per plant earlier, which had higher mean and IPCA scores nearer to zero. In AMMI 2 biplot (Fig. 4.4.16) the hybrid H-5 was nearer to IPCA origin, hence these two hybrids were stable over locations and other hybrid H-5, H-16, H-12, H-4 and H-13 had high IPCA scores.

H-7 is having high fresh stalk yield and stable, while H-3 & H-11 are having high fresh stalk yield and unstable. H-1, H-16, H-5, H-12, H-4 and H-13 low fresh stalk weight and stable while H-8, H-9, H-14, H-15, H-10, H-6, H-2 and check entry are having low fresh stalk weight and unstable.

4.6.5.9 Juice yield (l ha⁻¹)

ANOVA for juice yield (Table 4.26.3) revealed that only residual component was significant. The genotypes, environments and genotype x environment interaction were accounting for 47.53 *per cent*, 59.60 *per cent* and 50.11 *per cent* of the total variation, respectively. The ANOVA also indicated that G x E interaction was partitioned into a single IPCA. The IPCA was significant and explained 69.62 *per cent* of the total G x E interaction sum of squares.

The AMMI 1 biplot (Fig. 4.4.17), H-10 and H-11 were identified as stable hybrids which had higher mean and IPCA scores nearer to zero and hybrid H-6, H-2 are with higher mean but IPCA scores are far away from zero. In AMMI 2 biplot (Fig. 4.4.18), the H-12 and H-11 were nearer to IPCA origin, hence the hybrids were found to be stable over locations. Hybrid H-15 had high IPCA score with specific adaptation

H- 15, H- 6, H-2 & H-10 are having high juice yield and stable, though the H-3, H-7, H-9 & H-11 are having high juice yield performance are unstable. The hybrids H-13, H-16 & H- 14 are low juice yielders and stable while H-8, H- 5, H-12, H- 4 and check entry are low juice yielders and unstable. Location 1 and 2 have similar main effects and they are clustered into single group and had above average mean and negative IPCA scores.

4.6.5.10 Brix%

ANOVA for brix per cent was presented in (Table 4.26.4) revealed that genotypes, environments and residual component were significant. The genotypes, environments and genotype x environment interaction were accounting for 39.26 *per cent*, 11.21 *per cent* and 47.02 *per cent* of the total variation, respectively. The analysis further indicated that G x E interaction was partitioned into only one IPCA, which was significant and explained 68.65 *per cent* of the total G x E interaction sum of squares percentage.

The AMMI 1 biplot (Fig. 4.4.19), H-7 was identified as stable hybrid because of higher mean and IPCA scores nearer to zero while hybrids H-8, H-3, H-16 had higher mean but IPCA scores are far away from zero. Whereas, AMMI 2 biplot (Fig. 4.4.20), showed that the H-13 and H-4 were nearer to IPCA origin, hence these hybrids were stable over environments. Hybrids H-9, H-10 had high IPCA scores with specific adaptation.

Table 4.26.3. ANNOVA of AMMI model for characters 1000 grain weight, Fresh stalk yield, Juice yield in 16 F₁ hybrids of Sorghum [*Sorghum bicolor* (L.) Moench].

Source	df	7. 1000 Grain weight (g)		8. Fresh stalk yield (T ha ⁻¹)		9. Juice yield (l ha ⁻¹)	
		MS	Explained %	Ms	Explained %	Ms	Explained %
Trials	50	42.72		190.59			
Genotype	16	31.61	20.77%	265.13	44.27%	25077232.64	47.53%
Environment	2	283.12**	23.24%	312.6	6.52%	37694254.05	59.60%
G * E Interaction	32	33.24	43.68%	145.71	48.66%	7486471.87	50.11 %
IPCA 1	17	52.35	83.65%	189.20	68.98%	19868144.48	69.62%
Residual	15	11.59*	16.35%	96.43**	31.02%	26035343.39**	30.38%
Pooled residual	15	11.59		96.43		12878652.38	
Error	51	5.87		1.00		290359.80	
Total	101	24.11		94.86		12561088.93	

*Significant at 0.05 level

** Significant at 0.01 level

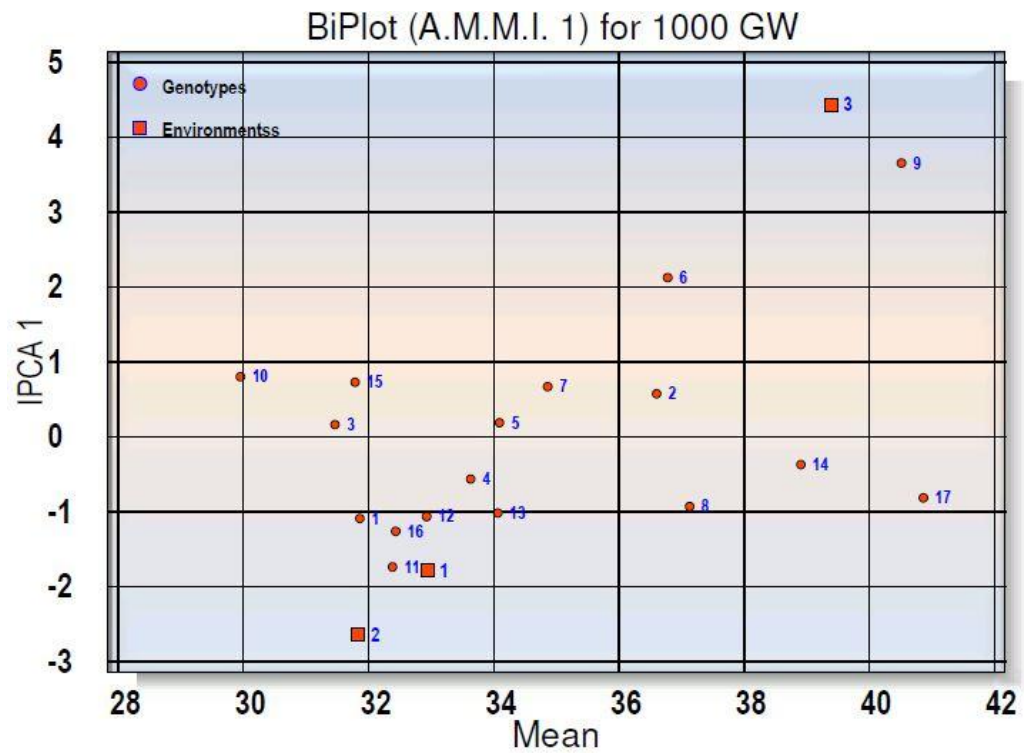


Fig. 4.4.13. Biplot (AMMI 1) for 1000 grain weight.

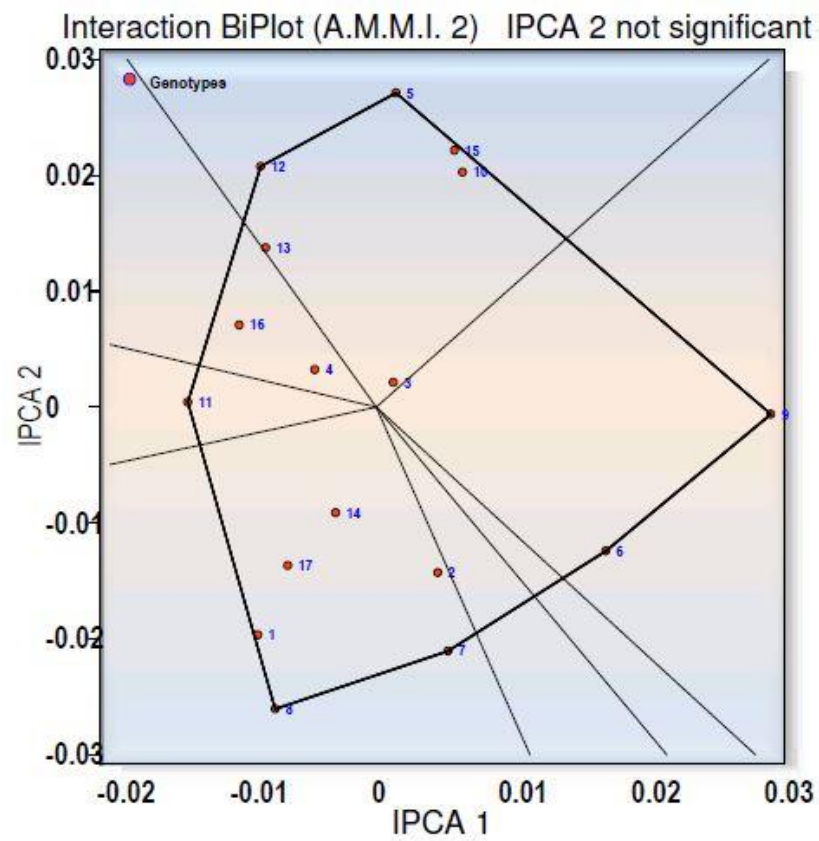


Fig. 4.4.14. Interaction Biplot (AMMI 2) for 1000 grain weight.

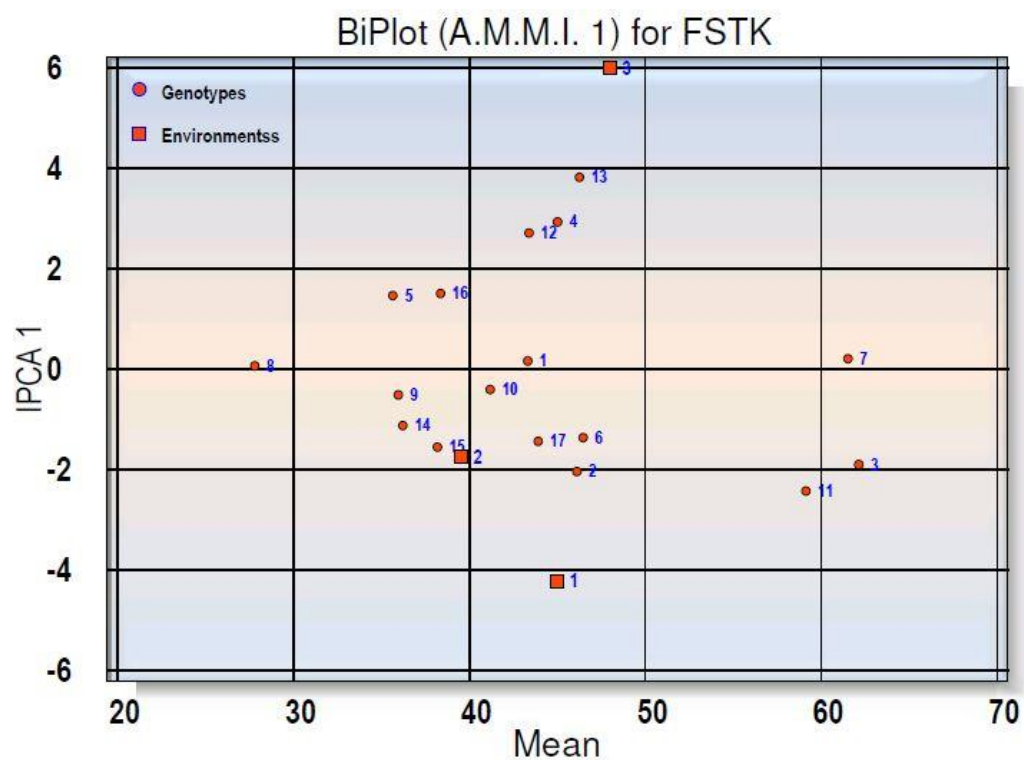


Fig. 4.4.15. Biplot (AMMI 1) for Fresh stalk yield.

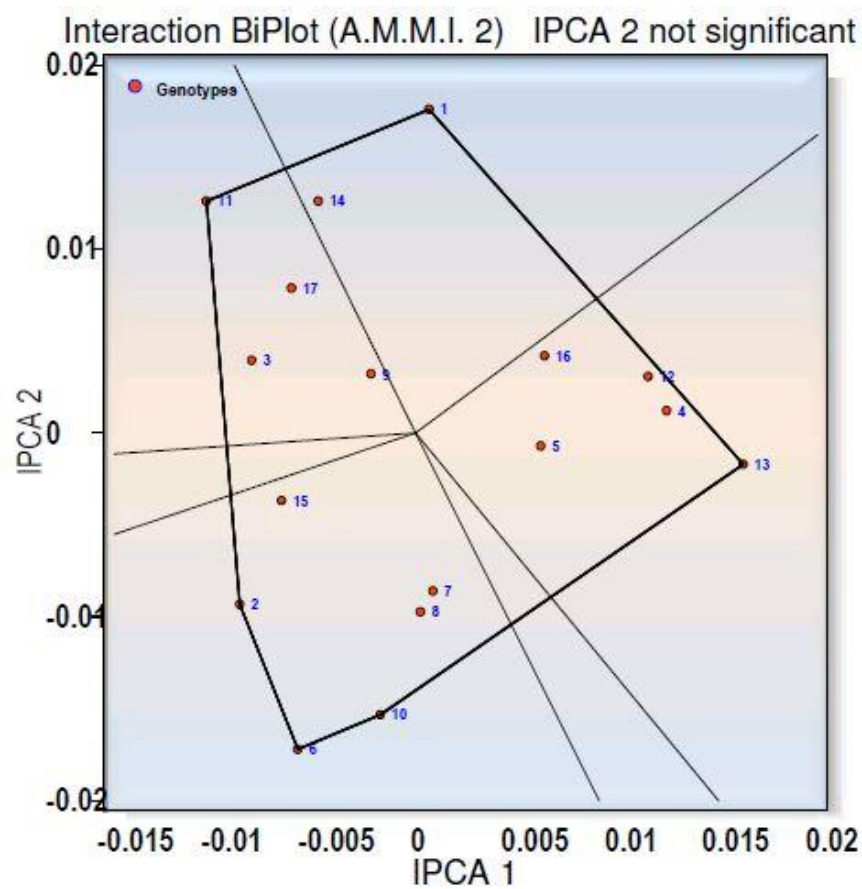


Fig. 4.4.16. Interaction Biplot (AMMI 2) for Fresh stalk yield

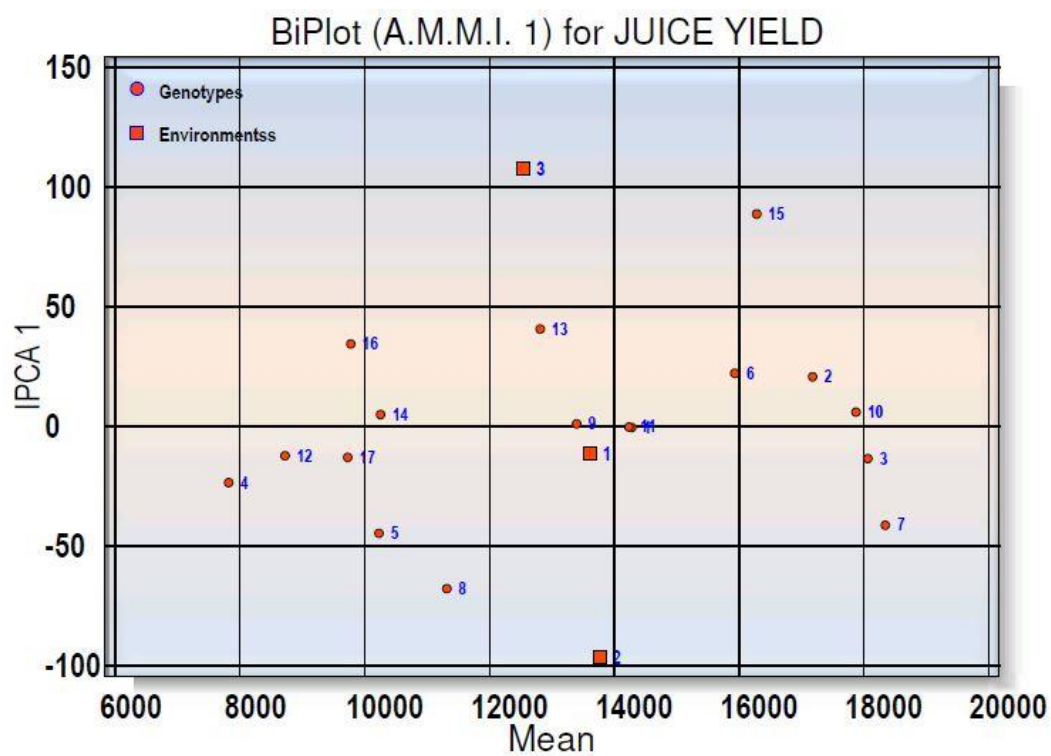


Fig. 4.4.17. Biplot (AMMI 1) for Juice yield.

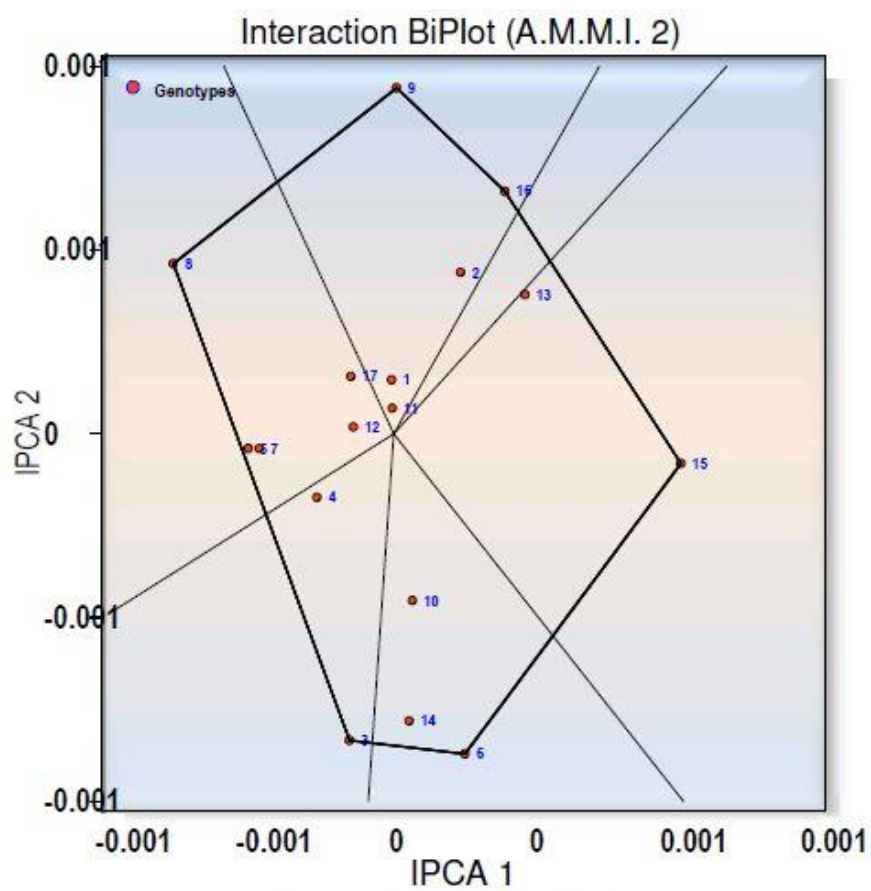


Fig. 4.4.18. Interaction Biplot (AMMI 2) for Juice yield.

H- 2 is having high brix per cent and stable, while H- 4, H-15, H-7, H-8, H-3, H-16 and hybrid check are having high brix per cent and unstable. H-9, H-10 and H-1 are having low brix per cent and stable while H-6, H-13, H-14, H-12 and H-5 are having low brix per cent and unstable. Location 1 and 2 have similar main effects and they are clustered into single group had above average mean and negative IPCA scores.

4.6.5.11 Total soluble sugars (%)

ANOVA for total soluble sugars (Table 4.26.4) showed that environments and residual component were significant. The genotypes, environments and genotype x environment interaction were accounting for 39.25 *per cent*, 11.20 *per cent* and 47.03 *per cent* of the total variation, respectively. The ANOVA also indicated that G x E interaction was partitioned into one IPCA which was significant and explained 68.67 *per cent* of the total G x E interaction sum of squares.

According to AMMI 1 biplot (Fig. 4.4.21), H-7 and H-8 were identified as stable hybrids which had higher mean and IPCA scores nearer to zero. Hybrids H-9, H-10 were having high IPCA scores which is showing specific adaptation. In AMMI 2 biplot (Fig. 4.4.22), H-13 and H-4 were nearer to IPCA origin, hence these hybrids were stable over locations.

H- 2 are having high total soluble sugars and stable, while H- 4, H-15, H-7, H-8, H-3, H-16 & H-11 are having high total soluble sugars and unstable. H-9, H-10, H-1 and hybrid check are having low total soluble sugars and stable while H-6, H-13, H-14, H- 12 and H-5 are having low total soluble sugars and unstable.

4.6.5.12 Ethanol yield (l ha⁻¹)

ANOVA for ethanol yield (Table 4.26.5) showed that environment and residual components were significant. The genotypes, environments and genotype x environment interaction were accounting for 48.85 *per cent*, 4.17 *per cent* and 45.72 *per cent* of the total variation, respectively and further indicated that G x E interaction was partitioned into single IPCA which too is significant and explained 67.21 *per cent* of the total G x E interaction sum of squares.

Table 4.26.4. ANNOVA of AMMI model for characters Brix %, Total soluble sugars in 16 F₁ hybrids of Sorghum [*Sorghum bicolor* (L.) Moench].

Source	Df	10. Brix%		11. Total Soluble Sugars (%)	
		MS	Explained %	MS	Explained %
Trials	50	8.01		6.12	
Genotype	16	10.08	39.26%	7.71	39.25%
Environment	2	23.04*	11.21%	17.61*	11.20%
G * E Interaction	32	6.03	47.02%	4.62	47.03%
IPCA 1	17	7.80	68.65%	5.97	68.67%
Residual	15	4.03**	31.35%	3.08**	31.33%
Pooled residual	15	4.03		3.08	
Error	51	0.20		0.15	
Total	101	4.06		3.11	

*Significant at 0.05 level

** Significant at 0.01 level

Table 4.26.5. ANNOVA of AMMI model for characters Ethanol and Grain yield in 16 F₁ hybrids of Sorghum [*Sorghum bicolor* (L.) Moench].

Source	DF	Ethanol yield (l ha ⁻¹)		Grain yield (T ha ⁻¹)	
		MS	Explained %	MS	Explained %
Trials	50			1.48	
Genotype	16	228028.54	48.85%	0.77	15.12%
Environment	2	155932.63*	4.17%	0.25	0.61%
G * E Interaction	32	106711.15	45.72%	1.91	75.13%
IPCA 1	17	134998.61	67.21%	2.30	63.76%
Residual	15	74652.03**	32.79%	1.48**	36.24%
Pooled residual	15	106711.15		1.48	
Error	51	1824.45		0.14	
Total	101	73941.84		0.80	

*Significant at 0.05 level

** Significant at 0.01 level

From the AMMI 1 biplot (Fig. 4.4.23), H-2 was identified as stable hybrid based on higher mean value and IPCA score near to zero. The AMMI 2 biplot (Fig. 4.4.24) has revealed that H-3 is having a higher mean value and was nearer to zero, while the H-14 and H-12 were nearer to IPCA origin, hence these hybrid were stable over locations. Hybrid H-15, H-13, H-16 & H-6 are having IPCA scores with specific adaptation only.

H- 11, H-15 & H-3 are having high ethanol yield and stable, while H- 2, H-7 & H-10 are having high yield and unstable. H-6, H-16, H-13 & H-14 are having low ethanol yield and stable while H-1, H-9, H- 8, H-5, H-4 , H-12 and check entry are low ethanol yields and unstable. Location 1 and 2 have similar main effects and they are clustered into single group had above average mean and negative IPCA scores.

4.6.5.13 Grain yield ($T\ ha^{-1}$)

ANOVA for grain yield (Table 4.26.5) showed that only residual component was significant. The genotypes, environments and genotype x environment interaction respectively accounted for 15.12 *per cent*, 0.61 *per cent* and 75.13 *per cent* of the total variation, and further indicated that G x E interaction was partitioned into only one IPCA, which was significant and explained 63.76 *per cent* of the total G x E interaction sum of squares.

The AMMI 1 biplot (Fig. 4.4.25), H-12 was identified as stable as they have higher mean and IPCA scores nearer to zero and followed by hybrids H-10, H-11, H-2. While hybrids H-15 had average mean with IPCA score with specific adaptation. In AMMI 2 biplot (Fig. 4.4.26), the H-12 and H-11 were found to be nearer to IPCA origin, hence these hybrids were stable over locations.

H- 9, H-5, H-11, H-10 and H-12 are having high grain yield and stable, while H- 8, H-7, H-4, H-3 are having high grain yield and unstable. H-15 is showing low grain yield and stable while H-6, H-14, H-1, H-13 and H-16 are showing low grain yield and unstable. Location 1 and 3 have similar main effects and they are clustered into single group had above average mean and negative IPCA scores.

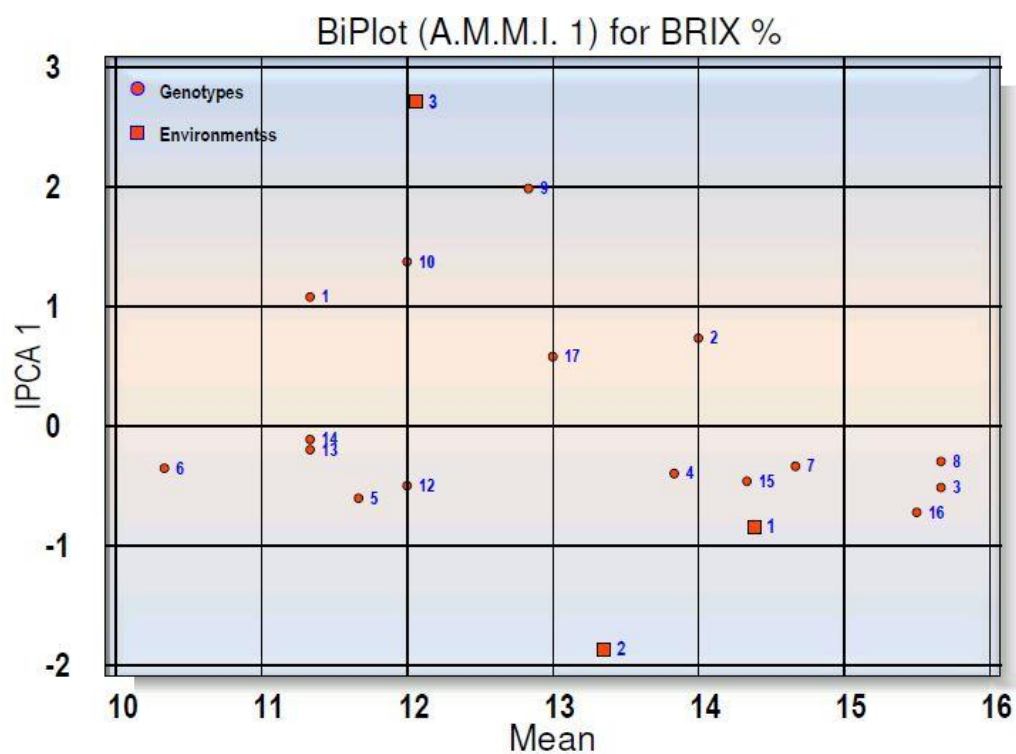


Fig. 4.4.19. Biplot (AMMI 1) for Brix %.

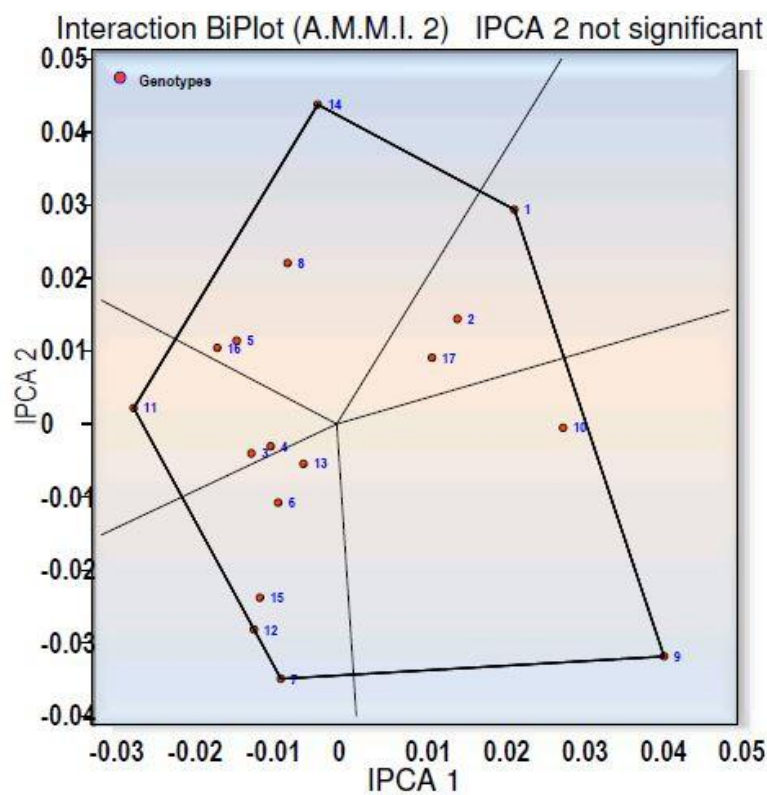


Fig. 4.4.20. Interaction Biplot (AMMI 2) for Brix %

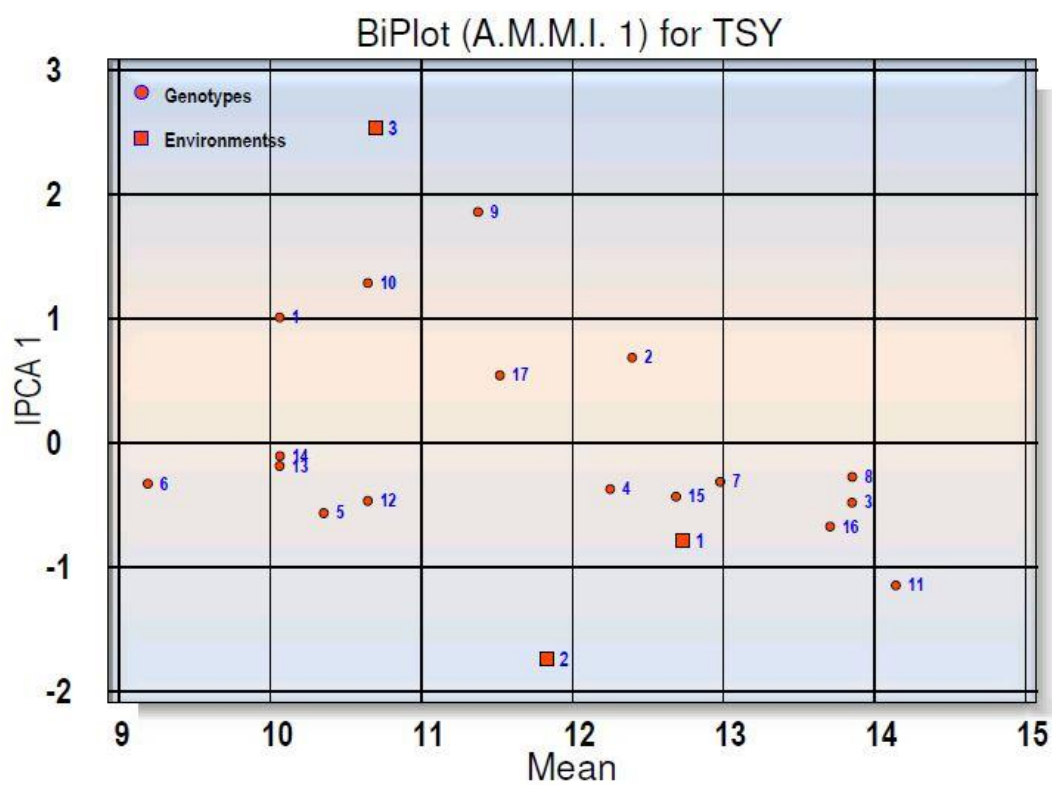


Fig. 4.4.21. Biplot (AMMI 1) for Total soluble sugars.

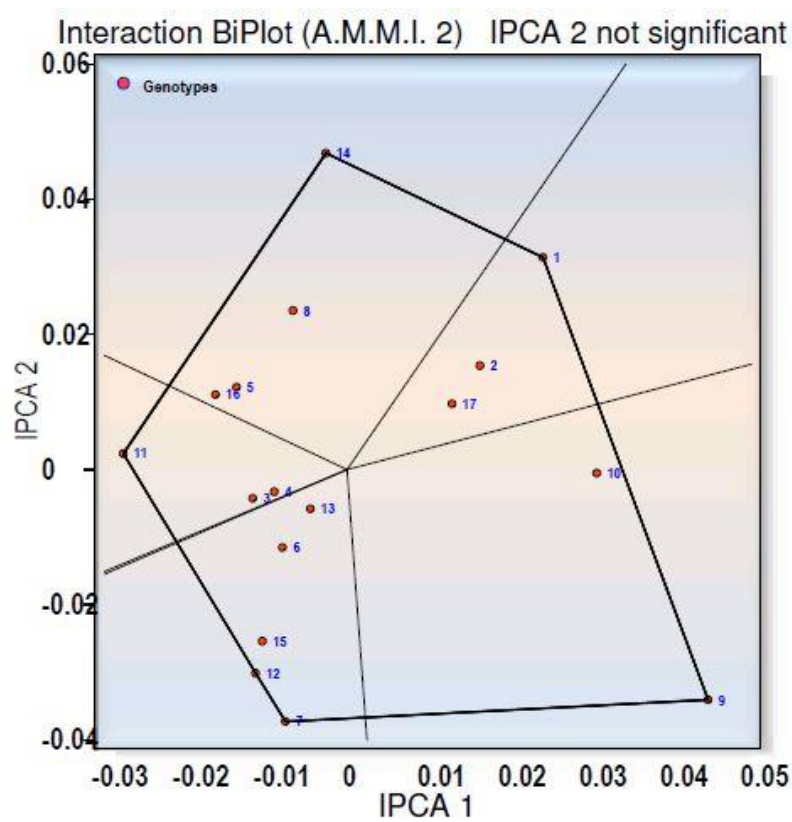


Fig. 4.4.22. Interaction Biplot (AMMI 2) for Total soluble sugars.

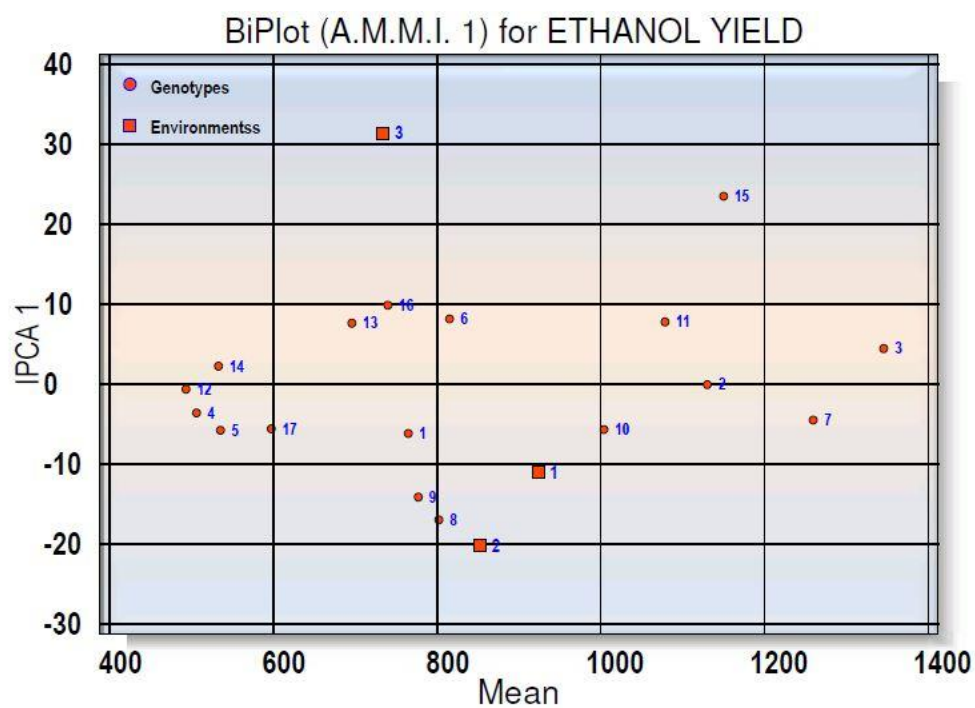


Fig. 4.4.23. Biplot (AMMI 1) for Ethanol yield.

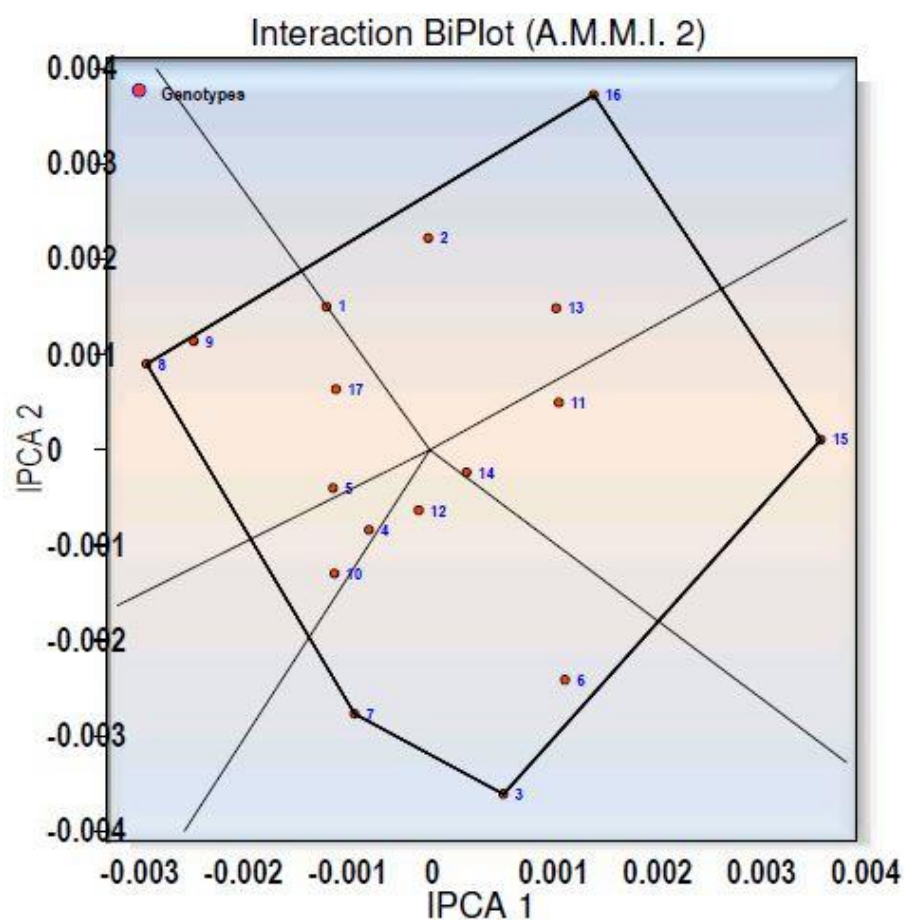


Fig. 4.4.24. Interaction Biplot (AMMI 2) for Ethanol yield.

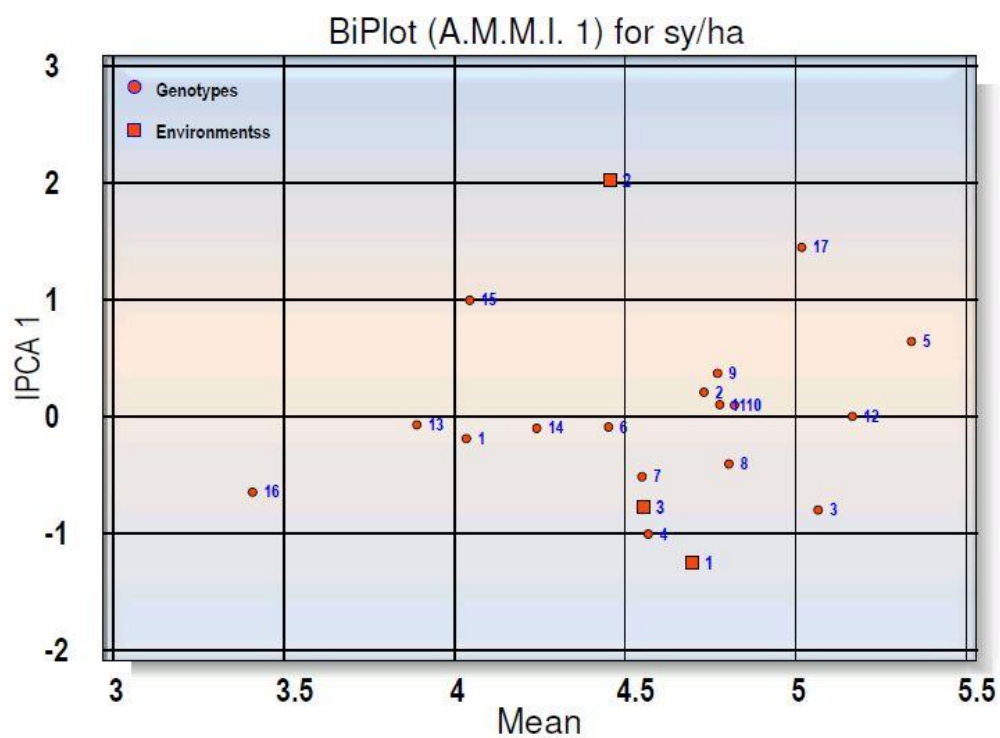


Fig. 4.4.25. Biplot (AMMI 1) for Grain yield .

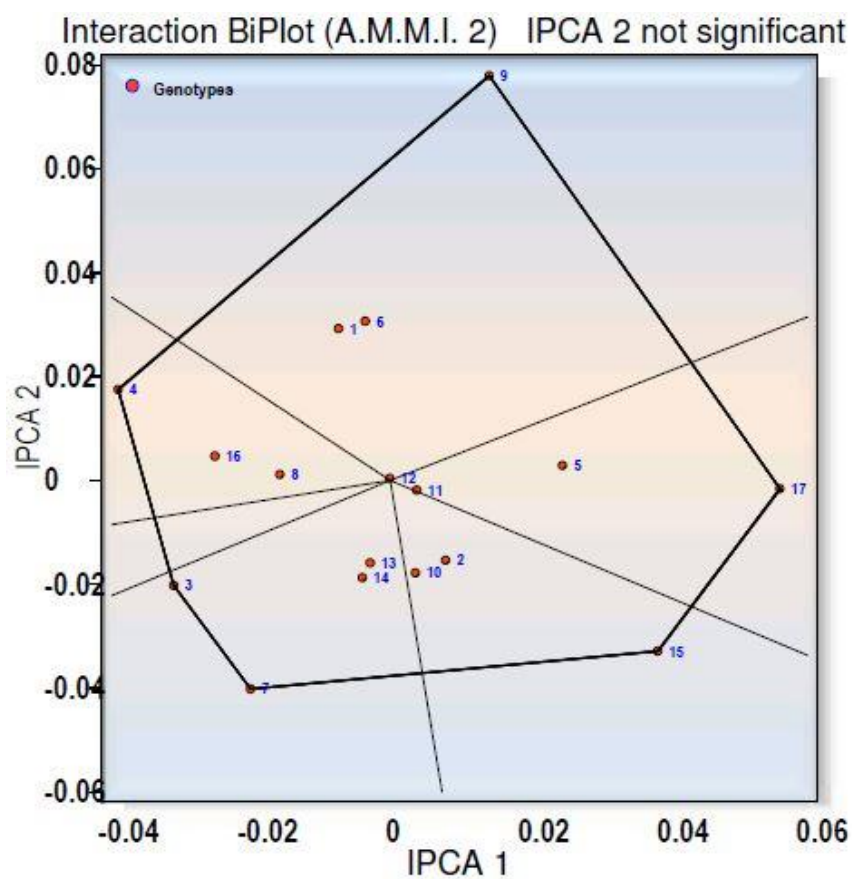


Fig. 4.4.26. Interaction Biplot (AMMI 2) for Grain yield

Conclusion: In AMMI analysis, the IPCA scores gave an indication of stability or adaptability of the genotypes over environments (Rashidi *et al.*, 2013). The genotypes having greater IPCA score indicates their specific adoption to a given environment while genotypes having scores close to zero are stable only in sampled environment. In this scenario H-2 for days to 50% flowering, H-3 and H-5 were stable over locations for days to maturity, H-10 and H-2 for plant height, H-7 and H-5 for no of nodes per plant, H-15 for stem girth, H-3 and H-4 for 1000 grain weight, H-5 for Fresh stalk yield, hybrids H-12, H- 10, H-11, H-2 for grain yield, H -7 for brix%, H- 7 & H- 8 for total soluble sugars and H-10 and H-11 for juice yield and H-2 and H-3 for ethanol yield.

When Eberhart and Russel's model is compared with the later AMMI analysis explains a higher proportion of the sum of squares of the G x E interaction and is more informative with regard to environments and cultivar performance. The AMMI model was found as a supportive tool in indicating G X E interaction. It enables clustering of genotypes based on similarity of response characteristics and detecting possible trends through environments. Hybrids which performed similar and different in Stability and AMMI analysis were presented in table: 4.26.6.

The classification for Eberhart and Russel's model and AMMI model was similar for the traits Days to 50% flowering, days to maturity, Plant height, number of nodes per plant. For remaining characters the AMMI classification doesn't present any similarity with the results obtained by Eberhart and Russel model. The stable performing hybrids 2, 14 and 12 which are tested in 3 locations may be utilized in future breeding programme in sorghum for improvement of ethanol yield and its component traits. The hybrids that give consistent performance under better environments may be utilized for trait manipulation and other breeding programmes need to be carried out in under targeted environment.

Table 4.26.6. Differential performance of F₁ hybrids in Eberhart and Russell's stability model vs AMMI stability model.

S. No.	Character	Hybrids which performed similar in Stability and AMMI analysis	Hybrids which performed different in Stability and AMMI analysis
1	Days to 50% flowering	H-2	H-14
2	Days to maturity	H-3, H-5	-
3	Plant height (cm)	H-2, H-10	-
4	Number of nodes per plant	H-5, H-7, H-16	H-2
5	Stem girth (cm)	-	H-11, H-12
6	Panicle weight (g)	H-8	-
7	1000 grain weight (g)	H-6	H-3, H-4, H-7
8	Fresh stalk yield (T ha ¹)	-	H-5, H-7
9	Juice yield(T ha ⁻¹)	-	H-10, H-11, H-12
10	Brix %	H-15	H-4, H-7, H-13
11	T.S.S (%)	H-15	H-4, H-7, H-8, H-13
12	Ethanol yield (T ha ⁻¹)	-	H-2, H-12, H-14
13	Grain yield(T ha ⁻¹)	H-8	H-11, H-12

4.7 GENERATION MEAN ANALYSIS

The choice of an efficient breeding programme depends to a large extent on knowledge of the type of gene action involved in the expression of the character. The knowledge on nature of gene action for ethanol yield and its component traits like Brix per cent and Juice content in the breeding material can provide useful information for selecting proper breeding procedure for future genetic enhancement. Genetic enhancement for increased ethanol yield and its attributing traits is very important to make sweet sorghum more profitable to the farmers and the industry, while sustaining grain yield and other important components. In the present study only single cross has been studied for 6 parameter model (The seed set in backcrosses was ample only in this cross)

4.7.1 Per se Performance

The mean values along with standard error and variances pertaining to six basic generations (P_1 , P_2 , F_1 , F_2 , BC_1P_1 and BC_2P_2) of the cross 'ICSB 14029 x ICSV 15006' of sorghum in respect of ethanol yield and its other component characters have been tabulated in Table 4.27

4.7.1.1 Days to 50 % flowering (days)

The mean performance of the two selected parents of P_1 (ICSB 14029) and P_2 (ICSV-15006) were different from each other. The former was found to be early in days to 50 % flowering with a mean value of 73.40 days compared to the P_2 which was late in days to 50 % flowering with a mean value of 83.75 days. Similarly the mean values of F_1 and F_2 are 79.00 and 73.25 days respectively. The mean value of F_1 is tending towards P_2 and is more than the mid parental value of 78.57, whereas the mean performance of F_2 is almost similar to P_1 . Similarly the BC_1P_1 and BC_2P_2 family generation mean values for this trait are slightly lower than the respective female parent and male parent and even less than mid parental value and hence tended towards earliness of female parent. The F_1 mean values greater than the respective mean mid parental values for this trait is indicating dominance. Further the BC_1P_1 and BC_2P_2 family means are also tending towards earliness.

4.7.1.2 Days to maturity (days)

The mean performance of the two selected parents of P₁ (ICSB 14029) and P₂ (ICSV-15006) were different from each other. The former was found to be early in days to maturity with a mean value of 116.50 days compared to the P₂ which was late in days to maturity with a mean value of 122.60 days. Similarly the mean values of F₁ and F₂ are 121.70 and 115.18 days respectively. The mean value of F₁ is tending towards P₂ and is more than the mid parental value of 119.55 days, whereas the mean performance of F₂ is almost similar to P₁. The F₁ mean values greater than the respective mean mid parental values for this trait is indicating dominance. Similarly the BC₁P₁ and BC₂P₂ family generation mean values for this trait are slightly higher than the female parent and lower than male parent and even less than mid parental value and hence tended towards early maturity of female parent. The F₁ mean values greater than the respective mean mid parental values for this trait is indicating dominance.

4.7.1.3 Plant height (cm)

The mean performance of F₁ was 233.56 cm which are intermediate in plant height when compared to parents P-1 (195.47 cm), P-2 (295.28 cm) while female parent is short when compared to male parent. F₂ recorded mean plant height of 207.69 cm, BC₁P₁ and BC₂P₂ recorded average plant height of 214.57 cm, 237.29 cm respectively and when compared to mid parental values F₁, F₂, BC₁P₁ and BC₂P₂ recorded lower values which indicates non allelic interactions.

4.7.1.4 Number of nodes per plant

The mean performance of P₁ (ICSB 14029) and P₂ (ICSV-15006) were differing in number of nodes per plant. Similarly the mean values of F₁ and F₂ are 14.30 and 12.51 respectively. The mean value of F₁ is lower than P₂ (15.05) and higher than P₁ (10.55) and is more than the mid parental value of 12.8. The F₁ mean values greater than the respective mean mid parental values for this trait is indicating dominance. Similarly the BC₁P₁ and BC₂P₂ family generation mean values for this trait are slightly higher than the female parent and lower than male parent. The F₁ mean values greater than the respective mean mid parental values for this trait is indicating dominance.

4.7.1.5 Stem girth (cm)

Female parent (ICSB 14029) has recorded average stem girth of 2.85 cm and male parent (ICSV 15006) with average stem girth of 3.23 cm. The F₁ recorded average stem girth of 2.63 cm while the mid parental value was 3.04 cm which was lower than

both the parents which is showing lack of dominance. F_2 has recorded average stem girth of 2.70 cm which is on par with F_1 . While BC_1P_1 and BC_2P_2 has recorded average stem girth of 2.70 cm and 2.85cm which is tending towards like P_1 .

4.7.1.6 Panicle weight (g)

The mean performance of P_1 (ICSB 14029) and P_2 (ICSV-15006) were almost alike with mean values of 47.62 g and 44.74 g. while the mean values of F_1 and F_2 are 48.31 g respectively. The mean value of F_1 (48.31 g) is higher than P_1 (47.62 g) and P_2 (44.74 g) and is more than the mid parental value of 46.18 g. The F_1 mean values greater than the respective mean mid parental values for this trait is indicating dominance. Similarly the BC_1P_1 and BC_2P_2 family generation mean values for this trait are slightly lower than the female parent and on par with the male parent.

4.7.1.7 1000 grain weight (g)

The range for 1000 grain weight for F_1 was (17.70 – 35.85g), F_2 was (14.35 – 32.76g) and were intermediate to both the parents. P_1 and P_2 has respective mean values of 24.12g and 22.79g. Similarly the mean values of F_1 and F_2 are 25.28 g and 23.91 g respectively. The mean value of F_1 is lower than the mid parental value of, whereas the mean performance of F_2 is also intermediate between both the parents. The F_1 mean values lower than the respective mean mid parental values for this trait. BC_2P_2 (22.12g) was similar like P_2 . BC_1P_1 (23.67g) was nearer to P_1 (24.12g).

4.7.1.8 Fresh stalk yield ($T\ ha^{-1}$)

The mean performance of the two selected parents of P_1 (ICSB 14029) and P_2 (ICSV-15006) were different from each other. The former was found to be low biomass type with a mean value $51.14\ T\ ha^{-1}$ compared to the P_2 which was high biomass type with a mean value of $62.42\ T\ ha^{-1}$. Similarly, the mean values of F_1 and F_2 are $58.09\ T\ ha^{-1}$ and $38.94\ T\ ha^{-1}$ respectively. The mean value of F_1 is higher than the mid parental value of $56.78\ T\ ha^{-1}$, whereas the mean performance of F_2 is also lower than the both the parents. Similarly, the BC_1P_1 and BC_2P_2 family generation mean values for this trait are less than mid parental value and overlapped with each other which indicate gene interactions.

Table 4.27. Range, mean with their standard error and variance of six generations of the sorghum [*Sorghum bicolor* (L.) Moench] cross ‘ICSB 14029 X ICSV 15006 in respect of 13 quantitative characters

Character	Generation					
	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
1. Days to 50% flowering (days)						
Range	72.00- 75.00	83.00 -85.00	76.00 -80.00	72.00 -79.00	70.00 – 74.00	72.00 – 85.00
Mean + SE	73.40 ± 0.33	83.75 ± 0.32	79.00 ± 0.580	73.25 ±0.47	72.46 ±0.43	77.39 ±1.79
Variance	0.568	0.51	1.684	3.556	1.29	22.470
2. Days to maturity (days)						
Range	115.00 -117.00	121.00 – 124.00	119 – 127	115.00 – 117.00	115.00 – 118.00	114.00 – 125.00
Mean + SE	116.50 ± 0.271	122.60± 0.468	121.70 ± 1.171	115.18 ±0.40	117.07 ± 0.30	118.50 ± 1.40
Variance	0.368	1.095	6.853	2.663	0.661	13.889
3. Plant height (cm)						
Range	180.80- 210.60	243.60 – 323.50	197.40 -304.30	172.60 -254.60	140.80 – 224.30	187.65 – 323.50
Mean + SE	195.47 ± 3.233	295.285 ± 8.364	233.560 ±12.818	207.69 ± 5.45	214.57 ± 11.55	237.29 ± 15.91
Variance	195.479	295.285	233.560	207.694	214.579	237.29
4. Number of nodes per plant						
Range	9.00 – 11.00	14.00 – 16.00	12.00 -15.00	10 – 14	9- 15	11.00 – 15.00
Mean + SE	10.55 ± 0.27	15.05 ± 0.27	14.30 ± 0.38	12.51 ± 0.40	12.28 ±0.76	13.78 ± 0.47
Variance	0.366	0.366	0.747	2.571	4.138	1.58
5. Stem girth (cm)						
Range	2.30 – 3.20	3.00 – 3.60	1.90 – 3.40	1.80 – 2.50	1.40 -3.20	1.80 – 3.60
Mean + SE	2.85 ±0.123	3.23 ± 0.071	2.635 ± 0.197	2.700 ± 0.105	2.750 ±0.159	2.85 ± 0.16
Variance	0.075	0.025	0.194	0.175	0.177	0.180
6. Panicle weight (g)						
Range	42.60 – 53.70	38.60 – 50.70	37.67 – 55.21	21.50 – 49.53	25.45- 52.40	22.70 -55.60
Mean + SE	47.62 ± 1.286	44.74 ±3.594	48.31 ±1.983	37.33 ± 1.900	45.15 ± 2.249	44.69 ±2.94
Variance	8.265	64.579	19.653	57.780	35.400	60.546

Character	Generation					
	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
7. 1000 grain weight (g)						
Range	20.80 – 27.70	16.20 – 29.80	17.70 – 35.85	14.35 – 32.76	17.20 – 35.85	10.40 – 31.45
Mean + SE	24.12 ± 0.930	22.79 ± 1.492	25.28 ± 2.262	23.91 ± 1.109	23.676 ± 1.470	22.123 ± 1.368
Variance	4.323	11.316	25.59	19.68	15.11	13.09
8. Fresh stalk weight (T ha⁻¹)						
Range	42.28 – 56.53	56.13 – 75.94	29.75 – 58.73	29.82 – 50.71	21.75 – 48.73	22.82 -75.94
Mean + SE	51.14 ± 1.938	62.42 ± 2.120	58.095 ± 3.431	44.943 ± 1.858	47.702 ± 3.338	48.559 ± 4.225
Variance	1.938	2.120	3.431	1.858	3.338	4.255
9. Juice yield (T ha⁻¹)						
Range	11170.36 – 13511.10	14992.58 - 19970.35	16562.95 - 23392.57	6755.55 – 21051.83	8562.95 – 19229.61	9567.0 – 20874.05
Mean + SE	12466.65 ± 362.96	17151.83 ± 605.435	19876.28 ± 895.31	14101.14 ± 921.59	14220.62 ± 1087.53	17104.74 ± 1358.02
Variance	658700.25	1832755.99	4007930.43	13589411.60	8279165.82	12.9538.71
10. Brix%						
Range	16-17	14-16	15 - 17	14 – 20	14 -16	14 -17
Mean + SE	16.70	15.60	15.75	16.31	14.64	15.60
Variance	0.221	0.358	0.408	2.726	0.460	0.840
11. Total soluble sugars (%)						
Range	14.15 – 15.02	7.15 – 9.15	13.27 – 15.02	12.40 – 15.02	12.40 -14.15	12.40 -15.02
Mean + SE	14.75 ± 0.183	13.80 ± 0.235	13.929 ± 0.250	13.765 ± 0.252	13.679 ± 0.435	13.929 ± 0.344
Variance	0.167	0.276	0.314	1.015	1.328	0.828
12. Ethanol yield (T ha⁻¹)						
Range	841.22 – 1080.41	1062.77 – 1503.93	1247.33 – 1761.65	445.84 – 1647.20	608.14 – 1448.15	737.19 – 1669.18
Mean + SE	979.47 ± 30.92	1260.219 ± 52.38	1472.61 ± 67.21	1055.78 ± 71.42	1001.53 ± 75.18	1273.93 ± 112.28
Variance	4780.42	13722.97	22589.77	81620.23	39571.00	88255.74
13. Grain yield (T ha⁻¹)						
Range	4.39 – 5.44	3.73 – 5.60	3.96 – 6.01	1.44 – 5.36	1.85 – 5.29	1.66 – 5.51
Mean + SE	4.13 ± 0.131	4.630 ± 0.219	4.84 ± 0.244	3.66 ± 0.2676	4.531 ± 0.287	4.00 ± 0.333
Variance	0.086	0.240	0.297	1.222	0.575	0.778

F_1 's range (29.75 – 58.73 T ha⁻¹) were found to be intermediate when compared to parents P-1 (42.28 – 56.53 T ha⁻¹), P-2 (56.13 – 75.94 T ha⁻¹). F_2 recorded low values (29.82 – 50.71 T ha⁻¹) when compared to F_1 and parents. The range of BC₁P₁ (21.75 – 48.73 T ha⁻¹) and BC₂P₂ (22.82 – 75.94 T ha⁻¹).

4.7.1.9 Juice yield (l ha⁻¹)

The mean performance of the two selected parents of P₁ (ICSB 14029) and P₂ (ICSV-15006) were different from each other. The female parent has mean value of 12466.65 l ha⁻¹ and male parent has average value of 17151.83 l ha⁻¹. Similarly the mean values of F_1 and F_2 are 19876.28 l ha⁻¹ and 14101.14 l ha⁻¹ respectively. The mean value of F_1 is more than the mid parental value of 14809.24 l ha⁻¹, whereas the mean performance of F_2 is almost similar to F_1 . The F_1 mean values greater than the respective mean mid parental values for this trait is indicating dominance. Similarly the BC₁P₁ (14220.62 l ha⁻¹) and BC₂P₂ (17104.74 l ha⁻¹) family generation mean values for this trait are higher than the female and similar to male parent. The F_1 mean values greater than the respective mean mid parental values for this trait is indicating dominance.

4.7.1.10 Brix%

The mean performance of the two selected parents of P₁ (ICSB 14029) and P₂ (ICSV-15006) were almost similar for each other. Similarly the mean values of F_1 and F_2 are 15.75 per cent and 16.31 per cent respectively. The mean value of F_1 is tending towards P₂ and is less than the mid parental value of 16.15 per cent, whereas the mean performance of F_2 is almost similar to P₁. Similarly the BC₁P₁ and BC₂P₂ family generation mean values for this trait are slightly lower than the respective female parent on par male parent and even less than mid parental value. The F_1 mean values greater than the respective mean mid parental values for this trait is indicating dominance.

The range for brix per cent ranged from 15 – 17 per cent in F_1 which is intermediate to both parents P₁ (16-17 Per cent), P₂ (14-16 Per cent). F_2 population has high range of brix (14-20 per cent) among the 6 populations. BC₂P₂ (14-17 per cent) was nearer to P₁. BC₁P₁ (14-16 per cent) was nearer to P₂.

4.7.1.11 Total soluble sugars (%)

Among the 6 populations, F_1 recorded TSS of 13.92 per cent and F_2 recorded TSS of 13.76 per cent was lower than P₁ TSS value of 14.75 per cent, when compared to mid parental values F_1 recorded low TSS per cent indicating lack of dominance while

BC₁ population has recorded 13.67 per cent and BC₂ population has recorded 13.92 % which is tending towards P₂ TSS value 13.80 per cent. Range of F₁ and F₂ varied from 13.27 to 15.02 and 12.40 to 15.02 respectively. Similarly the BC₁P₁ and BC₂P₂ family generation mean values for this trait are overlapped with each other which indicate gene interactions.

4.7.1.12 Ethanol yield (l ha⁻¹)

The average mean value for ethanol yield was differing for both parents, where high value of ethanol yield was recorded for P₂ (ICSV-15006) with 1260.21 l ha⁻¹ and low value of ethanol yield was recorded for P₁ (ICSB-14029) with 979.47 l ha⁻¹. F₁ (1472.61 l ha⁻¹) recorded average value which is higher than both the parents i.e., mid parental value. F₂ value (1005.78 l ha⁻¹) was intermediate between parents and lower than F₁. Similarly the BC₁P₁ (1001.53 l ha⁻¹) and BC₂P₂ (1273.93 l ha⁻¹) family generation mean values for this trait are higher than the female and similar to male parent. The F₁ mean values greater than the respective mean mid parental values for this trait is indicating dominance.

4.7.1.13 Grain yield (T ha⁻¹)

The mean performance of the two selected parents of P₁ (ICSB 14029) and P₂ (ICSV-15006) were similar for each other. The female parent recorded a mean value of 4.13 T ha⁻¹ compared to the P₂ with a mean value of 4.63 T ha⁻¹. Similarly the mean values of F₁ and F₂ are 4.84 T ha⁻¹ and 3.66 T ha⁻¹ respectively. The mean value of F₁ is higher than both the parents and is more than the mid parental value of 4.38 T ha⁻¹, whereas the mean performance of F₂ is lower than both parents. The F₁ mean values greater than the respective mean mid parental values for this trait is indicating dominance. Similarly the BC₁P₁ and BC₂P₂ family generation mean values for this trait are slightly higher than the female parent and lower than male parent and even less than mid parental value.

4.7.2 Scaling Tests and Joint Scaling Tests

The mean and variance of six generations viz., P₁, P₂, F₁, F₂, BC₁P₁ and BC₂P₂ of the cross 'ICSB 14029 x ICSV 15006' in respect of 13 traits were subjected to scaling tests as per the method of Mather (1949) and Joint scaling test as per the method of Cavalli (1952) to test the presence or absence of gene interaction in the inheritance of

these traits. The significance of any one of these scales is taken to indicate the presence of non-allelic interactions, which can be noted as: The significance of A and B scales indicates the presence of all the three types of non-allelic interactions viz., additive $\times$ additive [$i^{\wedge}$], additive $\times$ dominance [$j^{\wedge}$] and dominance $\times$ dominance [$l^{\wedge}$]. The significance of C scale suggests dominance $\times$ dominance [$l^{\wedge}$] type of interaction. D scales provide a test of [$i^{\wedge}$], type of interaction (additive $\times$ additive). (Singh and Chaudhary, 1977). The results of scaling tests and joint scaling test in respect of 13 traits have been tabulated in Table: 4.28 and 4.29, respectively and presented trait wise below.

4.7.2.1 Days to 50 % flowering (days)

The tests ‘A’ ‘B’ and ‘C’ are highly significant indicating inadequacy of additive-dominance model, which was further asserted by significance of additive component as well as high level of significance of chi-square value in joint scaling test indicating role of non-allelic interactions in the genetic control of the trait.

4.7.2.2 Days to maturity (days)

The inadequacy of simple additive-dominance model and presence of digenic or still higher order epistasis in the inheritance of this trait is confirmed by the presence of highly significant scaling tests ‘A’ ‘B’ and ‘C’, which was further confirmed by high level of significance of chi-square value obtained in Joint scaling test.

4.7.2.3 Plant height (cm)

‘B’ and ‘C’ tests are highly significant while ‘A’ and ‘D’ are nonsignificant negative. Additive component as well as Chi-square values were also highly significant specifying inadequacy of simple additive-dominance model and presence of gene interaction in the genetic control of this trait.

4.7.2.4 Number of nodes per plant

‘B’ and ‘C’ tests were highly significant. The additive- dominance components as well as chi-square value of joint scaling test were also highly significant, which clearly stipulates the major role of gene interaction in the inheritance of this trait.

4.7.2.5 Stem girth (cm)

None of the tests were significant for stem girth which indicates the adequacy of simple additive –dominance model. The dominance component of joint scaling test were also non-significant, which indicates absence of gene interaction of this trait.

4.7.2.6 Panicle weight (g)

The tests ‘A’ and ‘C’ are significant at 5 % and 1 % respectively, confirming the absence of additive-dominance model, significance of chi-square value in joint scaling test indicating role of gene interaction in the genetic control of the trait.

4.7.2.7 1000 grain weight (g)

Absence of significant values in ‘A’, ‘B’ ‘C’ and ‘D’ test indicates the absence of non-allelic interactions. Non significance of Additive and dominance components were also highly significant indicating adequacy of simple additive-dominance.

4.7.2.8 Fresh stalk yield (T ha⁻¹)

‘A’, ‘B’ are non-significant but ‘C’ test was highly significant. In joint scaling, the additive dominance components as well as chi-square value were also highly significant, which clearly stipulating major role of gene interaction in the inheritance of this trait.

4.7.2.9 Juice yield (l ha⁻¹)

Out of the four tests viz., A and C are highly significant and positive except D test which is negative. The additive dominance components and chi-square value of joint scaling test were also highly significant suggesting failure of additive-dominance model to explain the inheritance and presence of epistasis in the genetic control of this trait.

Table 4.28. Scaling tests for 13 characters in the cross ‘ICSB 14029 x ICSV 15006’ of Sorghum [*Sorghum bicolor* (L.) Moench] (Mather, 1949).

S. No.	Character	Scaling test			
		A	B	C	D
1	Days to 50% flowering (days)	7.471 ± 0.546 **	7.964 ± 1.822**	22.150 ± 1.131 **	-3.357 ± 1.035
2	Days to maturity (days)	4.057 ± 0.675**	7.300 ± 1.543**	21.750 ± 1.452**	-5.196 ± 0.828
3	Plant height (cm)	-0.118 ± 13.313	54.259 ± 17.662**	127.109 ± 17.417**	-36.484 ± 11.246
4	Number of nodes per plant	0.279 ± 0.804	1.779 ± 0.531**	4.138 ± 0.910**	-1.040 ± 0.604
5	Stem girth (cm)	-0.010 ± 0.197	0.151 ± .786	0.555 ± 0.296	-0.207 ± 0.154
6	Panicle weight (g)	5.641 ± 2.540*	3.681 ± 3.586	39.672 ± 4.692**	-15.175 ± 2.653
7	1000 seed weight (g)	2.061 ± 1.078	3.791 ± 1.969	1.785 ± 0.543	2.034 ± 1.360
8	Fresh stalk yield (T ha ⁻¹)	-0.164 ± 3.876	9.397 ± 4.709	45.983 ± 5.258**	-18.375 ± 3.281
9	Juice yield (l ha ⁻¹)	3901.686 ± 1.189.987**	2818.629 ± 1461.59	11766.470 ± 2079.30 **	-2523.076 ± 1267.311
10	Brix %	3.164 ± 0.312 **	0.136 ± 0.398	-1.450 ± 0.890	2.375 ± 0.466 **
11	Total soluble sugars (%)	1.329 ± 0.462**	-0.131 ± 0.384	1.335 ± 0.582**	-0.079 ± 0.375
12	Ethanol yield (l ha ⁻¹)	449.028 ± 83.794 **	184.958 ± 120.098	961.777 ± 160.774 **	-163.895 ± 98.318
13	Grain yield (T ha ⁻¹)	0.615 ± 0.318	1.462 ± 0.371**	4.511 ± 0.617**	-1.217 ± 0.353

Note: * and ** Significance at P = 0.05 and 0.01 respectively

Table 4.29. Joint scaling test for 13 characters in ‘ICSB 14029 x ICSV 15006’ cross of Sorghum (*Sorghum bicolor* L. Moench) (Cavalli, 1952).

S. No.	Character	M	D	H	χ^2
1	Days to 50% flowering (days)	77.946 **	5.393 **	-2.802	449.51**
2	Days to maturity (days)	119.121 **	2.628	-2.862	271.1**
3	Plant height (cm)	240.510 **	45.31**	-37.870	62.41**
4	Number of nodes per plant	12.678 **	2.201 **	1.122 **	27.1**
5	Stem girth (cm)	3.033**	0.186 **	-0.504	4.31*
6	Panicle weight (g)	43.492 **	-3.247	1.349	74.68**
7	1000 seed weight (g)	23.185**	-0.914	0.856	4.49**
8	Fresh stalk yield (T ha ⁻¹)	55.270 **	5.094 **	-19.598 **	86.48**
9	Juice yield (l ha ⁻¹)	14597.896 **	2275.706**	3791.579 **	38.09**
10	Brix %	16.033**	-0.323	-0.793	116.61**
11	Total soluble sugars (%)	14.232**	-0.448	-0.467	12.94**
12	Ethanol yield (l ha ⁻¹)	1098.085 **	138.720 **	240.940 **	54.55**
13	Grain yield (T ha ⁻¹)	4.596 **	-0.183	-0.201	60.59**

Note: * and ** Significance at P = 0.05 and 0.01 respectively

4.7.2.10 Brix %

‘A’ and ‘D’ tests are highly significant signifying the inadequacy of simple additive-dominance model to explain the genetic control of this trait was suggested high level of significance of chi-square value of joint scaling test indicating the presence of epistasis in the inheritance of this trait.

4.7.2.11 Total sugars estimation (%)

As indicated by the significance of ‘A’ and ‘C’ tests, Simple additive-dominance model failed to explain the inheritance of this trait which was further confirmed by the significance of chi-square value in joint scaling test. This strongly suggests major role of gene interaction in the inheritance of this trait.

4.7.2.12 Ethanol yield (T ha⁻¹)

A’ and ‘C’ tests are highly significant and positive. The chi-square values and additive as well as dominance components in the joint scaling test are also highly significant suggesting the role of gene interaction in the genetic control of this trait

4.7.2.13 Grain yield (T ha⁻¹)

B’ and ‘C’ tests are highly significant stipulating the inadequacy of additive-dominance model which was further confirmed by high level of significance of chi-square value suggesting the presence of gene interaction in the genetic control of this trait.

4.7.8 Estimation of Gene Effects

When, the scaling tests as well as joint scaling test were highly significant affirming the Inadequacy of the simple additive-dominance model to explain the genetic control, the perfect fit six-parameter estimates of digenic interaction model were estimated following the methods of Jinks and Jones (1958) and Mather and Jinks (1982). The six generations of the cross ‘ICSB 14029 x ICSV 15006’ were used to estimate the gene effects viz., $[m^*]$, $[d^*]$, $[h^*]$, $[i^*]$, $[j^*]$ and $[l^*]$ in respect of 13 quantitative traits. The gene effects estimated by using perfect fit model in respect of 13 quantitative traits have been tabulated in Table: 4.30 and presented character wise below.

4.7.8.1 Days to 50 % flowering (days)

The additive gene effect [d^*] (-4.929) is non-significant and negative. Among epistatic effects, dominance $\times$ dominance [l^*] (8.721) effect is relatively high and positively significant followed by additive $\times$ additive [i^*] (6.714) which was significant. Operation of complimentary gene interaction was evidenced from the same signs of [h^*] and [l^*] estimates. Baskheti and Arun Bhatt (2005), Rajguru *et al.* (2005) reported additive, dominance as well as digenic interactions.

4.7.8.2 Days to maturity (days)

As per the model, [d^*] component (-1.429) is negative and non-significant and [h^*] component (12.543) is positive and nonsignificant. The magnitude of dominance [h^*] effect was more compared to all other gene effects. Among, the three type of gene interaction, both [i^*] & [j^*] types are highly significant in positive direction. The same signs of [h^*] and [l^*] components indicated the presence of complementary type of epistasis in the genetic control of the trait. Shivani and Sreelakshmi (2013) observed additive genetic effects (d) for days to maturity.

4.7.8.3 Plant height (cm)

In the given parameter only dominance [h^*] gene effects (61.146) is highly significant. Significance of epistatic effects was also observed. Both additive $\times$ additive [i^*] (72.968) as well as additive $\times$ dominance [j^*] interaction (54.377) effects were significant. The significant opposite signs in [h^*] and [l^*] components indicated the presence of duplicate nature of epistasis. This trait can be improved by adopting selection in later generations. Baskheti and Arun Bhatt (2005), Rajguru *et al.* (2005) indicated additive, dominance and epistatic interactions.

4.7.8.4 Number of nodes per plant

Only dominance gene effect [h^*] (3.580) is highly significant and [d^*] component (-1.500) is nonsignificant in negative direction while all other components except mean [m^*] are non-significant. However, duplicate gene interaction was observed for this character based on opposite nature of both [h^*] and [l^*] estimates. Baskheti and Arun Bhatt (2005) indicated additive, dominance and epistatic interactions.

Table 4.30. Gene effects for 13 characters in the cross ‘ICSB 14029 x ICSV 15006’ of Sorghum [*Sorghum bicolor* (L.) Moench]

S. No.	Character	M	D	H	I	j	l	Type of Epistasis
1	Days to 50% flowering (days)	73.250 ± 0.236 **	-4.929 ± 0.921	7.139 ± 2.093**	6.714 ± 2.070**	0.493 ± 1.857	8.721 ± 2.262**	Complimentary
2	Days to maturity (days)	115.188 ± 0.204 **	-1.429 ± 0.721	12.543 ± 1.762	10.393 ± 1.657**	3.243 ± 1.467**	0.964 ± 3.229	Complimentary
3	Plant height (cm)	207.694 ± 2.727 **	-22.714 ± 9.835	61.146 ± 23.494 **	72.968 ± 22.491**	54.377 ± 20.175 **	-18.827 ± 43.023	Duplicate
4	Number of nodes per plant	12.516 ± 0.200 **	-1.500 ± 0.452	3.580 ± 1.227**	2.080 ± 1.208	1.500 ± 0.924	-0.023 ± 2.024	Duplicate
5	Stem girth (cm)	2.700 ± 0.052 **	-0.017 ± 0.113	0.007 ± 0.325	-	-	-	-
6	Panicle weight (g)	37.334 ± 0.950 **	0.458 ± 1.851	32.482 ± 5.481	30.350 ± 5.306**	-1.960 ± 4.165	-21.029 ± 8.766	Duplicate
7	1000 seed weight (g)	23.917 ± 0.555**	1.553 ± 1.547	-2.215 ± 3.228	-	-	-	-
8	Fresh stalk yield (T ha ⁻¹)	38.943 ± 0.929**	-0.856 ± 2.704	24.062 ± 6.821 **	36.750 ± 6.562**	9.562 ± 5.596	-27.516 ± 12.027	Duplicate
9	Juice yield (l ha ⁻¹)	14401.140 ± 460.798 **	-2884.117 ± 869.908	10113.190 ± 2579.893**	5046.152 ± 2534.622 **	-1083.0551 ± 1775.255	1674.172 ± 4053.559	Complimentary
10	Brix %	16.313 ± 0.206**	-0.964 ± 0.215	-5.510 ± 0.946	-4.750 ± 0.931	-3.029 ± 0.463	8.050 ± 1.239**	Duplicate
11	Total soluble sugars (%)	13.765 ± 0.126 **	-0.250 ± 0.277	-0.193 ± 0.763	0.157 ± 0.749	-1.461 ± 0.574	1.041 ± 0.831	Duplicate
12	Ethanol yield (l ha ⁻¹)	1055.787 ± 35.712**	-272.405 ± 67.567	680.556 ± 200.067 **	327.797 ± 196.63	-264.070 ± 138.514	306.195 ± 314.471	Complimentary
13	Grain yield (T ha ⁻¹)	3.660 ± 0.138 **	0.525 ± 0.220**	2.548 ± 0.720 **	2.433 ± 0.706 **	0.847 ± 0.458	-0.356 ± 1.074	Duplicate

Note: * and ** Significance at P = 0.05 and 0.01 respectively

4.7.8.5 Stem girth (cm)

None of the tests were significant for stem girth which indicates the adequacy of simple additive –dominance model. Baskheti and Arun Bhatt (2005) indicated additive, dominance and epistatic interactions which is deviating from the current reported results.

4.7.8.6 Panicle weight (g)

It is evident from six parameter model that only additive $\times$ additive [$i^{\wedge}$] component (30.35) is significant and others are nonsignificant. Operation of duplicate type of epistasis was evidenced from the estimates of [$h^{\wedge}$] and [$l^{\wedge}$], which had opposite signs.

4.7.8.7 1000 grain weight (g)

Absence of significant values in ‘A’, ‘B’ ‘C’ and ‘D’ test indicates the absence of non-allelic interactions.

4.7.8.8 Fresh stalk yield (T ha⁻¹)

As per the model, only [$h^{\wedge}$] component (24.062) is highly significant and positive while [$d^{\wedge}$] component (-0.856) is negative non-significant. Among, the three type of gene interaction, only [$i^{\wedge}$] type is highly significant in positive direction. The opposite signs of [$h^{\wedge}$] and [$l^{\wedge}$] components indicated the presence of duplicate type of epistasis in the genetic control of the trait. Audilakshmi *et al.* (2010) reported similar result for highly significant dominance component.

4.7.8.9 Juice yield (l ha⁻¹)

In the given model, only [$h^{\wedge}$] component (10113.190) is highly significant and positive while [$d^{\wedge}$] component (-2884.117) is negative non-significant. Among, the three type of gene interaction, only [$i^{\wedge}$] type (5046.152) is highly significant in positive direction. The same signs of [$h^{\wedge}$] and [$l^{\wedge}$] components indicated the presence of complementary type of epistasis in the genetic control of the trait. Similar results were reported by Audilakshmi *et al.* (2010) and Kumar *et al.* (2011)

4.7.8.10 Brix %

The additive (-0.964), dominance component (-5.510) were noticed nonsignificant and negative and only $[l^*]$ component (8.050) is positive significant. However, joint scaling test also indicated non significance of both additive and dominance gene effects. Duplicate epistasis was operating in the cross as evidenced from the estimates of $[h^*]$ and $[l^*]$ which had opposite signs. The additive and dominance components results quoted by Premalatha *et al.* (2006), Audilakshmi *et al.* (2010), Kumar *et al.* (2011) were significant for this trait which is deviating from the current result.

4.7.8.11 Total soluble sugars (%)

Both $[d^*]$ (-0.250) and $[h^*]$ (-0.193) gene effects are nonsignificant in negative direction. The dominance $\times$ dominance $[l]$ (1.041) type of interaction is significant and positive. The estimates of $[h^*]$ and $[l^*]$ components with opposite signs indicating the duplicate nature of epistasis for the trait. Sanjanareddy *et al.* (2011) reported both additive and dominant genes controlled overall sugar yield.

4.7.8.12 Ethanol yield (T ha⁻¹)

Negative and non-significant additive gene effect $[d^*]$ (-272.405) and positive significant is noticed for dominant $[h^*]$ component (680.58). However none of the epistatic components are highly significant. Complementary type of epistasis was found operating in the inheritance of biomass as evidenced by same signs of $[h^*]$ and $[l^*]$ components. Vinaykumar (2009) reported dominant gene effects for this trait.

4.7.8.13 Grain yield (T ha⁻¹)

The $[d^*]$ (0.525) & $[h^*]$ (2.548) component is highly significant and positive. Among interaction components, additive $\times$ additive $[i^*]$ component (2.433) is highly significant and positive. Duplicate gene interaction based on the significance of opposite signs of $[h^*]$ and $[l^*]$ components was noticed in the genetic control of this trait. Shivani and Sreelakshmi (2013), Iraddi *et al.* (2014), Karande and Lad (2015), Gaddimeedi *et al.* (2018) and Lad *et al.* (2019)

The mean performance of 6 generations indicated that the F₂ means were lesser than the F₁ means except for brix per cent and stem girth and between mid-parental values in respect of all the traits except panicle weight, grain yield indicating high

degree of inbreeding depression. These results depict the predominant role of non-additive gene action which includes both dominance as well as epistatic interactions.

The F_1 means were greater than the respective mid-parent mean values for all the given characters, indicating dominance for important traits like juice yield, ethanol yield and grain yield conforming the report Sudhirkumar *et al.* (2011). The BC_1P_1 and BC_1P_2 family means were tended towards their respective parents and overlapped with each other which indicate gene interactions. Chi-square significance of joint scaling test indicated the inadequacy of additive-dominance model which in turn indicated the presence of non-allelic interactions.

The scaling tests as well as chi square test from joint scaling test were highly significant in the cross ICSB 14029 x ICSV 15006' cross for 11 characters excluding stem girth and 1000 grain weight, indicating inadequacy of simple additive-dominance model and justifying the use of six parameter model for the detection of gene interactions.

The six generation mean analysis carried out for 13 quantitative characters indicated significance of dominance gene effects for days to flowering, plant height, Fresh stalk yield, juice yield, grain yield and ethanol yield. Significance of one or more interaction types is observed (additive $\times$ additive or additive $\times$ dominance or dominance $\times$ dominance) in all the 13 traits except nodes per plant, stem girth, 1000 grain weight, total sugars estimation and ethanol yield. Based on the signs of $[h^*]$ and $[l^*]$ gene effects, complementary gene interaction was evident in the inheritance of days to 50% flowering, days to maturity, juice yield, ethanol yield, while, duplicate gene interaction in the inheritance was evident for plant height, number of nodes per plant, panicle weight, Fresh stalk yield, brix %, total sugars estimation, grain yield indicating predominantly dispersed alleles at the interacting loci (Jinks, and Jones, 1958).

Conclusion: The present study of 13 characters for generation mean analysis suggested that dual gene effects (additive and dominance) were important but dominance gene effect had more profound effect. When gene interactions are significant *i.e.*, additive $\times$ additive, simple selfing in early generations will yield desired genotypes. If additive $\times$ dominance or dominance $\times$ dominance gene interactions are present, heterosis breeding will be useful, as in hybrids, heterozygous condition is fixed. (Audilakshmi *et al.* 2010).

Though, detection and estimation of additive, dominance and epistatic gene effects is possible through generation mean analysis, it does have limitations. In the presence of linkage, the estimates of additive $\times$ additive and dominance $\times$ dominance gene effects are biased to an unknown extent (Mather and Jinks, 1982). The speculation based on the magnitude of additive gene effects may not be advisable, because the distribution of positive and negative gene effects in the parents may result in different degrees of cancellation of gene effects in the expression of the generation means Audilakshmi *et al.* (2010). For the same reason, the magnitudes of additive gene effects do not accurately reflect the magnitude of additive variance. However, dominance [$\hat{h}$] and dominance $\times$ dominance [$\hat{l}$] are independent of the degree of gene distribution due to which the combined estimates of dominance [$\hat{h}$] and dominance $\times$ dominance [$\hat{l}$] could be considered to be the best representative of sign and magnitude of individual $\hat{h}$ and $\hat{l}$, respectively. So, practically these are the only components which can safely be used to determine the type of epistasis that may have influence on the observed performance of generations (Mather and Jinks, 1982). For the same reason, emphasis has been given to the characters plant height, Fresh stalk yield, brix %, juice yield, ethanol yield and grain yield which are governed by such gene effects for suggesting appropriate breeding method that could be followed to achieve higher expression of such characters.

Higher magnitude of dominance gene effects and dominance gene interactions could not be exploited for heterosis breeding due to presence of duplicate epistasis in the present crosses as it minimizes the manifestation of heterosis. (Kearsey and Pooni, 1996). Hence, selection for high ethanol yielding genotypes would be effective if dominance and epistatic effects were first reduced by few generations of selfing. Then biparental mating followed by intermating of selected progeny and selection in subsequent segregating generation or population improvement methods may possibly serve the purpose. Days to 50% flowering, Juice yield and ethanol yield expressed complementary epistasis along with dominance $\times$ dominance interaction. Usually, characters with non-additive gene action coupled with duplicate type of gene interaction, can be improved through recurrent selection or diallel selective mating.

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Chapter – V

SUMMARY AND CONCLUSIONS

Human dependency on fossil fuel is at its peak leading to the depletion of fossil fuel resources (petroleum) at an alarming rate. Therefore, in order to cut the gap of energy (fossil fuel) demand created by current day life style, the non-conventional energy source in the form of biofuel is one of the best options. Ethanol alone accounts for about 90 per cent of the total biofuel production in the world.

The bioethanol produced from agriculture sources provide eco-friendly energy. The present ethanol production is through sugarcane given that water availability is poised to become a major constraint to agricultural production in coming years, high input requiring cultivation of sugarcane becomes difficult and sweet sorghum offers a sustainable choice as it requires minimal water and purchased inputs. Sweet sorghum is similar to grain sorghum but with rich juicy sugar stalks, it becomes a potential raw material resource for bioethanol production. Unlike sugarcane, it can be grown on poor and marginal soils with minimum inputs and could yield three crops a year. Hence, in the present study, “Stability analysis in Sorghum [*Sorghum bicolor* (L.) Moench] genotypes” variability, diversity, correlation and path analysis, combining ability, stability analysis and generation mean analysis was studied for 13 quantitative characters. The summary of the results obtained are presented experiment-wise.

In the present investigation carried out, variability studies were carried out with 110 genotypes including 2 checks. Estimates of PCV were narrowly higher than the corresponding GCV values for the characters days to 50 % flowering, days to maturity and stem girth, while number of nodes per plant, fresh stalk yield (t/ha), grain yield (t/ha), brix %, T.S.S, juice yield (t/ha), ethanol yield (t/ha) showed moderate differences between PCV and GCV. Characters plant height (cm), 1000 grain weight, Panicle weight (gm) showed high magnitude of difference. Narrow and moderate difference between PCV and GCV was observed which duly indicated that the environment influence on these characters was less. Therefore, of phenotypic selection alone is effective for the improvement of these traits and selection based on phenotypic performance could be worth in achieving desired results. High heritability coupled with high genetic advance as percent of mean was observed for all the 13 characters studied. Thus, these traits are predominantly under the control of additive gene action and hence these characters can be improved by selection.

In the diversity study for 110 genotypes were clustered into 8 clusters indicating the presence of a wide range of genetic diversity. Cluster- I, among the 8 clusters was possessing the highest number of genotypes *i.e.*, 78 indicating the genetic similarity among them and is followed by Cluster- III with 15 genotypes, Cluster - II with 12 genotypes, Cluster - IV, V, VI, VII, VIII were monogenotypic indicating the uniqueness of the genotypes included in those clusters when compared to other genotypes included in the study. The highest inter-cluster distance (596.33) was observed between cluster II and cluster VIII followed by the cluster VII and cluster VIII (406.31), while the lowest inter cluster distance (50.54) was observed between cluster IV and cluster VII. The genotypes belonging to these clusters were separated by high statistical distance and the genotypes having high *per se* performance should be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. Stem girth has contributed maximum (22.49 %) to the genetic divergence followed by days to maturity (22.2 %), days to 50 % flowering (19.58 %), juice yield (10.39%), brix % (9.89%) followed by panicle weight (0.17%), grain yield (0.82%), ethanol yield (1.32%), plant height (1.48%). 1000 grain weight (2.22%), number of nodes (2.42%), fresh stalk weight (7.02%) whereas total soluble sugars (0%) didn't contribute to the divergence. The cluster means for brix %, juice yield, ethanol yield and days to 50 % flowering were considered as criteria and for crossing diverse parents were selected from various clusters. *i.e.*, from cluster IV, cluster V, cluster VI, cluster VII, and cluster VIII for hybridization programme. All these clusters are solitary.

The correlation results revealed that brix percent, total soluble sugars and juice yield had significant positive correlation with ethanol yield while negative association with grain yield, plant height, days to 50% flowering and days to maturity was observed.

Path coefficient analysis revealed that juice yield exerted the highest positive direct effect on ethanol yield followed by brix %, total sugar yield along with positive correlation for all the above mentioned characters.

In the line x tester analysis, *sca* variance component estimates were greater than that of *gca* for the characters no of nodes, fresh stalk yield (t/ha), stem girth (cm), 1000 grain weight (g), panicle weight(g), brix%, total soluble sugars, juice yield(l/ha) and grain yield(t/ha) indicating the non-additive control of genetic variation in these traits.

Female line 1 (ICSA-14029) was found to be promising general combiner for fresh stalk yield, brix%, total soluble sugars, juice yield, and ethanol yield with higher positive significant GCA effects. while line 2 (ICSA-14030) was good general combiner for panicle weight, juice yield and seed yield significantly and line 3 (ICSA-14033) for days to 50% flowering, no. of nodes, fresh stalk yield, stem girth and seed yield and negative non-significant for brix %, total soluble sugars, ethanol yield while line 4 (ICSA-14035) was negative significant for all the characters studied except stem girth and plant height indicating this line was poor combiner for all the characters.

Among the testers which are used as male parents, tester 3 (ICSV 15006) has shown positive significant *gca* for all the traits like number of nodes, plant height, fresh stalk weight, stem girth, panicle weight, brix per cent, total soluble sugars, juice yield ethanol yield followed by tester 2 (GGUB 28) possessing positive *gca* for juice yield and ethanol yield and negative *gca* for rest of the traits studied and Tester 4 (IS 29308) had positive significant *gca* for brix %, total soluble sugars. Tester 1 (SEVS-08) recorded positive significant *gca* for characters days to 50 per cent flowering, days to maturity, no. of nodes, plant height, 1000 seed weight and negative significant association for brix, total soluble solids, juice yield, ethanol yield and seed yield.

Among the hybrids, H-3 has excelled with high *sca* effects for brix%, total soluble solids, juice yield and ethanol yield followed by H-2 having high *sca* effects for brix per cent total soluble sugars, juice yield and ethanol yield, 1000 grain weight, panicle weight. H-8 has shown high *sca* effects for brix, total soluble sugars, juice yield, ethanol yield, days to maturity, 1000 grain weight, panicle weight and negative significant for no. of nodes, days to 50 % flowering, fresh stalk yield, stem girth. H-9 exhibited high *sca* effects for brix, total soluble sugars, juice yield and ethanol yield, 1000 grain weight, and number of nodes and negative for days to maturity, fresh stalk yield, stem girth while H-13 has shown significant *sca* effects for juice and ethanol yield respectively. High significant *sca* effects for grain yield was observed in H-5, and non-significant positive *sca* effects for grain yield were noticed for H-2, H-4, H-8, H-12, H-13, H-14, H-15 and H-16. Hence the following hybrids can be used for further improvement. Among the Hybrids H-3, H-2, H-8 and H-10 were found to be superior for juice, brix percent and ethanol content.

The range of heterosis over mid parent, better parent and commercial check was high with respect to ethanol productivity related traits particularly juice yield and brix % . However, it was deviating for no. of nodes, plant height, and 1000-grain weight which has shown negative heterosis. As far as ethanol and juice yields are concerned medium flowering and intermediate plant height are desirable. As observed in the correlation studies grain yield and ethanol yield are found to be contrary traits while in this study of hybrids there is an improvement in the juice, brix% and ethanol yield but heterosis is limited in the aspects of grain yield and 1000 grain weight.

Considering, the magnitude of standard heterosis with respect to juice yield, Brix and ethanol yield considered and following hybrids have performed well ICSA 14029 x ICSV-15006; ICSA 14030 x ICSV 15006; ICSA 14305 x ICSV-15006; ICSA 14029 x GGUB 28; ICSA 14030 x GGUB 28; ICSA 14033 x ICSV-15006.

Stability analysis through “Eberhart and Russell’s model” resulted that Bapatla location was found to be most favourable location for brix %, total soluble sugars, ethanol yield and seed yield. Guntur was the most favourable location for number of nodes per plant and juice yield while garikapadu was the favourable for days to fifty percent flowering, days to maturity, plant height, fresh stalk yield, stem girth, 1000 grain weight and panicle weight.

According to AMMI analysis the following hybrids were stable over locations identified for different characters like H-2 for days to 50% flowering, H-3 and H-5 for days to maturity, H-10 and H-2 for plant height, H-7 and H-5 for no of nodes per plant, H-15 and 19 for stem girth, H-3 and H-4 for 1000 grain weight, H-5 for fresh stalk yield , hybrids 12, 10,11, 2 for grain yield, H -7 for brix%, H- 7 & 8 for total soluble sugars and H-10 and 11 for juice yield and H-2 and 3 for ethanol yield.

The classification for Eberhart and Russel’s model and AMMI model was similar for the traits Days to 50% flowering, days to maturity, Plant height, number of nodes per plant. For remaining characters the AMMI classification doesn’t present any similarity with the results obtained by Eberhart and Russell’s model. The stable performing hybrids H-2, H-14 and H-12 which are tested in 3 locations may be further tested in the All India Trials on sweet sorghum before their commercial exploitation.

The mean performance of 6 generations under generation mean analysis indicated that the F_2 means were lesser than the F_1 means except for brix per cent and stem girth and between mid-parental values in respect of all the traits except panicle weight, fresh stalk weight, grain yield indicating high degree of inbreeding depression. These results depict the predominant role of non-additive gene action which includes both dominance as well as epistatic interactions.

The scaling tests as well as chi square test from joint scaling test were highly significant in the cross ICSB 14029 x ICSV 15006' cross for 11 characters excluding stem girth and 1000 grain weight, indicating inadequacy of simple additive-dominance model and justifying the use of six parameter model for the detection of gene interactions.

The six generation mean analysis carried out for 13 quantitative characters indicated significance of dominance gene effects for days to flowering, plant height, fresh stalk weight, juice yield, grain yield and ethanol yield. Significance of one or more interaction types (additive $\times$ additive or additive $\times$ dominance or dominance $\times$ dominance) in all the 13 traits except nodes per plant, stem girth, 1000 grain weight, total sugars estimation and ethanol yield. Based on the signs of $[h^*]$ and $[l^*]$ gene effects, complementary gene interaction was evident in the inheritance of days to 50% flowering, days to maturity, juice yield, ethanol yield, while, duplicate gene interaction in the inheritance was evident for plant height, number of nodes per plant, stem girth, panicle weight, 1000 grain weight, fresh stalk weight, brix %, total sugars estimation, grain yield indicating predominantly dispersed alleles at the interacting loci. Due to presence of duplicate epistasis in the present crosses it minimizes the manifestation of heterosis. Hence, selection for high ethanol yielding genotypes would be effective if dominance and epistatic effects were first reduced by few generations of selfing. Then biparental mating followed by intermating of selected progeny and selection in subsequent segregating generation or population improvement methods may possibly serve the purpose. Days to 50% flowering, Juice yield and ethanol yield expressed complementary epistasis along with dominance $\times$ dominance interaction.

Future line of work:

- The entry IS-3980 which has been identified as extra early genotype with 26 days to 50 % flowering and 53 days to maturity possibly could be tested in several locations. If found reliable can be used as a donor for earliness in breeding short duration varieties.
- Entry ICSV-15006 performance was high in respect of brix per cent, Juice and Grain yield and hence can be evaluated in multizones for its performance and can also be used as a restorer in hybrid programmes for genetic enhancement of sweet sorghum.
- Among the lines and testers studied Line ICASA-14029 and tester ICSV 15006 were found superior in their performance for ethanol and its attributing traits which can be used as parents.
- The following hybrid combinations ICASA 14029 x ICSV 15006, ICASA 14029 x GGUB 28, ICASA 14030 x SEVS-08 and ICSV 14033 x GGUB-28 were found to be superior for juice, brix percent and ethanol content.
- The stable performing hybrids ICASA14029 X GGUB-28, ICASA 14033 x IS 29308 and ICASA 14035 x GGUB-28 which are tested in 3 locations may be tested further in AICRP trials before their release and commercial exploitation.

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***Original not seen**

Note: The literature cited is in accordance with thesis guidelines formulated by Acharya N.G Ranga Agricultural University, Lam, Guntur, A.P.

Appendix - I

Average weather data during *Kharif and Rabi* seasons of 2017-18 and 2018 -19 during crop growth period

2017-18								2018-19						
Month	Week	Mean Temperature		Mean RH	Rainfall (mm)	Rainy days	Sunshine days (hrs/day)	Week	Mean Temperature		Mean RH	Rainfall	Rainy days	Sunshine days (hrs/day)
		Max	Min						Max	Min				
June	1-4	39.05	28.87	72.1	0.0	0	2.5	1-3	37.13	27.16	74.58	13.3	1	4.1
	5-11	37.72	26.50	73.5	33.00	3	2.0	4-10	37.12	26.92	73.21	11.80	-	3.9
	12-18	37.10	26.57	71.2	47.00	1	4.0	11-17	38.98	26.65	75.68	21.50	3	4.0
	19-25	52.32	40.77	70.3	1.90	0	3.5	18-24	38.77	27.47	71.13	2.5	1	3.9
	26-30	35.86	25.56	73.8	19.20	2	3.5	25-30	36.38	25.91	73.21	28.10	2	4.0
July														
	1-2	37.70	26.42	72.1	2.00	0	2.0	1-8	34.87	28.62	71.24	24.00	3	3.1
	3-9	34.78	24.58	73.6	5.00	1	2.0	9-15	31.80	31.14	73.52	40.70	4	2.9
	10-16	33.67	23.90	74.1	20.00	4	2.5	16-22	33.87	26.31	72.16	32.10	0	2.9
	17-23	32.30	24.35	71.6	22.00	5	2.5	23-29	37.04	26.70	72.35	5.1	1	2.87
	24-31	27.05	21.0	73.2	35.00	2	3.0	30-31	37.30	27.75	73.12	00.00	0	2.1

August														
	1-6	37.05	25.91	72.1	5.3	1.0	2.0	1-5	37.78	26.42	70.18	4.1	2	2.2
	7-13	34.14	24.45	72.5	104.10	4.0	2.0	6-12	34.21	24.92	69.35	71.8	1	2.0
	14-20	32.71	23.84	73.1	18.0	1.0	3.5	13-19	29.95	23.74	71.16	71.50	5	3.5
	21-27	32.24	24.51	74.1	108.70	3.0	3.0	20-26	32.91	25.42	70.25	11.00	1	3.4
	28-31	32.42	24.40	73.1	54.701	2.0	3.5	27-31	27.55	20.12	70.14	6.8	1	3.5
September														
	1-3	35.00	25.93	75.01	78.50	1	2.0	1-2	34.45	25.05	78.1	0.2	-	4.5
	4-10	33.44	25.77	78.23	35.71	1	2.0	3-9	35.51	25.74	76.2	7.5	1	4.0
	11-17	32.97	25.84	76.12	53.40	2	3.0	10-16	29.78	26.55	77.3	0	0	4.4
	18-24	34.10	25.98	78.12	4.5	1	4.5	17-23	32.72	24.01	77.3	50.60	4	4.2
	25-30	32.71	24.71	77.12	67.10	5	3.0	24-30	28.51	22.65	76.5	2.4	1	4.1
October														
	1-8	28.08	25.01	75.01	89.4	3	4.0	1-7	34.07	24.98	78.63	11.5	1	6
	9-15	28.07	25.65	76.23	9.4	1	3.25	8-14	34.75	24.80	77.62	2	-	5.8
	16-22	33.81	27.64	79.13	22.2	1	5	15-21	32.01	24.21	77.54	23.10	2	6.2
	23-29	33.45	23.74	78.24	--	0	4.75	22-28	32.84	22.45	78.85	-	-	5.9
	30-31	32.30	22.10	76.23	--	0	3.75	29-31	32.76	21.70	78.15	-	-	6.1

November														
	1-5	30.64	21.50	81.0	0.2	0	5.0	1-4	28.40	23.42	81.05	38.200	2	6.25
	6-12	31.78	21.31	79.03	1.3	0	4.5	5-11	32.22	22.82	79.86	0	0	5.8
	13-19	31.64	23.07	78.15	21.0	1	3.5	12-18	31.48	21.71	79.34	16.90	2	6.0
	20-26	31.92	22.45	76.33	9.7	1	4.0	19-25	30.57	22.01	78.15	1.0	-	6.2
	27-30	30.82	18.98	78.21	--	--	3.5	26-30	30.82	18.30	78.24	1.0	-	6.4
December														
	1-3	29.46	19.10	72.13	-	-	5.25	1-2	30.65	19.95	72.13	1.0	-	3.0
	4-10	30.82	17.92	73.92	-	-	5.0	3-9	29.98	21.65	73.34	-	-	2.5
	11-17	31.35	19.01	74.10	-	-	4.75	10-16	30.55	19.51	72.54	-	-	3.0
	18-24	30.27	16.67	72.58	-	-	4.75	17-23	26.58	18.25	75.31	47	1	2.5
	25-31	30.08	16.34	74.31	-	-	5.25	24-30	29.21	17.66	73.34	-	-	3.0
January														
	1-7	30.48	16.91	73.56	-	-	4.9	1-6	29.06	14.60	77.08	-	-	3.6
	8-14	25.67	18.17	74.15	-	-	5.35	7-13	29.72	15.68	75.4	-	-	4.0
	15-21	17.41	17.14	72.36	-	-	5.0	14-20	29.74	17.64	76.2	-	-	4.1
	22-28	30.05	24.41	70.13	-	-	5.25	21-27	29.81	18.41	75.4	-	-	3.8
	29-31	30.03	17.56	71.54	-	-	4.0	28-31	28.57	16.85	76.5	-	-	3.6

February														
	1-4	31.97	15.42	69.5	-	-	7.0	1-3	29.40	16.96	75.85	-	-	7.0
	5-11	30.61	19.30	70.2	-	-	7.2	4-10	30.32	19.54	74.85	-	-	6.5
	12-18	31.17	18.74	71.4	-	-	6.5	11-17	31.02	17.38	74.91	-	-	6.9
	19-25	26.64	17.84	68.9	-	-	7.0	18-24	32.71	18.70	73.92	-	-	6.8
	26-28	34.30	16.63	72.2	-	-	7.1	25-28	32.50	24.00	73.92	3.9	1	6.8
March														
	1-3	35.26	19.23	69.5	-	-	7.8	1-2	32.20	24.20	76.2	-	-	7.9
	4-11	37.62	21.45	72.2	-	-	7.2	3-10	42.08	28.64	75.14	-	-	8.0
	12-18	32.64	21.78	69.0	-	-	6.8	11-17	33.35	22.37	75.09	-	-	8.0
	19-25	33.84	22.91	70.2	-	-	7.0	18-24	32.85	24.42	74.23	-	-	8.1
	26-31	28.28	21.41	71.1	-	-	7.1	25-31	34.20	24.50	74.03	-	-	8.1
April														
	1-8	33.60	27.67	72.0	13.8	1	8.1	1-7	33.77	25.78	76.23	-	-	7.9
	9-15	33.80	24.68	71.5	39	1	7.9	8-14	34.55	26.21	75.14	-	-	8.0
	16-22	34.90	26.48	73.0	--	--	8.2	15-21	34.75	24.87	75.09	-	-	8.0
	23-30	45.12	31.51	71.1	-	-	8.3	22-28	35.50	26.60	74.23	-	-	8.1
								29-30	35.40	27.60	74.03	-	-	8.1

May														
	1-6	34.88	26.20	72.5	8.2	1	7.9	1-5	39.36	27.48	72.15	-	-	8.3
	7-13	35.64	28.32	73.4	-	-	8.0	6-12	39.48	29.24	71.08	-	-	8.3
	14-20	35.37	27.84	71.5	-	-	7.9	13-19	36.21	28.5	73.52	-	-	8.0
	21-27	36.03	27.88	72.5	-	-	8.0	20-26	36.10	28.94	73.45	-	-	8.0
	28-31	38.72	28.17	71.3	-	-	8.2	27-31	37.34	28.72	73.40	-	-	8.2

Appendix - II

Mean Performance of 16 hybrids in Bapatla location for 13 characters (E-I)

S.No.	Hybrids	Days to 50% flowering (Days)	Days to maturity (Days)	Plant height (cm)	Number of nodes per plant	Stem girth (cm)	Panicle weight (g)	1000 Grain weight (g)	Fresh Stalk yield (T ha ⁻¹)	Juice yield (l ha ⁻¹)	Brix %	Total soluble sugars (%)	Ethanol yield (l ha ⁻¹)	Grain yield (T ha ⁻¹)
H-1	ICSA 14029 x SEVS-08	81.50	122.50	242.50	9.50	2.05	35.76	29.62	33.39	13765.71	9.50	8.46	620.47	3.60
H-2	ICSA 14029 x GGUB 28	65.50	108.00	166.20	9.50	3.20	45.65	31.19	60.94	15303.69	13.50	11.96	975.00	5.03
H-3	ICSA 14029 x ICSV-15006	79.50	122.50	295.45	13.50	3.20	52.86	29.71	68.76	22742.57	17.50	15.46	1874.27	6.74
H-4	ICSA 14029 x IS 29308	89.00	122.50	247.20	11.00	2.00	45.81	33.34	32.81	8799.99	15.50	13.71	644.36	5.47
H-5	ICSA 14030 x SEVS -08	78.00	121.00	208.45	10.00	1.80	44.33	35.99	30.23	10237.03	12.50	11.08	601.93	4.59
H-6	ICSA 14030 x GGUB 28	63.00	104.50	153.00	10.50	3.50	42.22	29.38	61.96	21216.65	12.50	11.08	1254.19	3.85
H-7	ICSA 14030 x ICSV 15006	81.50	124.50	248.90	10.50	3.75	51.58	28.78	65.95	18399.98	18.50	16.33	1597.93	6.42
H-8	ICSA 14030 x IS 29308	87.50	127.50	258.50	9.00	1.70	47.93	33.16	33.48	8303.70	15.50	13.71	604.23	5.41
H-9	ICSA 14033 x SEVS-08	78.50	118.50	268.10	14.00	1.65	31.13	32.14	37.14	8540.73	14.50	12.83	584.14	2.31
H-10	ICSA 14033 x GGUB -28	61.00	111.00	173.60	11.50	3.15	54.46	29.74	52.55	20733.31	12.00	10.65	1119.19	5.32
H-11	ICSA 14033 x ICSV-15006	84.50	127.50	273.80	11.50	3.15	47.89	33.76	63.01	14148.13	18.00	15.89	1197.23	4.83
H-12	ICSA 14033 x IS-29308	90.50	124.50	278.05	12.50	1.30	48.02	33.62	31.04	8777.77	15.50	13.71	642.14	5.29
H-13	ICSA 14035 x SEVS-08	70.50	116.50	258.80	9.50	2.15	52.90	36.13	31.48	11496.29	13.00	11.52	705.17	4.55
H-14	ICSA 14035 x GGUB 28	62.00	113.50	103.05	7.50	1.45	54.75	36.44	34.09	14396.28	9.50	8.46	670.29	5.01
H-15	ICSA 14035 x ICSV-15006	76.00	121.00	282.70	12.00	3.10	45.68	31.99	47.70	18037.02	17.50	15.46	1484.19	3.84
H-16	ICSA 14035 x IS-29308	70.50	111.50	286.30	12.50	1.75	35.39	33.45	30.45	6844.44	16.50	14.58	530.83	4.21
CHK	CSH-22SS ©	86.00	118.00	311.30	14.50	2.25	42.92	38.52	46.33	9022.21	13.00	11.52	553.42	3.39
	Mean	76.76	118.53	238.58	11.12	2.42	45.84	32.76	44.78	13574.44	14.38	12.71	921.12	4.70
	C.V (%)	1.59	2.21	10.09	8.41	9.85	12.85	11.07	13.20	16.04	9.24	8.17	15.05	10.09
	CD @5%	2.59	5.56	51.04	1.98	0.51	12.48	7.69	12.54	4615.97	2.82	2.20	293.92	1.01
	SEM	0.86	1.86	17.02	0.66	0.17	4.16	2.56	4.18	1539.68	0.94	0.73	98.04	0.34

Appendix - III

Mean Performance of 16 hybrids in Guntur location for 13 characters (E-II)

S.No.	Hybrids	Days to 50% flowering (Days)	Days to maturity (Days)	Plant height (cm)	Number of nodes per plant	Stem girth (cm)	Panicle weight (g)	1000 Grain weight (g)	Fresh Stalk yield (T ha ⁻¹)	Juice yield (l ha ⁻¹)	Brix %	Total soluble sugars (%)	Ethanol yield (l ha ⁻¹)	Grain yield (T ha ⁻¹)
H-1	ICSA 14029 x SEVS-08	75.00	126.50	212.50	9.50	1.95	37.25	34.43	51.71	15155.54	11.00	9.77	788.49	3.40
H-2	ICSA 14029 x GGUB 28	63.50	113.00	134.55	10.00	1.85	54.57	34.06	38.03	21037.02	13.50	11.96	1342.03	5.10
H-3	ICSA 14029 x ICSV-15006	80.50	124.00	268.05	12.50	2.65	43.79	27.88	63.85	14548.13	16.50	14.58	1129.22	3.42
H-4	ICSA 14029 x IS 29308	97.50	129.50	204.40	12.50	1.80	36.96	31.83	36.63	5444.44	14.50	12.83	372.66	2.33
H-5	ICSA 14030 x SEVS -08	79.50	118.50	266.45	12.50	1.00	70.47	27.21	27.90	6744.44	13.50	11.96	397.34	6.51
H-6	ICSA 14030 x GGUB 28	53.50	94.50	177.40	9.50	1.45	37.87	29.88	31.23	15725.91	10.50	9.33	780.64	4.01
H-7	ICSA 14030 x ICSV 15006	78.00	123.50	277.25	13.50	1.85	38.04	32.95	50.04	14688.87	13.50	11.96	936.70	3.57
H-8	ICSA 14030 x IS 29308	71.50	120.00	261.30	11.00	0.70	43.46	40.10	15.70	6711.10	17.50	15.46	553.38	3.86
H-9	ICSA 14033 x SEVS-08	90.50	127.50	134.00	10.50	1.80	47.55	28.04	34.67	16962.95	7.50	6.71	606.91	5.05
H-10	ICSA 14033 x GGUB -28	70.50	124.50	127.60	12.00	1.35	38.35	28.32	25.67	17444.43	9.50	8.46	787.99	4.98
H-11	ICSA 14033 x ICSV-15006	81.50	121.50	250.70	10.50	3.00	47.89	34.06	68.82	14881.47	18.50	16.33	1295.71	4.87
H-12	ICSA 14033 x IS-29308	69.50	102.50	170.85	10.50	2.05	45.22	30.18	36.30	8044.44	11.50	10.21	438.84	5.05
H-13	ICSA 14035 x SEVS-08	94.50	137.50	161.65	9.50	1.95	42.55	32.11	33.61	18392.57	11.50	10.21	998.22	3.70
H-14	ICSA 14035 x GGUB 28	57.00	91.50	156.05	10.50	3.05	44.73	38.20	43.10	8674.07	12.00	12.40	572.45	4.00
H-15	ICSA 14035 x ICSV-15006	79.50	126.50	272.25	12.50	2.10	57.91	26.61	33.50	25029.60	14.00	12.40	1651.84	6.09
H-16	ICSA 14035 x IS-29308	75.50	108.50	286.45	13.50	1.75	23.56	31.99	34.24	15659.24	17.50	15.46	1287.40	1.96
CHK	CSH-22SS ©	92.00	129.00	306.50	15.00	2.05	63.02	41.92	47.28	9422.21	12.50	11.08	555.57	3.14
	Mean	77.03	118.74	215.76	11.50	1.90	45.48	32.34	39.55	13798.03	13.24	11.83	852.67	4.18
	C.V (%)	1.30	1.22	10.69	10.70	10.27	11.12	10.04	12.35	14.30	9.42	8.03	13.83	13.03
	CD @5%	2.13	3.08	48.88	2.61	0.41	10.72	6.88	10.35	4184.12	2.64	2.01	250.07	1.16
	SEM	0.71	1.027204	16.31	0.87	0.14	3.58	2.29	3.45	1395.64	0.88	0.67	83.41	0.39

Appendix - IV

Mean Performance of 16 hybrids in Garikapadu location for 13 characters (E-III)

S.No.	Hybrids	Days to 50% flowering (Days)	Days to maturity (Days)	Plant height (cm)	Number of nodes per plant	Stem girth (cm)	Panicle weight (g)	1000 Grain weight (g)	Fresh Stalk yield (T ha ⁻¹)	Juice yield (l ha ⁻¹)	Brix %	Total soluble sugars (%)	Ethanol yield (l ha ⁻¹)	Grain yield (T ha ⁻¹)
H-1	ICSA 14029 x SEVS-08	84.50	126.00	256.91	11.50	2.00	53.89	32.34	44.86	13918.50	13.50	11.96	885.69	5.10
H-2	ICSA 14029 x GGUB 28	67.50	106.50	235.66	9.50	1.6	61.15	44.06	39.39	15199.98	15.00	13.27	1073.91	4.07
H-3	ICSA 14029 x ICSV-15006	76.50	122.50	303.93	10.50	1.8	57.32	36.8	53.83	16859.24	13.00	11.52	1034.13	5.03
H-4	ICSA 14029 x IS 29308	87.50	121.50	331.79	8.50	3.15	56.85	35.735	66.60	9207.40	11.50	10.21	501.31	5.90
H-5	ICSA 14030 x SEVS -08	90.50	127.50	317.77	11.50	2.35	64.44	39.085	48.32	14199.99	9.00	8.02	606.54	4.92
H-6	ICSA 14030 x GGUB 28	71.50	113.50	185.87	7.00	2.85	70.04	51.085	45.75	10807.40	8.00	7.15	411.30	5.49
H-7	ICSA 14030 x ICSV 15006	80.00	122.00	286.88	12.50	3.25	67.56	42.86	68.62	21955.53	12.00	10.65	1244.50	3.66
H-8	ICSA 14030 x IS 29308	88.50	128.50	255.95	7.50	2.25	67.07	38.14	33.73	18933.31	14.00	12.40	1249.52	5.14
H-9	ICSA 14033 x SEVS-08	76.50	113.00	363.83	13.50	2.05	67.23	61.375	36.09	14688.87	16.50	15.45	1140.17	6.95
H-10	ICSA 14033 x GGUB -28	68.50	109.50	233.76	13.00	3.15	46.86	37.795	45.33	15451.84	14.50	12.83	1054.97	4.17
H-11	ICSA 14033 x ICSV-15006	71.50	116.50	292.03	10.50	2.75	49.97	29.33	46.10	13674.06	11.50	10.21	742.87	4.62
H-12	ICSA 14033 x IS-29308	90.50	128.50	321.55	14.50	3.15	57.42	32.49	62.34	9340.73	9.00	8.02	398.98	5.16
H-13	ICSA 14035 x SEVS-08	84.50	124.50	403.96	15.50	3.6	43.20	33.965	73.20	8548.14	9.50	8.46	384.47	3.43
H-14	ICSA 14035 x GGUB 28	60.50	98.50	260.86	10.00	2.2	47.45	42.09	30.47	7185.18	10.50	8.02	356.64	3.71
H-15	ICSA 14035 x ICSV-15006	83.50	124.50	187.93	9.00	2.55	36.14	39.26	33.34	5792.59	12.50	11.09	314.72	2.21
H-16	ICSA 14035 x IS-29308	88.50	133.50	256.07	12.00	2.75	43.96	31.37	50.39	5822.22	12.50	11.08	401.98	4.05
CHK	CSH-22SS ©	91.50	131.50	383.50	14.50	2.1	47.16	42.17	37.67	10733.32	13.50	11.96	683.59	3.82
	Mean	80.12	120.47	286.95	11.24	2.56	55.16	39.41	48.00	12489.31	12.12	10.72	734.43	4.55
	C.V (%)	1.13	1.12	10.11	11.67	9.05	11.23	12.05	14.10	15.14	11.51	8.70	14.68	14.63
	CD @5%	1.92	2.87	61.52	2.78	0.49	13.13	10.07	14.35	4007.27	2.96	1.98	228.62	1.41
	SEM	0.64	0.96	20.52	0.93	0.16	4.38	3.36	4.79	1336.65	0.99	0.66	76.26	0.47

