www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(3): 4121-4123

www.thepharmajournal.com
Received: 18-12-2022
Accepted: 31-01-2023

AW More
Department of Agriculture Botany, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India

LN Jawale
Sorghum Research Station, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India

DK Zate
Department of Agriculture Botany, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India

Corresponding Author:
AW More
Department of Agriculture Botany, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India

Genetic variability and heritability for juice yield and its contributing traits in sweet sorghum genotypes (*Sorghum bicolor* (L.) Moench)

AW More, LN Jawale and DK Zate

Abstract
The present experimentation was conducted to assess the genetic variability and heritability in 33 sweet sorghum genotypes at Sorghum Research Station, VNMKV, Parbhani during *kharif* 2019. Observations were recorded on eleven quantitative traits. The estimate of genotypic and phenotypic coefficient of variation were nearly equal in almost in all traits which indicates that the variability existing in these characters was due to genetic factors and there was less influence of environmental factor in the expression of these characters. High genotypic coefficient of variation was observed for juice yield followed by millable cane weight, grain yield, total fresh biomass and stem girth. Almost all the traits showed high estimate of heritability, however high heritability with high genetic advance was observed for juice yield, total fresh biomass, millable cane weight, grain yield, stem girth and juice extraction percentage indicating additive gene action and thus selection for these characters in genetically diverse material would be more effective for desired genetic improvement.

Keywords: Sweet sorghum, genotypic variation, heritability, genetic advance

Introduction

Sorghum is a major cereal crop in semi arid tropics. Cultivated sorghum are grouped in to four main types based on primary use of sorghum *viz*., Grain sorghum, sweet sorghum or Sorgos, Broom Sorghum and Sudan grass etc. Particular varieties of sorghum with an ability to accumulate 10-25 percent sugar in its stalk juice are referred to as sweet sorghum. It is also called as sorgos. As grain sorghum, sweet sorghum is a C4 plant with very low photorespiration has a high biomass production capacity. Beside the traditional use grain and fodder, sweet sorghum used to produce several alternate products *viz*., syrup jaggary, ethanol, sugar, alcohol, vine and sweetener. It has the potential to improve the rural livelihoods in India due to its potential industrial use for bio-ethanol production. Also the Government of India (GOI) approved the National Policy on.

Biofuels on December 24, 2009 and had proposed an indicative target to replace 20% of petroleum fuel consumption with biofuels. The commercial value of these crops is based on exploiting their stems which contains high amount of sugars (Billa *et al*., 1997). Many characteristics such as millable cane weight, juice extraction percentage, cane yield, juice yield, sucrose yield and grain yield have been proved as major contributors to its economic superiority (Bala *et al* 1996) [1]. Average cane yield and juice quality needs to be increased by using the existing germplasm resources of the sweet sorghum.

Progress in any crop improvement venture depends mainly on the magnitude of genetic variability and heritability present in the source material. The extent of variability is measured by GCV and PCV which provides information about relative amount of variation in different characters. High heritability indicates the effectiveness of selection based on phenotypic performance but does not necessarily mean high genetic gain for particular characters, Consideration of both heritability and genetic advance is more important for predicting effectiveness of selection than heritability alone. Hence the experiment was initiated to estimate genetic variability, heritability and genetic advance in the available sweet sorghum germplasm.

Material and Methods

Thirty genotypes of sweet sorghum collected from Indian Institute of Millet Research along with three checks PVK 400, SSV 84 and CSH 22 SS were used as experimental material for the present study.

All the genotypes were evaluated in randomized block design with two replication. Two rows of each genotype was sown with a distance of 60 cm between two rows and 15 cm between plant to plant and all recommended agronomical practices were followed to grow healthy crop. Observations were recorded on randomly selected five plants from each entry from each replication for eleven characters days to 50 per cent flowering, days to maturity, plant height (cm), stem girth (cm), internode length (cm), total fresh biomass (g/plant), millable cane weight (g/plant), grain yield (g/plant), brix at physiological maturity, juice extraction percentage (%) and juice yield (ml/plant). The mean values of all traits under consideration were used for statistical analysis. The genotypic and phenotypic coefficients of variation were calculated by the formula given by Burton (1952). The heritability was computed based on the methods given by Falconer (1960). Genetic advance and genetic advance as percentage of mean were estimated according to the formula given by Johnson *et al*. (1955) [5] and Hanson *et al*. (1956) [6]. Statistical analysis were done by using INDOSTAT software.

Results and Discussion

Analysis of Variance for juice yield and its attributing traits (Table 1) showed significant mean sum of squares due to treatment for all the traits indicating genotypes were differed significantly. The extent of variability in respect of genotypic and phenotypic coefficient of variation, heritability and genetic advance along with the range and mean of characters is depicted in Table 2. Results revealed very slight differences between phenotypic coefficient of variances and genotypic coefficient of variances for all the characters, suggesting the least influence of environment in the expression of these characters. Maximum range of variation was observed for juice yield, millable cane weight, total fresh biomass, plant height and grain yield. Higher estimates of genotypic and phenotypic coefficient of variation were observed for juice yield (39.36 & 39.46) followed by millable cane weight (28.42 & 28.79), grain yield (28.22 & 28.44), total fresh biomass (26.06 & 26.25) and stem girth (20.70 & 20.87) revealing that the genotypes have a broad base genetic background as well as good potential that will respond positively to selection in improving characters. Tomar *et al.* (2012) obtained similar results for fresh cane weight, millable cane weight, juice extraction percentage and juice yield. Kachapur and Salimath (2009) [7] reported highest GCV & PCV for juice yield, Veerbhadiran and Kennedy (2001a) [9] for grain yield and Patil *et al.* (1996) [8] for green cane yield.

The genotypic coefficient of variation alone does not indicate the proportion of total heritable variation. High heritability indicates the effectiveness of selection based on phenotypic performance but does not necessarily mean high genetic gain for particular characters, Consideration of both heritability and genetic advance is more important for predicting effectiveness of selection than heritability alone. High heritability with high genetic advance indicates preponderance of additive gene effect, in such cases selection may be effective. In present investigation, high estimate of heritability was observed for almost all the traits suggesting that the characters were under genotypic control. However, high heritability with high genetic advance as percent of mean was observed for juice yield (99.50 & 80.88), total fresh biomass (98.50 & 53.20), millable cane weight (97.50 & 57.80), grain yield (98.50 & 57.70), stem girth (98.40 & 42.29) and juice extraction percentage (93.60 & 36.01) indicating additive gene action and thus selection for these characters would be more effective for desired genetic improvement. Kachapur and Salimath (2009) [7] observed similar results for juice yield. The characters days to 50 per cent flowering, days to maturity, Non-reducing sugar and total soluble sugar had high heritability coupled with low genetic advance suggesting that the variability for these characters are governed by non-additive gene action indicating the limited scope for improvement of these traits through phenotypic selection. While, the characters plant height, internode length, brix at 50 per cent flowering, Brix at physiological maturity and reducing sugar showed high heritability with low genetic advance indicating additive and non- additive gene action involved in expression of these traits. These findings are in agreement with the results of Tomar *et al.* (2012) for internode length and brix.

it may be concluded that characters juice yield, total fresh biomass, millable cane weight and grain yield, stem girth had high PCV, GCV and high heritability coupled with high genetic advance indicating variation in these characters was most likely due to additive gene effects. Hence, simple directed selection may be effective to improve these traits.

Table 1: Analysis of Variance for Juice yield and its attributing traits studied in sweet sorghum

Source of variation	DF	Days to 50% flowering	Plant height (cm)	Stem girth (cm)	Internode length (cm)	Total fresh biomass (g/plant)	Millable cane weight (g/plant)	Grain yield (g/plant)	Brix at physiological maturity	Juice Extraction%	Juice Yield (ml/plant)
Replication	1	23.04	114.68	0.0007	7.46	1383.7	283.13	0.44	0.038	0.206	68.72
Treatments	32	68.87**	2524.2**	0.34**	13.13**	55225.9**	42812.4**	177.79**	6.80**	102.44**	12706.4**
Error	32	2.29	24.11	0.002	0.32	417.78	549.84	1.37	0.059	3.41	32.54

Table 2: Variability Parameters for Juice yield and its attributing traits studied in sweet sorghum

Sr. No.	Characters	Range	Mean	GCV	PCV	Heritability (bs), (%)	Genetic advance %	Genetic Advance as % of mean
1	Days to 50% flowering	64.00-90.00	80.46	7.17	7.41	93.50	11.46	14.28
2	Days to maturity	104.00-132.00	119.77	5.05	5.27	91.60	11.93	9.96
3	Plant height (cm)	185.00-371.00	276.89	12.76	12.89	98.10	72.14	26.05
4	Stem girth (cm)	1.07-2.46	2.008	20.70	20.87	98.40	0.84	42.29
5	Internode length (cm)	14.05-24.85	19.43	13.02	13.34	95.20	5.08	26.17
6	Total Fresh Biomass (g/plant)	238.81-877.00	635.24	26.06	26.25	98.50	338.44	53.20
7	Millable Cane Weight (g/plant)	168.93-737.95	511.42	28.42	28.79	97.50	295.63	57.80
8	Grain Yield (g/plant)	16.55-53.00	33.27	28.22	28.44	98.50	19.19	57.70

9	Brix at physiological maturity	12.25-20.30	16.00	11.47	11.57	98.30	3.75	23.43
10	Juice Extraction (%)	22.76-54.92	38.93	18.07	18.68	93.60	14.02	36.01
11	Juice Yield (ml/plant)	62.87-363.13	202.21	39.36	39.46	99.50	163.56	80.88

References

1. Bala RS, Biswas PK, Ratnavathi CV. Advances in value addition of Kharif sorghum. Crop Improv. 1996;23:169-177
2. Billa E, Koullas DP, Monties B, Koukios EG. Structure and composition of sweet sorghum stalk components. Ind. Crops Prod. 1997;6:297-302.
3. Burton GW. Quantitative inheritance in pearl millet (P *glaucum* L.) Agron. J. 1952;50:503.
4. Falconer D.S. Introduction to Quantitative Genetics. Oliver and Boyd Ltd., Edinburgh; c1960. p. 340.
5. Johnson HW, Robinson HF, Comstock RE. Genotypic and Phenotypic correlation in soybean and their implications in selection. Agron. J. 1955;47:477-482.
6. Hanson CH, Robinson HF, Comstock RE. Biometrical studies on yield in segregating populations of Korean lespedesa. Agron. J. 1956;48:268-272.
7. Kachapur RM, Salimath PM. Genetic studies on correlation and character association in sweet sorghum (*Sorghum bicolor* (L.) Monech) Green- Farming. 2009;2(6):343-346
8. Patil FB, Gadekar DA, Bhoite AG. Variability studies in forage sorghum. Journal of Maharashtra Agriculure University. 1996;21(3):320-330.
9. Veerabadhiran P, Kennedy VJF. Estimates of genetic Variability in selected genotypes in sorghum. Madras Agric. J. 2001a; 88(4/6):308.