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ASSESSMENT OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN ADVANCED GENERATION CLONES OF SUGARCANE AT KABIRDHAM DISTRICT OF CHHATTISGARH INDIA

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ABSTRACT

A sum of 15 clones (12 genotypes and 3 standards) of sugarcane were evaluated in the randomizedcomplete block design to study their yield and other yield attributed traits performance. Results revealed that the mean sum of squares of genotypes were highly significant for all the traits under investigation. Significant mean squares weredue to cane yield and its attributing traits revealed existence of considerable variability in the studied material for the improvement of various traits. This suggested that there might be greater opportunities for improvement through selection based on these traits. All traits in the current study PCV were found to be higher than GCV; among the different yield attributing traits, only germination % at 45 DAP was recorded the highest magnitude of PCV (21.38%) and none of the traits were recorded highest magnitude of GCV. Whereas, high heritability coupled with high genetic advance as percentage of mean was recorded forheight (cm) (82.22%&22.70%) and single cane wt. (kg) (70.56%&21.91%). These characters show additive gene action and improvement through direct selection could be possible for these traits.

Key words: Sugarcane, Variability, GCV, PCV, Heritability, Genetic Advance.

Introduction

Sugarcane is one of the major commercially important industrial crops in India, grown in both tropical and subtropical regions. It is a member of the Poaceae family and the botanical genus *Saccharum*, which includes three species that bears sugar : *S. officinarum*, also called “noble cane,” *S. sinense*, and *S. barberi*. It supplies raw materials for the production of alcohol and is the primary source of sugar, gur, and khandsari. It also works well as a replacement for other chemical and petroleum products. Due to its multi-purpose uses in different industries, the demand is increasing for the increased production of sugarcane and its sustainability in the country.After Brazil, India ranks second globally in terms of sugarcane production. Over the previous few decades, sugarcane production in the nation has grown steadily. In India, sugarcane is currently grown commercially on 5.88 mha of land, yielding 83.35 tonnes/ha (Anonymous, 2023).In Uttar Pradesh, Maharashtra, Karanataka, Tamil Nadu, Andhra Pradesh, Gujarat, Punjab, Haryana, Uttaranchal, and Bihar, the crop is primarily grown. Together, Uttar Pradesh and Maharashtra contributed over 69.65% of India’s total sugarcane production, making up nearly 68.70% of the country’s total sugarcane land (Anonymous, 2023).

Chhattisgarh state, which has been referred to as the “rice bowl” of the nation, is now set to create a niche for itself in the sugar industry. Some districts of Chhattisgarh, including Kabirdham (Kawardha), Surguja, and Balod districts, are primarily sugarcane-growing regions. The scope of sugarcane is bright in the Chhattisgarh; it is grown in 36.05 thousand hectares area, with an average productivity of 57.16 tons per hectare (Anonymous, 2023).

Sugarcane varieties in commercial cultivation are complex polyploid. The heterozygous and polyploidy nature of this crop has resulted in generation of greater genetic variability. The presence of genetic variability is an essential requirement for effective genetic improvement of any crop species. Success of any breeding programme is mainly based on available variability and intensity of selection imposed. Genotypic and phenotypic coefficients of variation along with heritability as well as genetic advance are very essential to improve any trait of sugarcane because this would help in knowing whether or not the desired objective can be achieved from the material (Tyagi and Singh, 1998). Statistics has offered various analytical techniques to assess the available variability. Thus, present work aims at studying on Sugarcane for its genetic variability and to evaluate the performance of different sugarcane clones. This information may lead to development of desirable plant type in future breeding endeavors.

Materials and Methods

The experimental material for this study comprised of 15 different clones (12clones and 3standards)of sugarcanewere evaluated in the randomized block design with three replications for their yield and other yield attributed traits performance.Every set of guidelines for growing a healthy sugarcane crop so that, the genetic parameters can be studied. In a plot with 4 rows, each 5 meters long, and 1.20 meters apart, two budded sets of every clone were planted. The observation taken on germination % at 45 DAP, number of millable canes/ plot, cane height (cm), single cane weight (kg), cane girth (cm), node length (cm), cane yield (t/ha), CCS (t/ha) and other biochemical analysis *viz*., juice%, brix%, purity%, and sucrose %. Five plants of each genotype were randomly tagged, and the morphological trait data was recorded. Prior to using a conversion method to determine it on a per hectare basis, yield and its related traits were originally recorded on a plot level.Analysis of variance as per the procedure given by Cochran and Cox, 1957 whereas, phenotypic variances, genotypic variances and heritability were analyzed statistically as per the procedure given by Burton, 1952 and Genetic advance was calculated by the formula given by Johnson *et al*., 1955 .

Results and Discussion

Analysis of variance

The average performance of the 15 sugarcane clones has been showed in the Table 1. According to the analysis of variance for cane yield and its attributing traits the mean sum of squares resulting from genotypes were highly significant for all the traits under investigation, including germination percentage at 45 DAP, number of millable canes/plot, height (cm), single cane weight (kg), girth (cm), node length (cm), cane yield (t/ha), CCS (t/ha), and other biochemical analysis such as juice%, brix%, purity%, and sucrose%.Significant mean squares due to cane yield and its attributing traits revealed existence of considerable variability in the material studied for the improvement of various traits. This suggested that there might be greater opportunities for improvement through selection based on

Table 1: Analysis of variance for yield and yield contributing traits in Sugarcane.

Source	df	Germination % at 45 DAP	No of millable canes/ plot	Height (cm)	Single cane wt. (kg)	Cane Girth (cm)	Node length (cm)	Cane yield (t/ha)	Juice %	Brix %	Purity %	Sucrose %	CCS (t/ha)
Rep.	2	1140.93	323.33	902.45	0.01	0.06	0.06	310.86	5.35	0.12	47.98	3.38	10.25
Gen.	14	15149.20**	24959.20**	51958.33**	2.53**	5.82**	17.39**	5217.57**	88.89**	46.88**	149.65*	32.10*	181.43**
Error	28	6609.07	9838.67	6987.66	0.64	2.00	5.64	3026.99	123.83	25.28	134.94	29.47	155.43

**Significant at P=1% & *Significant at P=5%, DAP= Date of Planting, CCS=Commercial Cane Sugar

Table 2: Genetic parameters of variability for yield and yield contributing traits in Sugarcane.

Characters	Mean	Range		GCV %	PCV %	Herita-bility	GA as % Mean
		Min	Max				
Germination % at 45 DAP	106.47	49	145	15.77	21.38	60.22	23.97
No of millable canes/ plot	208.20	155	266	10.49	13.83	57.59	21.02
Height (cm)	358.15	298.80	454.40	9.48	10.46	82.22	22.70
Single cane wt. (kg)	2.30	1.68	2.81	9.95	11.93	70.56	21.91
Cane Girth (cm)	9.00	8.22	9.88	3.76	4.79	61.59	7.79
node length (cm)	11.51	9.84	13.02	5.12	6.43	63.29	10.75
Cane yield(t/ha)	143.25	115.83	173.75	6.56	9.78	44.93	11.60
juice %	55.41	51.18	59.48	1.45	4.06	12.68	1.36
Brix%	20.72	18.20	23.80	4.36	6.33	47.45	6.18
Purity %	87.66	81.06	93.16	1.60	2.97	28.88	2.26
Sucrose%	18.14	15.23	21.07	3.54	6.67	28.20	4.97
CCS (t/ha)	17.94	12.42	25.52	8.76	15.78	30.79	12.83

these Traits. The study supports the findings of earlier researchers such as Patel *et al.* (2006), Gowda *et al.* (2016), Hiremath and Nagaraja(2016) and Agrawal and Kumar (2017).

Genotypic and phenotypic coefficients of variation

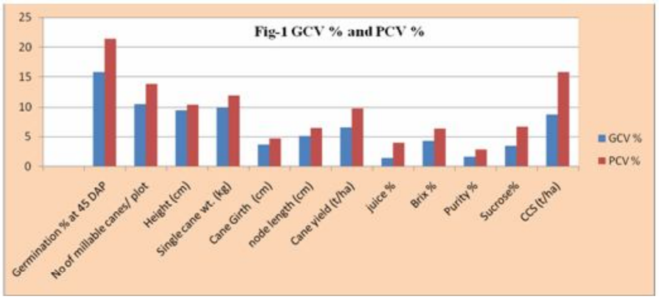
To evaluate the genetic variability, genotypic and phenotypic coefficient of variation is one which offers to estimate the extent of variability in material under investigation. The estimate of genotypic and phenotypic components of variation gives us an idea of relative extent of heritable and non heritable variation. Thus, the components of variation such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed. The PCV were marginally higher than the corresponding GCV.GCV and PCV are categorized as low (<10 %), moderate (10-20 %) and high (>20 %) as suggested by Sivasubramanian and Madhavamenon (1973).

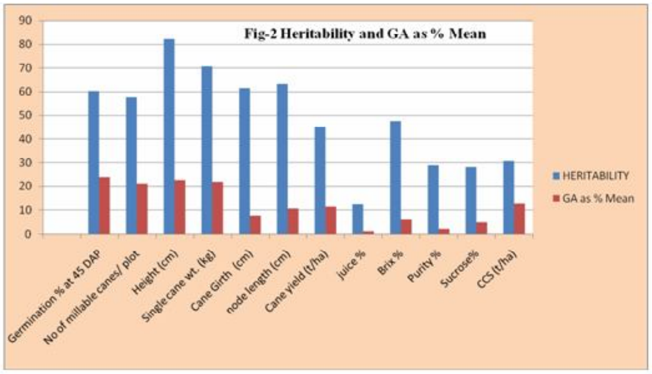
The estimates of genotypic and phenotypic coefficient of variation forCane yield and its attributing traits has been presented in Table2 and Fig 1 and discussed as follow:Among the different yield attributing traits, only germination % at 45 DAP was recorded the highest magnitude of PCV (21.38%) along with moderate GCV (15.77%). The moderate magnitude of PCV (13.83%) and GCV (10.49%) was observed for No. of milliable canes/plot whereas moderate PCV and low GCV was recorded for CCS (t/ha) (15.78% and 8.76%), single cane weight (kg) (11.93% and 9.95%), height (cm) (10.46% and 9.48%). Similar results were reported by Relisha and Balwant Kumar (2017). Low GCV and PCV were observed for Cane girth (cm) (4.79% and 3.76%), Node length cm(6.43% and 5.12%), Cane yield (t/ha) (9.78% and 6.56%), Juice % (4.06% and 1.45%), Brix% (6.33% and 4.36%), Purity% (2.97% and 1.60%) and Sucrose % (6.67% and 3.54%). Similar findings were also reported earlier by Kumari et al. (2020), Pandey *et al.*, (2018), Gowda *et al.*, (2016), Sanghera e*t al.*, (2014) andGhosh and Singh, (1996).

All characters in the current study PCV was found to be higher than GCV; however, for the following traits, the phenotypic and genotypic coefficients of variation differed very slightly: number of millable canes/ plot, cane height (cm), single cane weight (kg), cane girth (cm), node length (cm), cane yield (t/ha), juice%, brix%, purity%, and sucrose%, suggesting that these variables were less affected by the environment. Thus, it may be said that selection can be used to develop certain sugarcane traits in the desired direction based on phenotype.

Heritability and genetic advance

Success of improvement in any traits is based on





phenotypic selection, which depends upon the correspondence between phenotype and genotype. Hence, the selection intensity in a population relies upon the amount of heritable variation present in the population. Therefore, heritability estimates along with genetic advance considered useful in understanding the pattern of inheritance of quantitative traits. Estimates of heritability in broad sense and genetic advance as percentage of mean for yield and its components have been presented in Table 2 & Fig 2 and are discussed as follows:Heritability estimates along with genetic advance are normally more useful in predicting the gain under selection than that of heritability alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al*. 1955). An attempt has been made in the present investigation to estimate heritability in broad sense and categorized as low (<50%), moderate (50-70%) and high (>70%) as suggested by Robinson (1966).

The estimates of heritability in broad sense (h^2b) exhibited considerable variation for various traits and also presented in Table 2. In the present investigation high magnitude of heritability was recorded only for height (cm) (82.22) and single cane wt. (kg) (70.56%). moderate heritability was observed for germination% at 45 DAP, no. of milliable canes/plot, cane girth (cm), node length (cm) (63.29) whereas, the low heritability was observed for cane yield (t/ha) (44.93%), juice% (12.68%), brix% (47.45%), purity% (28.88%), sucrose% (28.20%) and CCS (t/ha) (30.79).However,traits, which showed low heritability, are difficult to improve.Similar results were reported by Pandey *et al.,* (2018), Sanghera *et al.,* (2014) and Mali and Patel (2013).

To facilitate the comparison of progress in various characters of different genotypes genetic advance was calculated as percentage of mean. Deshmukh *et al.,* (1986) classified genetic advance as per cent of mean as low (<10%), moderate (10-20%) and high (>20%). Traitslike Germination% at 45 DAP (23.97%), No. of milliable, Height (cm) (22.70%),Single cane wt. (kg) (21.91%) and canes/plot (21.02%) were exhibited high Genetic advance as percentage mean and moderate Genetic advance as percentage mean was observed forCCS (t/ha) (12.83%)followed by cane yield (t/ha) (11.60%) and node length (cm) (10.75%), whereas, low genetic advance as percentage mean was observed for cane girth (cm) (7.79%) followed by brix% (6.18%), sucrose% (4.97%), purity% (2.26%) and juice% (1.36%). These finding are in agreement with the finding of Pandey *et al.,* (2018), Sanghera *et al.,* (2014).

The heritability value alone however, provides no indication of the amount of genetic improvement that would result from selection of superior genotypes. The heritability estimates would be reliable if it is limited in a broad sense; additive and non additive gene effects are accompanied with high genetic advance. High heritability coupled with highgenetic advance as percentage of mean was found in height (cm) (82.22%) (22.70%) and single cane wt. (kg) (70.56%) (21.91%).Similar results were reported by Chandrakanth et al. (2006) and Kamath and Singh (2001).Moderate heritability with high values of genetic advance as per cent mean were reported for germination% at 45 DAP (60.22%) (23.97%), no. of milliablecanes/plot (57.59%) (21.02%). These characters show additive gene action and improvement through direct selection could be possible for these characters. Pandey (1989) had earlier reported the low genetic advance with moderate amount of heritability for stalk diameter suggesting a little scope in the improvement of this character. Low heritability with moderate genetic advance as per cent mean was found for CCS (t/ha) whereas, moderate heritability coupled with low genetic advance was observed for cane girth (cm) and node length (cm). Low heritability coupled with low genetic advance was found for cane yield (t/ha), juice%, brix%, purity% and sucrose% and this indicate that these traits were highly influenced by environment and selection would be ineffective for these characters. Thesefinding are similar reported by Pandey *et al.,* (2018).

Conclusions

The results of Analysis of variance (ANOVA) revealed that the mean sum of squares from genotypes were highly significant for all the traits under investigation. Significant mean squares due to cane yield and its attributing traits revealed existence of ample variability in the material studied for the improvement of various traits. All characters in the current study PCV were found to be higher than GCV, however, the phenotypic and genotypic coefficients of variation differed very slightly, indicated that these variables were less affected by the environment.High heritability coupled with High genetic advance as percentage of mean was recorded for height (cm) and single cane wt. (kg). These characters show additive gene action and improvement through direct selection could be possible for these characters. This suggested that there might be greater opportunities for improvement through selection based on these traits.

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