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Study of genetic variability for cane yield and its component characters in early maturing sugarcane clones (*Saccharum* spp.)

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Abstract
Thirty early maturing sugarcane clones were planted in a randomized block design during 2018-19 at ARS, perumallapalle, Tirupathi, Andhra Pradesh to study the variability in cane yield and its component traits. The characters studied were germination count at 30 DAP, tillers at 90 DAP, tillers at 120 DAP, shots at 240 DAP, NMC ('000/ha), cane length, cane diameter (cm), single cane weight (kg), number of nodes per cane, fibre per cent, Brix, sucrose, purity, CCS % at 8th and 10th months, cane yield and CCS yield (t/ha) at harvest. Analysis of variance revealed that significant differences observed for all the traits among the clones. The PCV is greater than GCV for most of the traits under study. The characters such as number of nodes per cane, cane length, CCS yield and cane yield showed high heritability coupled with high GAM indicates that presence of additive gene action and selection is effective for these traits. Hence these traits can be utilized for further selection and genetic improvement of early maturing clones.

Keywords: Genetic advance, heritability, genetic variability and early maturing sugarcane

Introduction
Sugarcane (*Saccharum spp*.) is a commercial crop next to cotton (Dagar *et al*. 2002) [6]. It is a perennial tropical tall grass belonging to family Poaceae, sub family Panicoideae, tribe Andropogoneae, sub-tribe Sacccharineae, and genus Saccharum (Watson *et al.* 1985) [18] of monocot origin, which is having a chromosome number of 2n=80-120 and it varies from species to species. It is also a valuable commercial crop of the tropics and subtropics accounting about 62 per cent of world sugar production. India is the second largest producer of sugar after Brazil with an area of 5.11 million hectare with an average cane yield of 78.24 tonnes per hectare while the production is 400.16 million tonnes during 2018-2019. (Anonymous, 2019) [3]. Whereas, in Andhra Pradesh sugarcane is grown in 0.10 million hectare area with production of 8.09 million tonnes and productivity of 79.32 tonnes per hectare during 2018-2019. (Anonymous, 2019) [3]. With day by day increase in the population the sugar demand also being increased. The requirement of entire population with the limited area is achieved only by increasing the productivity per unit area and time. Sugarcane plays a significant role in economy of sugarcane growing areas and hence improving the production will greatly help in economic growth of farmers and other stakeholders associated with sugarcane production. As an industrial crop sugarcane provides raw material for ethanol, pulp and paper and sugar industries. Only a fraction of it used for small scale industries for making local Khandasari and Gur. Sugarcane juice is used for making white sugar, jaggery (GUR) and many by products like bagasse and molasses. Bagasse can be used as a fuel, for production of wooden board, furfural, papers and plastics. Molasses is used in distillation units for preparation of ethyl alcohol and butyl alcohol. The recovery percent of sucrose ranges from 12-18% depending on the variety, soil conditions, time of maturity and cultural practices adapted by the farmers. The major problem in the sugarcane is the narrow genetic base of parents which may lead to greater inbreeding among progeny and reduction in genetic variability. The most significant work in sugarcane breeding from long time is being carried out by Sugarcane Breeding Institute, Coimbatore. They developed many high yielding varieties by interspecific hybridization and later selection of superior clones by way simple recurrent selection. Both cane and sugar yields are complex traits influenced by many components either directly or indirectly. Breeder should definitely know the association between cane and quality traits to improve the cane and sugar yields.

Sugarcane is a highly heterozygous and complex polyploid crop which leads to generation of more variability. Variability is measured by variance, GCV (genotypic coefficient variation), PCV (phenotypic coefficient of variation) and genetic advance as per cent of mean. The information regarding variability and heritability of traits is important for a breeder to make efficient selection among clones. Coefficient of variation with heritability along with genetic advance helps improving the traits by informing whether the particular objective is achieved or not with the available material.

Material and Methods

The material of the present investigation was comprises of thirty early maturing clones. All these clones were planted in a Randamized Block Design with two replications during 2018-19 at ARS, Perumallapalli, Tirupathi, Andhra Pradesh followed all the packages of practices to raise good sugarcane crop in order study the genetic parameters. Three budded sets of all the clones were planted in a plot of four rows of four meters length each with a spacing of 80 cm between the rows. Observations were recorded by selecting five canes of each clone from each replication for component traits of cane yield and quality parameters, viz., Germination per cent 30 days after planting (DAP), tillers at 90 DAP, tillers at 120 DAP, shoots count at 240 DAP, Number of millable canes ('000/ha), Number of nodes per cane, cane length, cane diameter (cm), single cane weight (kg), juice quality parameters viz. brix, sucrose, pol and CCS per cent at 10th month, cane yield and CCS yield (t/ha) at harvest.

The various genetic parameters phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV), heritability (h_2) in broad sense and genetic advance as percent of mean were calculated as suggested by Burton and Devane (1952). Lush (1940) and Johnson *et al*. (1955) [9, 10]. The data analysis was carried out with INDOSTAT software.

Statistical analysis

In order to assess and quantify the genetic variability for the characters of all the genotypes under study the statistical analysis was done as follows.

Analysis of variance

The differences among 30 genotypes in each trial for different characters were tested for significance by using analysis of variance technique (Panse and Sukhatme, 1961) [14].

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

Where,
Y_{ij} = Phenotypic observation on 'i'th genotype in 'j'th replication.
μ = General mean
g_i = Effect of ith genotype
γ_j = Effect of jth replication
e_{ij} = Random error associated with ith genotype and jth replication.

The analysis of variance for each character was carried out as follows:

Table 1: Analysis of variance for each character

Source of variation	Degree of freedom	Sum of squares	Mean sum of squares	'F' ratio
Replications	(r-1)	RSS	Mr	Mr/Me
Genotypes	(t-1)	VSS	$Mv = \sigma g^2 + \sigma e^2$	Mv/Me
Error	(r-1) (t-1)	ESS	$Me = \sigma e^2$	-
Total	(rt-1)	TSS		

Where,
r = Number of replications, t = Number of genotypes, Mr = Mean sum of squares due to replications, Mv = Mean sum of squares due to genotypes, Me = Mean sum of squares due to error

The significance test was carried out by referring to standard 'F' table values given by Fisher and Yates (1963).

Estimation of genetic parameters

The estimates of mean sum of squares from ANOVA were utilized for calculation of following parameters.

Variance

The genotypic and phenotypic variances were calculated as per the formulae proposed by Burton and Devane (1953) [4]
(i) Genotypic variance (σ_g^2) =

$$\frac{\text{MSS due to genotypes - MSS due to error}}{\text{Number of replications}}$$

(ii) Phenotypic variance (σ_p^2) = $\sigma_g^2 + \sigma_e^2$

σ_g^2 = Genotypic variance
σ_e^2 = Error variance

Genotypic and phenotypic coefficient of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the formulae given by Burton and Devane (1953) [4].

(i) GCV (%) = $\frac{\sigma_g}{\bar{X}}$ x 100
(ii) PCV (%) = $\frac{\sigma_p}{\bar{X}}$ x 100

Where, σ_g, σ_p and $\bar{X}$ were genotypic standard deviation, phenotypic standard deviation and general mean of the character, respectively.
Categorization of the range of variation was done as proposed by Sivasubramanian and Madhava menon (1973) [16]
Less than 10% - Low
10 - 20% - Moderate
More than 20% - High

Broad sense heritability

Heritability in broad sense refers to the proportion of genotypic variance to the total variance of the population. Heritability in broad sense [$h^2_{(b)}$] was calculated by the formula given by Lush (1949) [13].

Broad sense heritability = $\frac{\sigma_g^2}{\sigma_p^2}$ x 100

Where,
σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance
As suggested by Johnson *et al.* (1955) [9, 10], heritability estimates were categorized as
Less than 30% - Low
30 - 60% - Moderate
More than 60% - High

Genetic advance
Genetic advance refers to the expected genetic gain in the next generation by selecting the superior individuals under certain amount of selection pressure. From the heritability estimates, the genetic advance was estimated by the following formula given by Johnson *et al.* (1955) [9, 10].

$GA = k \sigma_p H$

Where
GA = Genetic advance
σ_p = Phenotypic standard deviation
H = Heritability (broad sense)
k = Selection differential at 5% selection intensity

Genetic advance as percent of mean (GA as percent mean)
Genetic advance as percent of mean was calculated as per the formula.

$$\text{GA as percent of mean} = \frac{GA}{\bar{X}} \times 100$$

Where,
GA = Genetic advance
$\bar{X}$ = Grand mean of the character

The range of genetic advance as percent of mean was classified as suggested by Johnson *et al.* (1955) [9, 10].
Less than 10% - Low
10 - 20% - Moderate
More than 20% - High

All the analysed statistical data being presented in table 1 and 2. Observed data are also presented in Graph 1 and 2 which showed Estimate of GCV, PCV and h² (broad sense), GAM of characters in early maturing Sugarcane clones respectively.

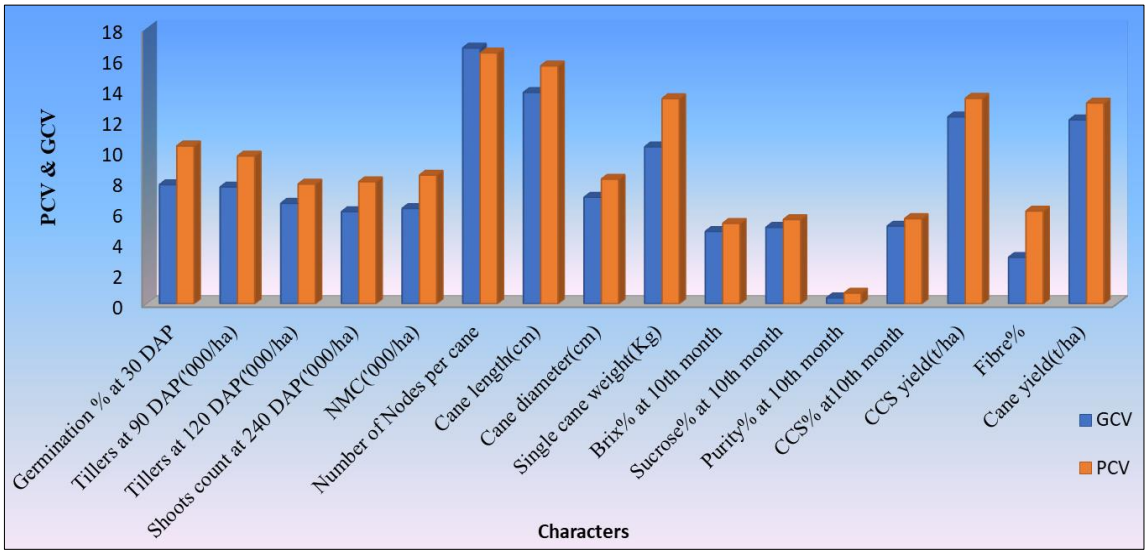

Fig 1: PCV and GCV for various traits

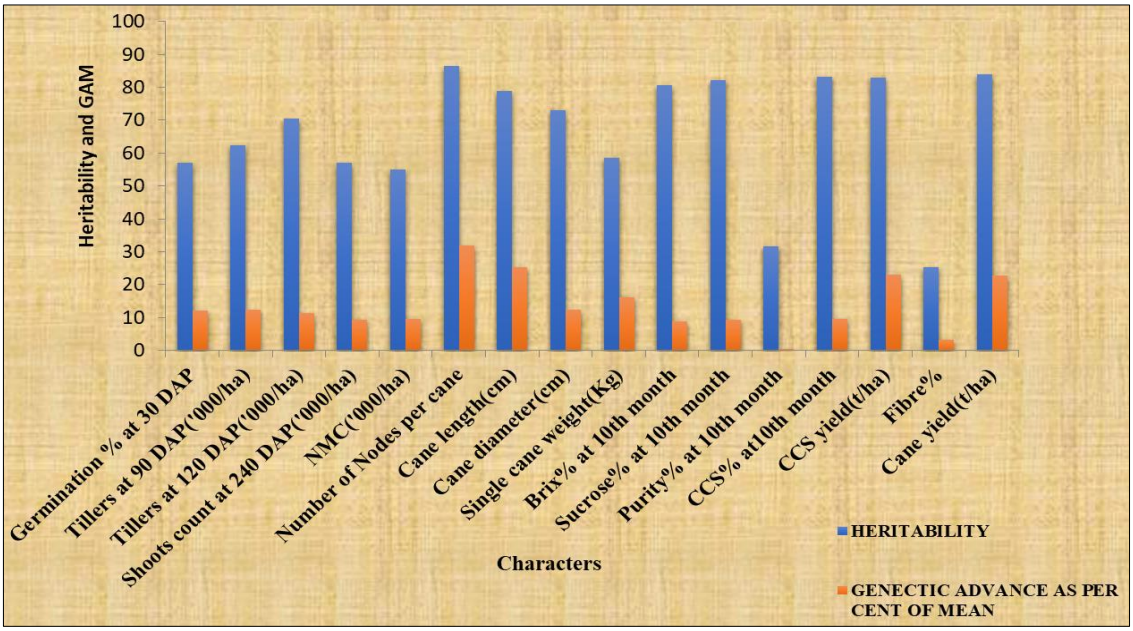

Fig 2: Heritability and genetic advance as percent of mean for various traits

Table 1: Analysis of variance for cane yield and quality characters in Sugarcane clones

Sl. No.	Characters	Mean sum of squares		
		Replications (df:1)	Treatments (df:29)	Error (df:29)
1	Germination % at 30 DAP	17.83	61.61**	17.05
2	Tillers at 90 DAP ('000/ha)	33.94	164.75**	38.22
3	Tillers at 120 DAP ('000/ha)	7.30	138.07**	23.94
4	Shoots count at 240 DAP ('000/ha)	0.36	131.93**	33.19
5	NMC ('000/ha)	39.47	101.70**	32.53
6	Number of Nodes per cane	0.26	30.55**	2.32
7	Cane length (cm)	261.20	1967.36**	233.04
8	Cane diameter (cm)	0.008	0.09**	0.01
9	Single cane weight (Kg)	0.02	0.04**	0.01
10	Brix % at 8th month	0.09	2.10**	0.26
11	Sucrose % at 8th month	0.03	1.61**	0.19
12	Purity % at 8th month	0.30	0.46*	0.24
13	CCS % at 8th month	0.008	0.77**	0.09
14	Brix % at 10th month	0.16	2.14**	0.23
15	Sucrose % at 10th month	0.16	1.86**	0.18
16	Purity % at 10th month	0.02	0.52*	0.27
17	CCS % at 10th month	0.08	0.94**	0.09
18	CCS yield (t/ha)	0.17	7.15**	0.68
19	Fibre %	1.07	1.02**	0.40
20	Cane yield (t/ha)	0.31	413.76**	36.31

*, ** Significant at 5% and 1%, respectively

Table 2: Mean, range, co-efficient of variation, heritability (broad sense), genetic advance and genetic advance as percent of mean for cane yield and quality characters in sugarcane clones

Sl. No.	Characters	Mean	Range		Variance		Coefficient of variation (%)		Heritability (%)	Genetic advance	Genetic advance as Percent of mean (%)
			Minimum	Maximum	Genotypic	Phenotypic	Genotypic	Phenotypic			
1	Germination % at 30 DAP	60.95	50	72.5	22.60	39.61	7.79	10.32	57.05	7.39	12.13
2	Tillers at 90 DAP ('000/ha)	104.19	89.84	123.44	63.27	101.50	7.63	9.66	62.34	12.93	12.41
3	Tillers at 120 DAP ('000/ha)	114.91	103.12	134.37	57.06	81.00	6.57	7.83	70.45	13.06	11.36
4	Shoots count at 240 DAP ('000/ha)	107.55	94.53	125.00	41.93	73.67	6.02	7.98	56.93	10.06	9.35
5	NMC ('000/ha)	99.59	80.84	113.31	38.54	70.12	6.23	8.41	54.89	9.47	9.51
6	Number of Nodes per cane	22.50	13.5	34	14.15	16.39	16.72	16.39	86.38	7.20	32.02
7	Cane length (cm)	213.54	131.66	272.5	870.35	1102.84	13.81	15.55	78.92	53.98	25.28
8	Cane diameter (cm)	2.85	2.46	3.45	0.03	0.05	6.96	8.15	72.98	0.35	12.25
9	Single cane weight (Kg)	1.20	0.89	1.52	0.01	0.02	10.26	13.41	58.53	0.19	16.17
10	Brix % at 10th month	20.67	17.50	22.85	0.95	1.18	4.73	5.26	80.60	1.80	8.74
11	Sucrose % at 10th month	18.50	15.6	20.6	0.85	1.04	5.00	5.51	82.11	1.72	9.33
12	Purity % at 10th month	89.58	88.6	90.55	0.12	0.39	0.39	0.70	31.63	0.41	0.47
13	CCS % at 10th month	12.93	10.85	14.40	0.43	0.52	5.08	5.57	83.13	1.23	9.54
14	CCS yield (t/ha)	14.76	11.6	19.05	3.25	3.93	12.22	13.43	82.85	3.38	22.92
15	Fibre %	14.00	12.45	14.80	0.18	0.72	3.04	6.06	25.21	0.44	3.14
16	Cane yield (t/ha)	114.26	87.35	141.05	188.88	225.04	12.02	13.12	83.93	25.93	22.69

Results and Discussions

Variability is the prime need of present sugarcane breeding programmes. As per overview in the table 1 it clearly indicates the significant differences observed for all the characters among all the clones under study. Similar results were also reported by earlier workers Hiremath and Nagaraja (2016) [8], Tena *et al.* (2016) [17], Agrawal and Kumar (2017) [1] and Kumar *et al.* (2017) [1]. It clearly indicates the presence of sufficient variability among all the clones for all the characters which is effective for selection for cane and sugar yield. So there is wide range of variation for cane and sugar yields which favors the selection of clones towards high cane and sugar yields. In the present investigation phenotypic coefficient of variation is higher than genotypic coefficient variation for all the characters which indicates the influence of non-genetic factors on expression of these traits. These results are in accordance with the findings of Relisha and Balwant Kumar (2017) [15]. Moderate PCV and GCV values observed for cane length followed by number of nodes per cane, CCS yield, cane yield and single cane weight. Similar results were reported by Relisha and Balwant Kumar (2017) [15]. High heritability coupled with low GAM were observed for tillers at 90 DAP, tillers at 120 DAP, cane diameter, brix%, sucrose% and CCS% at 10th month. The selection for these traits is not effective because presence of both additive and non-additive gene action genetic improvement for these traits is possible through heterosis breeding. These results are in accordance with the findings of Alam *et al.* (2017) [2], Agrawal and Kumar (2017) [1]. High heritability coupled with high GAM were observed for traits such as number of nodes per cane, cane length, CCS yield and cane yield indicates the selection for these traits is effective due to additive gene action. Similar results were reported by Chandrakanth *et al.* (2006) [5] and Kamath and Singh (2001) [11]. Hence, direct selection can be done through these characters for future improvement of clones for higher cane and sugar yield in

early maturing sugarcane clones.

Conclusion

The results of Analysis of variance (ANOVA) revealed that significant difference for mean sum of squares of all the characters under the study indicates the presence of ample variability among all the clones. High heritability and genetic advance as per cent of mean recorded for traits *viz.*, number of nodes per cane, cane length, CCS yield and cane yield indicating the prevalence of additive gene action hence crop improvement achieved by simple selection of these traits. Therefore, instead of 16 traits only four traits can be observed for further improvement in early maturing sugarcane clones.

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