



GENETIC VARIABILITY OF YIELD AND YIELD CONTRIBUTING CHARACTERS IN *Stylosanthes species*

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Abstract: The investigation variability of yield and yield contributing characters in *Stylosanthes species* was undertaken to study the magnitude of genetic variability of various components towards green forage yield. The ten observations were recorded on green forage yield and yield contributing characters viz., plant height (cm), plant spread (cm), number of primary branches per plant, leaf length (cm), leaf breadth (cm), length of leaf sheath (cm), leaf to stem ratio, green forage yield/plant (g), dry matter yield/plant (g), and crude protein yield/plant (g). The analysis of variance showed existence of considerable variability for all twelve characters. A wide range of variability was observed for almost all the characters studied. The genotypes RS-20-2, RS-20-11, RS-20-19, RS-20-20, RS-20-21, RS-20-22, RS-20-24, RS-20-25, RS-20-26, RS-20-27, RS-20-29 and RS-20-33 recorded higher green forage yield/plant, dry matter yield/plant and simultaneously other characters. Phenotypic coefficient of variation estimates was slightly higher than genotypic coefficient of variation. High genotypic and phenotypic coefficient of variation was observed for leaf to stem ratio followed by crude protein yield/plant, dry matter yield/plant, crude protein content and green fodder yield/plant indicating ample variability for these characters. All the characters except length of leaf sheath and number of primary branches per plant under study showed high estimates of broad sense heritability. High heritability estimates accompanied with high genetic advance was observed for the characters viz., leaf to stem ratio, crude protein yield/plant, crude protein content and dry matter yield/plant indicating inheritance of these characters due to additive gene action and direct selection of such traits necessary for crop improvement.

Keywords: *Stylosanthes*, variability, heritability, yield

I. INTRODUCTION

Stylosanthes popularly known as stylo, is an erect growing perennial forage legume native of Brazil. It grows 0.6 to 1.8 m tall. Stems are coarse and hairy becoming woody with age. Leaves are trifoliate with leaflets long; rather narrow varying in size, colour and hairiness. Flower which are borne in terminal clusters are small, yellow or orange. Pods are single seeded, seeds are yellowish brown, rather kidney shaped and larger than seeds of Lucerne. Seed count is 250 per g, chromosome number (2n) is 20 (Hopkinson and Walker, 1984). Improvement of feed quality and quantity has been major thrust and the genus *Stylosanthes* has been used for this purpose. *Stylosanthes* is also being successfully integrated in crop/pasture production system. The most important attributes of successful *Stylosanthes* genotypes used as pasture or lay in tropical America are resistance to disease, high seed yield and adaptation to infertile soils (Ferguson *et al.*, 1989). Genetic variability refers to distinctions between the genetic makeup of individuals in a population. Over the past four decades the genus *Stylosanthes* has received major focus across the tropics as a means of improving ruminant production. This was favoured by discovery of many “new” species which offered the required flexibility for growth in diverse agro-climatic situations. Improvement of feed quality and quantity has been major thrust and the genus *Stylosanthes* has been employed for this objective.

II. MATERIAL AND METHODS

The experiment was laid out in randomized block design (RBD) with two replications having forty three genotypes at Grass Breeding Scheme, Mahatma Phule Krishi Vidyapeeth, Rahuri- 413 722 (M.S.). The experimental material consisted of forty three genotypes of *Stylosanthes* including check Phule Kranti which were provided by Grass Breeding Scheme, MPKV, Rahuri.

Statistical analysis

Assessment of variability

a. Analysis of variance

The data collected on individual characters were subjected to the method of analysis of variance commonly applicable to the randomized block design (Panse and Sukhatme, 1985).

$$Y_{ij} = \mu + G_i + R_j + E_{ij}$$

Where,

- $i = 1, 2, \dots, G$
 $j = 1, 2, \dots, R$
 Y_{ij} = Observation on i^{th} genotype in j^{th} replication
 μ = General mean
 G_i = Effect of i^{th} genotype
 R_j = Effect of j^{th} replication
 E_{ij} = Random error associated with Y_{ij} observation

ANOVA Table:

Source	d.f.	MSS	Expected MS
Replications	$r-1$	RMS	$\sigma_e^2 + \sigma_r^2$
Treatments	$g-1$	GMS	$\sigma_e^2 + r\sigma_g^2$
Error	$(r-1)(g-1)$	EMS	σ_e^2

Where,

- r = Number of replications
 g = Number of genotypes
 σ_g^2 = Variance due to genotypes and
 σ_e^2 = Variance due to error

The genotype mean square (GMS) was tested against error mean square (EMS) by 'F' test for $n_1 = (g-1)$ and $n_2 = (r-1)(g-1)$ degrees of freedom, where, g = number of genotypes and r = number of replications. The characters showing significant differences were subjected to further analysis.

Estimation of S.E. and C. D.:

$$\text{S.E. of mean (S.E.m)} = \sqrt{\sigma_{e/r}^2}$$

$$\text{C.D.} = t \text{ at error d.f.} \times \text{S.E.m} \times \sqrt{2}$$

b. Estimation of mean and range

The mean values for each character were worked out by dividing the total by corresponding number of observations:

$$\bar{X} = \frac{1}{n} \sum_{i=1}^n X_i$$

Where,

- \bar{X} = Mean of character
 $\sum X_i$ = Total of all the observations for character
 N = Number of observations

The lowest and highest values of mean of each character represented the range.

c. Estimation of components of variation

The phenotypic and genotypic variances were calculated using the respective mean squares from variance table (Johnson *et al.*, 1955) as below.

$$\text{Environmental variance } (\sigma_e^2) = \text{EMS}$$

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{GMS} - \text{EMS}}{R}$$

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + \sigma_e^2$$

Where,

- GMS = Genotypic mean sum of square
 EMS = Error mean sum of squares
 r = Number of replications

d. Estimation of coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated as per Burton, (1952).

i) Genotypic coefficient of variation (GCV)

$$\text{GCV (\%)} = \frac{\sigma_g^2}{\bar{X}} \times 100$$

Where,

- σ_g^2 = Genotypic variance and,
 \bar{X} = Mean of character

ii) Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \frac{\sigma_p^2}{\bar{X}} \times 100$$

Where,

- σ_p^2 = Phenotypic variance and,
 \bar{X} = Mean of character

The high, medium and low GCV and PCV estimates were classified as:

Low : <10 per cent
 Medium : 10 to 20 per cent
 High : > 20 per cent

e. Estimation of heritability (b.s.)

Heritability in broad sense was estimated as suggested by Hanson *et al.*, (1956).

$$h^2(\text{b.s.}) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2 = Heritability

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The high, medium and low heritability estimates were classified on the basis of values given by Johnson *et al.*, (1955).

Low heritability = < 30 %

Moderate heritability = 30-60 %

High heritability = > 60 %

f. Genetic advance (G.A.)

Genetic advance (at 5 % selection intensity) was calculated using the formula given by Allard (1960).

i. Genetic advance (G.A.)

$$\text{G.A.} = k \times \frac{\sigma^2_g}{\sigma^2_p} \times \sqrt{\sigma^2_p}$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

k = Selection differential (at 5 % selection = 2.06)

$\sqrt{\sigma^2_p}$ = Phenotypic standard deviation

ii. G.A. as percentage of means (GAM)

$$\text{GAM} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,

$\frac{\text{G.A.}}{\bar{X}}$ = Genetic advance

\bar{X} = Character mean

GA (As percentage of mean) was classified as

Low : <10 per cent

Medium : 10 to 20 per cent

High : > 20 per cent

III. RESULTS AND DISCUSSION

1 Analysis of variance

The analysis of variance (Table 1) revealed significant genotypic differences for all twelve characters viz., plant height (cm), plant spread (cm), number of primary branches per plant, leaf length (cm), leaf breadth (cm), length of leaf sheath (cm), leaf to stem ratio, green forage yield/plant (g), dry matter content (%), dry matter yield/plant (g), crude protein content (%) and crude protein yield/plant (g) studied were significant, which indicated presence of appreciable amount of variability among *Stylosanthes* genotypes.

2 Mean performance

The mean values of forty three *Stylosanthes* genotypes for twelve different characters studied are included in the table 2.

2.1 Plant height (cm)

The average height of plants was 67.29 cm. The variation ranged from 53.60 cm (Phule Kranti) to 78.50 cm (RS-20-20). Thirty five genotypes significantly resulted in greater plant height than check Phule Kranti (53.60 cm).

2.2 Plant spread (cm)

The general mean for plant spread was 77.43 cm. The variation ranged from 64.70 cm (RS-20-4) to 96.60 cm (RS-20-24) for plant spread. Eighteen genotypes produced significantly more plant spread than check Phule Kranti (72.00 cm).

2.3 Number of primary branches per plant

The general mean for number of primary branches per plant was 11.34. The numbers of primary branches ranged from 9.50 (RS-20-37) to 14.20 (RS-20-20). The three genotypes viz., RS-20-20 (14.20), RS-20-24 (13.00) and RS-20-27 (13.20) had significantly higher number of primary branches per plant than Phule Kranti (11.34).

2.4 Leaf length (cm)

The leaf length average was 2.67 cm overall. It ranged from 2.29 cm (RS-20-36) to 3.07 cm (RS-20-24). Ten genotypes having significantly longer leaves than check Phule Kranti (2.73 cm).

2.5 Leaf breadth (cm)

The general mean for leaf breadth was 0.97 cm. It ranged from 0.75 cm (RS-20-4) to 1.13 cm (RS-20-20 and RS-20-39). None genotype produced significantly higher leaf breadth than check Phule Kranti (1.12 cm).

2.6 Length of leaf sheath (cm)

The general mean for length of leaf sheath was 2.51 cm. These lengths ranged from 2.20 cm (RS-20-17) to 2.75 cm (RS-20-21, RS-20-29 and RS-20-34). Twelve genotypes produced longer leaf sheaths than check Phule Kranti (2.40 cm).

2.7 Leaf to stem ratio

The general mean for leaf to stem ratio was 1.74. It ranged from 0.97 (RS-10-07) to 2.80 (RS-20-2). The four genotypes viz., RS-20-2 (2.80), RS-20-8 (2.58), RS-20-34 (2.63) and RS-20-40 (2.55) had significantly higher leaf to stem ratio than check Phule Kranti (2.00).

2.8 Green forage yield/plant (g)

The general mean for green forage yield/plant was 97.73 g. The yield of green forage varied from 80.85 g (RS-20-4) to 131.60 g (RS-20-24). The seventeen genotypes generated significantly higher green forage yield per plant than check Phule Kranti (84.80 g).

2.9 Dry matter content (%)

The average dry matter content across all genotypes was 28.62%. It ranged from 25.77% (RS-20-40) to 32.04% (RS-20-3). The eight genotypes viz., RS-20-2 (31.97%), RS-20-3 (32.04%), RS-20-4 (30.14%), RS-20-13 (30.65%), RS-20-19 (30.70%), RS-20-27 (30.86%), RS-20-28 (30.85%) and RS-20-37 (30.82%) had significantly higher dry matter per cent than check Phule Kranti (28.10%).

2.10 Dry matter yield/plant (g)

The general mean for yield dry matter/plant was 27.97 g. The range of dry matter yield is from 22.12 g (RS-20-31) to 36.78 g (RS-20-24). The dry matter yield/plant of the eighteen genotypes was significantly higher than check Phule Kranti (23.82 g).

2.11 Crude protein content (%)

The general mean for crude protein content was 17.37%. It ranged from 14.29% (RS-20-4) to 21.69% (RS-20-16). Fourteen genotypes had significantly higher crude protein content than check Phule Kranti (16.10%).

2.12 Crude protein yield/plant (g)

The general mean for crude protein yield/plant was 4.85 g. It ranged from 3.48 g (RS-20-4) to 7.28 g (RS-20-21). Significantly more crude protein yield/plant than check Phule Kranti (3.83 g) was produced by twenty two genotypes.

3 Components of genetic variability

By the estimation of mean coefficient of variation (genotypic and phenotypic), heritability and genetic advance variability was measured. Environment plays a paramount part in the expression of phenotypic and genotype facts, which are inferred from phenotypic observations. Hence, through biometric parameters like genotypic coefficient of variation, heritability (broad sense) and genetic advance, variability can be observed. Breeders would greatly benefit from this as they develop a selection program for crop development.

The range of mean values does not adequately represent the total variances in the studied material; hence, actual variance has to be estimated for the characters to understand the scope of existing variability. So the genotypic and phenotypic coefficient of variation which is calculated by considering the respective means, have been used for comparison. The values of coefficient of variation, heritability and genetic advance for all the 12 traits studied (Table 3), explained in detail here as follows.

3.1 Genotypic and phenotypic coefficients of variation

The genotypic and phenotypic coefficient of variation was recorded high for leaf to stem ratio (25.44% and 28.00%). Moderate genotypic and phenotypic coefficient of variation was observed in crude protein yield per plant (15.70% and 18.76%), dry matter yield per plant (11.69% and 13.90%), crude protein content (11.36% and 12.88%) and green forage yield per plant (10.62% and 12.58%). However, low genotypic and phenotypic coefficient of variation was observed for characters, plant spread (9.10% and moderate 10.13%), leaf breadth (8.85% and moderate 10.54%), number of primary branches per plant (6.15% and moderate 10.12%), plant height (7.39% and 9.49%), leaf length (7.37% and 7.64%), dry matter content (5.10% and 6.20%), length of leaf sheath (4.24% and 5.98%).

The environment had an impact on how the traits under study expressed themselves, as seen by the phenotypic coefficients of variation that were slightly greater than equivalent genotypic coefficients of variation.

The current results were in consistent with reports of Yadav *et al.* (1974) who also reported high to moderate values of PCV and GCV for green forage yield, plant height and leaf breadth and Patel *et al.* (2002) for green forage yield and dry matter yield in *Cenchrus ciliaris*. Bhagirath *et al.* (2011) reported high value of GCV and PCV for green forage yield, dry matter yield and number of leaves in *Cenchrus setigerus* genotypes. Whereas, Gore *et al.* (2016) observed high value of GCV and PCV for leaf to stem ratio and green forage yield; Kumar *et al.* (2020) for leaf to stem ratio, dry matter yield and green forage yield.

3.2 Heritability (bs) %

A measure of heritability is the amount of phenotypic variation brought on by the activity of genes. Heritability has been widely accepted by workers as a trustworthy signal for implementing effective improvements in the trait for which selection is used. The proportion of genetic variability, which parents pass down to their offspring, is shown by heritability. In general, heritability is defined by Lush (1949), as the percentage ratio of total genotypic variance to phenotypic variance.

The heritability (b.s.) estimates ranged between 36.93% to 93.20%. The character leaf length recorded the highest heritability (93.20%) followed by leaf to stem ratio (82.56%), plant spread (80.65%), crude protein content (77.69%), green

forage yield per plant (71.31%), dry matter yield per plant (70.71%), leaf breadth (70.45%), crude protein yield per plant (70.08%), dry matter content (67.70%) and plant height (60.63%). The characters length of leaf sheath (50.14%) and number of primary branches per plant (36.93%) had moderate estimate of heritability.

Present findings were in confirmatory with reports of Bhagirath *et al.* (2011) who additionally revealed significant heritability for dry matter yield, green forage yield in *Cenchrus setigerus*; Babu and Iyanar (2013) for number of leaves and crude protein content in guinea grass; Gore *et al.* (2016) for leaf to stem ratio and number of leaves in marvel grass and Udendra *et al.* (2020) for each of characteristics in grasses species.

3.3 Genetic advance

Johnson *et al.* (1955) suggested that heritability and genetic advance, when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression. It is stressed that genetic advancement and heritability should be used simultaneously since without it; heritability estimates would not be useful. Sufficient improvement through selection in genetically advanced generation cannot be achieved by high heritability alone.

The maximum value of genetic advance was observed for green forage yield (18.06) followed by plant spread (13.03). All the rest of characters recorded low values for genetic advance of which leaf breadth recorded the least value (0.15).

3.4 Genetic advance % of mean

The greatest magnitude of genetic advance as per cent mean was observed for leaf to stem ratio (47.62) followed by crude protein yield per plant (27.08), crude protein content (20.62) and dry matter yield per plant (20.24). The moderate value of genetic advance as per cent mean was observed for green forage yield per plant (18.48), plant spread (16.83), leaf breadth (15.30), leaf length (14.66) and plant height (11.86). The other traits *viz.*, dry matter content (8.64), number of primary branches per plant (7.70), length of leaf sheath (6.18) recorded low value of genetic advance as per cent mean.

High estimates of heritability along with high genetic advance as percent mean showed by leaf to stem ratio, crude protein yield per plant, crude protein content and dry matter yield per plant. High heritability coupled with moderate estimates of genetic advance as per cent mean was noticed in green forage yield per plant, plant spread, leaf breadth, leaf length and plant height. Selection for these traits will be successful since it suggests that additive gene action predominates in the control of these traits.

Comparable outcomes of high estimates of heritability with high genetic advance % of mean were in accordance with Bhagirath *et al.* (2011) for green forage yield and dry matter yield in *Cenchrus setigerus*; Babu and Iyanar (2013) for crude protein content in guinea grass; Gore *et al.* (2016) for leaf to stem ratio and number of leaves in marvel grass.

IV. CONCLUSION

Analysis of variance revealed that for all the 43 genotypes studied showed highly significant differences for all the twelve traits studied in *Stylosanthes species* indicating that there is enough variability present among all the 43 genotypes for those traits. Based on mean performance, the genotypes RS-20-2, RS-20-11, RS-20-19, RS-20-20, RS-20-21, RS-20-22, RS-20-24, RS-20-25, RS-20-26, RS-20-27, RS-20-29 and RS-20-33 were found superior for majority of the characters. There was slightly higher value for the phenotypic coefficient of variation than the corresponding genotypic coefficient of variation for all the twelve characters under study. High genotypic and phenotypic coefficient of variation was observed in leaf to stem ratio, crude protein yield/plant, dry matter yield/plant, crude protein content and green fodder yield/plant. High estimates of heritability combined with high genetic advance as per cent mean showed by leaf to stem ratio, crude protein yield/plant, crude protein content and dry matter yield/plant. It indicates effect of additive gene action for control of those traits and selection of such traits will be rewarding.

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Table 1: Analysis of variance for twelve characters of forty three *Stylosanthes* genotypes

Sr. No.	Characters	Replication	Genotypes	Error
	DF	1	42	42
1	Plant height (cm)	85.40*	65.54**	16.06
2	Plant spread (cm)	38.31	111.16**	11.91
3	No. of primary branches/plant	5.58*	1.80**	0.83
4	Leaf length (cm)	0.01	0.08**	0.003
5	Leaf breadth (cm)	0.02*	0.02**	0.003
6	Length of leaf sheath	0.04	0.03**	0.01
7	Leaf to stem ratio	0.08	0.43**	0.04
8	Dry matter content (%)	1.02	5.28**	1.02
9	Dry matter yield/plant (g)	5.42	25.79**	4.42
10	Crude protein content (%)	6.40*	8.90**	1.12
11	Crude Protein yield/plant (g)	0.08	1.41**	0.25
12	Green forage yield/plant (g)	133.38	258.90**	43.36

*, ** significant at 5% and 1% levels respectively

Table 2: Mean performance of forty three genotypes of *Stylosanthes* for green forage yield and its contributing characters

Sr. No.	Name of genotype	Plant height (cm)	Plant spread (cm)	No. of primary branches/plant	Leaf length (cm)	Leaf breadth (cm)	Length of leaf sheath (cm)	Leaf to stem ratio	Green forage yield /plant (g)	Dry matter (%)	Dry matter yield/plant (g)	Crude protein (%)	Crude protein yield/plant (g)
1	RS-20-1	68.20*	76.50	10.90	2.76	1.10	2.61	2.00	96.20	27.34	26.32	18.61*	4.90*
2	RS-20-2	71.25*	80.20*	11.00	2.76	1.08	2.63*	2.80*	101.30*	31.97*	32.37*	15.98	5.18*
3	RS-20-3	66.80*	73.80	11.40	2.78	1.07	2.47	2.40	91.60	32.04*	29.33*	16.39	4.80
4	RS-20-4	60.60	64.70	11.40	2.75	0.75	2.67*	1.78	80.85	30.14*	24.35	14.29	3.49
5	RS-20-5	62.40*	68.50	11.65	2.96*	1.08	2.49	2.07	85.20	26.81	22.87	16.97	3.88
6	RS-20-6	66.80*	73.60	11.60	2.92*	0.94	2.44	1.13	92.10	28.80	26.49	14.41	3.82
7	RS-10-07	73.30*	83.20*	11.40	2.73	0.86	2.58	0.97	104.60*	28.22	29.50*	14.98	4.44
8	RS-20-7	70.00*	78.40*	11.50	2.75	0.91	2.44	2.40	98.70*	30.02	29.60*	16.85	4.98*
9	RS-10-4	71.60*	81.20*	11.10	2.49	0.88	2.63*	1.40	101.90*	27.88	28.39*	14.48	4.11
10	RS-20-8	69.30*	77.40*	10.50	2.44	0.94	2.58	2.58*	98.65*	26.98	26.60	17.99	4.79
11	RS-20-9	60.40	70.60	10.10	2.34	0.91	2.31	1.35	87.50	29.17	25.55	17.88	4.58
12	RS-20-10	61.40	72.10	11.10	2.53	0.92	2.41	1.37	88.60	29.69	26.33	17.20	4.54
13	RS-20-11	72.80*	85.20*	10.90	2.60	0.95	2.62*	1.60	110.00*	27.11	29.79*	18.13	5.41*
14	RS-20-12	63.10*	68.00	10.60	2.48	0.76	2.50	1.50	84.90	29.32	24.98	15.98	3.97
15	RS-20-13	68.40*	76.00	11.00	2.68	0.88	2.43	1.82	95.00	30.65*	29.10*	14.52	4.22
16	RS-20-14	70.40*	77.40*	10.80	2.71	0.96	2.53	1.52	98.80*	28.10	27.78	19.74*	5.49*
17	RS-20-15	66.90*	75.70	9.60	2.93*	1.03	2.42	1.42	92.80	27.09	25.19	17.58	4.41
18	RS-20-16	65.60*	74.20	10.70	2.60	1.06	2.32	1.95	91.10	25.86	23.53	21.69*	5.11*
19	RS-20-17	65.90*	73.80	10.60	2.45	1.03	2.20	1.32	91.60	29.24	26.75	18.89*	5.05*
20	RS-20-18	66.60*	74.10	12.00	2.55	1.07	2.32	1.12	91.30	29.16	26.70	19.78*	5.29*
21	RS-20-19	75.70*	79.40*	12.00	2.69	0.90	2.64*	1.62	100.80*	30.70*	30.92*	15.96	4.94*
22	RS-20-20	78.50*	95.50*	14.20*	2.85*	1.13	2.70*	1.65	127.00*	28.14	35.71*	17.34	6.20*
23	RS-20-21	76.10*	91.70*	11.70	2.87*	1.00	2.72*	1.51	121.80*	29.40	35.77*	20.37*	7.28*
24	RS-20-22	71.90*	85.40*	12.10	2.97*	1.02	2.60	1.70	110.30*	28.09	31.06*	20.20*	6.25*
25	RS-20-23	68.50*	74.90	10.10	3.03*	0.96	2.62*	1.67	93.55	28.10	26.27	14.97	3.94
26	RS-20-24	78.20*	96.60*	13.00*	3.07*	0.85	2.59	1.12	131.60*	27.98	36.78*	17.42	6.42*
27	RS-20-25	65.00*	81.90*	12.80	2.87*	0.98	2.43	1.27	103.20*	27.43	28.27*	14.35	4.07
28	RS-20-26	73.40*	86.30*	12.70	2.81	0.89	2.50	1.95	111.00*	28.49	31.59*	15.49	4.89*
29	RS-20-27	71.50*	85.70*	13.20*	2.58	1.01	2.69*	1.67	107.60*	30.86*	33.24*	17.95	5.98*
30	RS-20-28	67.30*	79.40*	11.20	2.71	0.94	2.53	1.57	98.00	30.85*	30.22*	15.88	4.81

Sr. No.	Name of genotype	Plant height (cm)	Plant spread (cm)	No. of primary branches/plant	Leaf length (cm)	Leaf breadth (cm)	Length of leaf sheath (cm)	Leaf to stem ratio	Green forage yield /plant (g)	Dry matter (%)	Dry matter yield/plant (g)	Crude protein (%)	Crude protein yield/plant (g)
31	RS-20-29	74.90*	91.10*	12.10	2.45	0.95	2.72*	2.12	115.00*	30.10	34.63*	15.94	5.51*
32	RS-20-30	65.80*	72.00	11.80	2.31	1.04	2.34	1.55	90.20	28.23	25.45	15.01	3.80
33	RS-20-31	55.80	69.00	11.60	2.61	0.93	2.39	1.60	85.50	25.90	22.13	17.48	3.86
34	RS-20-32	59.70	73.40	11.50	2.59	0.90	2.48	1.22	92.00	26.10	24.04	20.86*	5.03*
35	RS-20-33	69.10*	83.90*	11.90	2.74	0.90	2.47	1.30	106.10*	25.93	27.49	20.43*	5.61*
36	RS-20-34	65.30*	76.20	11.70	2.88*	0.86	2.72*	2.63*	94.20	28.05	26.45	16.23	4.33
37	RS-20-35	59.90	72.80	10.70	2.52	0.90	2.62*	1.40	90.00	28.90	25.99	18.91*	4.92*
38	RS-20-36	65.00*	73.60	11.10	2.29	1.00	2.54	2.40	90.90	28.46	25.92	19.45*	5.04*
39	RS-20-37	67.30*	73.60	9.50	2.42	0.95	2.61	1.97	93.40	30.82*	28.77*	20.80*	5.98*
40	RS-20-38	57.60	67.30	9.80	2.40	0.95	2.45	1.63	84.50	29.82	25.20	14.69	3.70
41	RS-20-39	65.80*	73.40	10.50	2.82	1.13	2.39	2.40	94.20	28.91	27.22	19.85*	5.40*
42	RS-20-40	66.00*	72.00	11.40	2.54	1.12	2.34	2.55*	94.00	25.77	24.27	18.84*	4.56
43	P. Kranti	53.60	70.00	11.10	2.73	1.12	2.40	2.00	84.80	28.10	23.82	16.10	3.83
General mean		67.29	77.43	11.34	2.67	0.97	2.51	1.74	97.73	28.62	27.97	17.37	4.85
S.E. ±		2.83	2.44	0.64	0.04	0.04	0.08	0.14	4.66	0.71	1.49	0.75	0.35
C.D. 5%		8.09	6.96	1.84	0.11	0.11	0.21	0.41	13.29	2.03	4.24	2.13	1.01
C.V. %		5.96	4.46	8.03	1.99	5.73	4.22	11.69	6.74	3.52	7.52	6.09	10.26

* significant at 5% level

Table 3: Estimates of variability parameters for green forage yield and its contributing characters in forty three *Stylosanthes species* genotypes

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	ECV (%)	Heritability h ² (b.s.) (%)	Genetic Advance	Genetic Advance as % of mean
1	Plant height (cm)	67.29	53.60 - 78.50	7.39	9.49	5.96	60.63	7.98	11.86
2	Plant spread (cm)	77.43	64.70 - 96.60	9.10	10.13	4.46	80.65	13.03	16.83
3	No. of primary branches/plant	11.34	9.50 - 14.20	6.15	10.12	8.03	36.93	0.87	7.70
4	Leaf length (cm)	2.67	2.29 - 3.07	7.37	7.64	1.99	93.20	0.39	14.66
5	Leaf breadth (cm)	0.97	0.75 - 1.13	8.85	10.54	5.73	70.45	0.15	15.30
6	Length of leaf sheath	2.51	2.20 - 2.72	4.24	5.98	4.22	50.14	0.16	6.18
7	Leaf to stem ratio	1.74	0.97 - 2.80	25.44	28.00	11.69	82.56	0.83	47.62
8	Dry matter content (%)	28.62	25.77 - 32.04	5.10	6.20	3.52	67.70	2.47	8.64
9	Dry matter yield/plant (g)	27.97	22.12 - 36.78	11.69	13.90	7.52	70.71	5.66	20.24
10	Crude protein content (%)	17.37	14.29 - 21.69	11.36	12.88	6.09	77.69	3.58	20.62
11	Crude protein yield/plant (g)	4.85	3.48 - 7.28	15.70	18.76	10.26	70.08	1.31	27.08
12	Green forage yield/plant (g)	97.73	80.85 - 131.60	10.62	12.58	6.74	71.31	18.06	18.48

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