

## GENETIC VARIABILITY STUDIES FOR YIELD AND QUALITY COMPONENTS IN *CENCHRUS* GRASS (*CENCHRUS* SPP.)

ADLIN\*. S, C. BABU AND P. SUMATHI

Department of Forage Crops,  
Centre for Plant Breeding and Genetics  
Tamil Nadu Agricultural University, Coimbatore  
\*(e-mail : [adlins23@gmail.com](mailto:adlins23@gmail.com))

(Received : 16 October 2018; Accepted : 18 December 2018)

### SUMMARY

The present study was conducted to assess the magnitude of genetic variability in *Cenchrus* grass genotypes for fodder yield, its component traits and quality parameters. Significant genetic variability was observed among the germplasm studied. High PCV and GCV (>20 %) were observed for the traits like leaf length, leaf width, number of tillers per plant, 100 seed weight, green fodder yield per plant, crude fat content, calcium and magnesium content. In the present investigation, high heritability coupled with high genetic advance over mean was observed for the characters plant height, leaf length, leaf width, panicle length, internode length, number of tillers per plant, days to 50 per cent flowering, 100 seed weight, crude protein, crude fat, calcium, magnesium content and green fodder yield per plant suggesting the influence of additive gene action. Hence these traits may be considered as selection indices for *Cenchrus* grass improvement programme.

**Key words :** *Cenchrus* grass, PCV, GCV, heritability, genetic advance

*Cenchrus* grass (*Cenchrus* spp.) is a versatile grass species originated from grasslands of Africa. *Cenchrus* grass for many centuries has been the predominant plant species in "Korangadu", the traditional pastureland farming system existing in the semi-arid tract of Tamil Nadu state in South India (Vivekanandan, 2007). Though *Cenchrus* grass is in cultivation and a good variability is available, concerted efforts have not been made adequately to categorize this variability. As a result, the genetic improvement in *Cenchrus* grass for fodder yield and quality has become impasse. Hence an attempt was made to study the variability within the *Cenchrus* grass germplasm accessions for different biometrical traits which could be further utilized in breeding programme.

### MATERIAL AND METHODS

The experimental material consisted of 60 germplasm accessions of *Cenchrus* grass maintained at Department of Forage Crops, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. The accessions were planted using rooted slips on one side of the ridges of 4 metres length, adopting a spacing of 60×50 cm in a Randomized Block Design with two replications. All the agronomic practices were followed to maintain the

crop stand. The biometrical observations on fodder yield were recorded on single plant basis at the time of harvest. For recording single plant observations, three plants from each entry/replication were randomly selected. Average of these three plants in respect of plant height (cm), leaf length (cm), leaf width (cm), panicle length (cm), internode length (cm), number of nodes in main tiller, number of tillers per plant, days to 50% flowering, 100 seed weight (mg) and green fodder yield per plant (g) was observed. Same plants were subjected for the estimation of quality parameters such as crude protein (%), crude fibre (%), crude fat (%), calcium (%) and magnesium content (%). Statistical methods suggested by Burton (1952) for variability, Lush (1940) for heritability, Johnson *et al.* (1955) for genetic advance as percent of mean were adopted to find out the respective estimates. Further categorization of estimates was made based on the suggestions of Sivasubramanian and Madhavamenon (1973) for variability, Johnson *et al.* (1955) for heritability and genetic advance as percent of mean.

### RESULT AND DISCUSSION

Analysis of variance revealed highly significant differences among accessions for all the characters under investigation thereby indicating the

presence of a considerable magnitude of genetic variability among the experimental material (Table 1). The estimates of genetic parameters like phenotypic and genotypic coefficient of variation, heritability and genetic advance are presented in Table 2.

**Variability :** In general, the estimates of phenotypic coefficient of variation (PCV) were higher than the estimates of genotypic coefficient of variation (GCV) for all the traits under study indicating the environmental influence over the traits.

In the present study, high PCV and GCV (>20 %) was recorded for eight characters viz., leaf length, leaf width, number of tillers per plant, 100 seed weight, green fodder yield per plant, crude fat content, calcium and magnesium content and is depicted in Fig. 1. This discerning variability suggesting a greater scope of improvement for these traits and these traits could be used to make the selection more effective. Concomitant results were obtained by Jain *et al.* (2012), Jayabharathi (2015), Gore *et al.* (2016) and Santhosh *et al.* (2017).

Moderate levels of PCV and GCV were recorded for plant height, panicle length, internode length, days to 50 per cent flowering and crude protein content. Similar results were reported by Shanmuganatham *et al.* (2006), Jain *et al.*(2012),

Ramakrishnan *et al.*(2013), Jayabharathi (2015), Rana *et al.*(2016) and Santhosh *et al.* (2017).The moderate genotypic coefficients of variation pointing that moderate improvement of these traits by selection. Selection will be effective based on the heritable nature of these traits.

The characters viz., number of nodes and crude fibre showed moderate PCV and low GCV. Hence, direct selection may not be rewarding for improving crude fibre content and number of nodes in *Cenchrus* grass. It was observed that the genotypic coefficient of variation varied with the characters and this has brought out the presence of genetic diversity for different characters.

**Heritability and genetic advance :** The traits viz., plant height, leaf length, leaf width, panicle length, internode length, number of tillers per plant, days to 50 per cent flowering, 100 seed weight, crude protein, crude fat, calcium, magnesium contents and green fodder yield per plant recorded high heritability coupled with high genetic advance as per cent of mean and is furnished in Fig.2. This indicated the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance, since selection of these traits in breeding programme

TABLE 1  
Analysis of variance for different characters in Cenchrus grass genotypes

Source of variation Characters	d. f.	Mean sum of squares														
		PH	LL	LW	PL	IL	NN	NT	DF	SW	CP	CF	CFT	Ca	Mg	GFY
Treatment	59	322.25**	78.88*	0.09*	7.24*	1.45*	1.23*	524.36**	35.15*	13969.05**	4.60*	14.33*	1.59**	0.04**	0.026*	27066.98**
Error	59	22.985	12.38	0.014	1.02	0.27	0.22	62.63	7.26	1139.19	0.68	3.38	0.19	0.004	0.004	3762.38

\*, \*\*Significant at 5 and 1 per cent level, respectively.

(PH- Plant height, LL- Leaf length, LW- Leaf width, PL- Panicle length, IL- Internode length, NN- Number of nodes, NT- number of tillers per plant, DF - days to 50 % flowering, SW- seed weight, CP- Crude protein, CF- Crude fibre, CFT- Crude fat, Ca- Calcium, Mg- Magnesium, GFY- Green fodder yield).

TABLE 2  
Estimation of genetic variability parameters in Cenchrus grass genotypes

S. No.	Characters	PV	GV	PCV (%)	GCV (%)	h <sup>2</sup> bs (%)	GA	GAM
1.	Plant height (cm)	172.62	149.63	14.87	13.84	86.68	23.46	26.55
2.	Leaf length (cm)	45.64	33.25	24.52	20.92	72.85	10.14	36.79
3.	Leaf width (cm)	0.05	0.04	26.64	22.76	72.99	0.34	40.06
4.	Panicle length (cm)	4.14	3.11	17.76	15.40	75.22	3.15	27.52
5.	Internode length (cm)	0.86	0.59	14.28	11.81	68.35	1.31	20.11
6.	Number of nodes	0.73	0.50	10.68	8.89	69.35	1.22	15.25
7.	Number of tillers per plant	293.50	230.87	35.00	31.05	78.66	27.76	56.72
8.	Days to 50% flowering	21.21	13.95	15.01	12.17	65.76	6.24	20.33
9.	100 seed weight (mg)	7554.12	6414.93	31.36	28.90	84.92	152.04	54.86
10.	Crude protein (%)	2.64	1.96	17.52	15.09	74.13	2.48	26.76
11.	Crude fibre (%)	8.86	5.47	10.68	8.39	61.80	3.79	13.59
12.	Crude fat (%)	0.89	0.70	31.92	28.23	78.24	1.52	51.44
13.	Calcium (%)	0.03	0.02	27.59	25.47	85.17	0.29	48.41
14.	Magnesium (%)	0.02	0.01	30.35	25.78	72.16	0.18	45.11
15.	Green fodder yield/ plant (g)	15414.68	11652.30	32.04	27.85	75.59	193.34	49.89

would facilitate the improvement of both fodder yield and quality. The obtained results are in accordance with the results of Khan *et al.* (2002), Bedis *et al.* (2006), Bahadur *et al.* (2008), Vinodhana *et al.* (2013) and Santhosh *et al.* (2017).

High heritability with moderate genetic advance as percent of mean was recorded for number of nodes and crude fibre content. But Jayabharathi (2015) in *Cenchrus* spp. reported high heritability coupled with high genetic advance as per cent of mean for crude fibre content. This inferred that selection would be effective for these traits when favorable environment prevails as these traits appear to be under the control of non-additive gene actions.

In the present study, high heritability coupled with high genetic advance as per cent of mean was recorded by plant height, leaf length, leaf width, panicle length, internode length, number of tillers per plant, days to 50 per cent flowering, 100 seed weight, crude protein, crude fat, calcium, magnesium contents and green fodder yield per plant which implies that these characters were under the control of additive type of gene action. Therefore, selection of these traits would offer scope for improvement of both green fodder yield and quality in *Cenchrus* grass.

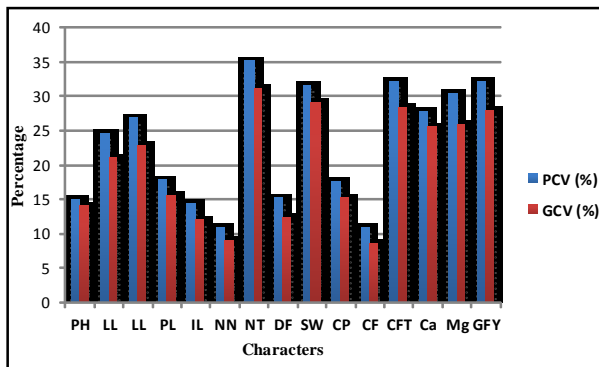


Fig. 1. Phenotypic and Genotypic Coefficient of Variation for 15 quantitative characters

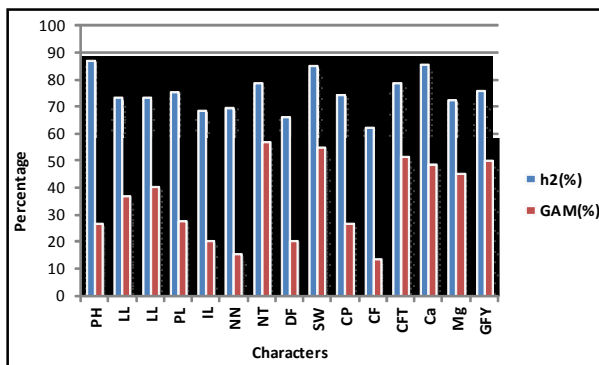


Fig. 2. Heritability and genetic advance as percentage of mean for 15 quantitative characters

## REFERENCES

- Bahadur, R.N and G.P. Lodhi. 2008 : Character association and path coefficient analysis in forage oat (*Avena sativa* L.). *Nat. J. Pl. Impv.* **10** : 30-33.
- Bedis, M.R., B.N. Ganvirand and P.P. Patil. 2006 : Genetic variability in finger millet. *J. Maharashtra Agric. Univ.*, **31** : 369-370.
- Burton, G.W. 1952 : Quantitative inheritance in grasses. *Proc. 6<sup>th</sup> Int. Grassland Cong.*, **1**: 24-84.
- Gore, V.R., P.P. Surana, and G.C. Shinde. 2016 : Genetic variability studies for forage yield and associated traits in marvel grass (*Dichanthium* spp.). *Forage Res.*, **42** : 172-175.
- Jain, S.K and P.R. Patel. 2012 : Genetic variability in land races of forage sorghum (*Sorghum bicolor* (L.) Moench) collected from different geographical origin of India. *Inter. J. Agric. Sci.* **4** : 182-185.
- Jayabharathi, P. 2015 : Genetic diversity assessment and screening of drought tolerant accessions in the genetic stocks of *Cenchrus* spp. analysis. M. Sc., (Ag.), Thesis, TNAU, Coimbatore.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955 : Estimation of genetic variability and environmental variability in soybean. *Agron. J.*, **47** : 314-318.
- Khan, A.K.F and K. Sukumar. 2002 : Variability, heritability, genetic advance in Napier grass. *Madras Agric. J.*, **88** : 461-464.
- Lush, J.L. 1940 : Intra-sire correlation and regression of offspring on dams as a method of estimating heritability of characters. *Proc. Amer. Soc. Anim. Prod.*, **33** : 293-301.
- Ramakrishnan, P., C. Babu and K. Iyanar. 2013 : Genetic diversity in Guinea grass (*P. maximum* Jacq.) for fodder yield and quality using morphological markers. *Int. J. Plant Biol Res.*, **2** : 1006-1011.
- Rana, H.R., K.N. Prajapathi, K.J. Suthar and H.R. Kher. 2016 : Study of variability, correlation and path analysis in forage sorghum. *The Bioscan.*, **8** : 259-263.
- Santhosh, K., C. Babu, S. Revathi and P. Sumathi. 2017 : Estimation of genetic variability, heritability and association of green fodder yield with contributing traits in fodder pearl millet. *Inter. J. Adv. Biol. Res.* **7** : 119-126.
- Shanmuganathan, M., A. Gopalan and K. Mohanraj. 2006 : Genetic variability and multivariate analysis in pearl millet (*Pennisetum glaucum* (L.) germplasm for dual purpose. *J. Agric. Sci.*, **2** : 73-80.
- Sivasubramanian, S. and Madhava Menon, P. 1973 : Genotypic and phenotypic variability in rice. *Madras Agric. J.*, **60** : 1093-1096.
- Vinodhana, N.K., M. Sathya and P. Sumathi. 2013 : Hierarchical clustering of pearl millet (*Pennisetum glaucum* (L.) R. Br) inbreds for morpho-physiological traits. *Int. J. Curr. Microbiol. App. Sci.*, **2** : 647-652.
- Vivekanandan, P. 2007 : Korangadu: A traditional pastureland farming system in the drylands of Tamil Nadu, South India. Sustainable-agriculture & Environmental Voluntary Action, Madurai, India.