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VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN FODDER PEARL MILLET

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ABSTRACT

Genotypic coefficient of variation, heritability and genetic advance were assessed in 28 genotypes of fodder pearl millet (Pennisetum glaucum.) The difference between the genotypes were-highly significant for all the 18 characters studied. Among the characters, stem weight, green fodder yield per plant, leaf weight, number of tillers per plant and number of leaves per plant showed high genotypic coefficients of variation. Stem weight, green fodder yield per plant, leaf weight, leaf stem ratio, plant height on the 30th day, plant height at harvest, crude protein content and dry matter content had high heritability combined with high genetic advance, These traits are the most suitable for improvement through selection.

KEY WORDS: Fodder pearl millet, Variability, Heritability, Genetic advance.

Pearlmillet (Pennisetum glaucum) an annual diploid (2n=14) assumes specific importance as a major grain cum fodder crop of the arid and semi-arid tracts of India and Africa. It can be fed to cattle without harm at any stage of growth (Krishnaswamy, 1962). Though it has dual utility value, breeding in the past was mainly concerned with increasing its grain yield but fodder aspect was considered as secondary. Studies on variability in Pennisetum glaucum have so far been carried out with grain types and such a study involving fodder types will be more purposeful and effective. Keeping this in view, 28 fodder pearlmillet genotypes were subjected to detailed investigation on variability, heritability and genetic advance.

MATERIALS AND METHODS

A set of 28 genotypes of fodder pearlmillet obtained from the breeder, All India Co-ordinated Research Project on Forage crops, Coimbatore, were grown at the school of Genetics, Tamil Nadu Agricultural University, Coimbatore during rabi 1991 in randomised block design with two replications. Selfed seeds of each genotype were sown with the spacing of 30 cm between rows and 15 cm between plants. Data were recorded at the time of 50 per cent flowering from five randomly selected competitive plants in each genotype in each replication for green fodder yield and its component characters. Representative samples from each replication were taken after the harvest for estimating dry matter, ash and crude fat contents (AOAC, 1970), crude protein content (Humphries, 1956), crude fibre content (Goering and Vansoest, 1970) and oxallic acid content (Talapatra et al., 1948). Standard statistical procedures were used for the analysis of variance, genotypic and phenotypic coefficients of variation (Burton, 1952), heritability (Hanson et al., 1956) and genetic advance (Lush, 1949; Johnson et al., 1955)

Table 1. Phenotypic and genotypic coefficients of variation, heritability and genetic advance for eighteen characters in fodder pearl millet

Characters	Mean	PCV	GCV	h2	GA	GA as per cent of mean
Plant height on 30th day (cm)	43.44	14.68	14.44	96.69	12.72	29.28
Days to 50 per cent flowering	48.75	6.70	5.90	77.54	5.22	10.71
Plant height at harvest (cm)	72.46	13.44	13.30	97.94	19.67	27.14
Number of tillers per plant	3.43	32.11	22.45	48.89	1.11	32.42
Number of leaves per plant	39.95	28.07	22.03	61.59	14.24	35.65
Leaf length (cm)	62.41	7.79	7.34	88.77	8.90	14.27
Leaf breadth (cm)	2.87	11.97	8.68	52.58	0.37	12.98
Stem diameter (cm)	0.93	15.58	8.33	28.57	0.09	9.73
Leaf weight (g)	60.22	25.65	23.21	81.84	26.07	43.29
Stem weight (g)	74.47	29.21	28.91	. 97.95	43.31	58.94
Leaf stem ratio	18.0	22.76	19.13	71.43	00.27	33.33
Green fodder yield per plant (g)	136.89	24.31	23.64	94.50	64.78	47,32
Dry matter content (%)	16.14	14.86	13.71	85.07	4.21	26.07
Ash content (%)	13.13	13.04	9.86	57.21	2.02	15.38
Crude protein content (%)	11.47	13.00	12.93	99.05	3.04	26.54
Crude fat content (%)	2.76	19.35	13.46	48.26	0.53	19.26
Crude fibre content (%)	24.12	15.49	12.49	64,99	5.01	20.76
Oxalic acid content (%)	1.84	16.12	9.41	34.02	0.21	11.29

RESULTS AND DISCUSSION

Data on mean, variability, heritability and genetic advance as percentage of mean are presented in Table 1. The analysis of variance revealed significant differences among genotypes for all the eighteen characters studied. The characters stem weight, green fodder yield per plant, leaf weight, number of tillers per plant and number of leaves per plant showed high PCV and GCV estimates. This suggests that the selection these characters would facilitate based on successful isolation of desirable types. Similar findings were reported for characters like green fodder yield, number of leaves and tillers, leaf weight, stem weight, days to 50 per cent flowering and stem diameter (Gupta and Athwal, 1966; Gupta and Sidhu, 1969; Sangha and Singh, 1973; Tyagi et al., 1980; Kumar, 1982; Shukla and Dua, 1983).

High heritability estimates were observed for crude protein content, stem weight, plant height on 30th day and green fodder yield per plant, leaf length, dry matter content, leaf weight, days to 50 per cent flowering and leaf stem ratio and selection based on phenotypic value would prove to be effective. Similar results were obtained by Gupta and Gupta (1971), Gupta and Nanda (1971), Hooda et al. (1978) and Shukla and Dua (1983).

Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson et al., 1955). In the present study, the highly heritable characters like stem weight, green fodder yield per plant, leaf weight, leaf stem ratio, plant height on the 30th day and at harvest, crude protein content and dry matter content had high genetic advance as per cent of mean indicating that these characters were under the influence of additive gene action (Johnson et al., 1955). Crude fibre content, ash content and crude fat content had moderate heritability coupled with moderate genetic advance, while moderate heritability and high genetic advance were recorded for number of leaves and tillers per plant rendering them unsuitable for improvement through selection. Low heritability combined with low genetic advance as percentage of mean was noted for stem diameter. It indicates that the scope for improving this trait through selection is very much limited and this may be attributed to the non-additive gene action (Johnson et al., 1955)

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ANALYSIS OF GENETIC DIVERGENCE IN FODDER PEARL MILLET

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ABSTRACT

Genetic diversity in fodder pearl millet (Pennisetum glaucum) was studied with 28 genotypes of different origin. The genotypes could be grouped into 5 distinct clusters. The clustering pattern showed that geographic diversity is not an index of genetic diversity. Crude protein content, leaf weight and dry matter content were important contributors to the divergence. On the basis of genetic distance and cluster mean values, nine genotypes have been identified for hybridisation and selection for the desirable traits.

KEY WORDS: Fodder Pearl Millet, Genetic Divergence, Analysis

Genetic divergence as measured Mahalanobis' (1936) generalized distance (D²) has been one of the important statistical tools to provide a rational basis for selection of parents in breeding programmes. A number of pioneering workers (Moll et al., 1962; Murthy and Arunachalam, 1966) have utilised this method of quantifying the degree of divergence between biological populations at the genotypic level and its role in breeding improved types. An attempt was made in this investigation to study the nature and magnitude of genetic divergence for green fodder yield and other related characters in fodder pearl millet (Pennisetum glaucum) genotypes.

MATERIALS AND METHODS

A set of 28 genotypes of fodder pearl millet obtained from the breeder, All India Co-ordinated Research Project on Forage Crops, Coimbatore were grown at the School of Genetics, Tamil Nadu Agricultural University during rabi 1991 in randomised block design with two replication. Selfed seeds of each genotype were sown with the spacing of 30cm between rows and 15cm between plants. Observation were made at the time of 50 per cent flowering from five randomly selected competitive plants for green fodder yield and its component characters. Representative plant samples from each replication were taken after the