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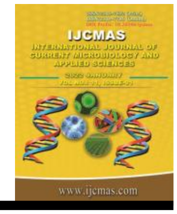

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Genetic Variability Study in ICRISAT Pearl Millet [*Pennisetum glauccum* (L.) R. Br.] Accessions for Green Fodder Yield and Related Traits

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A B S T R A C T

A field experiment was conducted with fifty pearl millet genotypes raised in a randomized block design with two replications at D block Research Farm, Department of Plant Breeding and Genetics, AC &RI, Killikulam to study the green fodder yield and its related traits. High magnitude of variation in the experimental material of this study was reflected by high values of mean and range for almost all the 12 characters. The results indicated that the genotypes IP11840, IP15257, IP11839, IP15322, IP20347, IP15341, IP10437 and IP17428 were the best identified genotypes for green fodder yield coupled with tallness, increased number of tillers per plant, more leaf length, more number of leaves per plant, more stem girth and internode length, more LAI, more leaf stem ratio which indicated that these genotypes can be selected as parents in pearl millet improvement programme for the development of elite varieties/hybrids. The traits plant height, number of tillers per plant, leaf length, leaf area index, number of leaves per plant, stem girth, internode length, dry fodder yield and green fodder yield exhibited high GCV and PCV. It showed more amount of genetic variations present between. Hence, selection towards these components will lead to development of dual purpose pearl millet varieties/hybrids.

Introduction

Currently, India has deficit of more than 50 per cent of green fodder and 25 per cent of dry fodder despite being the first in cattle and buffalo population (http//www.indiastat.com) in world. To sustain this animal population and to maintain its productivity, a large quantity of green fodder is required. Pearlmillet is one of the gifted crop plants of the tropical regions and that provide food, feed, stover/ dry fodder and fuel to millions of poor farmer families and their livestock. Its varieties are also cultivated for green fodder. Its grains are highly nutritious with high levels of metabolizable energy and protein, have high densities of iron and zinc, and more balanced amino acid profile than maize or sorghum. Grains are mainly used for human consumption in the form of diverse food, mostly as leavened and unleavened flat breads and porridges. Pearlmillet uses less water per unit of forage production, tolerates heat and drought. Therefore, it is generally grown in areas where environmental conditions, especially rainfall, temperature and soil fertility are too harsh to grow other cereals (Hanna and Cardona, 2001; Khairwal *et al.,* 2009; Amit *et al.,* 2012).

It is a well known fact that pearl millet is an excellent forage crop and it has great potential among the millets, as it is a rainy season cereal grass with large stem, leaves and heads with highly vigorous and quick growing habit. Its fodder is low in anti-quality factors like hydrocyanic acid and oxalic acid, while rich in protein, calcium, phosphorus and other minerals (Gupta, 1975; Arya *et al.,* 2009a and Amit *et al.,* 2012). Its green fodder is rich in protein, calcium, phosphorous and other minerals with oxalic acid within safe limits. A significant portion of pearl millet grain is also used for non-food purposes such as poultry feed, cattle feed and alcohol extraction.

Green fodders play important role in the profitability of the livestock production. Success of dairy farming is largely depends on the feed and fodder of high nutritional value. Scarcity of fodder is a major limiting factor in the livestock community due to increasing demand on land for food grains, oil seeds and pulses production.

At present, India faces net deficit of 35.7% green fodder, 10.9% dry crop residues and 44% concentrate feeds. (https://icar.org.in/files/Vision-2050-ICAR.pdf). To meet this requirement, high/multi-cut fodder yielding and nutritious varieties of fodder crops need to be identified. Under such circumstances pearl millet fits well for this purpose, as its high tillering potential and quick regenerative ability assures the possibility of multi-cutting which can assure year round supply of green/dry forage. Hence, there is urgent need to enhance productivity of forage crop to sustain feed for the livestock. The dry fodder and straw of pearl millet is also used to feed the livestock in marginal production environments, particularly during the dry season when green fodder/grazing is limited. Thus, the gap in fodder demand and its supply can be bridged to some extent by developing high fodder yielding cultivars of pearl millet (Arya *et al.,* 2009a).

Crop improvement program requires information on genetic variation, nature of association among yield and its component traits, and how traits influence each other to finally express the trait of interest. Limited correlation studies have been conducted on forage type pearl millet (Bhagirath *et al.,* 2007 and Kumar *et al.,* 2017) and in majority of path analysis studies in pearl millet, green forage yield (GFY) was considered as dependent variable for investigating direct and indirect effects of forage yield components traits in pearl millet (Govintharaj *et al.,* 2018).

Investigation on forage quality traits of pearl millet have indicated significant variation among dual-purpose hybrids, populations/OPVs and top cross hybrids (Bidinger and Blummel, 2007; Bidinger *et al.,* 2010; Rai *et al.,* 2012; Govintharaj *et al.,* 2018). Significant variability has been observed for biomass traits and also stover nitrogen, metabolizable energy and in vitro organic matter digestibility in new pearl millet germplasm (Gupta *et al.,* 2015 and Govintharaj *et al.,* 2018). Present study was aimed to determine the variability among forage related biomass to understand criteria for selection to identify the desirable genotypes with high yielding potential for forage quantity in crop improvement program of pearl millet.

Therefore, the present investigation was undertaken to study the genetic variability, heritability for green fodder yield and its components in fodder pearl millet genotypes.

Materials and Methods

The experimental material used in this study consisted of 50 promising Pearl millet genotypes received from ICRISAT, Hyderabad and were evaluated during *kharif* season. (June to August 2018). The details of the genotypes are given in Table.1. The experiment was carried out in Randomized Block Design with three replications. The seeds of 50 genotypes were directly sown in the field with a spacing of 45cm row to row and 15cm plant to plant spacing. Size of the field was 6×6 m. Each plot comprised of six lines. Normal and uniform cultural operations were followed to raise a good crop. The observations were recorded on the basis of five selected plants and average was taken for days to 50% flowering, plant height, number of tillers per plant, leaf length, leaf width, number of leaves per plant, stem thickness, internode length and spike length., green fodder yield and dry fodder yield. Mean values were used to compute the genetic parameters and statistical analysis of data was carried out for each character (Panse and Sukhatme 1967). The method suggested by Burton and De Vane (1953) was followed for computation of the GCV and PCV. Heritability in the broad sense was calculated according to the formula given by Allard (1960) and the genetic advance was estimated by the following formula given by Burton (1952). The mean values of individual genotypes were subjected to statistical analysis using statistical software's GENRES, Meta R and R studio software's.

Results and Discussion

Based on the mean performance, 50 pearl millet genotypes differed highly for all the 12 characters studied. Large variation among genotypes were found for the traits like plant height (110.31 cm. to 382.3 cm.), number of tillers per plant (3.0 –18.5), number of nodes per tiller (28.2 - 291.8) number of leaves per plant (28 – 165.6), leaf length (19.21 cm. – 62.64 cm.), leaf breadth (2.01 to 4.16 cm.), Internode length (7.52 - 28.62 cm), Leaf Area Index (1.36 – 64.40), Leaf stem ratio (0.2 – 0.36), stem girth (1.3 – 6.3cm),green fodder yield per plant (130 g. – 970g.) and dry matter yield per plant (77g. – 157g). This wide range of mean values observed for these characters would offer scope of selection for development of desirable genotypes and the significant variation could be attributed to the composition of the population, which is made up of diverse genotypes in the past.

The PCV were slightly higher than GCV indicating little influence of environment on the expression of characters (Table 2). In pearl millet, high PCV and GCV was recorded for all the traits studied except for leaf stem ratio. PCV and GCV was higher for all the traits discerning more variability and suggesting the greater scope of improvement for these traits and these traits could be used to make the selection effective. In the present study the trait green fodder yield, number of leaves per plant and dry matter yield per plant exhibited higher PCV and GCV. These findings were in accordance with Santosh *et al.,* (2017) and Thomas *et al.,* (2018). Moderate PCV and GCV was observed for the trait leaf width.

This indicates these characters can be improved by the vigorous selection. In Napier grass Santhosh *et al.,* 2017 observed moderate PCV and moderate GCV for 10 characters viz., plant height, number of nodes in main culm, number of tillers per plant, number of leaves per tiller, leaf width, leaf weight, stem weight, leaf stem ratio, dry matter per cent and crude protein content. In pearl millet moderate GCV and PCV were observed for plant height, leaf length, dry matter per cent and leaf width as reported by Bika *et al.,* 2015. The trait leaf stem ratio exhibited low PCV and GCV. This indicated the environmental influence to be more and selection may not be possible for its improvement. Contrary reports were given by Santhosh *et al.*, 2017 and Thomas *et al.*, 2018. High amount of GCV and PCV suggested greater scope of selection of superior genotypes for these traits.

The determination of heritable portions is not based on only the estimation of PCV and GCV, where the utility of heritability is increased when it is used to estimate genetic advance (Vinodhana *et al.,* 2013).

Table.1 List of ICRISAT Pearl millet accessions used in the current study

S. No.	Accessions	S.No.	Accessions
1	IP3080	26	IP15320
2	IP3476	27	IP15321
3	IP3604	28	IP15322
4	IP3613	29	IP15341
5	IP3616	30	IP15342
6	IP3625	31	IP15343
7	IP3627	32	IP15344
8	IP3628	33	IP15348
9	IP3636	34	IP15351
10	IP3645	35	IP15369
11	IP3663	36	IP15710
12	IP3665	37	IP17428
13	IP5836	38	IP20273
14	IP8327	39	IP20339
15	IP10437	40	IP20346
16	IP11839	41	IP20347
17	IP11840	42	IP20348
18	IP15257	43	IP20350
19	IP15285	44	IP20379
20	IP15288	45	IP20539
21	IP15290	46	IP20540
22	IP15301	47	IP20585
23	IP15302	48	IP21226
24	IP15306	49	PT4806
25	IP15307	40	PT4881

Table.2 Analysis of variance for different characters in Pearl millet

Traits	Mean sum of squares		
	Replications (df = 1)	**Genotypes (df = 1)**	**Error (df = 1)**
DFF	37.96	112.19**	17.51
PH	10.83	7052.26**	29.38
NTPP	6.68	29.88**	2.44
LL	22.74	271.94**	8.75
LW	0.05	0.66**	0.14
LAI	0.07	125.95**	1.21
NLPP	5.28	5791.48**	16.08
SG	0.95	5.24**	0.1
LSR	0.04	1.77**	0.003
INL	40.1	225.03**	0.17
DFY	17.81	3176.09**	8.63
GFY	0.81	9222.87**	0.7

Table.3 Genetic analysis in Pearl millet genotypes

Traits	Mean	Range	PCV (%)	GCV (%)	Heritability (%)	Genetic advance	Genetic advance as percentage of mean (%)
DFF	59.2	40-70	13.43	13.12	95.38	14.57	26.4
PH	207.91	110.31-383	33.41	28.05	70.45	85.4	48.49
NTPP	9	3-12	44.58	33.22	55.52	4.38	50.99
LL	41	11.21-62.64	29.11	28.65	96.85	20.84	52.55
LW	3.0	2 – 4.16	19.16	11.37	29.3	4.57	11.56
LAI	11.4	10.3-60.4	35.39	39.02	83.8	7.92	30.15
NLPP	87.3	10-160.5	62.22	62.04	97.36	89.14	97.45
SG	3.6	1.3 -6.3	43.55	42.52	95.32	3.15	85.51
LSR	0.23	0.2 – 0.36	9.59	7.46	60.54	7.18	11.96
INL	18.5	7.5 – 28.6	23.91	22.46	88.3	7.42	40.03
DFY	212.56	77-157.6	56.3	56.26	93.86	84.67	115.81
GFY	677.26	130- 970	58.85	58.79	99.99	92.22	121.22

DFF= Days to 50% flowering, PH=Plant height (cm), NTPP=Number of tillers per plant, LL= leaf length(cm), LW= leaf width (cm), LA= leaf area, NLPP=Number of leaves per plant, SG = stem girth, LSR = Leaf stem ratio, DFY – dry fodder yield(g) GFY = Green fodder yield(g)

The heritability estimates for the quantitative traits ranged from 29.3 (leaf width) to 97.36 (number of leaves per plant). High heritability (h2) with high genetic advance showed the predominance of additive gene action and greater response to phenotypic selection and improvement of such traits could be anticipated.

In this study, the high heritability combined with high genetic advance was observed for plant height, number of leaves per plant, green fodder yield and dry matter yield which showed that these characters were controlled by additive gene effects and phenotypic selection for these characters were likely to be effective. Similar results were reported by Santhosh *et al.*, 2017 and Thomas *et al.*, 2018. In this condition, selection will be more effective. Moderate heritability and genetic advance was observed for the trait leaf width and leaf stem ratio. In general the heritability estimates were high for most of characters.

High heritability was reported for leaf: stem ratio by Shanmuganathan *et al.*, (2006) and Ghazy *et al.*, (2012); for green fodder yield by Lakshmana and Guggari (2001); Khatri *et al.*, (2002); Bochaliya (2005); Shanmuganathan *et al.,* (2006); Vidyadhar *et al.*, (2007) and Gangaram (2011); for dry matter yield by Rathore (1993) and Nagar *et al.*, (2006) and for leaf area by Bochaliya (2005). Genetic advance as per cent of mean was high for all traits except stem thickness. Stem thickness recorded moderate level of genetic advance as per cent of mean (Bika *et al.*, 2015).

Heritability estimates along with genetic advance were more useful than heritability estimates alone in predicting this response to selection. High heritability along with high genetic advance as per cent of mean was observed for plant height, number of leaves per plant, green fodder yield and dry matter yield. In this condition, selection will be more effective. Moderate heritability and genetic advance was observed for the trait leaf width and leaf stem ratio where the response to selection will be poor.

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