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Genetic Variability in Distinct Genotypes of Forage Pearl Millet (*Pennisetum glaucum* (L.) R. Br.) for Forage Yield and Forage Yield Attributing Traits

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Abstract

The experiment was conducted during *kharif* (July–October, 2023) at Centre for Forage Research, S. D. Agricultural University, Sardarkrushinagar, Gujarat, India to study to appraise genetic variability in pearl millet genotypes for fodder yield and associating traits. Thirty forage pearl millet genotypes were evaluated for genetic parameters in terms of days to flowering, days to maturity, plant height (cm), number of tiller plant^{-1}, stem thickness (cm), number of leaf plant^{-1}, leaf length (cm), leaf: stem ratio, dry fodder content (%), dry fodder yield plant^{-1} (g), crude protein content (%), green forage yield plant^{-1} (g). Range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and genetic advance as per cent of mean were studied. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the traits indicating slight dominance of environment in the expression as compared to genetic contribution. Genotypic and phenotypic coefficient of variation were high for green forage yield plant^{-1}, dry fodder yield plant^{-1}, plant height, and number of tiller plant^{-1}. The high heritability with high genetic advance as a per cent of mean has been observed for green forage yield plant^{-1}, crude protein content, dry fodder yield plant^{-1}, leaf: stem ratio, leaf width, number of leaves plant^{-1}, plant height, number of tiller plant^{-1}, and stem thickness. This indicated that there is a lesser influence of environment in the expression of these traits and are predominantly governed by additive genes in their inheritance and selection for these traits will be effective for improvement of both forage yield and quality.

Keywords: Genetic variability, forage pearl millet, heritability, forage yield

1. Introduction

Pearl millet [*Pennisetum glaucum* (L.) R. Br.], a C_4 grass, is an extensively cross-pollinated diploid (2n=2x=14) with high photosynthetic efficiency and biomass production capacity (Varshney et al., 2017). Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is familiar in most parts of the country as bajra or bajri, and is also known as cat tail millet, spiked millet, and bulrush millet. Pearl millet is an important food and fodder crop grown in arid and semi-arid regions of Asia and Africa. In contrast to other C_4 cereals like maize and sorghum, pearl millet grows particularly well in arid areas that are usually harmful to other crops. Because of its exceptional adaptability, it can grow in regions with yearly precipitation ranging from 125 mm to 900 mm. The temperature range of 21°C to 35°C provides pearl millet with ideal growing circumstances (Singh et al., 2013). Pearl millet serves as a dual-purpose drought-resistant crop, particularly valuable for fodder production. The appeal of pearl millet's green fodder is augmented by its drought resilience and absence of hydrogen cyanide (HCN) content, rendering it safe for cattle consumption at all growth stages (Bhattacharya and Mandal, 2003). Notably, pearl millet outshines sorghum in this regard, making it a preferred choice. Pearl millet is excellent for producing silage, particularly in regions with dry spells during the rainy season (Shashikala et al., 2013). The richness of pearl millet's green fodder extends to its protein, calcium, phosphorus, and other mineral content, which remain within acceptable oxalic acid limits (Chauhan et al., 2008). Pearl millet is palatable to livestock, but its nutritive value depends on variety, growing conditions, and preservation methods (Nageswara Rao and Talwar, 1990). Several varieties have been developed to enhance forage yield, palatability, and digestibility (Blümmel and Lebzien, 2001).

Pearl millet is cultivated over 30 million ha in arid and semi-arid tropical regions. The area of cultivation of this crop is estimated to be >18 mha in Africa and >10 mha in Asia (Raheem et al., 2021). It is used as a staple food by nearly 90 million people in the African Sahelian region and the north-western part of India mainly Rajasthan, Haryana, and Gujarat (Srivastava et al., 2020). In India, it is cultivated with average grain productivity of 12.43 q ha^{-1} in around 6.93 mha area with production of around 8.61 million tons (Anonymous, 2020). Major pearl millet-producing states in India are Rajasthan (4.283 mt), followed by Uttar Pradesh (1.302), Haryana (1.079), Gujarat (0.961), and Maharashtra (0.66) (Satyavathi et al., 2013, 2021). These states contribute nearly 90% of the total grain production in India. The crop supports more than 100 million people around the world (Anonymous, 2021).

Improving the quantitative traits of any crop through breeding requires a thorough understanding of the crop's existing variability and the heritability of desirable traits found in the breeding material (Dey et al., 2021). To establish an effective breeding program, it is essential to analyse various parameters of genetic variability such as phenotypic and genotypic coefficient of variation, heritability, and genetic advance (Devi et al., 2022). The extent of variability is measured by GCV and PCV which provides information about relative amount of variation in different characters. Since heritability is also influenced by environment, the information on heritability alone may not help in pin pointing characters enforcing selection. Nevertheless, the heritability estimates in conjunction with the predicted genetic advance will be more reliable (Johnson et al., 1955). Therefore, in the present investigation, an attempt was made to investigate genetic variability in pearl millet genotypes for fodder yield and associating traits.

2. Materials and Methods

The present investigation on forage pearl millet was undertaken to study variability analysis using 30 genotypes. The experiment was conducted at Centre for Forage Research, S. D. Agricultural University, Sardarkrushinagar, Gujarat, India during *Kharif* (July–October, 2023) with three replications using a Randomized Block Design. Each entry was grown in one row with row to row-to-row distance was 30 cm and plant to plant distance was 15 cm. All recommended agronomic practices were followed for reaping good crops. The present study consisted of 30 diverse genotypes (Table 1) collected from germplasm materials maintained at the Main Forage Research Station, AAU, Anand. The genotypes were selected based on diverse performance for various traits. Data were recorded on randomly selected five plants from each genotype and the average value was used for the statistical analysis for 11 characters viz., plant height (cm), number of tiller plant^{-1}, stem thickness (cm), number of leaf plant^{-1}, leaf length (cm), leaf: stem ratio, dry fodder content (%), dry fodder yield plant^{-1} (g), crude protein content (%), green forage yield plant^{-1} (g).

Table 1: List of forage pearl millet genotypes used for the present research

Sl. No.	Genotype	Sl. No.	Genotype
1.	GAF-1	16.	ICMO-1604
2.	AFB-13	17.	RAJ BAJRA
3.	AFB-14	18.	BAJRA BAWAL
4.	AFB-15	19.	RBB-1
5.	AFB-16	20.	JMP-18-7
6.	AFB-4	21.	AFB-42
7.	AFB-17	22.	AFB-43
8.	AFB-18	23.	AFB-44
9.	AFB-19	24.	AFB-3
10.	AFB-20	25.	AFB-23
11.	ICMU-1616	26.	AFB-24
12.	BAIF	27.	AFB-25
13.	HC-20	28.	AFB-66
14.	AFB-21	29.	AFB-67
15.	AFB-22	30.	JAINT BAJARA

For the characters like days to flowering and days to maturity observations were recorded on a plot basis. The analysis of variance was estimated by Panse and Sukhatme (1978). The formula suggested by Burton (1952) was employed to calculate the phenotypic and genotypic coefficient of variation. Broad sense heritability was computed in per cent using the formula given by Allard (1960). The genetic advance expressed as per cent of the mean was calculated as per the formula by the method suggested by Johnson et al. (1955).

3. Results and Discussion

In the present investigation, the analysis of variance reported that there were significant differences present among genotypes for all the characters (Table 2), which illustrated that genotypes of forage pearl millet exhibited an ample amount of variability. Selection can be practiced for traits (Table 2) such as days to flowering, days to maturity, plant height (cm), number of tiller plant^{-1}, stem thickness (cm), number of leaf plant^{-1}, leaf length (cm), leaf: stem ratio, dry fodder content (%), dry fodder yield plant^{-1} (g), crude protein content (%), green forage yield plant^{-1} (g), as these traits revealed higher amount of variability for different genotypes. So, there is ample scope for improvement in breeding programmes. Substantial variation was reported by Thomas et al. (2018), Shalini (2019), and Parmar et al. (2022). The per se performance, range, GCV, PCV, heritability, and genetic advance as per cent of the mean of different genotypes for various traits are presented in Table 3 and represented graphically in Figure 1 and 2. Variation among pearl millet inbred lines was found for the characters like days to flowering (42.67–65.33 days), days to maturity (84.33–100.00 days),

Table 2: Analysis of variance (ANOVA) (mean sum of squares) for different characters of forage pearl millet genotypes

Sl. No	Characters	Mean sum of squares		
		Replication	Treatment	Error
1.	Days to flowering	4.04	91.14**	4.41
2.	Days to maturity	13.48	42.73**	4.33
3.	Plant height	18.04	779.12**	22.34
4.	Number of tiller plant^{-1}	0.04	1.04**	0.04
5.	Stem thickness	0.009	0.059**	0.004
6.	Number of leaf plant^{-1}	4.23	30.94**	3.90
7.	Leaf length	117.45	231.34**	40.10
8.	Leaf width	3.77	39.55**	4.09
9.	Leaf: Stem ratio	0.002	0.058**	0.004
10.	Dry fodder content	2.22	34.97**	7.19
11.	Dry fodder yield plant^{-1}	0.35	105.60**	7.04
12.	Crude protein content	0.05	3.79**	0.15
13.	Green forage yield plant^{-1}	96.36	1848.28**	124.39

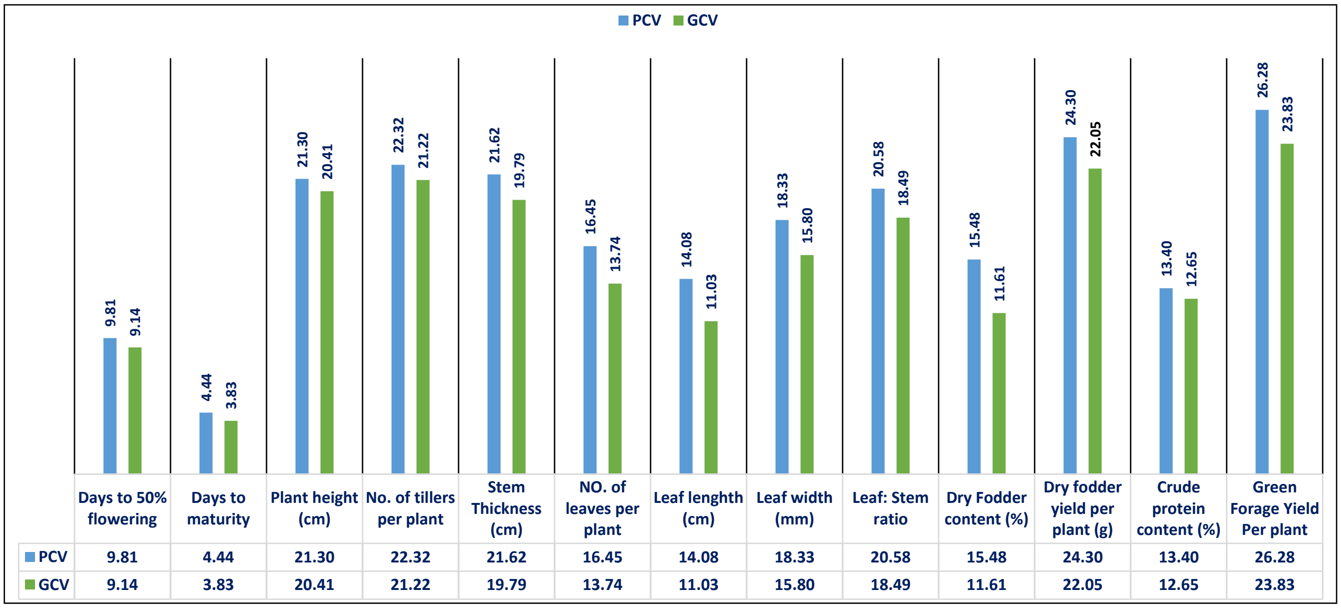
plant height (51.87–112.93 cm), number of tiller plant^{-1} (2.07–5.17), stem thickness (0.52–1.18 cm), number of leaf plant^{-1} (17.20–28.53), leaf length (47.00–83.80 cm), leaf width (12.07–30.87 mm), leaf: stem ratio (0.45–1.00), dry fodder content (19.61–35.45%), dry fodder yield plant^{-1} (16.17–38.63 g), crude protein content (6.70–11.36%), green forage yield plant^{-1} (57.20–174.60 g). The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters indicating slight dominance of environment in the expression as compared to genetic contribution.

The high estimates of phenotypic and genotypic coefficient of variations were observed for green forage yield plant^{-1} (26.28%, 23.83%), dry fodder yield plant^{-1} (24.29%, 22.05%), plant height (21.30%, 20.41%) and number of tiller plant^{-1} (22.32%, 21.22%). These results are in accordance with the results obtained by Balasaheb (2012), Lokhande (2015), Shalini (2019), Rani et al. (2022), Parmar et al. (2022). Moderate estimates of PCV and GCV were observed for the number of leaf plant^{-1} (16.45%, 13.74%), leaf length (14.08%, 11.03%), leaf width (18.33%, 15.80%), dry fodder content (15.48%, 11.61%), and crude protein content (13.40%, 12.65%). The findings are in close harmony with the results of Kalagare et al. (2021) for the number of leaf plant^{-1} and leaf length. Similar findings were observed by Shalini (2019) for leaf width and crude protein content. Low PCV and GCV were noticed for days to flowering (9.81%, 9.14%) and days to maturity (4.44%, 3.83%). The effectiveness of selection not only depends upon the variability but also the extent of variability transmitted from one generation to another generation.

Highest heritability coupled with high genetic advance per cent mean was registered for green forage yield plant^{-1} (g) (82.20%, 44.51%), crude protein content (%) (89.12%, 24.59%), dry fodder yield plant^{-1} (g) (82.36%, 41.22%), leaf: stem ratio (80.72%, 34.22%), leaf width (mm) (74.30%, 28.05%), number of leaves plant^{-1} (69.79%, 23.64%), plant height (cm) (91.86%, 40.30%), number of tiller plant^{-1} (90.42%, 41.56%), stem thickness (cm) (83.78%, 37.31%). This indicated that there is a lesser influence of environment in the expression of these characters and these traits are predominantly governed by additive genes in their inheritance and selection for these characters will be effective for improvement of both fodder yield and quality. High heritability along with high genetic advance was also reported by Shinde

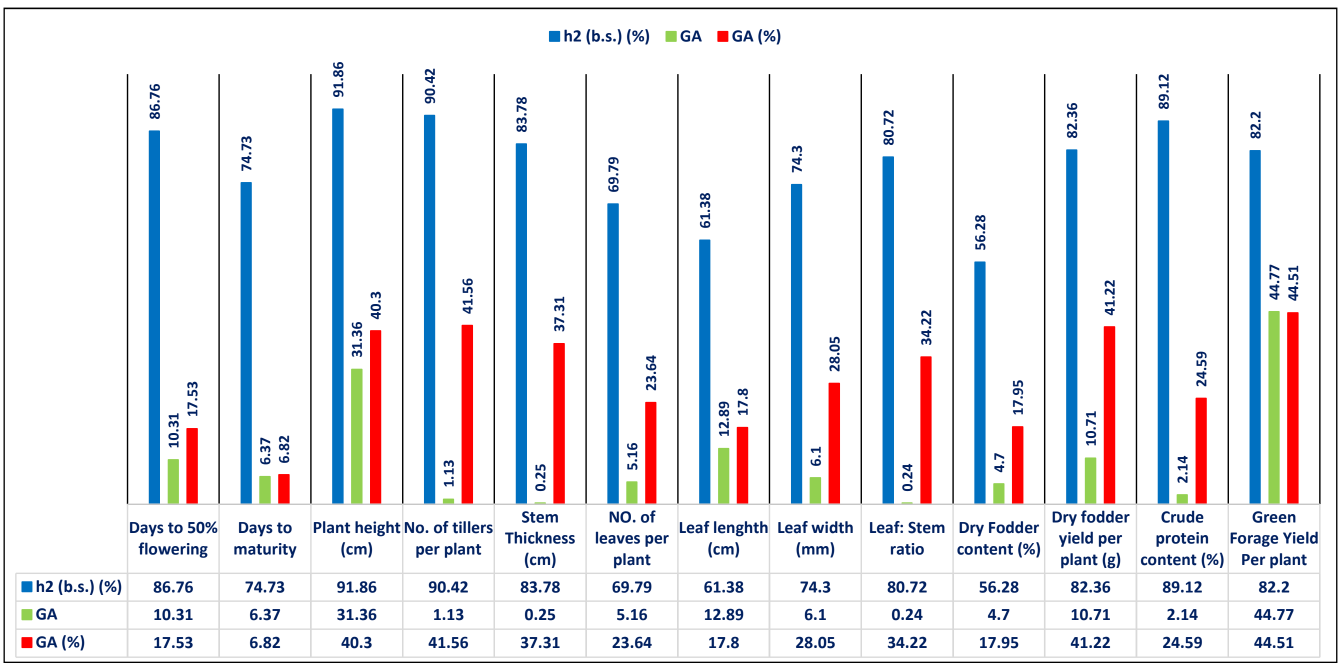
Table 3: Genetic parameters of variation for green forage yield and its contributing characters in forage pearl millet

Sl. No.	Characters	Range	PCV (%)	GCV (%)	h2 (b.s.) (%)	GA (%)
1.	Days to 50% flowering	42.67–65.33	9.81	9.14	86.76	17.53
2.	Days to maturity	84.33–100.00	4.44	3.83	74.73	6.82
3.	Plant height (cm)	51.87–112.93	21.30	20.41	91.86	40.30
4.	Number of tiller plant^{-1}	2.07–5.17	22.32	21.22	90.42	41.56
5.	Stem thickness (cm)	0.52–1.18	21.62	19.79	83.78	37.31
6.	Number of leaf plant^{-1}	17.20–28.53	16.45	13.74	69.79	23.64
7.	Leaf length (cm)	47.00–83.80	14.08	11.03	61.38	17.80
8.	Leaf width (mm)	12.07–30.87	18.33	15.80	74.30	28.05
9.	Leaf: stem ratio	0.45–1.00	20.58	18.49	80.72	34.22
10.	Dry fodder content (%)	19.61–35.45	15.48	11.61	56.28	17.95
11.	Dry fodder yield plant^{-1} (g)	16.17–38.63	24.29	22.05	82.36	41.22
12.	Crude protein content (%)	6.70–11.36	13.40	12.65	89.12	24.59
13.	Green forage yield plant^{-1} (g)	57.20–174.60	26.28	23.83	82.20	44.51



	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of tillers per plant	Stem Thickness (cm)	NO. of leaves per plant	Leaf lenghth (cm)	Leaf width (mm)	Leaf: Stem ratio	Dry Fodder content (%)	Dry fodder yield per plant (g)	Crude protein content (%)	Green Forage Yield Per plant
PCV	9.81	4.44	21.30	22.32	21.62	16.45	14.08	18.33	20.58	15.48	24.30	13.40	26.28
GCV	9.14	3.83	20.41	21.22	19.79	13.74	11.03	15.80	18.49	11.61	22.05	12.65	23.83

Figure 1: Graphical representation of genotypic, phenotypic, and environmental coefficient of variation for thirteen (13) characters in forage pearl millet



	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of tillers per plant	Stem Thickness (cm)	NO. of leaves per plant	Leaf lenghth (cm)	Leaf width (mm)	Leaf: Stem ratio	Dry Fodder content (%)	Dry fodder yield per plant (g)	Crude protein content (%)	Green Forage Yield Per plant
h2 (b.s.) (%)	86.76	74.73	91.86	90.42	83.78	69.79	61.38	74.3	80.72	56.28	82.36	89.12	82.2
GA	10.31	6.37	31.36	1.13	0.25	5.16	12.89	6.1	0.24	4.7	10.71	2.14	44.77
GA (%)	17.53	6.82	40.3	41.56	37.31	23.64	17.8	28.05	34.22	17.95	41.22	24.59	44.51

Figure 2: Graphical representation of broad sense heritability, genetic advance, and genetic advance expressed as per cent of mean for thirteen (13) characters in forage pearl millet

(2005) for L: S ratio, number of tillers plant^{-1}, and crude protein (%), dry matter yield and green forage yield in bajra x napier hybrids; Dhedhi et al. (2016) for dry fodder yield plant^{-1}; Chavan (2012) for number of internodes tiller^{-1}, dry matter yield, green forage yield and L: S ratio in bajra napier hybrid; Satapute et al. (2014) for plant height, number of tillers plant^{-1}, green forage yield plant^{-1} and dry matter yield plant^{-1}; Pattanashetti et al. (2015) for plant height, number of tillers plant^{-1}, number of leaves plant^{-1}, leaf width, stem thickness and green forage yield plant^{-1}; Parmar et al. (2022) for green forage yield plant^{-1}, leaf width, number of leaf plant^{-1}, and stem thickness; Rani et al. (2022) for green forage yield plant^{-1}, dry fodder yield plant^{-1}, stem thickness, number of tiller plant^{-1}. Moderate genetic advance accompanied by high heritability is shown by days to flowering (17.53%, 86.76%) and leaf length (17.80%, 61.38%), which indicate least influence of environment but having both additive and non-additive genes signify limited scope for improvement through selection. Moderate heritability coupled with moderate genetic advance expressed as per cent of the mean was observed for dry matter content (56.28%, 17.95%). The results are in concordance with Parmar et al. (2022).

4. Conclusion

Traits like green forage yield plant^{-1}, dry fodder yield plant^{-1}, plant height, and number of tiller plant^{-1} should be selected for genetic improvement as these recorded high genotypic coefficient of variation, phenotypic coefficient of variation, high broad sense heritability with high genetic advance as a per cent of mean.

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