

Genetic variability in birdwood grass (*Cenchrus setigerus*) for forage yield and its component traits

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Abstract

Identification of birdwood grass genotypes with higher forage yield is essential to boost the use of birdwood grass for direct consumption to milch animals and to sustain the arid rangeland. Twenty four germplasm lines along with one check (CAZRI 76) variety possessing high forage yield were evaluated for two seasons at CAZRI, RRS, Kukma, Bhuj. Analysis of data indicated that the germplasm differed significantly for all the traits. Genotypes viz., CAZRI-BH-CS- 15 and CAZRI-BH-CS-3 exhibited high *per se* performance for green fodder yield, dry fodder yield and their component characters. While assessing overall position in both the environments over pooled basis, the present study revealed high genetic advance as percentage of mean (genetic gain) alongwith high estimates of heritability and genotypic coefficient of variation for number of leaves per plant, green fodder yield (kg/ha) and dry fodder yield (kg/ha). On the basis of green and dry fodder yield, birdwood grass germplasm CAZRI-BH-CS-3, CAZRI-BH-CS-4, CAZRI-BH-CS-7, CAZRI-BH-CS-13, CAZRI-BH-CS-15, CAZRI-BH-CS-16, CAZRI-BH-CS-17, CAZRI-BH-CS-19 and CAZRI-BH-CS-24 appeared promising which could be gainfully utilized.

Keyword: Cenchrus setigerus, Germplasm, Genetic advance, Green fodder yield, Heritability

Introduction

Kachchh, the largest and the western most district of Gujarat state, has a very different terrain. Recurring drought, periodic seismicity, vast areas under salt marshes and ranns, undulating rocky terrain, shallow soil, high exploitation of potable ground water and depleting biodiversity pose serious threats to sustainable use of the land in the district (Devidayal *et al.*, 2009). Birdwood grass (*Cenchrus setigerus* vahl.) commonly known as *moda dhaman* in north western Gujarat is one of the major perennial grass species of

Indian arid zone range grasses. It forms the dominant species of Dichanthium-Cenchrus- Lasiurus grass cover and is known for its drought resistance (Vyas et al., 2003). Its fresh material at the early-bloom stage contained 18.6 per cent crude protein, 28.3 per cent crude fibre, 11.9 per cent ash, 1.9 per cent ether extract and 39.3 per cent nitrogen-free extract. Birdwood grass is an apomictic but pollination is necessary for endosperm formation and seed set. Breeding for higher forage yield in birdwood grass is important, keeping in view the sustained perennial rangeland management as well as the high demand of quality fodder to meet the fodder requirement of animal population. The areas under perennial grass are on the decline mainly because of competition from other lucrative crops, like cotton (Gossypium hirsutum L.) in the traditional birdwood grass belts. For sustaining the birdwood grass farming, efforts were initiated at the Bhuj station of Central Arid Zone Research Institute in the last two decade for developing higher- forage yielding, water use efficient birdwood genotypes for rainfed conditions. In view of this, an attempt was made to assess the genetic variability for green fodder yield, dry fodder yield and its components so as to identify superior germplasm of birdwood grass which could be utilized for future breeding programmes.

Materials and Methods

The present experiment was carried out at the research farm of Central Arid Zone Research Institute, Regional Station, Kukma, Bhuj (at 22° 41'11" to 24° 41' 47" N latitude and 68° 9' 46" to 71° 54'47" E longitude) during *kharif* season of 2004 and 2005. The soil of the experimental site was gravelly sand to loamy sand in texture with shallow depth (21 cm), low in organic C (0.38%), available N (214 kg/ha), P (7.0 kg/ha), and medium in available K (138.3 kg/ha) with a pH of 8.7. The range grass crop was raised strictly under rainfed conditions with basal dose of 45 kg N and 20 kg P_oO_e/

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ha. The germplasm were collected from the Banni, Naliya, Rapar and Khavda region of Kachchh. Twenty four germplasm lines were evaluated in a randomized block design with three replications along with one check, CAZRI 76. Each germplasm line was grown in 4 rows of 5 m length/ replication with row-to-row distance of 75 cm and plants spaced at 50 cm apart. The observations were recorded on 5 competitive plants from each plot for morphological characters, viz., plant height (cm), number of tillers per plant, number of leaves per plant, green fodder yield (kg/ha) and dry fodder yield (kg/ha). The mean values were used for statistical analysis. Analysis of variance in respect of various characters was done as suggested by Panse and Sukhatme (1978). Estimation of phenotypic and genotypic coefficient of variation and heritability in broad sense were made as suggested by Burton and De Vane (1953). Genetic gain (genetic advance as percentage of mean) is computed using formula suggested by Johnson et al. (1955).

Results and Discussion

The analysis of variance for all the traits showed highly significant difference among the germplasm indicating sufficient amount of variability in the materials (Table 1). Mean, range, genotypic and phenotypic coefficient of variation, heritability (in broad sense) and genetic advance analysed for pooled environment are shown in Table 2. The genotypic and phenotypic variation were higher for dry fodder yield (kg/ha) (Table 2). The highest genotypic and phenotypic coefficient of variation were observed for dry fodder yield (kg/ha) (29.01, 40.36), number of leaves per plant (31.26, 34.66) and green fodder yield (kg/ha) (25.29, 34.14) respectively. High genotypic and phenotypic coefficient of variation for dry fodder yield (kg/ha) and green fodder yield were also reported by Rajora et al. (2008) in birdwood grass. The results suggested that characters showing high value of genotypic and phenotypic coefficient variation can be improved by careful selection. High heritability estimates (broad sense) were focused for number of leaves per plant (81.37 %), green fodder yield (kg/ha) 54.87%, dry fodder yield (kg/ha) 51.68% and number of tillers per plant (51.67%) indicating that these characters were less influenced by the environmental factor and direct selection for these characters would be effective for further improvement.

Johnson *et al.* (1955) reported that heritability estimates along with genetic advance, were of more value than the former alone in predicting effect of selection. Thus, high heritability dose not necessary mean high genetic gain.

Panse (1957) reported that high genetic advance might be expected when heritability is mainly due to additive gene effect. Otherwise low genetic gain would mean that heritability is due to non-additive gene effects (dominance and epistasis). The heritability (broad sense) of number of leaves per plant (81.37 %) with maximum genetic advance (58.10 %) was observed which might be due to heritability with additive gene impact therefore selection may be effective (Table 2). These results are in agreement with the results obtained by Vyas et al. (2003) and Rajora et al. (2008) for number of leaves per plant, green fodder yield (kg/ha) and dry fodder yield (kg/ha). High heritability estimates coupled with moderate genetic advance as per cent of means was recorded for green fodder yield (kg/ha) and number of tillers per plant indicating the predominance of additive gene action for these characters.

Awasthi et al. (2009) reported that high heritability alongwith high genetic advance for number of leaves per plant, green fodder yield and dry fodder yield in fodder maize. Bhagirath et al. (2007) also reported that high heritability alongwith high genetic advance for green fodder yield and dry fodder yield in fodder pearlmillet.

The germplasm CAZRI-BH-CS-15 and CAZRI-BH-CS-3 provided higher green fodder yield (kg/ha) and dry fodder yield (kg/ha) as compared to check variety CAZRI 76 in the year over pooled analysis.

A relative comparison of heritability estimates and expected genetic advance will give an idea about the nature of gene action. Green fodder yield and dry fodder yield had high heritability estimates coupled with high genetic advance suggesting these characters were under control of additive gene action and potential possibilities exist for the improvement of these characters through simple selection.

While assessing overall position in both the environments over pooled basis, the present study revealed high genetic advance as percentage of mean (genetic gain) alongwith high estimates of heritability and genotypic coefficient of variation in number of leaves per plant, green fodder yield (kg/ha) and dry fodder yield (kg/ha). On the basis of green and dry fodder yield, birdwood grass germplasm CAZRI-BH-CS-3, CAZRI-BH-CS-4, CAZRI-BH-CS-7, CAZRI-BH-CS-13, CAZRI-BH-CS-15, CAZRI-BH-CS-16, CAZRI-BH-CS-17, CAZRI-BH-CS-19 and CAZRI-BH-CS-24 appeared promising which could be gainfully utilized.

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Table 1: Analysis of variance characters in birdwood grass

| Character | Replication MS* (2 df) | Treatment MS* (24 df) | Error MS* (48 df) | CD | |
|-----------------------------|------------------------|-----------------------|-------------------|---------|---------|
| | | | | P= 0.05 | P= 0.01 |
| Plant height (cm) | 90.62** | 167.59** | 23.09 | 7.75 | 10.25 |
| Number of tillers per plant | 20.42** | 43.03** | 6.97 | 2.75 | 3.64 |
| Number of leaves per plan | it 67.82** | 479.26 | 7.57 | 4.79 | 6.34 |
| Green fodder yield (kg/ha) | 230775.43** | 2780781.45** | 81495.23 | 661.89 | 874.99 |
| Dry fodder yield (kg/ha) | 50293.49** | 518787.69** | 21540.66 | 302.33 | 399.68 |

Table 2. Mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (b.s), genetic advance of promising germplasm from 24 total germplasm in birdwood grass (pooled data of 2 years)

| S. No | . Germplasm | Plant height | Number of | Number of | Green fodder | Dry fodder |
|-------|---------------------|--------------|-------------------|------------------|---------------|---------------|
| | | (cm) | tillers per plant | leaves per plant | yield (kg/ha) | yield (kg/ha) |
| 1. | CAZRI- BH -CS- 3 | 69.98 | 12.11 | 20.66 | 3578.06 | 1510.19 |
| 2. | CAZRI- BH -CS- 4 | 67.66 | 11.18 | 26.83 | 2692.05 | 1095.06 |
| 3. | CAZRI- BH -CS- 7 | 61.95 | 11.31 | 23.00 | 2553.05 | 947.56 |
| 4. | CAZRI- BH -CS- 13 | 58.36 | 6.93 | 26.33 | 2462.65 | 880.54 |
| 5. | CAZRI- BH -CS- 15 | 67.35 | 16.15 | 37.50 | 3700.35 | 1689.88 |
| 6. | CAZRI- BH -CS- 16 | 70.15 | 10.15 | 46.50 | 3169.14 | 1313.25 |
| 7. | CAZRI- BH -CS- 17 | 68.90 | 13.36 | 44.00 | 3506.68 | 1264.94 |
| 8. | CAZRI- BH -CS- 19 | 61.70 | 15.98 | 37.16 | 3118.21 | 1137.53 |
| 9. | CAZRI- BH -CS- 24 | 59.21 | 7.53 | 31.66 | 2854.88 | 865.32 |
| 10. | CAZRI 76 (C) | 68.40 | 13.15 | 26.50 | 3395.15 | 1328.59 |
| | Mean | 61.85 | 10.34 | 28.05 | 2524.28 | 942.65 |
| | SE± | 2.77 | 0.98 | 1.71 | 236.38 | 107.97 |
| | Range | 51.21 to | 5.46 to | 14.83 to | 1218.48 to | 430.25 to |
| | | 71.01 | 16.15 | 46.50 | 3700.35 | 1689.88 |
| | GCV (%) | 7.27 | 24.07 | 31.26 | 25.29 | 29.01 |
| | PCV (%) | 13.16 | 33.49 | 34.66 | 34.14 | 40.36 |
| | Heritability (b.s.) | 30.54 | 51.67 | 81.37 | 54.87 | 51.68 |
| | GA as % of mean | 8.28 | 35.65 | 58.10 | 38.59 | 42.96 |

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