



## Research article

# Harnessing agro-morphological and geographic diversity to develop a core collection of buffel grass (*Cenchrus ciliaris*)

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Received: 05<sup>th</sup> September, 2025

Accepted: 03<sup>rd</sup> June, 2026

## Abstract

*Cenchrus* is a diverse genus of major importance in forage production and ecological conservation, with *C. ciliaris* particularly valued in arid and semi-arid regions for its high biomass yield and drought tolerance. The ICAR-Indian Grassland and Fodder Research Institute conserves 613 *Cenchrus* germplasm accessions representing seven species from 30 countries. To enhance germplasm utilization and facilitate efficient management, a core collection was developed using geographic origin and 24 agro-morphological traits. Based on Ward's clustering method, the accessions were grouped into 58 clusters, from which 10% of accessions or at least one accession per cluster was selected. Consequently, a core set comprising 81 accessions (13.3% of the entire collection) was established. The representativeness of the core set was validated through mean comparison, variance homogeneity, frequency distribution, coincidence rate, variable rate, the Shannon-Weaver diversity index, and phenotypic correlation analysis. Statistical validation demonstrated that the developed core set effectively captured the diversity structure of the entire collection while maintaining key phenotypic correlations associated with co-adapted gene complexes. This core set constitutes a manageable and genetically diverse subset of *Cenchrus* germplasm, providing a valuable resource for trait discovery, forage improvement, and genomic studies.

**Keywords:** Buffel grass, *Cenchrus* sp., Core subset, Cluster analysis, Fodder, Genetic diversity, Rangeland, Shannon-Weaver diversity index

## Introduction

*Cenchrus*, a Panicoid C4 grass with origins in African bushlands, is now naturalized across tropical and subtropical regions, especially in arid and semi-arid zones (McIvor, 2005; Jorge *et al.*, 2008). Of the 22 recognized species, *C. ciliaris*, *C. setigerus* and *C. pennisetiformis* are most important for global forage production (Clayton and Renvoize, 1982). Among these, *C. ciliaris* is widely preferred for its high biomass, tolerance to drought and grazing, and ability to withstand fire (Marshall *et al.*, 2012). It exhibits apomixis, polyploidy, and wide polymorphism, with several ecotypes and cytotypes, and dominates grasslands of North Africa and the *Dichanthium-Cenchrus-Lasiurus* regions of India (Singh *et al.*, 2023a). The IGFRI maintains more than 600 accessions of *Cenchrus*, including indigenous and exotic

introductions (Sahay *et al.*, 2019). These genetic resources have contributed to the development and release of improved cultivars of *Cenchrus ciliaris*, namely Bundel Anjan-1, Bundel Anjan-3 and Bundel Anjan-4; and of *Cenchrus setigerus*, namely Bundel Dhaman-1, possessing desirable traits such as high forage yield, improved quality, rapid regeneration, frost tolerance and adequate sugar content for silage preparation (Roy *et al.*, 2020a; Singh *et al.*, 2023b).

However, evaluating such a large germplasm pool is costly and influenced by genotype × environment interactions, especially for complex traits like forage quality and stress tolerance. To address this, Brown (1989) proposed core collections, representing ~10% of entire set while capturing over 70% of the entire collection's genetic diversity. The Second Global Plan of Action

also emphasized the development of core subsets to enhance the conservation, evaluation and utilization of germplasm resources (FAO, 2011). Core collections reduce redundancy, facilitate systematic evaluation, and have been successfully applied in forage grasses and legumes, including *Bouteloua dactyloides* (Qian *et al.*, 2023), *Sehima nervosum* (Roy *et al.*, 2022), *Megathyrsus maximus* (Roy *et al.*, 2020b), *Heteropogon contortus* (Roy *et al.*, 2021a), *Dichanthium annulatum* (Roy *et al.*, 2021b), *Poa pratensis* (Johnson *et al.*, 1999), *Cynodon* spp. (Anderson, 2005), *Phleum pratense* (Casler, 2001), and *Medicago sativa* (Diwan *et al.*, 1994). These efforts have improved efficiency in identifying useful traits such as stress tolerance, forage quality, and biological nitrification inhibition (Bouton, 1996; Jung *et al.*, 1997; Villegas *et al.*, 2020).

In this context, the development of a core collection for *Cenchrus* provides a smaller but genetically representative subset of the large germplasm collection, enabling targeted evaluation for cultivar improvement, trait-specific accession identification, and advanced genomic research.

## Materials and Methods

**Plant material and evaluation:** A diverse germplasm collection of *Cenchrus*, comprising 613 accessions from 30 countries and representing seven species, served as the base material for developing the core collection (Table 1). The species included were *C. ciliaris*, *C. setigerus*, *C. pennisetiformis*, *C. prieurii*, *C. echinatus*, *C. mysuroides* and *C. biflorus*, with *C. ciliaris* accounting for nearly 90% of the accessions. The evaluation was conducted at the Central Research Farm of ICAR-IGFRI, Jhansi, India, situated in the semi-arid tropics (25°27' N, 78°37' E, 275 msl). The site received 700 to 1150 mm annual rainfall, concentrated from July to mid-September, with mean annual maximum and minimum temperatures of 32.3 and 17.4°C, respectively. Each accession was planted in a single 4 m row with 50 cm spacing between plants, and standard agronomic practices recommended for the species were followed.

All passport and evaluation data are archived in the Forage Genetic Resources Information System (FGRIS) of IGFRI, and a germplasm catalogue has been published (Mishra *et al.*, 2002; Anonymous, 2012). Based on passport data, the collection was stratified into eight geographic regions: Africa, Americas, Asia, Europe, Mediterranean, Oceania, Soviet Union, and Caribbean, while 48 accessions lacking origin data were grouped as 'unknown'. Observations were recorded on nine qualitative and 15 quantitative traits. Qualitative traits and days to 50% flowering were measured on a plot basis, while the remaining quantitative traits were recorded on five representative plants per accession. Additionally, accessions were screened for leaf spot resistance and frost

tolerance, classifying them into four categories: highly tolerant, tolerant, susceptible, and highly susceptible.

For core collection development, the proportional sampling strategy was adopted, which captures greater allelic diversity with lower variance (Grenier *et al.*, 2001; Upadhyaya *et al.*, 2009). In this approach, genetic distances among accessions were calculated using the least-distance stepwise sampling method, and accessions were grouped by hierarchical clustering. Approximately 10% of accessions were randomly selected, proportional to cluster size, to form the core set. Hierarchical cluster analysis was performed on standardized data using Ward's minimum variance method in SAS (PROC CLUSTER; SAS Institute, 1989).

**Validation of core collection:** Frequencies of geographic regions, countries within geographic regions, and qualitative traits in the entire and core collections were tested by the  $\chi^2$  test. The expected frequencies were tested against observed frequencies in the core collection for goodness of fit using  $\chi^2$  test. The means of the entire and core collections were compared using the Newman-Keuls procedure (Newman, 1939; Keuls, 1952) for quantitative traits. The homogeneity of variance for quantitative traits in the entire and core collections was tested following Levene's test (Levene, 1960). The coincidence rate (CR %) and variable rate (VR %) were calculated to compare the entire and core collection following Hu *et al.* (2000).

$$CR\% = \frac{1}{m} \sum_{j=1}^m \frac{R_c(j)}{R_e(j)} \times 100; \quad VR\% = \frac{1}{m} \sum_{j=1}^m \frac{CV_c(j)}{CV_e(j)} \times 100$$

Where, for jth trait,  $R_c$  is range of core collection,  $R_e$  range of the entire collection,  $CV_c$  is the coefficient of variation of core collection,  $CV_e$  coefficient of variation of entire collection; and m is the number of traits.

Shannon-Weaver diversity index ( $H'$ ) (Shannon and Weaver, 1949) as a measure of phenotypic diversity for each trait was calculated as follows:

$$H' = - \sum_{i=1}^n p_i \times \ln(p_i)$$

Where  $p_i$  = proportion of total number of accessions in the  $i^{th}$  class and n = number of phenotypic classes for a trait. The  $H'$  index was calculated separately in both entire and core collection to determine whether the diversity of each trait was retained in the core collection.

## Results and Discussion

**Cluster analysis:** The 613 accessions in the entire collection were grouped into 58 clusters. geographical regions wise, the number of clusters was 34 in Africa, 8 in Asia, 4 in the Americas and 6 in an unknown region. The Soviet Union, the Mediterranean, and Oceania were represented by two clusters in each region. The number

**Table 1.** Chi-square test for the frequency distribution of entire and core collection accessions in different geographic regions and countries within the geographic region

| Geographic region | Country within region | Accessions in entire collection | Accessions in core collection | df | Chi square | P-value |
|-------------------|-----------------------|---------------------------------|-------------------------------|----|------------|---------|
| Africa            | Botswana              | 10                              | 1                             | 1  | 0.041      | 0.839   |
|                   | Djibouti              | 7                               | 1                             | 1  | 0.228      | 0.633   |
|                   | Ethiopia              | 20                              | 2                             | 1  | 0.002      | 0.964   |
|                   | Ghana                 | 3                               | 1                             | 1  | 0.002      | 0.958   |
|                   | Jaire                 | 1                               | 1                             | 1  | 0.344      | 0.557   |
|                   | Kenya                 | 24                              | 4                             | 1  | 0.042      | 0.837   |
|                   | Madagascar            | 7                               | 1                             | 1  | 0.217      | 0.640   |
|                   | Malawi                | 13                              | 1                             | 1  | 0.012      | 0.911   |
|                   | Mali                  | 6                               | 2                             | 1  | 0.565      | 0.451   |
|                   | Namibia               | 3                               | 1                             | 1  | 0.002      | 0.958   |
|                   | Somalia               | 7                               | 2                             | 1  | 0.108      | 0.742   |
|                   | South Africa          | 60                              | 8                             | 1  | 0.005      | 0.980   |
|                   | Sudan                 | 1                               | 1                             | 1  | 0.344      | 0.557   |
|                   | Tanzania              | 156                             | 13                            | 1  | 2.746      | 0.097   |
|                   | Uganda                | 3                               | 1                             | 1  | 0.002      | 0.958   |
|                   | Zimbabwe              | 13                              | 2                             | 1  | 0.040      | 0.840   |
| Total             | -                     | 334                             | 42                            | 15 | 0.534      | 1.000   |
| America           | Argentina             | 1                               | 1                             | 1  | 0.344      | 0.557   |
|                   | Mexico                | 11                              | 1                             | 1  | 0.007      | 0.928   |
|                   | Paraguay              | 1                               | 1                             | 1  | 0.344      | 0.557   |
|                   | USA                   | 3                               | 1                             | 1  | 0.002      | 0.958   |
| Total             | -                     | 16                              | 4                             | 3  | 0.041      | 0.997   |
| Asia              | India                 | 171                             | 15                            | 1  | 2.347      | 0.125   |
|                   | Oman                  | 8                               | 2                             | 1  | 0.107      | 0.743   |
|                   | Pakistan              | 12                              | 1                             | 1  | 0.002      | 0.988   |
|                   | Philippines           | 3                               | 1                             | 1  | 0.002      | 0.958   |
|                   | Yemen                 | 2                               | 1                             | 1  | 0.072      | 0.787   |
| Total             | -                     | 196                             | 20                            | 4  | 1.318      | 0.858   |
| Europe            | Italy                 | 1                               | 1                             | 1  | 0.344      | 0.557   |
| Total             | -                     | 1                               | 1                             | 1  | 0.344      | 0.557   |
| Mediterranean     | Morocco               | 7                               | 2                             | 1  | 0.776      | 0.378   |
| Total             | -                     | 7                               | 2                             | 1  | 0.776      | 0.378   |
| Oceania           | Australia             | 6                               | 2                             | 1  | 1.298      | 0.254   |
| Total             | -                     | 6                               | 2                             | 1  | 1.298      | 0.254   |
| Soviet union      | -                     | 4                               | 2                             | 1  | 1.033      | 0.309   |
| Unknown           | -                     | 48                              | 7                             | 1  | 0.001      | 0.973   |
| Caribbean         | Antigua               | 1                               | 1                             | 1  | 0.344      | 0.557   |
| Total             | -                     | 1                               | 1                             | 1  | 0.344      | 0.557   |

of accessions representing each cluster ranged from one to 38. From each cluster, 10% or at least one accession was included in the core collection resulting in a core subset of 81 accessions. Africa is the primary centre of diversity for *Cenchrus*, and the composition of the core collection reflected that the majority of accessions were represented from Africa (48.2%), followed by Asia (24.6%). Europe and Caribbean regions were represented only by 1.2% of accessions in the core collection (Table 1). About 4.9% of accessions in the core collection were from America, and 2.4% of accessions were represented from the Mediterranean, Oceania, and the Soviet Union. The 'unknown' region was represented by seven accessions (8.6% of the core collection). The  $\chi^2$  values and heterogeneity were non-significant for all the geographic regions. Individual countries within each region also showed non-significant  $\chi^2$  values, indicating that all the countries were well represented in the core collection (Table 1).

**Species distribution:** The species distribution of the entire collection reflected the prevalence of *C. ciliaris* (90.2% accessions), followed by *C. setigerus* (7.8%), *C. prieurii* (0.97%), *C. mysuroides* (0.32%), *C. pennisetiformis* (0.32%), *C. echinatus* (0.16%) and *C. biflorus* (0.16%). In the core collection, *C. ciliaris* was represented by 70 accessions (86.4% of core collection), *C. setigerus* by four accessions (4.9%) and *C. prieurii* by three accessions (3.7%). The rest of the species was represented by one accession (1.2% of the core collection). The  $\chi^2$  values for the frequency distribution of accessions in the entire and core collections were non-significant for all seven species (Table 2), revealing that the sampling technique to constitute the core collection was adequate implying that constituted core collection is a reliable representative of the entire collection.  $\chi^2$  probabilities for frequency distribution of phenotypic classes in 9 qualitative traits ranged from 0.25 to 0.95 and were non-significant for all the traits (Table 3). Homogeneous distribution ( $p \geq 0.05$ ) of phenotypic classes of qualitative traits in the entire and core collection indicated that the proportional

**Table 2.** Chi-square value and probability for frequency distribution of species in the entire and core collections

| Species                   | Entire | Core | Chi square | P-value |
|---------------------------|--------|------|------------|---------|
| <i>C. ciliaris</i>        | 552    | 70   | 0.118      | 0.738   |
| <i>C. mysuroides</i>      | 2      | 1    | 0.738      | 0.390   |
| <i>C. setigerus</i>       | 45     | 4    | 0.233      | 0.629   |
| <i>C. prieuri</i>         | 11     | 3    | 0.217      | 0.640   |
| <i>C. pennisetiformis</i> | 1      | 1    | 2.065      | 0.150   |
| <i>C. echynatus</i>       | 1      | 1    | 2.065      | 0.150   |
| <i>C. biflorus</i>        | 1      | 1    | 2.065      | 0.150   |

**Table 3.** Chi-square value and probability for frequency distribution of classes in qualitative traits in entire and core collections

| S. No. | Traits            | df | Class | Entire | Core | Chi square | P-value |
|--------|-------------------|----|-------|--------|------|------------|---------|
| 1      | Early vigour      | 4  | 1     | 134    | 20   | 0.79       | 0.94    |
|        |                   |    | 2     | 246    | 32   |            |         |
|        |                   |    | 3     | 76     | 10   |            |         |
|        |                   |    | 4     | 157    | 18   |            |         |
|        |                   |    | 5     | 10     | 1    |            |         |
| 2      | Growth habit      | 2  | 1     | 148    | 23   | 0.94       | 0.70    |
|        |                   |    | 2     | 255    | 32   |            |         |
|        |                   |    | 3     | 210    | 26   |            |         |
| 3      | Leaf type         | 1  | 1     | 184    | 22   | 0.44       | 0.50    |
|        |                   |    | 2     | 429    | 59   |            |         |
| 4      | Leaf colour       | 5  | 1     | 80     | 14   | 4.1        | 0.66    |
|        |                   |    | 2     | 263    | 30   |            |         |
|        |                   |    | 3     | 194    | 23   |            |         |
|        |                   |    | 4     | 25     | 4    |            |         |
|        |                   |    | 5     | 42     | 8    |            |         |
| 5      | Culm formation    | 4  | 6     | 9      | 2    | 1.2        | 0.88    |
|        |                   |    | 1     | 136    | 20   |            |         |
|        |                   |    | 2     | 213    | 25   |            |         |
|        |                   |    | 3     | 181    | 25   |            |         |
|        |                   |    | 4     | 60     | 7    |            |         |
|        |                   |    | 5     | 23     | 4    |            |         |
|        |                   |    | 6     | 245    | 37   |            |         |
| 6      | Sheath hairiness  | 1  | 7     | 368    | 44   | 1.3        | 0.25    |
|        |                   |    | 1     | 245    | 37   |            |         |
| 7      | Bur colour        | 10 | 2     | 368    | 44   | 4.7        | 0.91    |
|        |                   |    | 1     | 114    | 15   |            |         |
|        |                   |    | 2     | 116    | 15   |            |         |
|        |                   |    | 3     | 237    | 33   |            |         |
|        |                   |    | 4     | 25     | 3    |            |         |
|        |                   |    | 5     | 40     | 5    |            |         |
|        |                   |    | 6     | 11     | 2    |            |         |
|        |                   |    | 7     | 14     | 1    |            |         |
|        |                   |    | 8     | 9      | 3    |            |         |
|        |                   |    | 9     | 25     | 2    |            |         |
| 8      | Spine arrangement | 5  | 10    | 7      | 1    | 1.1        | 0.95    |
|        |                   |    | 11    | 15     | 1    |            |         |
|        |                   |    | 1     | 129    | 19   |            |         |
|        |                   |    | 2     | 148    | 20   |            |         |
|        |                   |    | 3     | 147    | 19   |            |         |
|        |                   |    | 4     | 91     | 13   |            |         |
|        |                   |    | 5     | 90     | 9    |            |         |
| 9      | Leaf hairiness    | 1  | 9     | 8      | 1    | 0.77       | 0.38    |
|        |                   |    | 1     | 101    | 16   |            |         |
|        |                   |    | 9     | 512    | 65   |            |         |

**Table 4.** Range, means and variances of different quantitative traits in entire and core collections of *Cenchrus*

| Traits                       | Range     |            | Mean <sup>†</sup> |        | Variance <sup>‡</sup> |          |         |               |
|------------------------------|-----------|------------|-------------------|--------|-----------------------|----------|---------|---------------|
|                              | Entire    | Core       | Entire            | Core   | Entire                | Core     | F-value | F probability |
| Days to 50% flowering        | 46-189    | 47-175     | 91.42             | 91.37  | 1818.73               | 1892.90  | 0.00    | 0.99          |
| Plant height (cm)            | 21.6-162  | 27.2-145.3 | 72.47             | 69.78  | 852.35                | 908.04   | 0.55    | 0.46          |
| Number of tillers/plant      | 7.2-249   | 16-249     | 81.36             | 87.95  | 1772.24               | 1950.92  | 1.58    | 0.21          |
| Number of leaves/plant       | 4.6-14.5  | 5-13       | 8.93              | 8.94   | 2.93                  | 2.81     | 0.02    | 0.89          |
| Leaf length (cm)             | 5.2-55.7  | 5.6-46.6   | 18.61             | 17.09  | 71.95                 | 61.91    | 2.12    | 0.15          |
| Leaf width (cm)              | 0.4-1.7   | 0.43-1.4   | 0.70              | 0.72   | 0.03                  | 0.03     | 0.82    | 0.37          |
| Peduncle length (cm)         | 1.4-37    | 1.4-28.7   | 14.95             | 13.65  | 39.92                 | 34.18    | 2.78    | 0.10          |
| Spike length (cm)            | 2.5-15.2  | 2.5-15.2   | 7.53              | 7.04   | 5.35                  | 5.32     | 2.92    | 0.09          |
| Spike breadth (cm)           | 0.42-2.43 | 0.42-2.43  | 1.20              | 1.18   | 0.09                  | 0.09     | 0.35    | 0.56          |
| Number of spikes/plant       | 1-115     | 2-100      | 20.84             | 21.02  | 295.67                | 375.72   | 0.02    | 0.90          |
| Number of spikelets/spike    | 11-284    | 12-277.6   | 78.89             | 73.78  | 1410.59               | 1046.87  | 1.19    | 0.28          |
| Green fodder yield/plant (g) | 15-1450   | 20-1450    | 404.74            | 379.49 | 43897.58              | 42345.81 | 0.95    | 0.33          |
| Dry fodder yield/plant (g)   | 3.4-440   | 3.4-440    | 109.79            | 104.06 | 3834.82               | 3741.18  | 0.56    | 0.45          |
| Dry matter percentage        | 0.97-45.6 | 0.95-47.4  | 27.35             | 28.06  | 29.87                 | 34.78    | 1.06    | 0.30          |
| 100 Fasicle weight (g)       | 0.30-8.34 | 0.30-8.45  | 2.75              | 2.78   | 1.33                  | 1.47     | 0.03    | 0.86          |

<sup>†</sup>Means were tested by Newman-Keul test and were non-significant for all traits ( $P \geq 0.05$ ); <sup>‡</sup>Variances were tested by Levene test and were non-significant for all traits ( $P \geq 0.05$ )

sampling technique to constitute the core collection was appropriate and the total diversity of qualitative traits present in the entire collection is represented in the core collection.

**Diversity in core collections:** For examining the extent of diversity retained in the core collection as compared to the entire collection, differences between the means were compared using the Newman-Keuls procedure (Table 4). The differences between means were found non-significant for all the 15 quantitative traits. Variance of the entire and core collection were homogeneous for all the quantitative traits ( $p \geq 0.05$ ), resulting in zero variance difference (VD%), suggesting that a non-biased procedure was followed for defining the core collection and also that the diversity was fully represented in the core subset for all the quantitative traits (Table 4).

According to Hu *et al.* (2000), core collections having coincidence rate (CR%) and variable rate (VR%) more than 80% and 100%, respectively, are considered the best representative of the genetic diversity of the entire collection. The variable rate for the 15 quantitative traits was higher (>100%) in the core collection, resulting in an average 102.93% VR for all traits (Table 5). The high CR (86.07%) indicated how precisely the variability of

quantitative traits has been captured in the core collection from the entire collection (Table 5). The Shannon-Weaver diversity index ( $H'$ ) was used as a measure of phenotypic diversity of each trait. This index is used in diversity studies as a measure of allelic richness and evenness. A low value of  $H'$  indicates an extremely unbalanced frequency class for a particular trait and a lack of genetic diversity (Upadhyaya *et al.*, 2007). The  $H'$  indices computed for the 15 quantitative and 9 qualitative traits showed a similar pattern of diversity among the entire as well as the core collection, and no significant differences were observed for any of the traits (Table 5). The average  $H'$  index for all the 24 traits in the core collection (0.48) was comparable to that in the entire collection (0.47). Among the qualitative traits, bur colour and sheath hairiness had the highest and lowest  $H'$  values in the core (0.64 and 0.24) and entire collections (0.63 and 0.23), respectively. Similarly, among the quantitative traits, green fodder yield/plant and leaf width showed the maximum and minimum values for the  $H'$  index, respectively, in both the core (0.74 and 0.43) and entire collection (0.73 and 0.41). The similar trend of  $H'$  index in the entire and core collection indicated that the developed core set adequately captured the overall diversity available in the entire collection. Brown (1989) emphasized that

*Core set of buffel grass*

**Table 5.** Coincidence rate (CR %), Variable rate (VR %) and Shannon-Weaver diversity index ( $H'$ ) in entire and core collection of *Cenchrus*

| Traits                       | CR%   | VR%    | $H'$ index        |                 |
|------------------------------|-------|--------|-------------------|-----------------|
|                              |       |        | Entire collection | Core collection |
| <b>Quantitative</b>          |       |        |                   |                 |
| Days to 50% flowering        | 89.5  | 104.1  | 0.59              | 0.61            |
| Plant height (cm)            | 84.1  | 106.5  | 0.55              | 0.56            |
| Number of tillers/plant      | 96.4  | 110.1  | 0.65              | 0.67            |
| Number of leaves/plant       | 80.8  | 95.9   | 0.46              | 0.48            |
| Leaf length (cm)             | 81.2  | 86.0   | 0.51              | 0.53            |
| Leaf width (cm)              | 74.6  | 125.1  | 0.41              | 0.43            |
| Peduncle length (cm)         | 76.7  | 85.6   | 0.54              | 0.55            |
| Spike length (cm)            | 100.0 | 99.4   | 0.62              | 0.59            |
| Spike breadth (cm)           | 100.0 | 108.2  | 0.53              | 0.55            |
| Number of spikes/plant       | 86.0  | 127.1  | 0.61              | 0.61            |
| Number of spikelets/spike    | 55.8  | 74.2   | 0.52              | 0.54            |
| Green fodder yield/plant (g) | 99.7  | 96.5   | 0.73              | 0.74            |
| Dry fodder yield/plant (g)   | 100.0 | 97.6   | 0.62              | 0.63            |
| Dry matter percentage        | 94.8  | 116.4  | 0.56              | 0.58            |
| 100 Fasicle weight (g)       | 71.5  | 111.2  | 0.57              | 0.55            |
| Average                      | 86.07 | 102.93 | 0.56              | 0.57            |
| <b>Qualitative</b>           |       |        |                   |                 |
| Early vigour                 | -     | -      | 0.28              | 0.29            |
| Growth habit                 | -     | -      | 0.26              | 0.28            |
| Leaf type                    | -     | -      | 0.32              | 0.33            |
| Leaf colour                  | -     | -      | 0.36              | 0.36            |
| Culm formation               | -     | -      | 0.39              | 0.40            |
| Sheath hairiness             | -     | -      | 0.23              | 0.24            |
| Bur colour                   | -     | -      | 0.63              | 0.64            |
| Spine arrangement            | -     | -      | 0.42              | 0.43            |
| Leaf hairiness               | -     | -      | 0.32              | 0.33            |
| Average                      |       |        | 0.36              | 0.37            |

core subsets should be derived using characterization data and eco-geographic information, while Galway (1995) highlighted the critical role of passport data. In this study, the core collection was assembled using 24 agro-morphological traits and stratification across eight agro-geographic regions. According to the neutral allele theory, a subset comprising ~10% of the total collection is expected to retain 75 to 90% of the genetic diversity (Brown, 1989; Bisht *et al.*, 1998). The *Cenchrus* core developed here represents 13.3% of the entire germplasm and conserves more than 95% of the total diversity.

An adequate and proper sampling, essential in developing a representative core collection, should consider the phenotypic associations arising out of co-adapted gene complexes (Ortiz *et al.*, 1998). The constituted core collection preserved 35, out of 54 significant correlations

( $P= 0.05$ ;  $p = 0.01$ ) observed in the entire collection indicating that the co-adapted gene complexes governing these phenotypic associations are properly assembled in the core collection. However, it should be noted that with large number of degrees of freedom, correlation coefficients with a smaller magnitude are significant in the entire collection. Therefore, it was not surprising that many of the weak associations were not significant in smaller core subset. Correlation values greater than 0.707 and lesser than -0.707 are considered biologically significant (Skinner *et al.*, 1999). In our study, we found such strong relationship in the entire collection and core collection between number of tillers per plant and green fodder yield (Table 6) suggesting that tillers/plant could serve a useful purpose in choosing the high biomass producing accessions.

Table 6. Phenotypic correlation coefficients between 15 quantitative traits in *Cenchrus* entire (above diagonal) and core collection (below diagonal)

| Traits <sup>†</sup> | DFF     | PH       | NTP     | NLP     | LL       | LW       | PL      | SL       | SB      | NSP     | NSS      | GFY     | DFY     | DM%      | HFW      |
|---------------------|---------|----------|---------|---------|----------|----------|---------|----------|---------|---------|----------|---------|---------|----------|----------|
| DFF                 | -       | 0.020    | 0.190** | 0.060   | -0.080   | -0.020   | 0.050   | 0.030    | 0.080   | 0.010   | 0.050    | -0.080  | -0.110  | -0.120   | -0.170** |
| PH                  | 0.150   | -        | -0.070  | 0.180   | 0.250**  | 0.260**  | 0.430** | 0.280**  | 0.080   | 0.040   | 0.302**  | 0.290** | 0.220** | -0.170** | -0.080   |
| NTP                 | 0.070   | 0.120    | -       | 0.070   | -0.290** | -0.190** | -0.130* | -0.260** | 0.040   | 0.002   | -0.190** | 0.743** | -0.020  | 0.090    | -0.193** |
| NLP                 | -0.080  | 0.270    | 0.080   | -       | 0.160**  | 0.090**  | 0.110** | 0.102**  | 0.123** | -0.002  | 0.140**  | 0.120** | 0.102** | -0.050   | 0.173**  |
| LL                  | -0.050  | 0.160    | -0.130  | 0.201   | -        | 0.480**  | 0.325** | 0.630**  | 0.060   | 0.070   | 0.440**  | 0.290** | 0.280** | 0.010    | 0.102**  |
| LW                  | -0.002  | 0.311**  | -0.180  | 0.250*  | 0.540**  | -        | 0.402** | 0.380**  | 0.002   | 0.020   | 0.370**  | 0.210** | 0.230** | 0.050    | 0.090    |
| PL                  | 0.201   | 0.460**  | 0.030   | 0.230*  | 0.430**  | 0.330**  | -       | 0.450**  | 0.102** | 0.030   | 0.390**  | 0.170** | 0.160** | 0.020    | 0.001    |
| SL                  | 0.080   | 0.280*   | -0.190  | 0.060   | 0.532**  | 0.430**  | 0.370** | -        | 0.260** | -0.030  | 0.410**  | 0.173** | 0.153** | -0.040   | 0.050    |
| SB                  | 0.030   | 0.220*   | 0.090   | 0.140   | 0.220*   | 0.160    | 0.090   | 0.430**  | -       | 0.120** | 0.080    | 0.050   | 0.020   | 0.120**  | 0.160**  |
| NSP                 | -0.010  | 0.070    | 0.080   | 0.080   | 0.030*   | 0.023    | 0.102   | -0.040   | 0.120   | -       | 0.060    | 0.070   | 0.060   | 0.010    | 0.040    |
| NSS                 | 0.221*  | 0.530*   | -0.090  | 0.260*  | 0.423**  | 0.380**  | 0.442** | 0.330**  | 0.210   | 0.102   | -        | 0.270   | 0.080   | -0.040   | -0.160** |
| GFY                 | -0.040  | 0.260*   | 0.821** | 0.470** | 0.240*   | 0.390**  | 0.140   | 0.160    | 0.080   | 0.170   | 0.220    | -       | 0.447** | -0.080   | -0.120** |
| DFY                 | -0.10   | 0.170    | 0.102   | 0.431** | 0.250*   | 0.412**  | 0.120   | 0.140    | 0.060   | 0.080   | 0.190    | 0.570** | -       | 0.230**  | 0.012    |
| DM%                 | -0.250* | -0.310** | -0.080  | -0.120  | -0.040   | -0.080   | -0.070  | -0.150   | -0.130  | 0.110   | -0.150   | -0.220* | 0.365** | -        | 0.060    |

\*Significant at  $P \leq 0.05$ ; \*\* Significant at  $P \leq 0.01$ ; †DFF: Days to 50% flowering; PH: Plant height; NTP: Number of tillers per plant; NLP: Number of leaves per plant; LL: Leaf length; LW: Leaf width; PL: Peduncle length; SL: Spike length; SB: Spike breadth; NSP: Number of spikes per plant; NSS: Number of spikelets per spike; GFY: Green fodder yield per plant; DFY: Dry fodder yield per plant; DM%: Dry matter percentage; HFW: 100 fascicle weight

## Conclusion

The evaluation and clustering of the *Cenchrus* collection provided valuable insights for developing an efficient core set. In buffel grass, where breeding is still at an early stage, systematic assessment of this core collection will aid in selecting promising genotypes for cultivar development. As *Cenchrus* includes both sexual and apomictic species, variability can be exploited either through phenotype-based selection or hybridization where sexual forms exist. The constituted core collection of *C. ciliaris* offers significant potential, especially with the availability of sexual forms. Integrating molecular and phenotypic characterization will enable identification of superior parental combinations for forage yield, quality, and biofuel traits, while also facilitating molecular mapping and structured breeding efforts.

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