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# Barnyard millet global core collection evaluation in the submontane Himalayan region of India using multivariate analysis

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## ARTICLE INFO

### Article history:

Received 16 April 2015

Received in revised form 22 July 2015

Accepted 6 August 2015

Available online 15 August 2015

### Keywords:

Agro-morphological variation

Barnyard millet core germplasm

Cluster analysis

*Echinochloa* spp

Principal component analysis

## ABSTRACT

Barnyard millet (*Echinochloa* spp.) is one of the most underresearched crops with respect to characterization of genetic resources and genetic enhancement. A total of 95 germplasm lines representing global collection were evaluated in two rainy seasons at Almora, Uttarakhand, India for qualitative and quantitative traits and the data were subjected to multivariate analysis. High variation was observed for days to maturity, five-ear grain weight, and yield components. The first three principal component axes explained 73% of the total multivariate variation. Three major groups were detected by projection of the accessions on the first two principal components. The separation of accessions was based mainly on trait morphology. Almost all Indian and origin-unknown accessions grouped together to form an *Echinochloa frumentacea* group. Japanese accessions grouped together except for a few outliers to form an *Echinochloa esculenta* group. The third group contained accessions from Russia, Japan, Cameroon, and Egypt. They formed a separate group on the scatterplot and represented accessions with lower values for all traits except basal tiller number. The interrelationships between the traits indicated that accessions with tall plants, long and broad leaves, longer inflorescences, and greater numbers of racemes should be given priority as donors or parents in varietal development initiatives. Cluster analysis identified two main clusters based on agro-morphological characters.

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## 1. Introduction

Barnyard millet (*Echinochloa* spp.) is one of the oldest domesticated millets in the semiarid tropics of Asia and Africa. Two main species, *Echinochloa esculenta* (A. Braun) H. Scholz; syn. *Echinochloa utilis* Ohwi et Yabuno (Japanese barnyard millet) and *Echinochloa frumentacea* Link; syn. *Echinochloa colona* var.

*frumentacea* (Link) Ridl. (Indian barnyard millet) are cultivated and grown as cereals. It is a staple cereal in areas where climatic and edaphic conditions are unsuitable for rice cultivation [1]. In India, barnyard millet is grown in the Himalayan region from the north to the Deccan plateau in the south. It is generally cultivated in hill slopes and undulating fields of hilly, tribal, or marginal areas, where

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Peer review under responsibility of Crop Science Society of China and Institute of Crop Science, CAAS.

few options exist for crop diversification. In addition to the two domesticated species, the genus includes about 20–30 annual and perennial wild species distributed worldwide [2,3], many of which can grow in wet or well-watered situations and compete successfully with rice.

Barnyard millet has a wide adaptation capacity and can grow up to an altitude of 2000 m above mean sea level during summer season [4]. Diversity in barnyard millet has fast eroded, owing to a considerable reduction in acreage and changing socio-cultural and economic dimensions of the farming community in India [5]. Many efforts have been made to preserve the crop diversity *ex situ*, but information about on-farm and *in situ* conservation of all small millets is scarce [6].

The classification of the genus *Echinochloa* on the basis of inflorescence morphology into two species, four subspecies, and eight races is simple and reliable and helps to elucidate not only the patterns of variation but also the paths of evolutionary history. However, it is difficult to categorize the variation in germplasm collections for economic purposes [7]. Multivariate methods are useful for characterization, evaluation, and classification of plant genetic resources when a large number of accessions are to be assessed for several characters of agronomic and physiological importance [8]. The utility of multivariate methods for handling morphological variation in germplasm collections has been demonstrated in many crop plants (finger millet [9]; sorghum [10]; barnyard millet [4]). The information

generated can be useful for identifying groups of accessions that have desirable characters for crossing, planning efficient germplasm collecting expeditions, establishing core collections, revealing the patterns of variation in germplasm collections, and investigating aspects of crop evolution [8,11–15].

The present study describes the characterization of a recently developed barnyard millet global core germplasm collection [16] and identification of groups of accessions with similar quantitative characters, using a range of multivariate statistical methods, for genotypes grown in the submontane Himalayan region where this crop occupies a special place as food and fodder [17].

## 2. Materials and methods

### 2.1. Plant materials

The 95 germplasm accessions used include 89 accessions from the barnyard millet core collection developed by ICRISAT and six check genotypes [16]. The accessions with their source countries are presented in Table S1.

The crop was raised from July to November, 2011 and 2012 at the experimental farm of the ICAR-Vivekananda Institute of Hill Agriculture (79° 39' E latitude and 25° 35' N longitude, 1250 m above sea level). During 2011, a single row of each accession was planted in an augmented design, whereas in

**Table 1 – Qualitative trait analyses in a barnyard millet core germplasm collection based on two years of data.**

Trait	Classification	Number of accessions	Origin with accession <sup>a</sup>
Growth habit	Erect	89	India—51, Japan—18, Russia—3, Egypt—1, Pakistan—1, Malawi—1, Cameroon—1, Syrian Arab Republic—1, and Origin unknown—12
	Decumbent	5	Japan—5
	Prostrate	0	
Plant pigmentation	Green	81	India—42, Japan—20, Russia—3, Egypt—1, Pakistan—1, Malawi—1, Syrian Arab Republic—1, and Origin unknown—12
	Pigmented	13	India—9, Japan—3, and Cameroon—1
Degree of culm branching	Low	86	India—51, Japan—18, Egypt—1, Pakistan—1, Malawi—1, Cameroon—1, Syrian Arab Republic—1, and Origin unknown—12
	Medium	5	Japan—4; Russia—1
	High	3	Japan—1; Russia—2
Inflorescence shape	Cylindrical	37	India—23, Japan—4, Russia—3, Egypt—1, Malawi—1, and Origin unknown—5
	Pyramidal	56	India—28, Japan—18, Syrian Arab Republic—1, Pakistan—1, Cameroon—1, and Origin unknown—7
	Globose	1	Japan
Inflorescence compactness	Open	40	India—22, Japan—10, Syrian Arab Republic—1, Pakistan—1, and Origin unknown—6
	Intermediate	43	India—28, Japan—10, Russia—1, Malawi—1, and Origin unknown—3
	Compact	11	India—1, Japan—3, Russia—2, Egypt—1, Cameroon—1, and Origin unknown—3
Lower raceme shape	Straight	52	India—25, Japan—14, Russia—3, Syrian Arab Republic—1, Pakistan—1, Cameroon—1, and Origin unknown—7
	Curved	41	India—26, Japan—8, Egypt—1, Malawi—1, and Origin unknown—5
	Slender	1	Japan
Lower raceme branching	Absent	88	India—51, Japan—17, Russia—3, Egypt—1, Pakistan—1, Malawi—1, Cameroon—1, Syrian Arab Republic—1, and Origin unknown—12
	Present	6	Japan

<sup>a</sup> Numbers following country names are those of accessions from that country of origin for that trait classification.

2012 two rows of each accession were planted in an alpha lattice design with two replications. Five blocks constituted one replication with 19 accessions in each block. The row length was 3 m with a row-to-row spacing of 22.5 cm. Thinning was applied within a month after sowing to maintain a plant-to-plant spacing of 7.5 cm within rows.

Fertilizer was applied at 40:20:0 (N:P:K) kg ha<sup>-1</sup>, where the entire amount of phosphorus and half of the nitrogen was applied as a basal dose during field preparation. The remaining half of the nitrogen was applied as top dressing 45 days after sowing and after the second weeding. Manual weeding was performed twice during the crop season, 20 and 40 days after sowing.

## 2.2. Data recording

Data were recorded for 7 qualitative and 16 quantitative traits, following the descriptors of barnyard millet [18]. For every accession in a plot, five individual plants were used for recording the data, except for days to flowering and days to maturity, which were recorded on a plot basis.

## 2.3. Statistical analysis

The agro-morphological data of each year separately as well as the pooled data were analyzed. The data could not be subjected to a combined analysis of variance, owing to the unavailability of replicated data in the first year. The adjusted mean values of the first and second years were used for further analysis. The adjusted mean values of the two years were pooled and mean values were computed for combined analysis. Statistical analyses were performed using JMP 2009 (JMP, Version 9.0.0. SAS Institute Inc., Cary, NC) and SPSS (Statistical Package for Social Science, SPSS Inc., Chicago, IL). For multifactorial comparison, principal component analysis (PCA) was used to display the correlations between the various morphological and related parameters and their relationship with different barnyard millet genotypes. Two-way cluster analysis was performed with JMP 2009. One accession (IEc 566) did not set seeds and was not included in the analysis.

## 3. Results and discussion

The qualitative trait data showed that the predominant growth habit in barnyard millet is erect with green plant pigmentation. Culm branching was low in most of the accessions belonging to the *E. frumentacea* group. Medium and high culm branching was observed in eight accessions of Japanese and Russian origin. Among inflorescence traits, a pyramidal open shape with straight lower racemes was abundant. The five accessions having branching in the lower raceme were all of Japanese origin (Table 1). The qualitative trait data showed marked differences between Japanese accessions in comparison to other accessions, indicating them to be of a group of different origin: *E. esculenta*.

Morphological characterization is important for identification of accessions with desirable traits intended to be employed directly as cultivars or as trait donors for use in crop improvement programs [19]. We found a wide range of variation in agronomic performance among the accessions evaluated. The mean, range, genotypic variance, error variance, heritability ( $h^2_{bs}$ -broad-sense) and coefficient of variation (CV) of quantitative traits are presented in Table 2. In the analysis of quantitative traits, the coefficient of variation varied from 0.79% for days to maturity to 36.43 for basal tiller number. The  $h^2_{bs}$  estimates ranged from 70.14 for inflorescence length to 99.87 for days to maturity. All of the studied traits exhibited high heritability. Sonnad et al. [20] also observed high heritability for all quantitative traits in finger millet.

The highest five-ear grain weight was found in check variety PRJ 1 (24.25 g) followed by all accessions of Indian origin up to the yield level of 17.54 g. The accessions from Japan were low-yielding, except for PRJ 1, IEc 552 (17.52 g), and IEc 530 (16.71 g). We observed a range of 58–91 for days to maturity, 1.14–9.28 for basal tiller number, 2.57–9.17 mm for culm thickness, 79.68–156.85 cm for plant height, 4.19–9.16 for number of nodes, 12.28–31.26 cm for flag leaf length, 1.38–3.02 cm for flag leaf width, 6.86–14.42 cm for flag leaf sheath length, 8.09–29.84 cm for peduncle length, from –0.47 to 19.0 cm for panicle exertion, 12.12–24.02 cm for inflorescence

**Table 2 – Variance components of a barnyard millet core germplasm collection.**

Trait	GM	Range	CV (%)	$h^2_{bs}$ (%)	$\sigma^2_g$	$\sigma^2_e$
Days to 50% flowering	51.23	30.79–67.90	2.50	99.39	90.40	1.64
Days to maturity	76.07	58.02–90.98	0.79	99.87	95.28	0.36
Basal tiller number	2.26	1.14–9.28	36.43	87.08	1.53	0.68
Culm thickness (mm)	5.42	2.53–9.17	10.01	94.36	1.64	0.29
Plant height (cm)	125.12	79.68–156.85	7.30	92.39	338.12	83.45
Number of nodes	6.76	4.19–9.16	8.22	93.20	1.41	0.31
Flag leaf length (cm)	22.56	12.28–31.26	12.50	86.46	16.92	7.95
Flag leaf width (cm)	2.09	1.38–3.02	10.95	89.86	0.15	0.05
Flag leaf sheath length (cm)	9.34	6.86–14.42	15.77	78.56	2.65	2.17
Peduncle length (cm)	15.18	8.09–29.84	18.16	89.65	21.97	7.60
Panicle exertion (cm)	5.90	–0.47–19.00	25.99	94.66	13.90	2.35
Inflorescence length (cm)	16.27	12.12–24.02	18.46	70.13	7.06	9.02
Inflorescence width (cm)	3.89	2.36–5.79	14.83	82.47	0.52	0.33
Raceme number	31.26	8.73–49.74	11.86	96.29	118.88	13.74
Lower raceme length (cm)	3.19	1.78–6.16	17.02	92.59	1.22	0.29
Five-ear grain weight (g)	12.83	4.20–24.25	32.42	80.24	23.43	17.31

length, 2.36–5.79 cm for inflorescence width, 8.73–49.74 for raceme number, 1.78–6.16 cm for lower raceme length, and 4.20–24.25 g for five-ear grain weight in the global core germplasm collection (Table 2). The normal maturity duration of released varieties of barnyard millet in this ecology is 80–90 days. While, we observed several accessions with less than 64 days to maturity (Table 5), which can be used in the breeding program for earliness in crop maturity. Most of these early accessions were of Japanese and Russian origin. We observed high variation for grain yield, also reported previously [21–23]. The availability of genetic diversity in the core germplasm collection provides an opportunity to select best genotypes for different environments.

### 3.1. Principal component analysis

Interrelationships among the different parameters were evaluated by principal component analysis (PCA). The first three PCA components provided a reasonable summary of the data and explained 73% of the total variation, and subsequent components contributed 5% or less (Table 3). The first principal component (PC1) was the most important and explained 45% of the total variation. PC1 was attributed to days to flowering, days to maturity, culm thickness, plant height, number of nodes, flag leaf length, flag leaf width, inflorescence length, raceme number, and five-ear grain weight for largest positive loadings. Basal tiller number, flag leaf sheath length, peduncle length, panicle exertion, and lower raceme length had largest negative loadings. As a result, the first PC differentiated the accessions mainly by the contribution of high values for culm thickness, number of nodes, and raceme number. The second PC explained an additional 15.75% of the total variation and was attributed to positive loadings of plant height, flag leaf length, flag leaf sheath length, peduncle length, panicle exertion, inflorescence length, inflorescence width, and lower raceme length. The third PC, which explained 11.7% of the total variation, differentiated the accessions by higher numbers of basal tillers and narrow flag leaves and low levels of grain yield. Three fourths of the parameters occupied the right side of the biplot and one fourth were observed in the upper left side (Fig. 1).

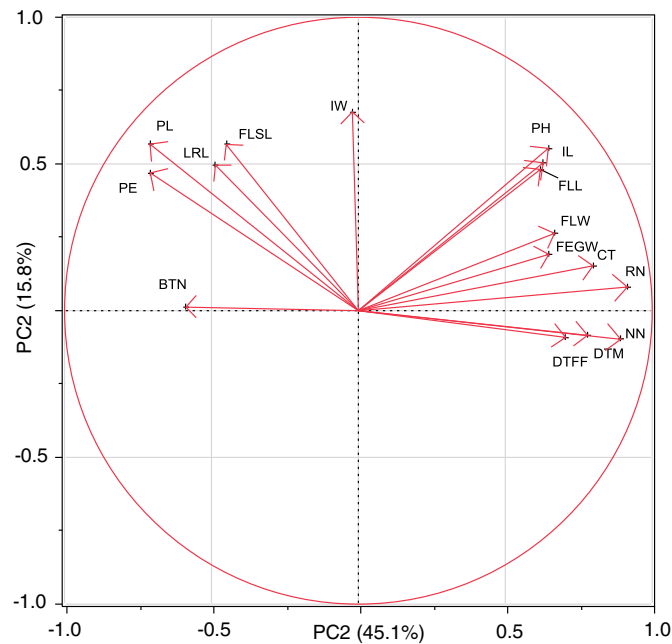
Three major groups were detected on the basis of projection of the accessions on the first two principal components. The majority of Indian and origin-unknown accessions were on the right-hand side in the biplot, whereas most of the Japanese accessions, namely, IEc 455, IEc 487, IEc 435, IEc 448, IEc 449, IEc 452, IEc 471, IEc 516, IEc 423, IEc 498, IEc 552, IEc 404, IEc 521, IEc 530, and PRJ 1 were on the top left. Six accessions from Japan (IEc 436, IEc 519, IEc 517, IEc 511, IEc 537, and IEc 561), three from Russia (IEc 330, IEc 331, and IEc 338), and one each from Cameroon (IEc 624), Egypt (IEc 353), and the Syrian Arab Republic (IEc 346) constituted the third cluster (Fig. 2).

Principal component analysis revealed that days to flowering, days to maturity, culm thickness, plant height, number of nodes, flag leaf length, flag leaf width, inflorescence length, raceme number, and five-ear grain weight contributed most to genetic diversity. A scatterplot of PC1 and PC2 showed overlapping of accessions of Indian origin with accessions of unknown origin along with one accession from Pakistan. A possible explanation

**Table 3 – Principal component analysis based on morphological and agronomic traits of 94 barnyard millet accessions, and significant loadings (in bold) of the first three principal components from mean data of two years.**

Trait	PC1	PC2	PC3
Days to 50% flowering	<b>0.705</b>	–0.091	<b>0.521</b>
Days to maturity	<b>0.780</b>	–0.084	<b>0.479</b>
Basal tiller number	– <b>0.587</b>	0.012	<b>0.556</b>
Culm thickness	<b>0.798</b>	0.153	–0.046
Plant height	<b>0.646</b>	<b>0.553</b>	0.223
Number of nodes	<b>0.893</b>	–0.098	0.220
Flag leaf length	<b>0.619</b>	<b>0.481</b>	–0.018
Flag leaf width	<b>0.667</b>	0.264	–0.556
Flag leaf sheath length	– <b>0.450</b>	<b>0.566</b>	– <b>0.379</b>
Peduncle length	– <b>0.709</b>	<b>0.567</b>	0.020
Panicle exertion	– <b>0.708</b>	<b>0.469</b>	0.170
Inflorescence length	<b>0.629</b>	<b>0.504</b>	0.062
Inflorescence width	–0.021	<b>0.677</b>	<b>0.399</b>
Raceme number	<b>0.916</b>	0.081	0.015
Lower raceme length	– <b>0.487</b>	<b>0.496</b>	0.134
Five ear grain weight	<b>0.648</b>	0.192	– <b>0.542</b>
Eigen value	7.2278	2.5209	1.8682
Percent of total variation	45.174	15.755	11.676
Cumulative value	45.174	60.929	72.605

for this overlap may be that all accessions of unknown origin either originated in the Indian subcontinent or have similar morphologies. Given that the separation of accessions was based mainly on agro-morphological traits, all the Indian accessions along with accessions of unknown origin and one accession each of Pakistan and Malawi grouped together. These accessions possibly belong to the *E. frumentacea* group. The Japanese accessions formed a second group, indicating them to be of the *E. esculenta* group. The third group contained a mix of accessions from Russia, Japan, Cameroon, and Egypt. The reason for the clear separation of Indian and Japanese accessions was their trait morphology and growth habitat. The accessions of Indian and unknown origin in the first group were characterized by thicker culms, taller plants, greater number of nodes, longer flag leaves, longer inflorescence, greater number of racemes, and late maturity. The Japanese accessions in the second group, in contrast, typically had longer flag leaf sheath, longer peduncles, high panicle exertion, and early maturity. The third group comprised accessions with lower values for all traits except basal tiller number. This finding matches previous observations that the races of *E. colona* do not correspond to geographic, ecological, or ethnological divisions, but are instead based on morphology [24]. *E. frumentacea* accessions are generally of longer growth duration and are adapted to both temperate as well as tropical climatic conditions, whereas *E. esculenta* accessions are adapted to temperate ecology and perform poorly in tropical conditions. Our results of three different groups in the barnyard millet global core collection are in agreement with results of Wallace et al. [25] who also obtained three groups using multidimensional scaling and PCA in SNP data generated by genotyping by sequencing in the same core germplasm. The accessions in the third group were speculated to be results of seed contamination [25], but hybrids between these two species are known to be sterile [26]. We accordingly propose that the third group consists of accessions belonging to wild, weedy species of *Echinochloa*,



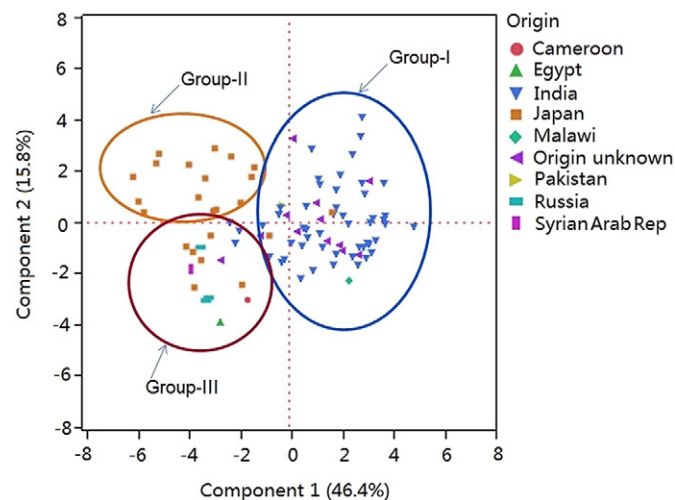
**Fig. 1 – Loading plot of PC1–PC2 for 94 barnyard millet genotypes. DTFF, days to 50% flowering; DTM, days to maturity; BTN, basal tiller number; CT, culm thickness; PH, plant height; NN, number of nodes; FLL, flag leaf length; FLW, flag leaf width; FLSL, flag leaf sheath length; PL, peduncle length; PE, panicle exertion; IL, inflorescence length; IW, inflorescence width; RN, raceme number; LRL, lower raceme length; FEGW, five-ear grain weight.**

given their higher basal tiller numbers, weak culms, low yield, and values for yield component traits.

### 3.2. Relationship between traits

The correlation coefficients between traits are presented in Table 4. Character associations may be used to identify a few traits that are less relevant and could be of low priority in germplasm evaluation [19]. The evaluation data provides a valuable opportunity for assessing relationships among traits to test the similarity between different groups [27]. This practice simplifies work and saves resources. Association studies among different traits are important for barnyard

millet breeders in effective selection of desirable genotypes. Of the 120 character associations estimated, five associations, namely peduncle length with panicle exertion (0.925), days to maturity with days to flowering (0.852), number of nodes with raceme number (0.801), days to maturity with number of nodes (0.796) and culm thickness with raceme number (0.790) had high estimates, indicating that in future characterization of barnyard germplasm, tedious observations such as of panicle exertion, number of nodes, and culm thickness may be avoided. Upadhyaya et al. [19] also observed a strong association of peduncle length with panicle exertion in finger millet and emphasized recording observations of the easy trait, peduncle length, and not panicle exertion. Gupta et al.



**Fig. 2 – Score plot of PC1–PC2 for 94 barnyard millet genotypes.**

**Table 4 – Correlation coefficients among grain yield-associated component traits in barnyard millet based on mean data of two years.**

Trait	DTFF	DTM	BTN	CT	PH	NN	FLL	FLW	FLSL	PL	PE	IL	IW	RN	LRL
DTM	0.852**														
BTN	-0.193	-0.243*													
CT	0.611**	0.542**	-0.529**												
PH	0.562**	0.552**	-0.331**	0.661**											
NN	0.788**	0.796**	-0.496**	0.703**	0.655**										
FLL	0.311**	0.461**	-0.366**	0.440**	0.536**	0.400**									
FLW	0.226*	0.254*	-0.589**	0.685**	0.423**	0.440**	0.618**								
FLSL	-0.485**	-0.565**	0.137	-0.150	-0.018	-0.536**	-0.088	-0.011							
PL	-0.549**	-0.573**	0.443**	-0.437**	-0.068	-0.658**	-0.174	-0.340**	0.632**						
PE	-0.505**	-0.482**	0.507**	-0.510**	-0.089	-0.624**	-0.192	-0.424**	0.434**	0.925**					
IL	0.428**	0.455**	-0.325**	0.553**	0.604**	0.454**	0.652**	0.466**	-0.069	-0.224*	-0.244*				
IW	0.002	0.113	0.173	-0.090	0.333**	0.007	0.340**	-0.018	0.135	0.245*	0.257*	0.316**			
RN	0.721**	0.689**	-0.486**	0.790**	0.672**	0.801**	0.580**	0.617**	-0.317**	-0.565**	-0.570**	0.572**	0.013		
LRL	-0.289**	-0.372**	0.304**	-0.304**	-0.045	-0.400**	-0.247*	-0.290**	0.419**	0.491**	0.410**	-0.048	0.455**	-0.489**	
FEGW	0.233*	0.245*	-0.615**	0.578**	0.357**	0.456**	0.432**	0.765**	-0.026	-0.368**	-0.464**	0.442**	-0.067	0.589**	-0.175

DTFF, days to 50% flowering; DTM, days to maturity; BTN, basal tiller number; CT, culm thickness; PH, plant height; NN, number of nodes; FLL, flag leaf length; FLW, flag leaf width; FLSL, flag leaf sheath length; PL, peduncle length; PE, panicle exertion; IL, inflorescence length; IW, inflorescence width; RN, raceme number; LRL, lower raceme length; FEGW, five-ear grain weight.

\*\* Significant at the 0.01 probability level (2-tailed).

\* Significant at the 0.05 probability level (2-tailed).

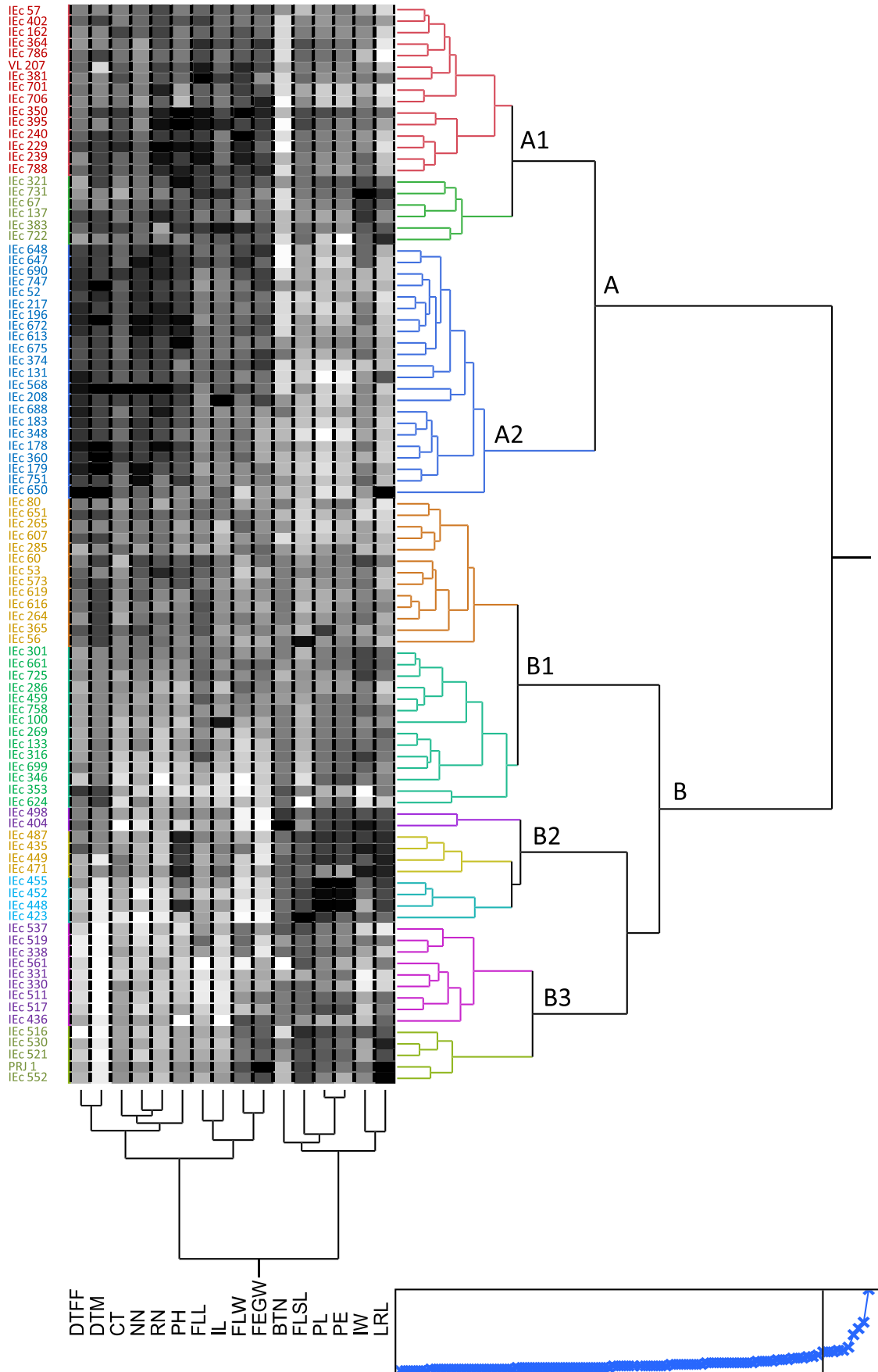


Fig. 3 - Two way hierarchical clustering of 94 barnyard millet core accessions.

[4] found a positive association of grain yield with raceme number and flag leaf width. In finger millet too, a positive association of finger number per ear with grain weight per ear was observed [20]. These associations suggest that raceme number and flag leaf width will be effective selection indices for grain yield. In addition, culm thickness and flag leaf width were highly positively correlated with five-ear grain weight, revealing the roles of biomass and photosynthesis, respectively, in sink development.

### 3.3. Cluster analysis

Two-way cluster analysis separated the accessions as well as traits into two major groups (Fig. 3). Group A contained 43 accessions, of which eight (IEc 786, IEc 701, IEc 706, IEc 788, IEc 731, IEc 722, IEc 747, and IEc 751) were of unknown origin, one each were from Japan (IEc 402) and Malawi (IEc 348) and the rest were Indian. This group was further subdivided into two groups. Group B contained 51 accessions of diverse origins. This group was subdivided into three subgroups (B1, B2, and B3) representing 27, 10, and 14 accessions, respectively. Subgroup B1 contained one accession each from Pakistan (IEc 661), Japan (IEc 459), Cameroon (IEc 624), Egypt (IEc 353) and Syrian Arab Republic (IEc 346) and four accessions (IEc 264, IEc 725, IEc 699) of unknown origin, and the rest were Indian. Subgroups B2 and B3 contained all Japanese accessions except for three lines from Russia.

Two-way cluster analysis broadly separated the accessions based on trait variation. The first group A contained accessions with late maturity, high culm thickness, more nodes, taller plants, larger and broader flag leaves, larger inflorescences, more racemes, and high five-ear grain weight. This group contained all Indian and origin-unknown accessions, clearly indicating that Indian and origin-unknown accessions can be used as donors for these traits. The accessions in group B had more basal tillers, longer flag leaf sheaths, longer peduncles, high panicle exertion, wider inflorescences, and longer lowest racemes. The subgrouping in cluster B also showed separation of accessions based on geographical origin. All the accessions from Japan and Russia were grouped together in subgroups B2 and B3, whereas B1 contained accessions of Indian, origin-unknown, Syrian Arab Republic, Egypt and Cameroon origin. This diversity may be due to migration of material from one region to another, and some ecological conditions could also influence the traits. The check genotypes VL 207 (*E. frumentacea*) and PRJ-1 (*E. esculenta*) occupied A1 and B3 clusters, respectively, clearly indicating the separation of the two different species of *Echinochloa* by hierarchical clustering. The results are in agreement with Wallace et al. [25] where the separation of two species was based on SNP data and the intermediate accessions were reported to be seed mixtures. But, in our opinion, the intermediate (based on trait values) accessions among both species are potential candidates for exploiting trait variation for genetic improvement of the crop.

Overall, there was a high level of genetic diversity of morphological and agronomic characters in the barnyard millet core collection. Gowda et al. [28] also observed high diversity in small millet germplasm collections of ICRISAT and identified trait-specific diverse lines in foxtail and finger

millet. We too identified some promising trait donors (Table 5) which could be efficiently used in breeding programs for the improvement of this orphan crop. The PCA and cluster analyses provided a simplified classification of barnyard millet core accessions for use in breeding. Categorizing germplasm accessions into morphologically similar and presumably genetically similar groups is useful for selecting parents for crossing [15]. Crossing accessions belonging to different clusters would maximize opportunities for transgressive segregation because of the higher probability that unrelated genotypes will contribute unique desirable alleles at multiple loci [8,9,29,30]. Thus, the grouping of accessions by multivariate methods in the present study will be of practical value to barnyard millet breeders in allowing them to choose elite accessions from different clusters as parental lines for crossing programs.

### Acknowledgments

We thank Dr. M.V.C. Gowda, Project Coordinator, AICSMIP, UAS, Bangalore, India for initiating and facilitating the movement of barnyard millet core germplasm from ICRISAT. Authors are also

**Table 5 – Promising trait donors identified from mean data of barnyard millet core germplasm evaluation.**

n	Promising accession
DFFF < 40	IEc 516, IEc 519, IEc 338, IEc 330, IEc 511, IEc 331, IEc 561, IEc 537, IEc 452, IEc 521, IEc 517, IEc 346
DTM < 64	IEc 537, IEc 561, IEc 511, IEc 517, IEc 330, IEc 331, IEc 516, IEc 338, IEc 519, IEc 521, IEc 455, IEc 423, PRJ 1, IEc 552, IEc 449, IEc 530, IEc 452, IEc 448, IEc 436, VL 207
BTN > 4	IEc 404, IEc 498, IEc 353, IEc 537, IEc 471, IEc 449
CT > 7.0	IEc 568, IEc 229, IEc 690, IEc 360, IEc 350, IEc 383, IEc 162, IEc 208, IEc 178, IEc 240
PH > 145.0	IEc 395, IEc 350, IEc 613, IEc 196, IEc 321, IEc 229, IEc 788, IEc 672, IEc 487, IEc 471, IEc 448, IEc 568
NN > 8	IEc 568, IEc 196, IEc 751, IEc 179, IEc 672, IEc 647, IEc 52, IEc 747, IEc 690, IEc 675, IEc 183, IEc 348, IEc 217, IEc 613, IEc 208, IEc 360, IEc 178
FLL > 30.0	IEc 381, IEc 350, IEc 239, IEc 395
FLW > 2.5	IEc 240, IEc 350, IEc 239, IEc 229, VL 207, IEc 383, IEc 647, IEc 381, IEc 701, IEc 788, IEc 395
FLSL > 11.5	IEc 423, IEc 56, IEc 516, IEc 452, PRJ 1, IEc 395, IEc 448
PL < 10.0	IEc 348, IEc 131, IEc 374, IEc 650, IEc 179
PE < 2.0	IEc 722, IEc 131, IEc 348, IEc 650, IEc 374, IEc 568, IEc 647
IL > 20.0	IEc 208, IEc 383, IEc 100, IEc 395, IEc 731, IEc 381
IW > 5.0	IEc 731, IEc 471, IEc 404, IEc 435, IEc 137
RN > 45	IEc 568, IEc 229, IEc 178, IEc 395, IEc 239, IEc 688, IEc 648, IEc 196, IEc 217, IEc 350
LRL > 6.0	IEc 650, PRJ 1, IEc 552
FEGW > 19.0	PRJ 1, IEc 706, IEc 350, IEc 788, IEc 648, IEc 364, IEc 395, IEc 675, IEc 374

DFFF, days to 50% flowering; DTM, days to maturity; BTN, basal tiller number; CT, culm thickness; PH, plant height; NN, number of nodes; FLL, flag leaf length; FLW, flag leaf width; FLSL, flag leaf sheath length; PL, peduncle length; PE, panicle exertion; IL, inflorescence length; IW, inflorescence width; RN, raceme number; LRL, lower raceme length; FEGW, five-ear grain weight.



grateful to Prof. James Nelson from Kansas State University, United States for English editing of the manuscript.

## Supplementary material

Supplementary material to this article can be found online at <http://dx.doi.org/10.1016/j.cj.2015.07.005>.

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