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Geographical Gaps and Diversity in Deenanath Grass (*Pennisetum pedicellatum* Trin.) Germplasm Conserved at the ICRISAT Genebank

HD Upadhyaya*, KN Reddy, Sube Singh, M Irshad Ahmed, Vinod Kumar and Senthil Ramachandran
Genetic Resources Unit, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru-502324, Andhra Pradesh

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The genebank at ICRISAT, India conserves 134 accessions of Deenanath grass (*Pennisetum pedicellatum* Trin.) from eight countries. A predicted probability map developed using FloraMap indicated 194 provinces in 21 countries of Asia and Africa as geographical gaps. All aceessions were annual and days to 50% flowering ranged from 43 to 109 days, number of total tillers/plant from 275 to 2,247 and number of productive tillers per plant from 114 to 1261. Accession IP 21821 produced maximum total tillers (2,247) and IP 21850 scored maximum (9) for forage yield potential. Early flowering (43 days) and high tillering (2,247) accessions of cluster 1 were considered as a promising source for early cuttings of green fodder. Mean diversity (H\`) for quantitative traits (H\`=0.591 $\pm$ 0.010) was higher than that for qualitative traits (H\`=0.284 $\pm$ 0.089). Early flowering, high tillering habit and higher levels of resistance to downy mildew make the Deenanath grass important.

Key Words: Crop wild relative, Germplasm, Mapping, Probability, Variation

Introduction

Crop wild relatives (CWR) are important components of agro-ecosystems as potential gene contributors for breeding programs. When the levels of resistance to various biotic and abiotic stresses in cultivated germplasm are low or the range of genetic variability is narrow and selection pressure results in virulent biotypes of the pests and diseases, the discovery and incorporation of additional genes for resistance from wild species becomes key to sustain crop productivity. Despite their importance, compared to landraces wild species have not received due attention from germplasm collectors. World's genebanks are conserving only a fraction of the total genetic variability that exists in CWR and only a small proportion of conserved accessions have been characterized. The economic impacts of wild relatives in crop improvement have been towards increasing disease resistances in wheat (Malik *et al*., 2003), rice (Brar and Khush, 1997) and potato (Pavek and Corsini, 2001). They have also been used to raise the nutritional value of some crops, such as protein content in durum wheat (Kovacs *et al*., 1998), calcium content in potato (Bamberg and Hanneman, 2003) and provitamin A in tomato (Pan *et al*., 2000).

Pearl millet, an important crop of the semi-arid tropics (SAT), has immense potential for adaptation to extreme limits of agriculture and its importance is expected to increase under changing climate scenarios (Lane *et al*., 2007). The primary genepool of pearl millet includes cultivated *Pennisetum glaucum* ssp. *glaucum*, the wild progenitor *P. glaucum* ssp. *monodii* and the weedy form *P. glaucum* ssp. *stenostachyum*. Hanna (1989) reported the development of a stable male sterile cytoplasm A_4 from the ssp. *monodii*. *Pennisetum purpureum* (napier grass) is the only known species in the secondary genepool. It is a rhizomatous perennial, with desirable characters like resistance to most pests, vigorous growth and outstanding forage yield potential (Hanna, 1992). The tertiary genepool consists of the remainder of the wild *Pennisetum* species including *P. pedicellatum* Trin., also called as Deenanath grass. It is widely distributed in West Africa and India. It is known as a weed in grain sorghum crops in northern Australia. In north of Cameroon, it is an important weed in field crops (Schmelzer, 1997). *Pennisetum pedicellatum* is a profusely tillering annual with big fluffy inflorescences (Fig. 1). It is quick growing, luscious, leafy and thin-stemmed grass and grows well even on poor, eroded soils in areas receiving 500-1500 mm annual rainfall (Mukherjee *et al*., 1982). As a high yielding grass of a short duration, it fits in well in the small period left in between two arable crops. Usually, one cut is taken after 80-90 days of sowing. *P. pedicellatum* was also considered as an important source for higher levels of downy mildew resistance (Singh and Navi, 2000).

**Author for Correspondence: Email:* H.Upadhyaya@CGIAR.ORG

Fig. 1. Plant of *Pennisetum pedicellatum*

To ensure the availability of large genetic diversity to the crop improvement programs, there is a need for collection, conservation, characterization, evaluation, documentation and distribution of plant genetic resources. The genetic variability accumulated over centuries is at risk, mainly due to replacement of landraces and wild relatives with improved varieties, climate change and concomitant natural catastrophes (droughts, floods, fire hazards etc.), human settlements, overgrazing, destruction of plant habitats for irrigation projects etc. (Upadhyaya and Gowda, 2009). Critical assessment of existing collections to identify geographical gaps, assess agronomic performance and launching germplasm collecting missions in the unexplored and under-explored areas is important to increase the variability. ICRISAT genebank being the world repository for the germplasm of its mandate crops and their wild relatives including pearl millet, assembled a total of 134 accessions of *P. pedicellatum* from India (57), Cameroon (56), Niger (14), Mali (3) and one each from Central African Republic, Mauritania, Tanzania and USA. Geographical distribution of any species is often scanty and patchy and makes it difficult to assess and map its occurrence in nature. In the present study, identified geographical gaps in *P. pedicellatum* germplasm assembled at ICRISAT genebank and evaluated to assess the diversity to enhance the utilization of germplasm in pearl millet improvement.

Materials and Methods

The present study was carried out with 134 accessions of *Pennisetum pedicellatum* assembled at ICRISAT genebank from eight countries. Passport data of the collection, particularly for information on precise location of collecting sites and corresponding geographic coordinates was updated verifying all records, collection reports and catalogs. Using the Microsoft Encarta®, an electronic atlas (MS Encarta Interactive World Atlas, 2000), geographic coordinates were retrieved to fill the gaps for accessions having location information and the accuracy of coordinates for 121 accessions was verified by plotting all accessions on political map. FloraMap, a GIS tool developed at Centro Internacional de Agricultura Tropical (CIAT) (Jones and Gladkov, 1999) was used to predict the probable areas of *P. pedicellatum* occurrence and identify geographical gaps in the collection. The basic input in the FloraMap software is the geographic coordinates (latitude and longitude) of the sampling site with a unique identifier (accessions number). The FloraMap system is based on calculating the probability that a climate record belongs to a multivariate normal distribution described by the climates at the collection points of a calibration set of organisms. With its user-friendly software linked to agroclimatic and other databases, biodiversity specialists can create maps showing the most likely distribution of any particular species in nature. FloraMap assigns climate data (monthly rainfall, minimum and maximum temperature, diurnal range in temperature) to each of the collection sites from the database provided along with the tool. Principal component analysis is used to reduce the dimensionality of this 36 dimensional dataset (set of 12 of the three variables) for each collection site and select first few components, which contribute to the maximum variation of the climatic characteristics. Also these few components are uncorrelated or orthogonal. Weights can be allocated to each of the three variables depending on the climate of the country/region. A probability density function is calculated on these few uncorrelated variables to find out the probability of finding a location for the population. While working on the passport dataset equal weights were allocated to the three climatic variables (monthly rainfall, minimum and maximum temperature, diurnal range in temperature) and an exponential transformation with a power of 0.3 to 0.5 was applied to the monthly rainfall data. The probability map was generated and the probabilities greater than 70% were considered for interpretation and recommendation for germplasm collection. While estimating the probability of *P. pedicellatum* occurrence, multiple accessions with same coordinates were treated as single collection site. Collection sites or sampled sites were overlaid on the probability image and the provinces with high probability (>70%) areas, where no collection or few collections have been made, were identified. All the provinces identified were shown (shaded area) in the map along with the collection sites of past collections.

All the 134 accessions were characterized during 2007 rainy season under field conditions on ICRISAT farm (17^0 48'N) in alfisol-Patancheru Soil Series (Udic Rhodustolf) field at Patancheru (18^ON, 79^OE, 545 m above sea level, and 600 km away from sea), Andhra Pradesh, India. The seeds were germinated in small cups with red soil mix and seedlings having 2-4 leaves were transplanted after 10-15 days in a single row of 8-m length with a row to row distance of 100 cm and plant to plant distance of 75 cm within the row during July. Crop received a basal dose of DAP @ of 150 kg ha^{-1} and 100 kg urea as top dressing 20 days after transplanting. Life saving irrigation was provided. The crop was protected from weeds. For each accession, five representative plants were selected to record observations on days to 50% flowering, plant height (cm), total tillers (no.), productive tillers (no.), stem thickness (mm), leaf blade length (cm), leaf blade width (cm), panicle length (cm), panicle thickness (mm), panicle exsertion (cm), 1000-seed weight (g), stem color, leaf blade pubescence, leaf blade shape, leaf color, panicle shape, bristle length (on 1-9 score, 1 = smallest and 9 = longest), green fodder yield potential (on 1-9 score, 1 = poor and 9 = good), and seed shape and color (IBPGR and ICRISAT, 1993).

Data on agronomic traits were analyzed using Residual Maximum Likelihood (REML) method considering accessions as random (random model) in GenStat 12 (Patterson and Thompson, 1971). Balanced Linear Unbiased Predictors (BLUPs) were calculated for each accession and each trait (Schonfeld and Werner, 1986). Principal component analysis (PCA) was carried out using standardized data of 11 quantitative traits using GENSTAT 5.1. Cluster analysis according to Ward (1963) was performed using scores of first 10 principal components. The mean, range and variances were calculated for 11 agronomic characters among the clusters and the entire collection. The means for different traits were compared using the Newman-Keuls procedure (Keuls, 1952; Newman, 1939). Homogeneity of variances was tested by Leven's test (Leven, 1960). The Shannon-Weaver diversity index (H`) (Shannon and Weaver, 1949) was estimated for each of the nine qualitative traits and the 11 quantitative traits over all the accessions to measure and compare phenotypic diversity.

Results

Overlaying of collection sites on the predicted probability image developed using FloraMap revealed that the existing collections are only from few areas in the primary and secondary centers of diversity for pearl millet (Fig. 2). In addition, it also revealed that many high probability areas were found in Africa and Asia, where no collections have been made in the past. In addition, high predicted probability (>70%) areas were also detected in Laos, Myanmar and Thailand in Asia and Mozambique and Madagascar in Africa. The probability image identified 8 provinces in India, 10 provinces in Laos, 14 provinces in Myanmar, 3 provinces each in Nepal and Thailand in Asia as the important source regions. Similarly, a total of 156 provinces in 16 countries in Africa, mainly Mali (38 provinces), Burkina Faso (29 provinces) and Senegal (23 provinces) were found as the important source regions for *P. pedicellatum* germplasm and need exploration (Table 1).

About 50 per cent of accessions (67) produced green stems and remaining produced purple stems. Only three accessions (IP 21850, IP 21861 and IP 21846) produced stems of >7.5 mm thickness. Three accessions (IP 21849, IP 22072 and IP 21836) produced leaves longer than 50 cm. IP 21853 flowered late (in 106 days) and grew to a maximum height of 248 cm and found as the promising source for green fodder yield. IP 21853, IP 21861, IP 21850, IP 21849, IP 21862, IP 21845 and IP 21864 grew more than 230 cm. IP 21821 produced maximum total tillers (2247 tillers) followed by IP 21866 (1791), IP 22220 (1772), IP 22071 (1766), IP 22091 (1736). Only one accession (IP 21850) scored maximum (9) for forage

Table 1. Provinces with high probability for occurrence of *Pennisetum pedicellatum* in different countries

Country	Provinces identified
India	Andhra Pradesh, Bihar, Chattisgarh, Jharkhand, Karnataka, Maharashtra, Orissa and West Bengal
Laos	Oudomxay, Vientiane (Munic.), Bokeo, Luang Prabang, Vientiane 2, Khammouane, Savannakhet, Xiangkhouang, Vientiane and Sayabouri
Myanmar	Arakan (Rakhine), Bago (Pegu), Chin, Irrawaddy, Kachin, Kawthulei (Karen), Kayah, Magwe, Mandalay, Mon, Sagaing, Shan, Tenasserim and Yangon
Nepal	East, Central and West
Thailand	Central, Northern and Northeastern
Benin	Atakora and Borgou
Burkina Faso	Seno, Boulgou, Gourma, Bougouriba, Kadiogo, Kouritenga, Gnagna, Tapoa, Sourou, Ganzourgou, Namentenga, Sanguie, Comoe, Soum, Mou Houn, Yatenga, Poni, Nahouri, Zoundweogo, Kenedougou, Oubritenga, Houet, Sanmatenga, Passore, Bazega, Sissili, Boulkiemde, Bam and Kossi
Cameroon	Adamoua, Extreme-Nord and Nord
Chad	Ouaddai, Chari-Baguirmi, Mayo-Kebbi, Logone Orienta, Logone Occiden, Tandjile, Moyen-Chari, Salamat and Guera
Gambia	North Bank, Upper River, Maccarthy Island, Lower River and Western
Guinea	Kindia, Labe and Kankan
Guinea-Bissau	Gabu, Bafata, Bissau, Biombo, Oio and Cacheu
Madagascar	Antananarivo, Mahajanga and Toliary
Malawi	Southern
Mali	Niafunke, Goundam, Youvarou, Niono, Douentza, Sikasso, Macina, Tenenkou, Koro, Nara, Mopti, San, Nioro, Koutiala, Bandiagara, Bla, Segou, Djenne, Diema, Yelimane, Kadiolo, Kayes, Kolondieba, Bankass, Yorosso, Banamba, Dioila, Baraoueli, Kolokani, Koulikoro, Tominian, Kenieba, Bafoulabe, Bougouni, Yanfolila, Kita, Kati and Kangaba
Mauritania	Hodh ech Chargui, Hodh el Gharbi and Assaba
Mozambique	Nampula, Zambezia, Cabo Delgado, Manica, Sofala and Tete
Niger	Tillabery, Dosso, Zinder, Tahoua and Maradi
Nigeria	FCT, Yobe, Taraba, Borno, Sokoto, Katsina, Adamwara, Plateau, Kebbi, Kaduna, Niger, Jigawa, Bauchi and Kano
Senegal	Thies, Kebemer, Tivaouane, Bambey, Diourbel, Mbacke, Linguere, Foundiougne, Fatick, Bakel, Kolda, Mbour, Matam, Kedougou, Gossas, Kaffrine, Velingara, Kaolack, Nioro-Du-Rip, Tambacounda, Sedhiou, Bignona and Ziguinchor
Sudan	Equatoria, Upper Nile, Darfur, Bahr el Ghazal, Central and Kordufan

yield potential and 23 accessions scored 8 on a 1-9 scale, 1 being the poorest and 9 as the best. All accessions produced brown colored seed either with elliptical shape (123 accessions) or obovate (11 accessions) shape.

REML Analysis

Residual Maximum Likelihood (REML) indicated that genetic variance components were highly significant for all the traits indicating the considerable diversity in the collection (Table 2). All accessions were annual and completed life cycle in one season and days to flowering ranged from 43 to 109. Similarly, important traits like plant height (73-248 cm), number of total tillers/plant from (275 to 2247), leaf blade length (16-53 cm) and leaf blade width (1-2.3 cm), which contribute for fodder yield had shown large variation.

Cluster Analysis

Principal component analysis (PCA) carried out using standardized data of 11 quantitative traits captured 71% of total variation from first three principal components (PCs). A hierarchical cluster analysis conducted on the scores of these three PCs resulted in three clusters (Table 3). The accessions from Cameroon (15), India (14), Niger (13), Mali (2) and Mauritania (1) formed the first cluster with 45 accessions; accessions from Cameroon (26) and one accession each from India, Mali and Tanzania formed the second cluster having 29 accessions and accessions from India (42), Cameroon (15), and one accession each from Central African Republic, Niger and USA formed the third cluster with 60 accessions. Clustering of accessions revealed no effect of geographic origin on agronomic performance. Accessions in cluster 1 were highly diverse with high range of variation for days to 50% flowering, plant height, total tillers, stem thickness, panicle exsertion and 1000 seed weight. Accessions in cluster 3 showed high range of variation for leaf blade length and width and panicle length.

Means and Variances

Newman-Keuls test of significance for mean values indicated significant differences among the clusters for all characters except panicle exsertion (Table 2). Cluster 1 was found as the best source for early flowering and high tillering accessions, whereas cluster 2 was found as the good source for late flowering accessions, with tall thick stems long and broad leaves forming an important source of high fodder yield. Cluster 3 was found as promising for panicle and seed traits. Homogeneity of variances of all the traits were tested by Leven's test (Leven, 1960) and were heterogeneous for days to 50% flowering, plant height, productive tillers/plant, leaf blade width, panicle thickness and 1000-seed weight indicating significant differences among the clusters for these traits. Variances

Table 2. Range, mean and variances for different traits of *P. pedicellatum* germplasm assembled and evaluated at ICRISAT genebank

Trait	Entire collection	Cluster 1 (45)	Cluster 2 (29)	Cluster 3 (60)	F value	P	$\delta^2 g$
Range							
Days to 50% flowering.	43-109	43-109	88-107	72-103			
Plant height (cm)	73-248	73-218	192-248	124-217			
Total tillers (no.)	275-2247	500-2247	420-1248	275-1056			
Productive tillers (no.)	114-1261	223-1261	167-742	114-637			
Stem thickness (mm)	2.7-8	2.7-6.4	4.7-8.0	3.5-7			
Leaf blade length (cm)	16-53	16.4-41.7	35.4-53.0	24.5-51.7			
Leaf blade width (cm)	1-2.33	1.0-2.3	1.4-2.4	1.2-2.2			
Panicle length (cm)	10-20	10.4-17	10.4-17	12-20.4			
Panicle thickness (mm)	5-20	4.7-18.4	5-9.7	8.4-20			
Panicle exsertion (cm)	(-)6.7-3.7	(-)6.7-3.7	(-)4.4-3.7	(-)6-3			
1000-Seed weight (g)	0.2-2.1	0.2-2.1	0.3-1.2	0.4-2			
Mean[1]							
Days to 50% flowering.	89±1.0	79.2c	98.2a	92.8b			
Plant height (cm)	181±3.0	153.1c	221.1a	182.9b			
Total tillers (no.)	823±28.0	1095.0a	779.0b	639.5c			
Productive tillers (no.)	420±18.0	579.6a	336.9b	341.4bb			
Stem thickness (mm)	5.1±0.1	4.2c	5.9a	5.4b			
Leaf blade length (cm)	36±1.0	29.1c	41.3a	38.5b			
Leaf blade width (cm)	1.7±0.0	1.5b	1.8a	1.8a			
Panicle length (cm)	15±0.0	13.7b	14.4bb	15.9a			
Panicle thickness (mm)	11±0.0	11.4b	7.5c	13.2a			
Panicle exsertion (cm)	-0.3±0.2	0.2a	-0.1a	-0.8a			
1000-Seed weight (g)	1.1±0.1	1.0b	0.6c	1.5a			
Variance[2]							
Days to 50% flowering.	126.7	138.9	37.4	35.8	6.76	0.002	70.71**
Plant height (cm)	1122.5	993.4	234.4	291.5	9.32	0.0002	515.00**
Total tillers (no.)	104557.6	117690.9	45513.7	34707.4	2.83	0.063	64889.00**
Productive tillers (no.)	41966.9	52220.5	14540.9	19666.7	4.69	0.010	29505.00**
Stem thickness (mm)	1.2	0.8	1.0	0.6	1.45	0.238	0.67**
Leaf blade length (cm)	56.8	37.2	16.2	36.1	0.01	0.989	32.16**
Leaf blade width (cm)	0.1	0.1	0.1	0.1	6.56	0.002	0.05**
Panicle length (cm)	3.3	2.7	2.3	2.0	0.54	0.587	2.28**
Panicle thickness (mm)	14.8	15.6	1.4	10.2	14.02	<0.0001	10.09**
Panicle exsertion (cm)	4.9	4.7	4.7	4.8	1.77	0.175	4.70**
1000-Seed weight (g)	0.3	0.3	0.1	0.1	11.02	<0.0001	0.16**

[1] Means were tested using Newman-Keuls test. Means followed by different letters were significant at p=0.05;
[2] Variances were tested using Leven’s test.

for days to 50% flowering, plant height, tillering, stem thickness, leaf blade length, panicle length and width and 1000-seed weight was high in cluster 1. Variance for leaf blade width was similar in all clusters and it was high for panicle exsertion in cluster 3.

Phenotypic Diversity

The Shannon-Weaver diversity index (H`) was calculated to compare phenotypic diversity for nine qualitative and 11 quantitative traits (Table 4). The diversity values (H`) were variable among traits. Among the qualitative traits, fodder yield potential had the highest diversity (H`= 0.696± 0.089) and among quantitative traits, stem thickness had the highest diversity (H`=0.632 ± 0.010). Mean diversity for quantitative traits (H`=0.591 ± 0.010) was higher than that for qualitative traits (H`=0.284 ± 0.089).

Discussion

Increasing the variability by launching germplasm collection missions in unexplored and under explored areas is essential to ensure the availability of large genetic variability to the crop improvement scientists. The activities of genetic resources for cultivated and wild relatives' germplasm are basically same. However, the collection strategy for CWR involve difficulties in identification of geographic distribution of species, precise location, time of maturity etc., which need to be gathered from different floras, herbaria, catalogs, literature and through correspondence. Because, the wild relatives are rather uncommon in natural vegetation and location data are often very old and not precise, it is not always feasible to follow the strategy recommended for the collection of cultivated species. The use of GIS tools to analyze of passport data and corresponding climate data to map the potential distribution of a species is a powerful method to assist germplasm collectors and genebank managers.

FloraMap, a GIS tool is very useful to know the geographical distribution of species and has been useful for identification of geographical gaps in the *P. pedicellatum* collection at ICRISAT genebank in the present study. The probability image developed using FloraMap has indicated a total of 38 provinces in five countries in Asia and a total of 156 provinces in 16 countries in Africa as the important source regions for *P. pedicellatum* germplasm and need exploration (Fig. 2) (Table 1). The probability map generated in the present study matched quite closely to the origin and dispersal of pearl millet supporting the prediction of *P. pedicellatum* occurrence in different regions (Appa

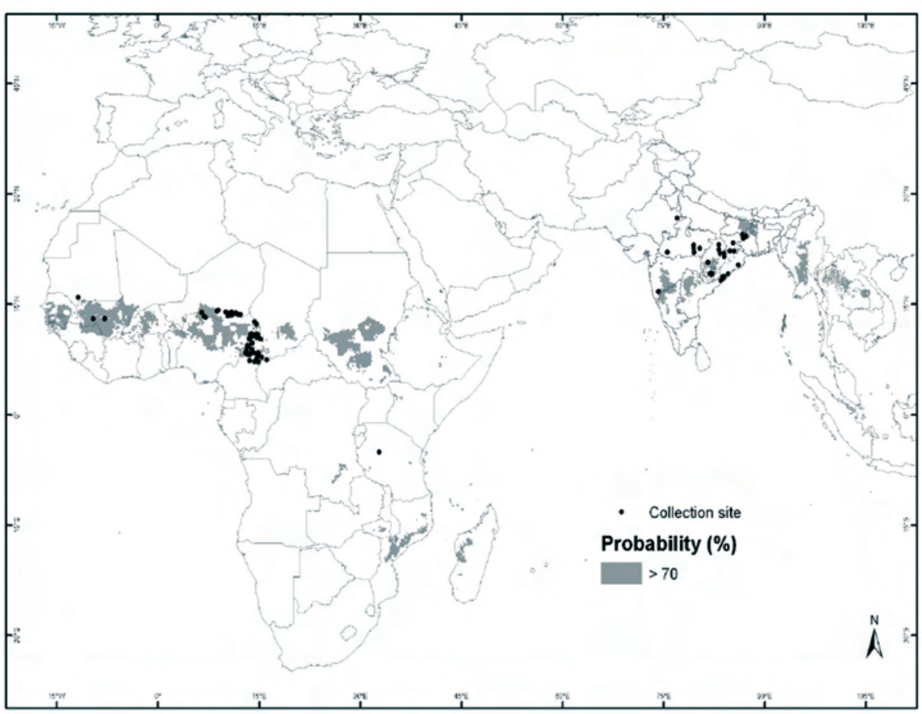

Fig. 2. Geographical distribution of *Pennisetum pedicellatum* collection at ICRISAT genebank and the high (>70%) probability areas of its occurrence (shaded area)

Table 3. Cluster wise *P. pedicellatum* accessions from different countries conserved at the ICRISAT genebank

Cluster No.	Country	IP No.
1	Cameroon	21811, 21812, 21813, 21814, 21816, 21817, 21820, 21821, 21822, 21824, 21832, 21834, 21858, 21859, 21860
	India	21795, 21805, 21806, 21863, 21881, 21883, 21884, 22071, 22074, 22075, 22082, 22085, 22091, 22220
	Mali	21866, 22088
	Mauritania	22148
	Niger	21867, 21868, 21869, 21870, 21871, 21872, 21873, 21874, 21875, 21876, 22092, 22094, 22095
2	Cameroon	21809, 21815, 21828, 21829, 21831, 21838, 21839, 21840, 21842, 21843, 21844, 21845, 21846, 21847, 21848, 21849, 21850, 21851, 21852, 21853, 21854, 21855, 21856, 21857, 21861, 21862
	India	21807
	Mali	21865
	Tanzania	21864
3	C. African Rep.	21803
	Cameroon	21810, 21818, 21819, 21823, 21825, 21826, 21827, 21830, 21833, 21835, 21836, 21837, 21841, 21941, 22090
	India	21789, 21790, 21791, 21792, 21793, 21794, 21796, 21797, 21798, 21799, 21800, 21801, 21802, 21804, 21808, 21877, 21878, 21879, 21880, 21882, 21885, 21886, 21887, 21888, 21889, 21890, 21891, 21892, 21893, 22072, 22073, 22076, 22077, 22078, 22079, 22080, 22081, 22083, 22084, 22086, 22087, 22219
	Niger	22093
	USA	22089

Table 4. Shannon-Weaver diversity (H`) for different traits in *P. pedicellatum* germplasm assembled and characterized at ICRISAT genebank

Trait	Diversity index (H`)
Qualitative traits	
Stem color	0.426
Leaf blade pubescence (P/A)	0.290
Leaf color	0.000
Leaf blade shape	0.375
Panicle shape	0.019
Bristle length (1-9 score)	0.625
FYP (1-9 score)	0.696
Seed shape	0.123
Seed color	0.000
Mean-qualitative traits	0.284
Se±	0.089
Quantitative traits	
Days to 50% flowering	0.589
Plant height (cm)	0.625
Total tillers (no.)	0.556
Productive tillers (no.)	0.563
Stem thickness (mm)	0.632
Leaf blade length (cm)	0.591
Leaf blade width (cm)	0.619
Panicle length (cm)	0.613
Panicle thickness (mm)	0.566
Panicle exsertion (cm)	0.611
1000-Seed weight (g)	0.534
Mean-quantitative traits	0.591
Se±	0.010
Mean-all traits	0.453
Se±	0.053

Rao and de Wet, 1999; Brunken, 1977). Schmelzer (1997) reported the occurrence of *P. pedicellatum* in parts of Cap Verdiane islands, Ethiopia, Tanzania, western and northern Australia. Though, the GIS tools provide precise cartographic representation of eco-geographic regions and of the germplasm collecting sites (Marilia *et al*., 2003), it is important to go through different flora and fauna, catalogs and literature for the distribution of species before embarking on actual germplasm collection. Generally, different species mature at different times. Therefore, the overall knowledge of CWR is essential to collect different species in one collection mission and make the collection mission a success.

Although resistance sources were identified in cultivated germplasm, their resistance could be overcome when the inoculum's levels are high. Singh and Navi (2000) screened 539 accessions of pearl millet wild relatives belonging to 12 species for resistance to downy mildew (*Sclerospora graminicola* (Sacc.) J. Schröt) at ICRISAT, Patancheru and reported that all (129) but two accessions of *P. pedicellatum* as completely free from the disease. Wild species are more important when they possess resistance to biotic and/or abiotic stresses in addition to traits of agronomic importance. Large variation observed for important traits in the *P. pedicellatum* collection is useful in crop improvement programs. Early flowering (43 days) and high tillering (maximum 2,247 total tillers) accessions of cluster 1 were considered as a promising source for early cuttings of green fodder. It can be used for short-term production only due to its poor regeneration capacity (Bhagavandoss *et al*., 1989). *P. pedicellatum* can stand several cuts a year for green fodder and is generally used as cut-and-carry green forage at ear emergence but it can also be made into silage and hay (Schmelzer, 1997). It responds to nitrogen fertilization and grows well under mixed cropping with cowpea (*Vigna unguiculata*) or rice bean (*Vigna umbellata*) and thus provides optimum quality forage for dairy cattle (Mukerjee *et al*., 1982). On the other hand, Prasad *et al*. (1990) reported highest green fodder yield of 53.30 t/ha and 11.50 t dry fodder/ha by cross-sowing with cowpea. Shukla *et al*. (1988) reported 32.12 t fresh fodder and 6.08 t dry matter/ha by sowing on ridges.

There has been only limited exploitation of wild species in tertiary genepool of pearl millet due to cross incompatibility with the cultigens. Crosses between cultivated pearl millet and *P. pedicellatum* are difficult, but are sometimes possible by using special techniques. Inter-specific crosses usually result in high male and female sterility. Attempts to produce inter-specific hybrids between pearl millet and species of the tertiary genepool using conventional techniques were not successful (Dujardin and Hanna, 1989). If required, recent advances in biotechnology could be used to transfer useful traits from *P. pedicellatum* to cultivated pearl millet (Sharma and Ortiz, 2000). The availability of sources of resistance to downy mildew in the cultivated pearl millet may meet the present requirement, but for future needs of higher levels of resistance, we may have to depend on species of tertiary genepool, particularly on *P. pedicellatum*. Therefore, currently, the need in wild *Pennisetum* research is to adequately and systematically collect the *P. pedicellatum* germplasm representing all areas of its occurrence. When compared with other *Pennisetum* species, *P. pedicellatum* produces more tillers than that of ssp. *monodii*, and grows tall facilitating more green fodder yield in a short period. Of the 12 *Pennisetum* species screened for downy mildew, only *P. pedicellatum* had shown no downy mildew incidence in almost all accessions. In addition, *Pennisetum glaucum* ssp. *monodii* stems are weak and susceptible to lodging. Therefore, early flowering, high tillering habit, tallness and higher levels of resistance to downy mildew makes the *P. pedicellatum* important in future pearl millet research for fodder.

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