

GENETIC DIVERSITY STUDY IN BARNYARD MILLET (*ECHINOCHLOA FRUMENTACEA* (ROXB.) LINK) GERMPLASM UNDER SODIC SOIL CONDITION

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Abstract

The present study was aimed to estimate the nature of genetic diversity existing in 99 barnyard millet genotypes including two commercial check varieties *viz.*, MDU1 and CO (KV) 2 under sodic soil condition. Mahalanobis D²analysis grouped the genotypes into 13 clusters with respect to 12 biometrical traits. Cluster I was the largest, consisting of 39 genotypes followed by cluster XIII with 35 genotypes. Cluster XII and XI had 4 and 3 genotypes, respectively. The remaining (9) clusters II, III, IV, V, VI, VII, VIII, IX and X included only 2 genotypes per cluster. Cluster XI recorded the highest intra-cluster distance followed by cluster XIII. The maximum inter-cluster distance was observed between clusters I and XI followed by clusters VIII and XI. The traits grain yield per plant and plant height contributed maximum to the genetic diversity. Principal component analysis revealed that the traits plant height, flag leaf length, lower raceme length and ear length contributed maximum towards variability in PCA axis I and II. Thus, selection of genotypes as parents from these genetically diversified clusters for breeding programmes could result in heterotic hybrids and could generate good amount of genetic variability in barnyard millet genotypes under the sodic soil condition.

Key words: Barnyard millet, cluster analysis, diversity, PCA, sodic soil.

Introduction

Small millets, which include finger millet, foxtail millet, barnyard millet, kodo millet, proso millet and little millet are crops of subsistence agriculture. These belong to the neglected and underutilized crop genetic resources, which plays a vital role for sustainable agriculture (Padulosi *et al.*, 1999; Mal, 2007; Dutta *et al.*, 2007). These crops have been under cultivation by tribal and dry land farmers since time immemorial and have accumulated tremendous diversity owing to the selection pressure imposed due to their diversified cultivation systems. Being a crucial component in the dry land farming system, small millets also respond to irrigation. Moreover, when compared to the major cereals like wheat, rice and maize, millets have superior nutrition and unique adaptation to biotic and abiotic stress (Rao, 1989). India is the largest producer of millets

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in the world accounting to 10.5 million metric tonnes (Kumar *et al.*, 2016). Millets are C₄ plants that can utilize water and nitrogen effectively and sustain in hot, drought prone arid and semiarid regions of Africa, Asia and America (Dwivedi *et al.*, 2012). They have low glycemic index, better amino acid profile and are free from gluten which makes them ideal for diabetic patients (Padulosi *et al.*, 2009). Lessons learnt from Green Revolution suggests that locally adapted species and landraces are needed to enhance the variability to cope up with rainfall, marginal soils and other abiotic and biotic stresses (Martini-Bettolo, 1988; Qualset *et al.*, 1995; Thrupp, 1998; Toledo and Burlingame, 2006; Burke *et al.*, 2009).

Continued progress of crop improvement needs genetic diversity. The recent genetic erosion of small millets and their lower economic competitiveness compared with major cereals (Padulosi *et al.*, 2009) are caused by many factors such as low productivity, non availability of high-yielding varieties, lack of production and processing technologies and introduction of highyielding commercial crops, that have contributed heavily towards a narrow food security basket (Upadhyaya et al., 2016; Hart, 2007; Gautam et al., 2008; Gruere et al., 2007). Barnyard millet (Echinochloa frumentacea) is a vital small millet crop due to its fast growing nature, excellent climate resilient capacity and nutrient potential (Gupta et al., 2010). It is one of the important crops that is traditionally cultivated as multipurpose crop in places where rice does not grow well. In India, it is generally cultivated as supplemental crop which is remunerative for subsistence farmers (Manimekalai et al., 2018; Goron, 2015). It is grown in two different agro-ecologies, from Himalayan region in the North to Deccan plateau region in the south (Sood et al., 2015; Gupta et al., 2009).

The genus *Echinochloa* belongs to the family Poaceae which consist of two domesticated species namely *Echinochloa frumentacea* and *E.utilis*, commonly known as Indian barnyard millet and Japanese barnyard millet respectively. Cytogenetic studies have confirmed that *E. colona* (Jungle rice) is the possible progenitor of *E. frumentacea* and have basic chromosome number x=9 (Hilu, 1994; Yabuno, 1987). The sub species *E. frumentacea* has four races *viz., robusta, stolonifera, intermedia and laxa* (Dwivedi *et al.*, 2012) which were recognized by De Wet *et al.*, (1983) based on the morphological characters.

Globally, 37 percent of the arable land (1500 M. ha.) is sodic (Khan and Duke, 2001; Szabolcs, 1989; Leland and Eugene 1999). Sodic soil possess high pH (> 8.5) and exchangeable Na (ESP >15%) content and it exhibits poor physical and chemical features that adversely influence water infiltration and air exchangeability in the soil (Szabolcs, 1993; Waskom et al., 2003; Ogle, 2010). As a consequence of this phenomenon, the wilting point in the soil increases and the plants suffer from water deficiency, even in wet soils, owing to the swelling of clay saturated with sodium ions (Pessarakli and Szabolcs, 1999). In sodic soil, plants suffer from micronutrient deficiency (e.g., Cu, Fe, Mn and Zn) as the solubility of micronutrients is at an all time low. Sodic soils are characterized by poor physical conditions, nutritional imbalance, ion toxicity, surface crusting, poor hydraulic conductivity, reduced infiltration rate and compaction of subsoil. These circumstances hinder seed germination and frequently restrict vegetative growth (Grattan and Grieve, 1999; Ansari et al., 1999; Pessarakli and Szabolcs, 1999).

Though genetic diversity among barnyard millet genotypes have been studied by several researchers, there

is paucity of information about nature and magnitude of diversity in the crop for problem soils like sodicity. Hence a study was undertaken to assess genetic diversity among 99 barnyard millet genotypes for yield contributing traits in sodic soil condition. The information generated could be useful in identification of diverse barnyard millet genotypes for exploitation as parents in hybridisation programmes for developing varieties for sodic soil conditions.

Materials and Methods

The present study was carried out during Summer (2018) to identify diverse barnyard millet genotypes in natural sodic soil (pH : 9.07, EC : 0.95dS/m and ESP : 43.69%) at Anbil Dharmalingam Agricultural College and Research Institute, Trichy, Tamil Nadu. The experimental material involved 97 germplasm lines of barnyard millet obtained from Indian Institute of Millets Research (IIMR), Hyderabad, Telangana and two commercial check varieties viz., MDU1 and CO(KV) 2. The experiment was laid out in randomized block design with two replications and the recommended crop management practices were followed. Observations were recorded on 12 biometrical traits viz., days to fifty percent flowering, days to maturity, plant height (cm), number of productive tillers, number of leaves on main tiller, ear length (cm), ear width (cm), flag leaf length (cm), flag leaf width (cm), lower raceme length (cm), thousand grain weight (g) and grain yield per plant (g) as per the descriptors of Barnyard millet (IPGRI, 1983). For every accession, five randomly selected plants per replication were used for recording the data, except for days to fifty percent flowering and days to maturity, which was recorded on plot basis.

The data collected were subjected to analysis of variance (ANOVA) as suggested by Panse and Sukhatme (1967). The replicated data were subjected to D² analysis (Mahalanobis, 1936) for estimation of genetic divergence and intra and inter cluster distances. Grouping of all the barnyard millet genotypes into different clusters was carried out as per the procedure proposed by Radhakrishna Rao (1952). All the analyses were carried out using GENRES software. The Principal Component Analysis (PCA) was carried out as per Radhakrishna Rao (1952).

Results and Discussion

The genetic diversity analysis gives information about germplam diversity and genetic relationships among accessions that would support the plant breeders for selecting elite genotypes for breeding programme and for germplams conservation (Vivekananda and Subramanian, 1993; Govindaraj *et al.*, 2015; Manimekalai *et al.*, 2018). The diversity of parents is of utmost importance which would give predictive knowledge of genetic variation to yield desirable recombinants in the progenies (Jaiswal *et al.*, 2010).

The ANOVA for 12 morphometric traits among 99 genotypes revealed that the mean sum of squares due to genotypes were highly significant for all the studied characters which indicated significant variations among the genotypes under sodic soil condition. Based on D² analysis, the 99 barnyard millet accessions were grouped into 13 clusters (Table 1). Among the 13 clusters, cluster I was the largest, consisting of 39 genotypes followed by cluster XIII with 35 genotypes. Cluster XII and XI had 4 and 3 genotypes, respectively. The remaining (9) clusters II, III, IV, V, VI, VII, VIII, IX and X included only 2 genotypes per cluster. This indicated wide genetic diversity among the genotypes. Genotypes falling in the same cluster are more closely related than the ones falling in different cluster groups.

The intra cluster distance ranged from 2.06 to 12.97 (Table 2). The maximum and minimum intra cluster distances were observed in cluster XI (12.97) and cluster II (2.06), respectively. Higher intra cluster distance indicated high degree of divergence within that cluster

(cluster XI) and low intra cluster distance implied lesser genetic diversity among the cluster constituents (cluster II). Thus the barnyard millet accessions present in cluster II *viz.*, BAR 340 and 357 are closely related to each other and the accessions BAR 242, BAR 351 and BAR 353 present in cluster XI are diverse among themselves. The maximum inter cluster distance was observed between cluster I and cluster XI (18.44) while it was minimum between cluster V and cluster VI (2.70). Hybridisation between genotypes of the divergent clusters *viz.*, clusters I and cluster XI could result in wide spectrum of beneficial segregants. This is in accordance with the views expressed by Nirosha *et al.*, (2016). But for exploitation of heterosis, selection of genotypes showing moderate diversity is advisable (Shahidullah *et al.*, 2009).

Cluster mean values for different characters are presented in table 3. Cluster XIII had maximum cluster means for most of the desirable characters *viz.*, ear width, flag leaf length, flag leaf width, grain yield per plant. Cluster XII also had high cluster mean for lower raceme length, flag leaf length, ear width and plant height. Cluster XI had highest mean value for grain yield per plant and thousand grain weight. From the result, it was observed that the genotypes in cluster XI *i.e.*, BAR 242, BAR 351and BAR 353 were of medium stature and high yielding which could be used for grain yield improvement

Table 1: Clustering pattern of 99 Barnyard millet germplasm by D² analysis under sodic soil condition.

Clusters	Number of	Name of the genotypes									
	genotypes										
		BAR-84	BAR - 120	BAR - 154	BAR-191	BAR-199	BAR - 208	BAR-219	BAR-229		
		BAR-87	BAR-123	BAR - 160	BAR-193	BAR-200	BAR-209	BAR-220	BAR-236		
Ι	39	BAR-91	BAR-131	BAR - 178	BAR-195	BAR-203	BAR-213	BAR-222	BAR-241		
		BAR-111	BAR-151	BAR - 183	BAR-197	BAR-206	BAR-214	BAR-223	BAR-394		
		BAR-119	BAR-152	BAR - 190	BAR-198	BAR-207	BAR-215	BAR-228			
I	2	BAR-340	BAR-357								
Ш	2	BAR-348	BAR-383								
IV	2	BAR-327	BAR-396								
V	2	BAR-279	BAR-373								
VI	2	BAR-296	BAR-392								
VII	2	BAR-376	BAR-384								
VIII	2	BAR-289	BAR-315								
IX	2	BAR-273	BAR-280								
X	2	BAR-338	BAR-365								
XI	3	BAR-242	BAR-351	BAR - 353							
XII	4	BAR-248	BAR-249	BAR - 329	BAR - 369						
		BAR-252	BAR-270	BAR - 295	BAR - 358	BAR-371	BAR - 390	BAR-581			
		BAR-254	BAR-277	BAR - 308	BAR - 359	BAR-372	BAR - 399	BAR-1088			
ХШ	35	BAR-263	BAR-278	BAR - 314	BAR-366	BAR-382	BAR-424	BAR-1365			
		BAR-264	BAR-288	BAR - 317	BAR-367	BAR-388	BAR-427	CO(KV)2			
		BAR-269	BAR-293	BAR - 350	BAR-370	BAR-389	BAR-568	MDU 1			

or as parents in hybridization programme. Cluster III consisted of BAR 348 and BAR 383 which showed high mean value for ear width, number of productive tillers and lower raceme length. Hence, outstandingly performing genotypes present in these clusters could be utilized as potential parents for improvement of grain yield in barnyard millet under sodic condition. Similar results were obtained by Anuradha *et al.*, (2014); Arya *et al.*, (2018) in barnyard millet; Suryanarayana *et al.*, (2014) in finger millet and Shanmuganathan *et al.*, (2006) in pearl millet.

The percent contribution of each character towards divergence is presented in table 4. Among the yield contributing traits major contributors towards divergence were grain yield per plant (58.46 %) followed by plant height (17.30%), lower raceme length (4.99%), thousand

grain weight (4.37 %), flag leaf width (3.46 %) and ear width (3.44 %). Similar pattern was observed in barnyard millet by Arya *et al.*, (2018), Anuradha *et al.*, (2014). De *et al.*, (1988) opined that traits contributing maximum towards the D² values need to be given more emphasis for deciding the clusters to be taken for the purpose of choice of parents for hybridization. Thus the characters indicated above should form the criteria for selection of parents for hybridization programme (Shanmuganathan *et al.*, 2006). Remaining characters like days to fifty percent flowering, days to maturity, ear width, flag leaf length, number of leaves on main tillers and number of productive tillers did contributed less towards the total divergence which showed that the genotypes possessed unique features for most of the traits studied.

Table 2: Intra (Diagonal and bold) and inter cluster distance values for 13 clusters

Clusters	Ι	П	Ш	IV	V	VI	VII	VIII	IX	Χ	XI	XII	XIII
Ι	8.81	7.90	7.24	6.89	9.21	7.02	7.67	7.76	7.22	9.35	18.44	8.50	11.15
I		2.06	5.04	4.09	4.16	3.35	4.45	4.00	3.89	3.65	14.61	7.08	8.91
Ш			2.17	4.23	5.94	3.81	5.41	4.96	3.95	6.24	16.28	6.10	9.03
IV				2.33	5.76	2.70	3.56	3.50	3.04	5.37	16.98	6.22	9.41
V					2.60	5.23	5.59	4.54	5.79	3.46	14.56	8.36	9.42
И						2.63	3.93	3.94	3.29	4.90	15.60	5.89	8.82
VII							2.71	3.77	3.62	4.74	16.35	6.84	9.28
VIII								2.83	3.81	4.66	17.12	7.43	9.80
IX									2.91	5.33	16.40	6.23	9.26
X										3.00	14.14	8.21	9.34
XI											12.97	16.60	15.66
XII												8.46	10.10
XIII													11.41

Table 3: Cluster mean for 13 characters in barnyard millet germplasm

Clusters	Characters											
	Days to	Days	Plant	Ear	Ear	Lower	Flag	Flag	Number	Number	Thousand	Grain
	fifty	to	height	length	width	raceme	leaf	leaf	of leaves	of pro-	grain	yield/
	percent	maturity	(cm)	(cm)	(cm)	length	length	width	on main	ductive	weight	plant
	flowering					(cm)	(cm)	(cm)	tiller	tillers	(g)	(g)
Ι	37.47	88.80	52.68	10.13	1.80	1.80	12.96	1.29	4.95	5.41	2.18	9.19
Π	35.50	85.50	44.02	8.91	1.21	1.40	9.86	1.14	4.75	5.25	2.05	13.29
Ш	36.50	87.75	45.23	9.75	2.32	1.84	12.19	1.18	4.50	5.50	2.20	10.57
IV	36.25	87.00	46.11	9.80	1.51	1.37	12.55	1.26	4.00	4.75	2.09	9.58
V	38.75	92.50	37.31	8.09	1.47	1.07	11.28	1.18	5.00	3.75	2.09	13.30
VI	36.75	88.50	47.63	9.54	1.62	1.45	11.39	1.22	4.00	4.75	2.23	11.43
VII	37.50	90.00	46.72	10.07	1.59	1.30	11.71	1.26	4.25	3.50	1.64	10.59
VIII	36.50	87.75	40.78	8.32	1.43	1.21	9.87	1.12	4.50	3.75	1.90	9.64
IX	35.75	87.75	44.95	9.16	1.59	1.69	12.54	1.07	4.00	4.25	1.82	10.49
X	36.00	86.75	38.51	8.94	1.38	0.96	10.00	1.23	4.25	4.25	1.85	13.87
XI	37.33	89.17	48.38	10.26	1.72	1.63	12.64	1.48	4.50	4.67	2.35	27.13
XII	37.00	88.25	52.38	10.53	2.05	1.85	14.27	1.30	4.13	4.63	2.22	11.12
XIII	37.69	100.87	50.14	10.63	2.05	1.79	13.09	1.49	4.89	4.81	2.13	14.17

 Table 4: Contribution of 12 morphological characters to genetic divergence in barnyard millet germplam under sodic soil condition.

S.	Characters	No. of	% contri-
No.		1st rank b	ution (%)
1	Days to fifty per cent flowering	61	1.26
2	Days to maturity	20	0.41
3	Plant height (cm)	839	17.30
4	Ear length (cm)	12	0.25
5	Ear width (cm)	167	3.44
6	Lower raceme length (cm)	242	4.99
7	Flag leaf length (cm)	81	1.67
8	Flag leaf width (cm)	168	3.46
9	Number of leaves on main tiller	101	2.08
10	Number of productive tillers	112	2.31
11	Thousand grain weight (g)	212	4.37
12	Grain yield/plant (g)	2836	58.46

 Table 5: Eigen values, factor scores and contribution of principal component axes.

Principal components	PC1	PC2	PC3	PC4	PC 5
Eigen values	5.46	1.50	1.26	0.97	0.79
Percentage of variation	45.51	12.52	10.48	8.04	6.60
Cumulative percentage	45.51	58.03	68.50	76.55	83.15
DTFF	-0.31	-0.41	0.03	-0.40	0.04
DTM	-0.31	-0.42	0.09	-0.36	0.11
PH	-0.37	0.26	-0.05	-0.09	-0.05
EL	-0.35	0.26	0.12	0.11	-0.15
EW	-0.32	0.05	0.15	0.06	-0.24
LRL	-0.27	0.29	-0.10	-0.18	-0.61
FLL	-0.37	0.12	0.13	0.17	0.11
FLW	-0.29	0.03	0.19	0.50	0.31
NLMT	-0.32	0.03	0.01	-0.11	0.48
NPT	-0.08	0.27	-0.70	-0.31	0.23
TGW	-0.17	-0.18	-0.59	0.46	0.04
GYPP	-0.13	-0.56	-0.22	0.25	-0.38

(DTFF- Days to fifty percent flowering; DTM- Days to maturity; PH- Plant height; EL- Ear length; EW- Ear width; LRL- Lower raceme length; FLL- Flag leaf length; FLW- Flag leaf width; NLMT- Number of leaves on main tillers; NPT-Number of productive tillers; TGW- Thousand grain weight; GYPP- Grain yield per plant; PC- Principal components.)

The PCA analysis revealed the interactions and the contribution of the traits towards diversity among the genotypes. It was observed that about 83 percent of the total variation was explained by five major principal components (Table 5 and Fig. 1). The principal components PC4 and PC5 recorded Eigen vector values of less than 1 hence these two components were eliminated to have a smaller lot. PC1 explained 45.51 percent of variation followed by PC2 (12.52%) and PC3



Fig. 1 Screen plot showing Eigen value variance





(10.48%). The traits plant height (-0.37), flag leaf length (-0.37) and ear length (-0.35) were negatively related to PC1. Lower raceme length (0.29), plant height (0.26) and ear length (0.26) are positively related to PC2. Flag leaf width (0.19), ear width (0.15) and flag leaf length (0.13) are positively related to PC3. As first two principal components had a cumulative percentage of 58.03 percent, the traits were highly correlated. Similar results were obtained for PCA analysis by Gupta *et al.*, (2009); Sood *et al.*, (2015) in barnyard millet and Suman *et al.*, (2019) in finger millet. The biplot was plotted between



Fig. 3 Grouping of 99 barnyard millet germplasm by principal component analysis

PC1 and PC2 which revealed that traits plant height and ear length contributed positively towards the total divergence (Fig. 2). The genotypes were well dispersed along the biplot indicating the significant variation between the genotypes.

Apart from the D² analysis, grouping of genotypes into various clusters were carried out using Ward's method. A total of twelve clusters were formed of which cluster seven was the largest with four sub clusters (19 genotypes) followed by cluster twelve with three sub clusters (15 genotypes). According to eucleadian's distance matrix clusters one and twelve comprise of diverse set of genotypes. Cluster eleven had high yielding germplasm accessions of barnyard millet with two sub clusters (4 genotypes: BAR 242, BAR 264, BAR 351 and BAR 353). Hybridization among genotypes from these clusters could result in better segregants (Fig. 3).

Conclusion

The traits grain yield per plant and plant height contributed maximum to the genetic diversity. Distribution of barnyard millet in to various clusters indicated the presence of considerable genetic diversity for most of the traits among the genotypes. The clusters XI and I were the distant clusters and clusters V and VI were the least divergent clusters. The clusters XIIII and XII possessed the high mean values for many of the traits studied. With respect to grain yield per plant the clusters XI, XIII and V appeared to be the superior clusters. As per the D² statistic and principal component analysis, the accessions of cluster XI (BAR 242, BAR 351 and BAR 353) and cluster I (BAR 183, BAR 223, BAR 228) can be exploited as diverse parents in crossing programme for development of hybrids and good recombinants for grain yield per plant. It could generate good amount genetic variability in barnyard millet genotypes under the sodic soil condition.

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References

- Ansari, R., S.M. Alam, S.S.M. Naqvi, N.E. Marcar and S. Ismail (1999). Response of woody species to salinity. *Handbook* of Plant and Crop Stress, (Pessarakli, M. Ed.), 931-946.
- Anuradha, N., T.S.S.K. Patro, K. Udaya Bhanu, J. Madhuri and A. Sowjanya (2014). Multivariate analysis in barnyard millet (*Echinochloa frumentacea* (Roxb.) Link). *International Journal of food, Agricuture and Veterinary Science*, 4: 194-199.
- Arya, R., A. Bhatt and V. Kumar (2018). Study of Genetic Divergence in Barnyard millet (*Echinochloa frumentacea* (Roxb.) Link) Germplasm. *International Journal of Bio-Resource and Stress Management*, **9**: 192-196.
- Burke, M.B., D.B. Lobell and L. Guarino (2009). Shifts in African crop climates by 2050 and the implications for crop improvement and genetic resources conservation. *Global Environmental Change*, **19**: 317-325.
- De-Wet, J.M.J., K.P. Rao, M.H. Mengesha and D.E. Brink (1983). Domestication of sawa millet (*Echinochloa colona*).

Economic Botany, 37: 283-291.

- De, R.N., R. Seetharaman, M.K. Sinha and S.P. Banerjee (1988). Genetic divergence in rice. *The Indian Journal of Genetics and Plant Breeding*, **48**: 189-194.
- Dutta, M., B.S. Phogat and B.S. Dhillon (2007). Genetic improvement and utilization of major underutilized crops in India. *Breeding of Neglected and Underutilized Crops, Spices and Herbs. Science Publishers, Enfield (NH), USA*, 251-298.
- Dwivedi, S.L., H.D. Upadhyaya, S. Senthilvel, C.T. Hash, K. Fukunaga, X. Diao, D. Santra, D. Baltensperge and M. Prasad (2012). Millets: genetic and genomic resources. In: Janick J (ed) Plant breeding reviews. Wiley-Blackwell, New York, pp 247–375.
- Gautam, R., R. Suwal, and B.R. Sthapit (2008). Securing family nutrition through promotion of home gardens: underutilized production systems in Nepal. In: *International Symposium* on Underutilized Plants for Food Security, Nutrition, Income and Sustainable Development, 806: pp. 99-106.
- Goron, T.L. and M.N. Raizada (2015). Genetic diversity and genomic resources available for the small millet crops to accelerate a New Green Revolution. *Frontiers in plant science*, **6**: 157.
- Govindaraj, M., M. Vetriventhan and M. Srinivasan (2015). Importance of genetic diversity assessment in crop plants and its recent advances: An overview of its analytical perspectives. *Genetics research international*, pp. 431-487.
- Grattan, S.R. And C.M. Grieve (1999). Mineral nutrient acquisition and response by plants grown in saline environments. *Handbook of plant and crop stress*, **2:** 203-229.
- Gruere, G.P., L. Nagarajan and E.D.I. King (2007). Collective Action and Marketing of Underutilized Plant Species: The Case of Minor Millets in Kolli Hills, Tamil, Nadu, India. *Capri working paper*, no. 69.
- Gupta, A., V. Mahajan, M. Kumar and H.S. Gupta (2009). Biodiversity in the barnyard millet (*Echinochloa frumentacea* Link, Poaceae) germplasm in India. *Genetic resources and crop evolution*, **56**: 883-889.
- Gupta, A., V. Mahajan and H.S. Gupta (2010). Genetic resources and varietal improvement of small millets for Indian Himalaya. *Biodiversity Potentials of the Himalaya*, Gyanodaya Prakashan, Nainital, India, 305-316.
- Hart, N. (2007). Inviting all the world's crops to the table. pp. 4-28.
- Hilu, K.W. (1994). Evidence from RAPD markers in the evolution of *Echinochloa* millets (Poaceae). *Plant Systematics and Evolution*, **189**: 247-257.
- Jaiswal, J.P., A. Mamta, K. Anil and R.S. Rawat (2010). Assessing genetic diversity for yield and quality traits in indigenous bread wheat germplasm. *Electronic Journal of Plant Breeding*, 1: 370-378.

- Khan, M.A. and N.C. Duke (2001). Halophytes–A resource for the future. *Wetlands Ecology and Management*, **9:** 455-456.
- Kumar, P.A., H.A. Pushpadass, M.E.E. Franklin, H.V. Simha and B.S. Nath (2016). Effect of enzymatic hydrolysis of starch on pasting, rheological and viscoelastic properties of milk-barnyard millet (*Echinochloa frumentacea*) blends meant for spray drying. *International Journal of Biological Macromolecules*, **91**: 838-845.
- Leland, E. and V. Eugene (1999). Crop response and management of salt-affected soils. *Handbook of plant and crop stress*, 169.
- Mahalanobis, P.C. (1936). On the generalized distance in statistics. National Institute of Science of India.
- Mal, B. (2007). Neglected and underutilized crop genetic resources for sustainable agriculture. *Indian Journal of Plant Genetic Resources*, 20: 1-14.
- Manimekalai, M., M. Dhasarathan, A. Karthikeyan, J. Murukarthick, V.G. Renganathan, K. Thangaraj, S. Vellaikumar, C. Vanniarajan and N. Senthil (2018). Genetic diversity in the barnyard millet (*Echinochola frumentacea*) germplasms revealed by morphological traits and simple sequence repeat markers. *Current Plant Biology*, 14: 71-78.
- Martini-Bettolo, G.B. (Ed.) (1988). Towards a second green revolution. From Chemical to New Biological Technologies in Agriculture in the Tropics. *Proceedings of the International Meeting*, Rome, Italy, 8-10 September 1986. 530 p. Elsevier Publ.
- Nirosha, R., S. Thippeswamy, V. Ravindrababu, V.R. Reddy and B. Spandana (2016). Genetic diversity analysis of zinc, iron, grain protein content and yield components in rice. *Electronic Journal of Plant Breeding*, 7: 371-377.
- Ogle, D. (2010) Plants for saline to sodic soil conditions. USDA. Natural Resources Conservation Service. Boise, Idaho. Technical Note No.9A, p10150.
- Padulosi, S., P. Eyzaquirre and T. Hodgkin (1999). Challenges and strategies in promoting conservation and use of neglected and underutilized crop species. *Perspectives on new crops and new uses*, 140-145.
- Padulosi, S., B. Mal, S. Bala Ravi, J. Gowda, K.T.K. Gowda, G. Shanthakumar and M. Dutta (2009). Food security and climate change: role of plant genetic resources of minor millets. *Indian Journal of Plant Genetic Resources*, 22:1.
- Panse, V. G. and P.V. Sukhatme (1967). Statistical methods foragricultural workers. *Indian Council for Agricultural Research. New Delhi, Indlca.*, 87-89.
- Pessarakli, M. and I. Szabolcs (1999). Soil salinity and sodicity as particular plant/crop stress factors. *Handbook of plant and crop stress*, **2:** 1-15.
- Qualset, C., P. McGuire and M. Warburton (1995). In California: Agrobiodiversity'key to agricultural productivity. *California Agriculture*, **49:** 45-49.

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- Radhakrishna Rao, C. (1952). Advanced statistical methods in biometric research. A Division of Macmillan Publishing Co, Inc New York; Collier-Macmillan Publishers; London. pp. 390.
- Rao, M.V. (1989). The small millets: their importance, present status and outlook. In: Advances in Small Millets. (Riley K W; Gupta S C; Seetharam A; Mushonga J N, eds), pp 271–287. Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi.
- Shahidullah, S.M., M.M. Hanafi, M. Ashrafuzzaman, M.R. Ismail and A. Khair (2009). Genetic diversity in grain quality and nutrition of aromatic rices. *African Journal of Biotechnology*, 8: 1238-1246.
- Shanmuganathan, M., A. Gopalan and K. Mohanraj (2006). Genetic variability and multivariate analysis in pearl millet (*Pennisetum glaucum* L. R. Br.) germplasm for dual purpose. *Journal of Agricultural Sciences*, 2: 73-80.
- Singh, R.K. and B.D. Chaudhary (1977). Biometrical methods in quantitative genetic analysis Kalyani Publishers. *New Delhi*, **304**: 92-101.
- Sood, S., R.K. Khulbe, A.K. Gupta, P.K. Agrawal, H.D. Upadhyaya and J.C. Bhatt (2015). Barnyard millet-a potential food and feed crop of future. *Plant Breeding*, **134**: 135-147.
- Sood, S., R.K. Khulbe, A.K. Gupta, P.K. Agrawal and H.D. Upadhyaya (2015). Barnyard millet global core collection evaluation in the submontane Himalayan region of India using multivariate analysis. *The Crop Journal*, 3: 517-525.
- Suman, A., S.S. Surin and E. Ahmad (2019). Finger millet germplasm characterization and evaluation using principal component analysis. *International Journal of Chemical*

Studies, 7: 1002-1005.

- Suryanarayana, L., D. Sekhar and N.V. Rao (2014). Genetic variability and divergence studies in finger millet (*Eleusine* coracana L. Gaertn.). International Journal of Current Microbiology and Applied Sciences, 3: 931-936.
- Szabolcs, I. (1989). *Salt-affected soils*. CRC Press, Inc., Boca Raton. pp. 274-424.
- Szabolcs, I. (1993). Soils and salinization. In: Pessarakli M (ed) Handbook of plant and crop stresses. Dekker, New York, Basel, Hong Kong, 3-11.
- Thrupp, L.A. (1998). *Cultivating diversity: agrobiodiversity and food security*. World Resources Institute, Washington, DC, USA. pp.127-131.
- Toledo, Á. and B. Burlingame (2006). Biodiversity and nutrition: A common path toward global food security and sustainable development. *Journal of Food Composition and Analysis*, **19:** 477-483.
- Upadhyaya, H.D., M. Vetriventhan, S.L. Dwivedi, S.K. Pattanashetti and S.K. Singh (2016). Proso, barnyard, little and kodo millets. In *Genetic and Genomic Resources for Grain Cereals Improvement*, Academic Press. pp. 321-343.
- Vivekanandan, P. and S. Subramanian (1993). Genetic divergence in rainfed rice. *Oryza*, **30**: 60-60.
- Waskom, R.M., T. Bauder, J.G. Davis, A.A. Andales and G.E. Cardon (2003). Diagnosing saline and sodic soil problems. Crop series. Soil; no. 0.521. Fort Collins, CO: Colorado State University Cooperative Extension.
- Yabuno, T. (1987). Japanese barnyard millet (*Echinochloa utilis*, Poaceae) in Japan. *Economic Botany*, **41**: 484-493.