www.ThePharmaJournal.com

The Pharma Innovation



ISSN (E): 2277- 7695 ISSN (P): 2349-8242 NAAS Rating: 5.03 TPI 2018; 7(7): 944-945 © 2018 TPI www.thepharmajournal.com Received: 06-05-2018 Accepted: 07-06-2018

Suryanarayana L

Senior Scientist (Plant Breeding), Regional Agricultural Research Station, ANGRAU, Chintapalle, Visakhapatnam District, Andhra Pradesh, India

Sekhar D

Senior Scientist (Agronomy), Regional Agricultural Research Station, ANGRAU, Chintapalle, Visakhapatnam District, Andhra Pradesh, India

Correspondence Suryanarayana L

Senior Scientist (Plant Breeding), Regional Agricultural Research Station, ANGRAU, Chintapalle, Visakhapatnam District, Andhra Pradesh, India

Genetic divergence studies in little millet (*Panicum* sumatrense L.)

Suryanarayana L and Sekhar D

Abstract

Twenty three genotypes of little millet were evaluated for genetic diversity using Mahalanobis D^2 statistics for five quantitative traits during *kharif*, 2011. The data was subjected to Mahalanobis' D^2 statistics, all the 23 genotypes in the present study were grouped into six clusters. Maximum number of genotypes (8) were included in cluster VI followed by cluster-I (7), cluster-II, III, IV and V with two genotype in each cluster. Considering the inter cluster distances, it was highest between cluster IV and V (163.09) followed by V and VI (145.69). Among the five characters studied, grain yield (q/ha), days to 50% flowering and plant height (cm) contributed maximum towards the total divergence and were found to be responsible for primary differentiation.

Keywords: Little millet, genetic divergence, D²-statistics

Introduction

Little millet (*Panicum miliare* L.) is grown in India under various agro ecological situations and is commonly known as sama. It is mainly grown in the states of Karnataka, Maharashtra, Tamilanadu, Andhra Pradesh, Madhya Pradesh, Jharkhand, Odisha, Gujarat and Chhattisgarh. In the state of Andhra Pradesh the crop is mainly grown in hill slopes by tribal farming community in High Altitude and Tribal Areas, the productivity is low due to poor soil fertility. Though, the crop has been important over centuries, more concentrated research efforts are required to evolve improved varieties and develop production technology.

Progress in any crop improvement mainly depends on the degree of divergence for the desired characters existing in the germplasm collection. The knowledge on characters influencing divergence is an important aspect for a breeder. Information on the nature and degree of genetic divergence would help the plant breeder to choose right parents for breeding programmes. It has become possible to quantify magnitude of genetic diversity among germplasm with the help of advanced biometrical methods such as multivariate analysis (Rao, 1952) ^[5] based on Mahalanobis' (1936) ^[2] D² statistics.

Material and Methods

Seeds of 23 little millet genotypes including 4 checks were raised in Randomized Block Design (RBD) in three replications with spacing of 22.5×10 cm at Regional Agricultural Research Station, Chintapalle during *kharif*, 2011. Each genotype was grown in 10 lines of 3 m length. All the recommended package of practices were followed to raise a healthy crop. Observations were recorded on plant height (cm), number of productive tillers, days to 50% flowering, days to maturity and grain yield (q/ ha).

The genetic divergence among the genotypes was computed by means of Mahalanobis' D^2 statistics. Intra and inter cluster distance, cluster means and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary (1985)^[7].

Results and Discussion

The ANOVA revealed highly significant differences among the twenty three genotypes for five characters indicating the existence of sufficient amount of diversity among genotypes. The 23 genotypes were grouped into six clusters using Tocher's method with a criterion that the intra cluster average D^2 values should be less than the inter-cluster D^2 values. The distribution of 23 genotypes into six clusters was at random with maximum number of 8 genotypes grouped in cluster VI followed by Cluster I with 7 genotypes and cluster II, III, IV and V with two genotypes in each cluster (Table 1).

The average intra and inter cluster distances revealed that inter cluster distance was greater than intra cluster distance (Table 2). The maximum intra cluster distance was observed in the cluster I (49.32) followed by cluster VI (23.632), cluster V (3.023), cluster IV (2.394), cluster III (2.271) and cluster II (2.268). The intra cluster distance in cluster I was highest indicating the presence of wide genetic diversity among the genotypes present within this cluster. Similar findings were reported by Shinde et al., (2013)^[6], Devaliya et al., (2017)^[1] and Mahanthesha et al., (2017)^[3] in finger millet, Nirubana et al., (2017)^[4] in kodo millet. The inter cluster D² values ranged from 5.44 (between cluster II and III) to 163.09 (between cluster IV and V). Genotypes grouped in the same cluster presumably differ little from one another as the aggregate of characters measured. Based on the intra and inter cluster distances among the groups it is suggested to make crosses between the genotypes of cluster II and cluster V or VI after confirming their general combining ability to evolve transgressive segregants for yield and yield

components.

The knowledge on characters influencing divergence is an important aspect to a breeder. The per cent contribution towards genetic divergence by five contributing characters is presented in Table 3. Character wise rank has shown that no single character alone had a greater contribution to total genetic divergence. The maximum contribution towards genetic divergence was displayed by grain yield (q/ha) (46.24%) followed by days to 50% flowering (26.08), plant height (13.04), number of productive tillers (9.88) and days to maturity (4.74) in the decreasing order of values, respectively. The cluster mean values for five characters are presented in Table 4. High mean values for plant height, number of productive tillers and grain yield (q/ha) were seen in cluster III, while days to 50% flowering and days to maturity were seen in cluster V. Thus involving the genotypes of outstanding mean performance from these clusters will be useful in development of high vielding variety with better quality.

Table 1: Cluster composition of 23 little millet genotypes
--

Cluster No	No of genotypes in each cluster	Cluster members		
Cluster 1	7	GV-2-1, RLM-42, DLM-14, TNAU-152, DLM-18, BL-3, BL-6.		
Cluster 2	2	CO-2, BL-5.		
Cluster 3	2	TNAU-140, OLM-203.		
Cluster 4	2	RLM-41, JK-8.		
Cluster 5	2	GV-2, TNAU-142.		
Cluster 6	8	RLM-40, BL-2, BL-4, RLM-141, RLM-186, TNAU-157, TNAU-159, Peda Sama.		

 Table 2: Average intra and inter cluster D² values among six clusters in little millet

	Ι	II	III	IV	V	VI
т	49.32	26.4	34.087	37.204	108.744	37.562
1	(7.023)	(5.138)	(5.838)	(6.1)	(10.428)	(6.129)
Π		2.268	5.447	14.46	124.034	13.327
		(1.506)	(2.334)	(3.804)	(11.137)	(3.651)
III			2.271	25.506	139.76	19.398
			(1.507)	(5.05)	(11.822)	(4.404)
IV				2.394	163.099	15.833
1 V				(1.547)	(12.771)	(3.979)
v					3.023	145.699
					(1.739)	(12.071)
VI						23.632
v I						(4.861)

Table 3: Contribution of characters towards genetic divergence

Character	No of times ranked first	% Contribution	
Plant height (cm)	33	13.0435	
No of productive tillers	25	9.8814	
Days to 50% flowering	66	26.087	
Days to maturity	12	4.7431	
Grain yield (q/ha)	117	46.2451	
Total	253	13.0435	

 Table 4: Cluster means for five characters in 23 genotypes of little millet.

Cluster No	Plant height (cm)	No of productive tillers	Days to 50% flowering	Days to maturity	Grain yield (q/ha)
Ι	135.929	4.381	66	89.095	3.388
II	145.467	4.75	59.667	83.167	3.493
III	154.567	5.233	59	82.833	4.16
IV	108.733	4.567	58.833	83	3.317
V	153.817	3.8	91.167	114.833	2.43
VI	129.7	4.879	59.875	83.458	3.465

References

- Devaliya SD, Singh M and Intawala CG. Genetic divergence studies in finger millet (*Eleusine coracana* L.). Int. J Curr. Microbiol. App. Sci. 2017; 6(11):2017-2022.
- 2. Mahalanobis' PC. On the generalized distance in statistics. Proceedings of National Institute of Sciences (India). 1936; 12:49-55.
- 3. Mahanthesha M, Sujatha M, Pandravada SR, Meena AK. Study of genetic divergence in finger millet (*Eleusine coracana* (L.) germplasm. International Journal of Pure and Applied Bio Sciences. 2017; 5(3):373-377.
- Nirubana V, Ganesamurthy K, Ravikesavan R, Chitdeshwari. Genetic diversity studies in kodo millet (*Paspalum scorbiculatum* L.) germplasm accessions based on biometrical and nutritional quality traits. Int. J Curr. Microbiol. App. Sci. 2017; 6(10):832-839.
- Rao CR. Advanced Statistical Methods in Biometric Research. Edn l. John Wiley and Sons, New York, 1952, 36-38.
- Shinde SR, Desai SV, Pawar RM. Genetic diversity pattern in finger millet (*Eleusine coracana* L.). Electron. J Plant Breed. 2013; 4(3):1242-1245.
- 7. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. 1985, 102-157.