



E-ISSN: 2278-4136

P-ISSN: 2349-8234

www.phytojournal.com

JPP 2020; 9(1): 1950-1953

Received: 07-11-2019

Accepted: 09-12-2019

N Anuradha

Acharya NG Ranga Agricultural University, Agricultural Research Station, Vizianagaram, Andhra Pradesh, India

TSSK Patro

Acharya NG Ranga Agricultural University, Agricultural Research Station, Vizianagaram, Andhra Pradesh, India

U Triveni

Acharya NG Ranga Agricultural University, Agricultural Research Station, Vizianagaram, Andhra Pradesh, India

P Joga Rao

Acharya NG Ranga Agricultural University, Agricultural Research Station, Vizianagaram, Andhra Pradesh, India

S Rajkumar

Acharya NG Ranga Agricultural University, Agricultural Research Station, Vizianagaram, Andhra Pradesh, India

Corresponding Author:**N Anuradha**

Acharya NG Ranga Agricultural University, Agricultural Research Station, Vizianagaram, Andhra Pradesh, India

Trait association and genetic variability in browntop millet

N Anuradha, TSSK Patro, U Triveni, P Joga Rao and S Rajkumar

Abstract

Browntop millet (*Brachiaria ramosa* (L.) Stapf.) is one of forgotten crop with very small grains which is mainly used as food and fodder. It is a climate resilient crop which can come well with limited water. It is highly valued for its high fiber and mineral content in grains. Genetic variability of a crop plays an important role in crop improvement. Hence, present study was attempted to assess the genetic variability and associations of various economic traits at Agricultural Research Station, Vizianagaram. Significant differences for all twelve traits studied were noticed among 10 browntop millet genotypes. GCV ranged from low (4.63 for plant height) to moderate (12.99 for days to 50% flowering) indicating low to moderate variability. The difference in GCV and PCV was very narrow (less than 0.2) for days to 50% flowering and days to maturity indicating least influence of surrounding environment which was further supported by high value of broad sense heritability (more than 95%) while grain and fodder yield recorded moderate heritability with moderate GAM indicating the presence of both additive and non additive gene action. Selection for high grain and fodder yield can be relied upon selection for more number of days to 50% flowering and days to maturity as grain and fodder yield are significantly associated in positive direction with days to 50% flowering and days to maturity.

Keywords: Brown top millet, *Brachiaria ramosa*, genetic variability, heritability

Introduction

Brown top millet (*Brachiaria ramosa* (L.) Stapf.) or signal grass belong to the family poaceae. it is a tetraploid with basic chromosome number of four (Basappa *et al.*, 1987) [6]. Though it is a weed in many places, it is grown as feed for game birds in some parts of America and it is grown as crop for human consumption and fodder to animals in few parts of southern India (Kimata *et al.*, 2000) [12]. In the past it used to be a major staple crop in much wider areas (Fuller, *et al.*, 2004) [9]. Recently it is gaining importance among public as nutritional grain because of its high fibre content in the grain. Its growing popularity among public made the Government sector working on small millets to include it as one of the small millet in AICRP system for conducting trials and developing varieties during 2018-19. It is also considered as illegal wife of little millet since it mimics little millet and is mostly seen in the little millet crop (Sakamoto 1987) [17].

In India, it is cultivated mainly in Karnataka, Andhra Pradesh and to some extent in Tamil Nadu. It is drought resistant, heat tolerant and can be grown even in degraded soils with scarce water resources. It fits into any cropping system and it can also be used as a cover crop as it easily spreads like grass striking roots wherever it touches the ground covering the ground and holding the soil firmly, thus preventing soil erosion. The grain matures within 75-90 days, while for forage it is hardly 50 days duration with rapid forage production. Two types of browntop millet are under cultivation, one with compact panicles ($2n=38$) and another with open type of panicles ($2n=28$). It is mostly grown in arecanut and coconut plantations to prevent rodent damage because of its sharp leaf edges. The crop can pose a challenge to the changing climate. (Sujata *et al.*, 2018) [20].

Materials and methods

In the present investigation, ten genotypes were evaluated at Agricultural Research Station, Vizianagaram, Andhra Pradesh during *kharif*, 2018 in complete randomized block design (RCBD) under three replications with a spacing of 22.5×10 cm per each entry. Fertilizers, 40-20-0 NPK kg/ha and need based plant protection measures were taken to raise a healthy crop. Observations were recorded on days to 50% flowering, plant height (cm), No. of productive tillers/plant, panicle length, No. of primary rachis in the panicle, peduncle length (cm), flag leaf length (cm), flag leaf width (cm), days to maturity, grain yield (q/ha) and fodder yield (q/ha).

Analysis of variance and summary statistics were calculated as per Panse and Sukathme (1967) [15]. Analysis of variance may not reveal the absolute variability and this could be accessed through standardizing the phenotypic and genotypic variances by obtaining the coefficients of variability. Hence, the components of variation such as genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were computed as per Burton and Devane (1953) [7]. Further it is essential for selection to separate out the environmental influence from the total variability. This indicates the accuracy with which a genotype can be identified by its phenotypic performance and thus heritability in broad sense was computed as per Allard (1960) [11]. The estimates of heritability alone fail to indicate the response to selection. Therefore, the heritability estimates appeared to be more meaningful when accompanied by estimates of genetic advance. Hence the genetic advances as per cent mean (GAM) was also estimated. Heritability and genetic advancement were categorized into low, medium and high as per Johnson *et al.*, (1955) [10]. Selection depends on many interrelations and hence phenotypic correlations were calculated according to Falconer (1981) [8].

Results & Discussions

Analysis of various help us to know whether real differences are existing among the genotypes or the difference among genotypes for a trait is due to other factors like environmental factors or due to experimental error (Sharma, 2006) [18].

The present study revealed that real significant difference (Table 1) were existing among 10 different brown top millet genotypes for all twelve traits studied. Similar variations were reported by Anuradha *et al.*, (2017a, 2018) [2, 19], Singamstti *et al.*, (2018) [19] in finger millet and Anuradha *et al.*, (2017b) [3] in pearl millet. Replications were also significant for No. of productive tillers/plant and peduncle length indicating that the blocking was quiet apt in reducing the error due to edaphic factors.

Mean values of all ten brown top millet genotypes were given in Table 2. Early maturity was observed for TNBr 002 (68 days) and GPUBT 2 while GPUBT 1 and HB 2 were late maturing genotypes. Short plant height was recorded in TNBr 001 (145 cm) and tall height in GPUBT 2 (174.2 cm). Highest Number of tillers were observed for GPUBT 5 (12.5) while long panicle length was recorded in KMBT 1 and GPUBT 4 (20.0 cm). No. of primary rachi in inflorescence were more for GPUBT 1 (19.5) while lower number were recorded in TNBr 002. Longer peduncle length was recorded in GPUBT 5 while longest (20.5cm) and widest flag leaf length was recorded in GPU BT 4 (20.5cm and 3.0 cm respectively). Highest grain yield was recorded in GPUBT 4 (12.5 q/ha) followed by GPUBT 6 (12.0 q/ha) while early maturing genotypes TNBr 002 and TNBr 001 recorded 8.4 and 8.5 q/ha grain yield respectively. Browntop millet is also valued for fodder yield. So fodder yield of all ten genotypes were taken where GPUBT 3 (69.8 q/ha) followed by KMBT 1 (67.8 q/ha) and GPUBT 1 (67.5 q/ha) recorded higher fodder yield.

Analysis of Variance (Anova) and mean values alone does not give the information on quantity of variation present among the population. Variability can better be understood in terms of Genotypic Coefficient of Variation (GCV) which is due to genetic cause alone and Phenotypic Coefficient of Variation which is due to both genetic and environmental causes. GCV and PCV are unit less quantities which help us to compare the amount of genetic and phenotypic variation present among different traits. PCV and GCV (Table 3) ranged from low to

medium for twelve traits studied. PCV was slightly higher than GCV for days to 50% flowering (13.07, 12.99) and days to maturity (10.51, 10.36) indicating that whatever differences are existing among genotypes are due to genetic factors and these two traits are not much influenced by environmental factors. It was also evident from the high heritability values of 98.7% and 97.19% for days to 50% flowering and days to maturity respectively which further emphasise the real genetic nature of the variation. Hence, even though these two traits had moderate variations, but almost all the variation is heritable. Similar results were reported earlier by Patil *et al.*, (2013); Jyothsna *et al.*, (2016), Mahanthesha *et al.*, (2017) [16, 11, 13] in millets. The variation for plant height was recorded as low (PCV=9.16, GCV=4.63) further the heritability of the trait was near to low (25.48) and with wide difference between GCV and PCV indicating that it is very difficult for selection to operate in improving this trait

No. of productive tillers/plant also had low GCV, a wide difference of GCV (6.99), PCV (11.43) and moderate heritability indicating that the variation which is due to genetic cause is low and that too it is inflated by the influence of environment which hinders the easy improvement of the trait through simple selection. No. of primary rachi in the panicle, peduncle length flag leaf length and flag leaf width also recorded low GCV and moderate heritability values indicating that these traits can be improved only to a limited extent. Grain yield and fodder yield recorded moderate variability (GCV 10.72 and 11.02 for grain yield and fodder yield respectively) along with moderate heritability (>20% and <60% for grain yield and fodder yield respectively) indicating some amount of variability which is genetic and inherited moderately though environment has its role in determining the trait.

GCV, PCV and heritability alone cannot give the total information on how the trait is inherited and what are the breeding strategies to be followed for improvement of a trait. Genetic Advance of mean in combination with heritability suggests the nature of gene action. So, in this context GAM was estimated. Days to 50% flowering, days to maturity recorded high heritability with high GAM indicating more of additive gene action for these two traits. Hence simple selection process like pure line selection and mass selection can be followed for their improvement. Plant height, No. of productive tillers/plant, peduncle length and flag leaf width recorded to have moderate heritability with low GAM indicating non additive gene action. Hence, response to selection is difficult and one has to go for recombination breeding and make selections at later generations (Nadarajan, 2005) [14].

Panicle length, No. primary rachi in the panicle, flag leaf length, fodder yield and grain yield recorded moderate heritability with moderate GAM indicating presence of additive and non additive components of genetic variation. Hence selection of these traits is not so simple and is possible through population improvement or has to depend on other associated traits which are easily heritable.

In order observe the association with other traits for considering simultaneous selection of various traits correlations were studied. Days to maturity was highly correlated (Table 4) in significant positive direction with days to 50% flowering, panicle length, flag leaf length, flag leaf width, grain yield and fodder yield. Panicle length was strongly associated in positive direction with days to maturity, No. of productive tillers/plant, No. of rachis in inflorescence, flag leaf length, flag leaf width and grain yield. Fodder yield

recorded significant positive associations with days to 50% flowering, days to maturity and flag leaf length while the grain yield potential of a genotype recorded significant positive associations with days to 50% flowering, days to maturity, panicle length, flag leaf length and flag leaf width.

Since days to 50 % flowering and days to maturity are having high heritability and are predominantly governed by additive nature of gene action, having strong positive association with grain yield & fodder yield, these two traits can be relied upon for improvement of grain & fodder yield in the present population.

Table 1: Anova of 10 browntop millet genotypes

Source of Variations	df	Mean Squares											
		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of productive tillers	Panicle length (cm)	Length of primary rachis	No. of primary rachi in a panicle	Peduncle length (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Grain Yield (q/ha)	Fodder Yield (q/ha)
Treatments	9	168.45**	242.11**	310.43	2.97*	7.16**	0.95	13.22*	2.19*	12.86**	0.20*	5.81*	219.06*
Replications	2	0.03	1.90	118.91	11.12**	1.82	0.25	0.91	10.43**	4.98	0.18	4.51	22.02
Error	18	0.74	2.31	153.23	1.06	1.39	0.57	4.88	0.85	2.82	0.07	1.93	88.89

*significant at 5% level & ** significant at 1% level

Table 2: Mean values and summary statistics of 10 browntop millet genotypes

S. No	Entries	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of productive tillers	Panicle length (cm)	Length of primary rachis	No. of primary rachi in a panicle	Peduncle length (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Grain Yield (q/ha)	Fodder Yield (q/ha)
1	GPUBT-2	64.0	92.0	174.2	9.4	17.7	6.2	16.0	10.2	17.2	2.8	11.1	63.6
2	GPU BT-6 ©	61.3	90.3	154.0	11.6	18.9	6.5	15.4	9.9	20.1	3.2	12.0	52.6
3	GPUBT-5	61.7	90.3	161.5	12.5	19.0	6.9	17.3	11.5	17.4	2.7	11.6	64.3
4	KMBT-1	57.7	88.7	151.6	12.0	20.0	6.1	18.3	10.2	19.4	2.9	11.1	67.8
5	GPUBT-4	58.3	87.7	150.7	12.0	20.0	7.6	17.7	11.2	20.5	3.0	12.5	63.0
6	GPUBT-1	58.7	92.0	173.2	12.1	19.0	6.7	19.5	10.0	18.7	2.9	10.1	54.0
7	HB-2	62.0	91.7	156.6	12.4	19.1	7.1	17.9	10.9	19.7	2.9	11.0	67.5
9	GPUBT-3	64.0	91.3	151.5	10.9	17.2	7.0	17.6	10.7	20.2	2.9	9.7	69.8
9	TNBr 001	45.0	70.7	145.3	10.9	17.1	6.0	17.3	8.5	14.6	2.4	8.5	46.4
10	TNBr 002	43.0	68.3	146.5	10.4	15.0	5.9	11.9	11.1	15.5	2.4	8.4	48.7
	Minimum	43.0	68.3	145.3	9.4	15.0	5.9	11.9	8.5	14.6	2.4	8.4	46.4
	Maximum	64.0	92.0	174.2	12.5	20.0	7.6	19.5	11.5	20.5	3.2	12.5	69.8
	Mean	57.57	86.3	156.5	11.41	18.31	6.59	16.9	10.41	18.34	2.81	10.61	59.76
	CD (5%)	1.47	2.61	21.23	1.77	2.03	1.29	3.79	1.58	2.88	0.47	2.38	16.17
	CD (1%)	2.02	3.57	29.09	2.42	2.78	1.77	5.19	2.16	3.95	0.64	3.26	22.15
	CV (%)	1.49	1.76	7.91	9.04	6.45	11.45	13.07	8.83	9.16	9.71	13.08	15.78

Table 3: Genetic parameters of 10 browntop millet genotypes

S. No	Parameter	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of productive tillers	Panicle length (cm)	Length of primary rachis	No. of primary rachi in a panicle	Peduncle length (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Grain Yield (q/ha)	Fodder Yield (q/ha)
1	GCV	12.99	10.36	4.63	6.99	7.57	5.43	9.87	6.42	9.97	7.36	10.72	11.02
2	PCV	13.07	10.51	9.16	11.43	9.95	12.67	16.38	10.92	13.54	12.19	16.91	19.25
3	ECV	1.49	1.76	7.91	9.04	6.45	11.45	13.07	8.83	9.16	9.71	13.08	15.78
4	H ² (Broad Sense)	98.70	97.19	25.48	37.41	57.94	18.36	36.28	34.59	54.23	36.47	40.18	32.80
5	Genetic Advance	15.30	18.16	7.53	1.00	2.17	0.32	2.07	0.81	2.78	0.26	1.49	7.77
6	GAM	26.58	21.04	4.81	8.81	11.87	4.79	12.24	7.78	15.13	9.16	14.00	13.01

Table 4: Phenotypic correlation of 12 traits in 10 browntop millet genotypes

Traits	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of productive tillers	Panicle length (cm)	Length of primary rachis	No. of primary rachi in a panicle	Peduncle length (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Grain Yield (q/ha)
Days to maturity	0.97**										
Plant height (cm)	0.57	0.63									
No. of productive tillers	0.24	0.36	-0.08								
Panicle length (cm)	0.60	0.71*	0.26	0.71*							
Primary branch length of a panicle	0.58	0.58	0.09	0.56	0.55						
No. of primary Branches in a panicle	0.50	0.61	0.33	0.56	0.74*	0.48					
Peduncle length (cm)	0.33	0.30	0.07	0.28	0.11	0.54	-0.18				
Flag leaf length (cm)	0.74*	0.78**	0.11	0.48	0.68*	0.71*	0.45	0.37			
Flag leaf width (cm)	0.78**	0.83**	0.28	0.39	0.72*	0.56	0.41	0.18	0.92**		

Grain Yield (q/ha)	0.72*	0.74*	0.30	0.44	0.82**	0.60	0.33	0.39	0.71*	0.80**	
Fodder Yield (q/ha)	0.77**	0.73*	0.21	0.25	0.50	0.53	0.45	0.53	0.65*	0.47	0.52

References

- Allard RW. Principles of Plant Breeding. John Wiley and Sons Inc., New York, 1960, 485.
- Anuradha N, Patro TSSK, Divya M, Sandhya Rani Y, Triveni U. Morphological diversity analysis in finger millet (*Eleusine coracana* (L.) Gaertn.). *Frontiers of Crop Improvement Journal*. 2017a; 5(1):67-70
- Anuradha N, Satyavathi CT, Meena MC, Sankar SM, Bharadwaj C, Bhat J *et al.* Evaluation of pearl millet [*Pennisetum glaucum* (L.) R. Br.] for grain iron and zinc content in different agro climatic zones of India. *Indian Journal of Genetics and Plant Breeding (The)*. 2017b; 77(1):65-73.
- Anuradha N, Patro TSSK, Divya M, Sandhya Rani Y, Triveni U. Genetic Variability, Heritability and Association in Advanced Breeding Lines of Finger Millet [*Eluesine coracana* (L.) Gaertn.]. *International Journal of Chemical Studies*. 2018a; 5(5):1042-1044
- Anuradha N, Patro TSSK, Divya M, Sandhya Rani Y, Triveni U. Genetic Variability, Heritability and Correlation of quantitative traits in Little Millet Genotypes. *Journal of Pharmacognosy and Phytochemistry*. 2018b; 6(6):489-492
- Basappa GP, Muniyamma M, Chinnappa CC. An investigation of chromosome numbers in the genus *Brachiaria* (Poaceae: Paniceae) in relation to morphology and taxonomy. *Canadian J. Botany*. 1987; 65:2297-2309
- Burton GW, Devane EW. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agronomy Journal*. 1953; 45:478-481.
- Falconer DS. *Introduction to Quantitative Genetics*. 2nd ed. Longman, London, 1981.
- Fuller DQ, Korisettar R, Venkatasubbaiah PC, Jones MK. Early plant domestications in southern India: some preliminary archaeo botanical results. *Vegetation History and Archaeo botany*. 2004; 13:115-29.
- Johnson HW, Robinson HF, Comstock RE. Estimate of genetic and environmental variability in Soybeans. *Agronomy Journal*. 1955; 47:314-318.
- Jyothsna S, Patro TSSK, Sandhya Rani Y, Neeraja B, Ashok S, Triveni U. Studies on genetic parameters, character association and path analysis of yield and its components in little millet (*Panicum sumatrense*). *International Journal of Agriculture Sciences*. 2016; 8(5):1018-1020.
- Kimata M, Ashok EG, Seetheram A. Domestication, cultivation and utilization of two small millets, *Brachiaria ramosa* and *Setaria glauca* (Poaceae), in South India. *Econ Bot*. 2000; 54:217-227
- Mahanthasha M, Sujatha M, Ashok Kumar Meena, Pandravada SR. Studies on Variability, Heritability and Genetic Advance for Quantitative Characters in Finger millet [*Eleusine coracana* (L.) Gaertn] germplasm. *Int. J. Curr. Microbiol. App. Sci*. 2017; 6(6):970-974.
- Nadarajan N. *Quantitative genetics and biometrical techniques in plant breeding*. Kalyani Publishers, 2005.
- Panse VG, Sukathme PV. *Statistical Method for Agricultural Workers*. ICAR, New Delhi, 1967, 381p.
- Patil AS, Mane VA. Studies on the genetic variation of yield and contributing traits in finger millet [*Eleusine coracana* (L.) Gaertn]. *Progressive research*. 2013; 8(sp.):526-528.
- Sakamoto S (ed.). A preliminary report of the studies on millet cultivation and its agro-pastoral culture complex in the Indian subcontinent. Kyoto: Kyoto University Research Team for the Studies on Millet Cultivation and Its Agro-pastoral Culture Complex in the Indian Subcontinent, 1987.
- Sharma JR. *Statistical and biometrical techniques in plant breeding*. New Age International (P) Ltd, Publishers, New Delhi, India, 2006.
- Singamsetti A, Patro TSSK, Anuradha N, Divya M. Studies on Genetic Variability for Yield and Yield Attributing Traits in Finger millet (*Eluesine coracana* L. Gaertn). *International Journal of Current Microbiology and Applied Sciences*. 2018; Special Issue-7:90-95.
- Sujata B, Prabhu CG, Nandini C, Prabhakar, Thippeswamy V. Browntop Millet- A Review. *Agricultural Research & Technology: Open Access Journal*. 2018; 14(5):555937. doi: 10.19080/ARTOAJ.2018.14.555937.