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GENETIC VARIABILITY STUDIES FOR QUANTITATIVE TRAITS OF MAINTAINER (B) LINES IN PEARL MILLET [*Pennisetum glaucum* (L.) R. Br.]

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ABSTRACT
The present investigation was carried out during kharif 2015-16 at Regional Agricultural Research Station, Vijayapur, Karnataka with 48 genotypes of pearl millet [*Pennisetum glaucum* (L.) R. Br.] in a randomized block design with two replications to estimate the genetic variability, heritability and genetic advance for nine quantitative traits. Analysis of variance revealed significant differences among the genotypes for all the traits studied indicating the presence of sufficient variability in the studied material. The PCV was higher than GCV and the difference between PCV and GCV was narrow for most of the characters revealing little influence of the environment in the expression of these traits. High magnitude of PCV and GCV were observed for traits like panicle weight (24.71 & 25.57), stover weight per plot (30.35 & 35.12) and grain yield per plot (21.93 & 26.78) respectively. Suggesting the existence of wide range of genetic variability in the germplasm for these traits and thus the scope for improvement of these characters through simple selection would be better. High heritability coupled with high genetic advance as per cent of mean was observed for characters *viz*., panicle girth, panicle weight and stover weight per plot, grain yield per plot and 1000 seed weight. Indicating predominance of additive gene action for these characters. Hence, Simple selection based on phenotypic performance of these characters would be more effective.

KEY WORDS: Pearl millet, Variability, Heritability, Genetic Advance.

INTRODUCTION
Pearl millet [*Pennisetum glaucum* (L.) R.Br.] is extensively cultivated for grain as well as fodder in the dry areas of north-western and southern India and along with periphery of the Sahara. It is the fourth most important staple food after rice, wheat and maize in India. To sustain food wealth and cattle production, pearl millet varieties need to be improved for grain and fodder yield with better quality. Genetic variability for grain yield and its contributing components and understanding their inter-relationship is essential to develop high yielding varieties of pearl millet.

The development of an effective plant breeding programme is depending upon the assessment of polygenic variation, selection of elite genotypes, choice of parents and breeding procedures. Crop improvement depends upon the magnitude of genetic variability and the extent to which desirable characters are heritable. Genetic variability for yield and yield components is essential in the base population for successful crop improvement (Allard, 1960). Yield and yield components are quantitative characters and are poly genetically inherited which are greatly influenced by environment. The phenotype of a character is the resultant of interaction between genotype and environment. Partitioning of observed variability into heritable and non-heritable components is essential to get a true indication of the genetic variation of the trait. Genetic parameters such as Genotypic, Phenotypic coefficient of variation (PCV and

GCV) are useful in detecting the amount of variability present in the available genotypes. Heritability and genetic advance help in determining the influence of environment in expression of the characters and the extent to which improvement is possible after selection (Robinson *et al*., 1949). The total variability can be partitioned into heritable and non heritable components with the help of genetic parameters like phenotypic and genotypic coefficient of variation, heritability and genetic advance. Heritable variation can be effectively studied in conjunction with genetic advance. High heritability alone is not enough to make efficient selection in segregation, unless the information is accompanied for substantial amount of genetic advance (Johnson *et al*., 1955). Keeping these things in view, the present study has been carried out to access amount of variability present in pearl millet maintainer lines.

MATERIALS & METHODS
Experimental material consist of 48 diverse maintainer (B) lines received from ICRISAT, Patencheru (**Table. 1**) and were sown during *kharif* 2014-15 in Randomized Block Design with two replication at Regional Agricultural Research Station, Vijayapur (Karnataka, India). The recommended packages of practices were followed to raise the crop. Each germplasm line was sown in two rows of 4 m. length with 45 X 15 cm spacing. The observation on days to 50 per cent flowering, plant height (cm), panicle length (cm), panicle girth (cm), panicle weight (g/panicle),

grain yield/plot (kg), stover yield/plot (kg), number of productive tillers (No.'s) and 1000 seed weight (g) were recorded on five randomly selected plants for all the lines in each replication.

Statistical analysis

Statistical analysis was done on the mean values of five randomly selected plants in each progeny rows. The statistical software (WINDOSTAT version 8.0) was used to work out ANOVA, genetic parameters and the statistical methods adopted were as follows

Genotypic coefficient of variation (GCV) = $\dfrac{\sigma^2_g}{\bar{X}}$ X 100

Phenotypic coefficien of variation (PCV) = $\dfrac{\sigma^2_p}{\bar{X}}$ X 100

Where, σ^2_g = Genotypic variance, σ^2_p = Phenotypic variance, $\bar{X}$ = General mean of the character

GCV and PCV values were categorized as low, moderate and high as indicated by Sivasubramanian and Menon (1973).

0-10%: Low
10-20%: Moderate
20% and above: High

Heritability in broad sense was estimated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage (Hanson et al., 1956).

Heritability (h²) = $\dfrac{Vg}{Vp}$ X 100

Where, Vg = Genotypic variance, Vp = Phenotypic variance

The heritability percentage was categorized as low, moderate and high as followed by Robinson et al. (1949), as follows.

0 – 30 per cent   : Low
30 – 60 per cent   : Moderate
> 60 per cent   : High

Genetic advance

The extent of genetic advance to be expected by selecting five per cent of the superior progeny was calculated by using the following formula given by Robinson et al. (1949).

GA = i σ_p h²

Where, i = efficacy of selection which is 2.06 at 5 per cent selection intensity

σ_p = phenotypic standard deviation, h² = heritability in broad sense.

Genetic advance as per cent of mean

GA as per cent of mean = (GA /$\bar{X}$) x 100

Where, GA = genetic advance, $\bar{X}$ = general mean of character

The GA as per cent of mean was categorized as low, moderate and high as following by Johnson et al. (1955) as follows.

0 - 10 per cent   : Low
10 - 20per cent   : Moderate
20 and above   : High

RESULTS & DISCUSSION

Analysis of variance for the experiment involving 48 pearl millet maintainer lines for 9 quantitative characters revealed that the mean sum of squares were highly significant for all the traits studied (**Table 2**), indicating presence of significant variability in the genotypes which can be exploited through selection.

The extent of variability with respect to 9 characters in different genotypes measured in terms of mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) along with the amount of heritability (h), expected genetic advance and genetic advance as per cent of mean (GAM) are presented in (**Table 3**). Results revealed high mean and wide range of expression of different characters indicating sufficient variability existed in the present material selected for the study and indicating the scope for selection of suitable initial breeding material for crop improvement (Janaki et al., 2013).

The trend of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for all the characters remained similar in all the characters. The phenotypic coefficient of variation (PCV) was though higher than genotypic coefficient of variation (GCV) for all the characters under study (Table 2) but the narrow range of difference indicated that most of the characters were least influenced by the environment (Janaki et al. 2015).

High values of GCV and PCV were obtained for the characters Viz., Panicle weight (24.71 & 25.57), Stover weight per plot (30.35 & 35.12) and Grain yield per plot (21.93 & 26.78). Indicating variation for these characters contributed markedly to the total variability. Further, narrow range of difference between PCV and GCV indicated that any selection pressure operated on these characters may help to realize improvement at early generation. High PCV and GCV values were reported in pearl millet by Sumathi et al. (2010) and Vinodhana et al. (2013) for panicle weight, stover weight, productive tillers per plant and ear length; Lakshmana et al., 2003 for grain yield per plant; Borkhataria et al., 2005 for ear girth and grain yield per plant.

The coefficient of variation indicates only the extent of total variability present for a character and does not demarcate the variability into heritable and non-heritable portion. Hence, the estimate of heritability, which indicates precisely the heritable expected gain, assumes importance. The extent of variability, which could be transferred from parent to offspring, would suggest how for the variation in heritable portion has close bearing on response to selection. High heritability is an indication of presence of higher proportion of fixable additive variance in the population. Heritability value is of much use to breeder, as it indicates the accuracy with which a genotype can be evaluated by its phenotypic expression. The heritability estimates ranged from 16.6 for number of productive tillers to 93.8 for panicle weight. High estimates of heritability were recorded for characters viz., panicle girth (85.1%), Panicle weight (93.8 %) and Stover weight per plot (74.7 %), Grain yield per plot (67.0%) and 1000-seed weight (72.2 %). Sumathi et al., 2010, Mukesh et al., 2013 and Kumar et al., 2014 also obtained similar results in pearl millet.

TABLE 1. List and pedigree details of maintainer (B) lines of pearl millet used in the study

Sl.No.	Genotype	Pedigree (B lines)
1	CPBLT-101	(ICMB 0133 X HHVDBCHS-10-1-2-1-1-1-3-B)-2-1-3-2-1
2	CPBLT-102	[[(ICMV 88908-11-12-3-2-B x B-bulk)-8-B-3)]843B x ICMPS 900-9-3-2-2)-41-2-5-5 S2-34-1-2-1-1 X B-bulk)-5-B-B]-11-1-1-B-B X ICMB 04111]-54-2-
3	CPBLT-103	(SRC II C3 S1-19-3-2 X HHVBC)-12-4-1-3-2-1-B-5-B-3-B-B
4	CPBLT-104	(ICMB 01888 X ICMB 01222)-16-1-2-2-1-B-B
5	CPBLT-105	(SRC II C3 S1-19-3-2 X HHVBC)-3-5-1-2-B
6	CPBLT-106	[SRC IIC3 S1-103-1-1 X HHVBC)-20X (8IB X ICMP 451)-5-4-2]-3-2-3-1-B-B
7	CPBLT-107	[SRC IIC3 S1-1-1-2 X HHVBC)-2-2-1-1-1-B-B X (8IB X 40I7-5-4-B)-12-3-1-3]-2-3-1-2-2
8	CPBLT-108	(NC D2 S1-2-2-2-3-4-B X ICMB 97333)-1-2-3-3
9	CPBLT-109	(ICMB 93333 X ICMB 01222)-20-2-B-5-B-1-B
10	CPBLT-110	(DMR 133 x HTBC 48-B-1-1-1-5)-19-2-B-B x ICMB 04111]-145-6-2-4
11	CPBLT-111	[8IB X 40I7-6-1-1)-3-1-3-3-1-1-B-B X ICMB 04111]-86-4-4
12	CPBLT-112	9ICMB 94333 X ICMB 01222)-47-1-B-B-B
13	CPBLT-113	(ICMB 01888 X ICMB 01222)-4-4-B-B-B-B-1
14	CPBLT-114	[[(843B X ICTP 8202-161-5)-20-3-B-B-3 X B-bulK]-2-B-9 X [(ICMB 96555 X LaGrap C2 S1-32-1)-10 X IP 14758-2-1]-8-2]-1-1-1-2
15	CPBLT-115	(ICMB 96555 X IP 10437)-9-2-5-1-B-1-B-1-3-B
16	CPBLT-116	(EBC-Gen-S1-40-2-2-1 X B-bulk)-28-B-B-3-B-B-3
17	CPBLT-117	[[(ICMV 88908-11-12-3-2-B X B-bulk)-8-B-3 X {(843B X ICMPS 900-9-3-2-2)-41-2-5-5 S2-34-1-2-1-1 X B-bulk)-5-B-B]-11-1-1- B-B X ICMB
18	CPBLT-118	[SRC IIC3 S1-1-1-2 X HHVBC)-2-2-1-1-1-B-B X (8IB X 40I7-5-4-B0-12-3-1-3)-2-3-1-2-3
19	CPBLT-119	ICMB 93333
20	CPBLT-120	ICMB 01666
21	CPBLT-121	JMSB-101
22	CPBLT-122	JMSB-2007
23	CPBLT-	JMSB-20082

Table 1. (Contd...)

24	**TPBLT -101**	(HHVDBC HS-246-1-2-1-1-2 X ICMB 98444)-4-3-2-1
25	**TPBLT -102**	(ICMB 01666 X ICMB 01222)-49-1-2-B-2
26	**TPBLT -103**	(B X B) F2 S1 109-2-3-3-1-4-2
27	**TPBLT -104**	(HHVDBC HS-246-1-2-1-2 X ICMB 01222)-4-2-1-1
28	**TPBLT -105**	(ICMB 01333 X HHVDBC HS-10-1-2-1-1-1-3-B)-2-1-3-2-4
29	**TPBLT -106**	(ICMB 01888 X ICMB 01222)-16-1-2-B-1-3
30	**TPBLT -107**	([ICMB 95111 X (ICMB 96555 X IP 10437)-3] X B-bulk (3981-3989/S06 G1)}-3-2-4-B X ICMB 08999-13
31	**TPBLT -108**	{78-7088/3/SER3 AD//B282/(3/4)EB X PBLN/S95-359]-7-4-B-B-2-B-B X HHVDBC HS-10-1-2-1—1-1-4-1-1}-16-2-1-2
32	**TPBLT -109**	(ICMB 04888 X HHVDBC HS-10-1-21-1-1-2-B)-1-2-3-2
33	**TPBLT -110**	([(ICMB 95111 X (ICMB 96555 X IP 10437)-3]-7-2-1-B-2-15-1]X B-bulk(3981-3989/S06 G1)}-3-2-1-B X HHVDBC HS-10-1-2-1-1-1-3-B)-14-1-5-1
34	**TPBLT -111**	(ICMB 04888 X HHVDBC HS-120-1-2-1-2-B-2-B)-5-5-2-2
35	**TPBLT -112**	NC D2 S1-20-2-2-1-1-5-3-B
36	**TPBLT -113**	(HHVDBC HS-10-1-2-1-1-4 X [ICMB 99555 X {78-7088/3/SER3 AD//B2A2/(3/4)EB X PBLN/S95-359}-19-5-B-B]-13-2-B-B-B}-22-1-4-2-2
37	**TPBLT -114**	{MC 94 S1-81-1-B X HHVBC)-4-4-1 X (MC 94 S1-81-1-B X ICMB 02777}-8-1-B-4-1
38	**TPBLT -115**	{(ICMB 96555 X IP 10437)-3-4-1-2-8 X [(ICMB 96555 X LaGrap C2 S1-32-1)-10 X IP 14758-2-1]}-8-3-2-4-1-2
39	**TPBLT -116**	[(MC 94 S1-34-1-B X HHVBC)-10-4-32-2-B-B-2 X (ICMR 312 S1-1-5-3-B X HHVBC)-7-1-1-B-B-B]-21-B-1-4-1-2-1-3
40	**TPBLT -117**	{[78-7088/3/SER3 AD//B282/(3/4)EB X PBLN/S95-359}-7-4-B-B-2-B-B X HHVDBC HS-10-1-2-1-1-4-1-3}-17-1-2
41	**TPBLT -118**	{[78-7088/3/SER3 AD//B282/(3/4)EB X PBLN /S95-359] -7-4-B-B-2-B-B X HHVDBC HS-10-1-2-1-1-1-4-1-2)-8-1-5
42	**TPBLT -119**	ICMB 00555
43	**TPBLT -120**	ICMB 01777
44	**TPBLT -121**	JSMB-200042
45	**TPBLT -122**	JSMB-20091
46	**TPBLT -123**	JSMB-20101
47	**TPBLT -124**	ICMB 02333 B
48	**TPBLT -125**	ICMB 263 B

TABLE 2. ANOVA, Mean sum of squares for yield and its component traits in 48 pearl millet maintainer lines (B)

Sl. No.	Character	Replication	Treatment	Error	S. Em.±	C.V. (%)	C.D. @5%	C.D. @1%
1	Days to 50 per cent flowering	0.09	40.85**	7.79	1.95	5.97	3.93	5.24
2	Plant height (cm)	642.57	826.14**	318.86	12.49	15.09	25.13	33.54
3	Panicle girth (cm)	0.33	2.21**	0.33	0.40	6.18	0.81	1.08
4	Panicle length (cm)	26.07	59.69**	6.49	1.78	10.66	3.58	4.78
5	Panicle weight (g)	7.88	211.32**	3.88	1.37	5.41	2.77	3.70
6	Stover weight per plot (kg)	0.03	0.89**	0.27	0.36	29.01	0.74	0.99
7	Grain yield per plot (kg)	0.01	0.25**	0.03	0.12	12.51	0.25	0.33
8	1000-grain weight (g)	0.09	6.06**	2.09	1.01	12.66	2.03	2.71
9	Number of productive tillers	1.89	0.49**	0.13	0.25	17.09	0.51	0.69

Note: * Indicates significance at 5per cent probability level.
** Indicates significance at 1per cent probability level

TABLE 3. Estimates of genetic variability parameters for productivity traits in pearl millet maintainer (B) lines

Sl. No.	Character	Mean	Range Min	Range Max	^{2}p	^{2}g	GCV (%)	PCV (%)	h^2_{bs} (%)	GA	GAM
1	Days to 50 per cent flowering	46.73	46.5	84	24.32	16.52	8.69	10.55	67.90	6.09	14.77
2	Plant height (cm)	118.27	49.5	159.3	572.50	253.64	13.46	10.23	44.30	21.83	18.46
3	Panicle length (cm)	23.89	14.25	29.75	16.28	9.79	13.09	16.79	60.1	4.99	20.91
4	Panicle girth (cm)	9.32	6.96	12.66	1.27	0.94	10.39	12.09	73.8	1.71	18.39
5	Panicle weight (g/panicle)	36.40	7.0	55.37	107.60	103.72	27.97	28.49	96.40	20.59	56.58
6	Stover weight per plot (kg)	1.81	0.67	3.24	0.58	0.31	30.68	42.66	52.70	0.83	45.87
7	Grain yield per plot (kg)	1.44	0.98	2.39	0.14	0.11	23.11	26.29	77.00	0.64	41.88
8	1000-seed weight (g)	11.42	8.12	16.7	4.09	1.98	12.32	17.67	48.70	2.02	17.71
9	Number of productive tillers	2.15	1.37	3.25	0.31	0.17	19.60	26.00	56.80	0.65	30.43

The estimates of heritability when accompanied by estimates of genetic advance are more meaningful from the point of expected gain and type of selection method to be followed. Moderate genetic advance was observed for the characters like plant height, panicle length and number of productive tillers, whereas traits *viz.,* panicle girth, panicle weight and stover weight per, grain yield per plot and 1000-seed weight recorded high estimates indicating the predominance of additive gene action and hence direct phenotypic selection is useful with respect to these traits. Similar results were earlier reported by Shanthi *et al*. (2014), Govindaraj *et al*. (2010) and Vinodhana *et al*. (2013).

Johnson *et al*. (1955) suggested that high heritability coupled with high genetic advance as percent of mean (GAM) is more useful than heritability alone in predicting the resultant effect during selection of best individual genotype. In the present experiment, high heritability coupled with high genetic advance as a per cent of mean was observed for Panicle girth, Panicle weight and Stover weight per plot, Grain yield per plot and 1000 seed weight. Indicating predominance of additive gene action for these characters. Hence, Simple selection based on phenotypic performance of these characters would be more effective. This is in conformity with the earlier reports of Vinodhana *et al*. (2013) for 1000 seed weight and stover weight per plot. Lakshmana *et al*. (2003) for grain yield, panicle girth and panicle weight.

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