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Univariate and character association studies in elite 'B' and 'R' lines against *maldandi* cytoplasm in *Rabi* sorghum

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Abstract

Present study comprised of 42 B lines and 13R lines of *Rabi* sorghum (*Sorghum bicolor* (L) Moench). The phenotypic variance was more than genotypic variance for all the characters. Exhibition of high genotypic and phenotypic variance, heritability and genetic advance were observed for the characters *viz.*, panicle weight, grain yield per plant, 1000 seed weight and number of seeds per panicle showing additive gene effects were governing these traits. Positive and significant correlation exhibited between grain yield and panicle width, panicle weight, 1000 seed weight and number of seeds per panicle at phenotypic level, while the peduncle length exhibited negative correlation with grain yield.

Keywords: *Maldandi* cytoplasm, phenotype, grain yield, phenotypic variance, heritability, genotypic

Introduction

In the era of climate change, C4 plants have a role in combating global warming because of their higher optimal temperature and higher photosynthetic efficiency. Sorghum [*Sorghum bicolor* (L.) Moench] being a C4 plant with higher photosynthetic efficiency and abiotic stress tolerance (Reddy *et al.*, 2009) [16] adapted to a diverse set of environments ranging from arid and semiarid to tropical regions throughout the world. Among the cereals, sorghum is one of the far-reaching crops cultivated globally for food, fodder, feed, and fuel. The total production and productivity of sorghum are 4.77 million tons and around one ton per hectare, respectively from an area of 4.82 m ha (India Stat, 2019-20). Of the several cytoplasm's available in sorghum, only A1 (*milo*) CMS system is predominantly used for commercial production of hybrids (Reddy *et al.* 2007) [17] though it lacks good grain quality. In addition to the A1 cytoplasm several other CMS sources like A2, A3, A4, Indian A4, A5, A6, 9E, and KS were described in sorghum, among these *maldandi* (A4) cytoplasm is known for its grain quality with shoot fly resistance. There has been identified maintainers and restorers on A4 cytoplasm and need to increase productivity of as well as cytoplasmic base of sorghum by utilizing variability and heritability present among these genotypes. Breeding program will be more effective if the breeder have a sound knowledge of association between yield and yield attributing traits. In this study, an effort has been made to assess the genetic variability in B and R lines of sorghum for utilizing cytoplasmic genetic male sterility to develop high yielding hybrids having *maldandi* cytoplasmic background.

Materials and Methods

The experimental material comprised of B and R lines on *maldandi* cytoplasm as reported by Verma *et al.* 2022. Out of 54 germplasm lines, 42 were B lines and 13 were R lines and M 35-1 as check. These 55 genotypes were grown with two replication in Randomized Block Design during *Rabi* 2019 at Botany garden MARS, Dharwad. Each line was grown in single row of 4 meter length at 45 cm apart. Plant to plant distance was maintained at 15 cm. Observations were scored based on five randomly selected plants for the characters *viz.*, days to 50 % flowering, plant height, number of leaves, peduncle length, panicle length, panicle width, primaries per panicle, 1000 seed weight, number of seeds per panicle and grain yield per plant. The data was subjected to statistical analysis using WINDOSTAT software to estimate mean, range, ANOVA, variability parameters. The copilot package in R Studio was used to conduct correlation analysis, and all no significant correlations at the 0.05 level of significance were cross-marked in the correlation plot.

Results and Discussion

The analyses of variance for all the character are listed in Table 1. Considerable amount of differences in their mean performance in all the traits studied was observed across all the genotypes. All the treatments exhibited significant differences at 5 and 1 % for all the traits revealed presence of good amount of variability in these characters which helps in selection of vibrant and promising genotypes for further genetic improvement which endorsed the earlier findings of Kumar and Singh (1986) [9], Prabhakar (2003) [11] and Arunkumar *et al.*, (2004) [2].

Genotypic and phenotypic variation

The results of estimated genetic variability, heritability and genetic advance for grain yield per plant and other traits are

presented in table 2. In this investigation, GCV was lower than the PCV for all the traits which stipulated that all the characters were severally influenced by the environment though their differences were in lower magnitude. Good amount of genotypic and phenotypic coefficient of variation were observed for panicle weight, grain yield per plant, peduncle length and panicle length. These results endorsed earlier findings of Nimbalkar *et al.*, (1988) [10] and Hemlata Sharma *et al.*, (2006) [7]. Variation in the traits contributed markedly to the total variability (Biradar *et al.*, 1996) [3]. Contradictorily, Low GCV & PCV were observed for Number of leaves per pant (10.64 % & 14.57 %) and days to 50 % flowering (10.50 % & 11.55 %) Kjein and Rosenow (2006) [18] also reported similar results.

Table 1: Analysis of variance for yield and its attributing traits in B and R lines of *Maldandi* cytoplasm

Sources of variation	DF	Days to 50 per cent flowering	Peduncle length (cm)	Panicle Length (cm)	Panicle width (cm)	Primaries Panicle ¹	Number of leaves	Plant Height (cm)	Panicle weight (g)	Grain yield plant ¹ (g)	1000 seed weight (g)	Number of seeds panicle ¹
Replicates	2	166.91**	2.42	28.03	77.28	190.16	3.75	4719.79**	389.79	382.56**	8.52	127077.10
Treatments	55	143.45**	273.48**	86.84**	128.38**	371.78**	2.39**	3294.91**	1058.83**	1088.21**	122.51**	433759.22**
Error	54	13.58	20.26	4.29	12.05	52.58	0.72	271.02	61.35	41.95	3.52	36119.50
CD at 5 %		7.39	9.02	4.15	6.96	14.53	1.71	33.00	15.70	12.98	3.76	381.02

** indicates significant at 1 per cent

Table 2: Estimates of genetic components of variation for yield and its attributing traits in B and R lines of *Maldandi* cytoplasm

Traits	Days to 50 % flowering	Peduncle Length (cm)	Panicle Length (cm)	Panicle Width (cm)	Primaries Panicle ¹	Number of Leaves	Plant Height (cm)	Panicle Weight (g)	Grain yield plant ¹ (g)	1000 Seed Weight (g)	Number of Seeds Panicle ¹
Range	57.00-95.50	22.00-69.40	11.85-52.37	22.70-60.85	35.00-90.00	6.50-11.75	137.50-312.00	33.77-149.25	25.12-142.25	17.75-46.15	1171.28-3036.74
Mean	76.6864	43.0259	23.19	39.32	60.44	8.57	229.98	73.64	63.80	31.68	2004.08
GCV	10.50	26.15	27.9	19.39	20.90	10.64	16.90	30.32	35.84	24.34	22.24
PCV	11.55	28.16	29.9	21.30	24.10	14.57	18.36	32.13	37.25	25.05	24.18
h ² (bs) %	82.70	86.20	90.60	82.80	75.20	53.40	84.80	89.00	92.60	94.44	84.60
GA	15.09	21.52	13.00	14.29	22.57	1.37	73.76	43.41	45.33	15.43	844.98
GAM at 5 %	19.68	50.01	54.29	36.35	37.34	16.02	32.07	58.94	71.05	48.71	42.16

GCV: Genotypic Coefficient of Variation
 PCV: Phenotypic Coefficient of Variation
 h² (bs) %: Broad Sense Heritability
 GA: Genetic Advance
 GAM: Genetic Advance over Mean

Heritability and Genetic Advance:

Heritability values indicate only the magnitude of inheritance of the quantitative characters, while the genetic advance helpful in formulating the selection procedure to be adopted (Johnson *et al.* 1955) [8]. In this study, high heritability coupled with high genetic advance was reported for the characters gain yield per plant (92.60 % & 45.33 %), panicle weight (89 % & 43.41 %), plant height (84.80 % & 73.76 %) and number of seeds per panicle (84.60 % & 844.98 %). This ensures the abundance of additive gene effect and implicitly ensures the environment influence on these traits is minimal. Selection for these traits based on phenotype will be effective and more interest should be given on these traits while expecting genetic diversity (Rao and Patil 1996) [12]. These findings were in line with earlier reports of Raut *et al.* (1994) [13] revealed high genetic advance for plant height and days to 50 % flowering. Kumar and Singh (1986) [9] also reported high heritability for plant height, panicle weight, 1000 grain weight. Cheralu and Rao (1989) [5] observed high genetic advance for grain yield and panicle weight.

Contradictorily, low heritability and low genetic advance observed for the traits like number of leaves (53.40 % & 1.37 %), primaries per panicle (75.20 % & 22.57 %) and days to

50 % flowering (82.70 % & 15.09 %) ensuring the dominance of non-additive gene effects and restricted scope for selection. Similar results were reported by Shinde *et al.*, (1979) [14] and Prabhakar (2003) [11] for days to 50% flowering.

Correlation

The phenotype of the plant is result of interaction of a large number of factors. Final yield is the sum of effects of several component factors. Correlation coefficient helps in determining the direction of selection and the number of traits to be considered. In this investigation, panicle weight, 1000 seed weight, panicle girth and seeds per panicles have shown positive correlation with grain yield per plant revealing increase in the grain yield is because of increase in one or more characters (Fig 1). Similar results were reported by Patil (1985) [19] for number of primaries and secondaries and panicle weight, Bohra *et al.*, (1986) [4] for panicle length. On the other hand, peduncle length was negatively associated with grain yield per plant. As the number of seeds per panicle increases panicle girth, panicle weight and 1000 seed weight also increases. In total all these traits amounts to increases in the grain yield. Thus these traits are considered as vital for improving grain yield.

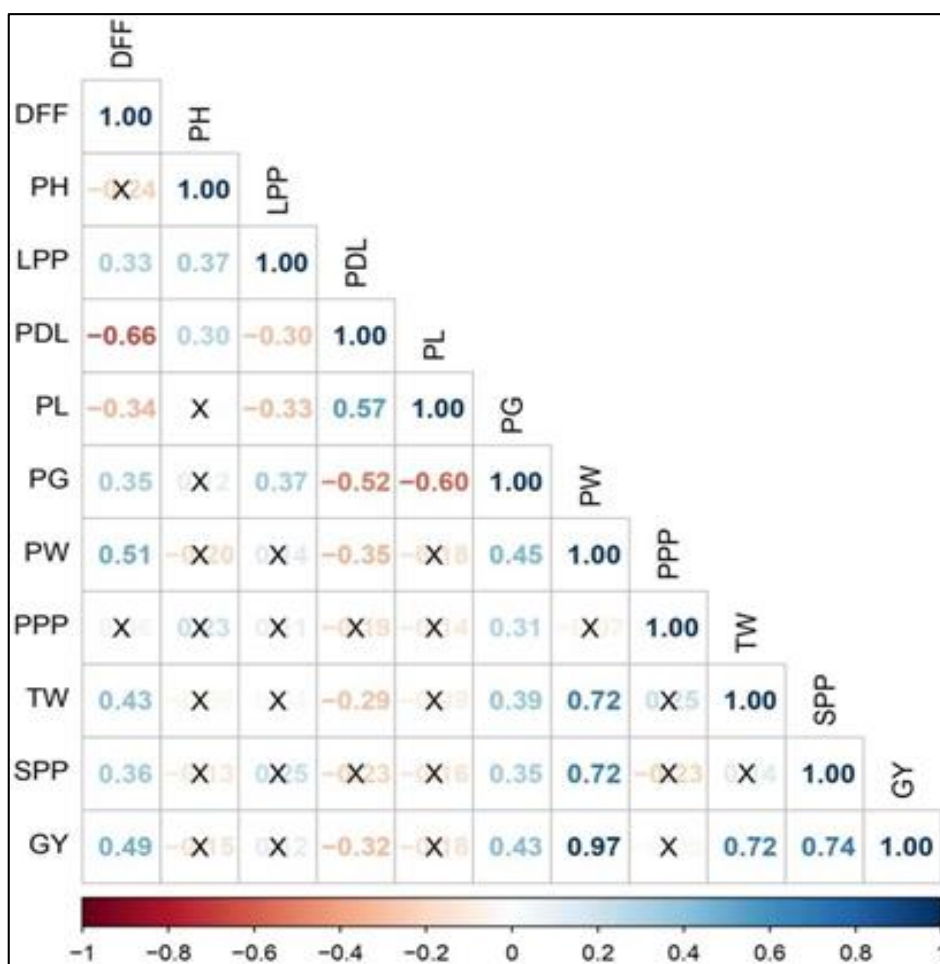


Fig 1: Correlation analysis between various traits under study in the B and R lines of *maldandi* cytoplasm

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