

Research Note

Genetic variability, diversity and principal component analysis in B and R lines of *rabi* sorghum [*Sorghum bicolor* (L.) Moench]

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Abstract

Hybrid technology is exploited in *kharif* (rainy) sorghum while the same is not the scenario in *Rabi* sorghum which is still dominated by landraces and varieties which have poor yield potentiality. Considering the necessity of development of heterotic hybrids, an attempt was made to screen hybrid parents (B and R lines) to assess variability and genetic diversity, for productivity traits. The study was conducted with 32 B and R lines at Regional Agricultural Research Station, Vijayapur during 2021-22. PCV was observed to surpass GCV across all traits. The traits grain yield per plant, fodder yield per plant, grain number per plant, and harvest index exhibited notably high PCV and GCV. Plant height, panicle length, panicle harvest index, and harvest index recorded high heritability and genetic advance, suggesting their control by additive gene action and potential for improvement *via* selection. Cluster analysis classified the 32 genotypes into four groups. PCA condensed 14 traits into five principal components, capturing 81.50% of total variation. The genotypes remained scattered in all four quadrants in PCA- Biplot, showing large genetic variability in quantitative traits studied.

Keywords: Genetic variability, heritability, diversity, clusters, PCA and *rabi* sorghum

Sorghum bicolor (L.) Moench, also known as jowar, is one of the five most significant cereal crops grown worldwide. It is primarily grown in semiarid tropics and subtropics. The crop is grown on 40.93 mha worldwide with total grain production of 61.36 million metric tonnes and a productivity of 1499 kg/ha, (Food and Agricultural Organisation, 2021). Sorghum has been grown in India for millennia in both the *kharif* (rainy) and *rabi* (post-rainy) seasons.

Yield improvement in *Kharif* sorghum realized due to high productivity and successful exploitation of hybrid

technology. However, the *post-rainy* sorghum grain productivity in India is low due to biotic and abiotic constraints, as well as low genetic variability among the genotypes. Much of the area cultivated during *post-rainy* season is under landraces with low yield potential. Furthermore, sorghum is grown with receding soil moisture after the rains have stopped. As a result, end-of-season moisture stress is a significant production constraint. Low temperature tolerance early in the season, response to photoperiod sensitivity (short day length), flowering and maturity independent of temperature fluctuations and sowing dates (thermo- insensitivity), tolerance to shoot fly

and aphids among insects, charcoal rot and rust among diseases, and grain quality traits (bold lustrous grain with thin pericarp) are critical for the *post rainy* season crop (Reddy *et al.*, 2010). The landrace derived variety M 35-1 that has continued to be popular over five decades since its release, possesses all the above characteristics required for *post rainy* season adaptation. The crop breeding efforts on genetic improvement for yielding ability in *rabi* sorghum although resulted into development of heterotic hybrids by involving temperate sorghums but the improved *post rainy* season sorghum hybrids are not popular with farmers as they do not match M 35-1 for grain quality, shoot fly resistance, cold tolerance and drought tolerance. Among the improved cultivars, hybrid parents and hybrids *per se* are more temperature sensitive than varieties. The situation necessitates development of *Rabi* hybrids with high yield (grain and fodder) coupled with improved *rabi* adapted traits.

Hybridization involving genetically diverse parents is known to provide an opportunity for bringing together gene constellations resulting in desirable transgressive segregants in advanced generations (Kumar *et al.*, 2010). The genetic diversity among the genotypes can be ascertained using Mahalanobis D^2 statistic. The effectiveness of selection is also determined by the amount of genetic variability with respect to particular character. In order to select a suitable breeding procedure, an assessment of heritable and non-heritable components in the overall variability observed is required. By examining components of variation such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and anticipated genetic advance (GA), the heritable portion of the overall observed variation can be determined.

In the present study, an attempt was made to screen hybrid parents (B and R lines) in *rabi* sorghum to assess variability, genetic diversity, and principal component analysis of various productivity traits.

The present investigation was carried out during *rabi* season of 2021–22 at the Regional Agricultural Research Station, Vijayapur. The study included a set of 32 elite sorghum genotypes, involving 14 B lines, 17 R lines and varietal check M 35-1. The experiment was laid out in a randomized block design with two replications. Each plot consisted of two rows of three meters each, spaced 60 cm apart. All recommended agronomic and plant protection practices were followed regularly as needed for better crop stand and expression. Observations on plant height (PH) (cm), SPAD at physiological maturity (SPAD-PM), panicle length (PL) (cm), panicle breadth (PB) (cm), panicle weight (PW) (g), grain yield per plant (GYPP) (g/plant), fodder yield per plant (FYPP) (g/plant), seed set percentage (SSP) and pollen fertility percentage (PFP), grain number per plant (GNPP) and 100-seed weight (100-SW) (g) were recorded on randomly chosen five plants in each entry. Days to 50% flowering (DFF) was recorded on plot basis. Genetic variability analysis and cluster analysis were carried out using the “variability” and “biotools” packages, respectively, in R software (Popat *et al.*, 2020; da Silva, 2021).

In the current study, an attempt was made to assess the genetic variability for productivity traits, including SSP and PFP in hybrid parents (B & R lines) of *rabi* sorghum. The genotypic mean sum of squares with respect to all 14 reproductive traits studied were significant among the genotypes, indicating sufficient variability present in the experimental material (Table 1).

The GCV was lesser than PCV for all the traits studied (Fig. 1). Elangovan and Babu (2015), Manonmani *et al.* (2002), Swamy *et al.* (2018) and Ganapathi (2007) also reported the same. Traits like DFF, PH, PL, PB, 100-SW, panicle harvest index (PHI), SSP and PFP showed narrow range of GCV and PCV indicating that these traits are less influenced by environment and hence phenotypic variability can be used as reliable measure of genotypic variability.

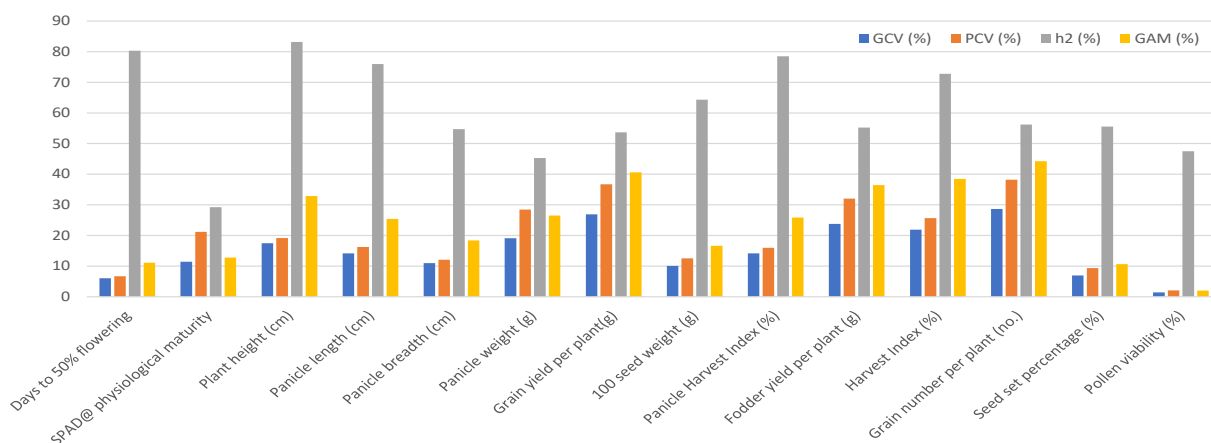


Fig.1. Genetic variability parameters of yield and its component traits of B and R lines in *rabi* Sorghum

Table 1. Summary statistics and mean squares for yield and its component traits of B and R lines in *rabi* Sorghum

S. No.	Traits	Mean	Range		Replication MSS	Genotypes MSS	Error MSS	C.V%	C.D@ 5%	S.Em.±
			Min.	Max.						
1	Days to 50% flowering	70.22	62.50	78.50	4.00	40.22**	4.39	2.98	4.27	1.48
2	SPAD @ physiological maturity	18.25	10.67	28.433	31.26	19.40*	10.61	17.85	6.64	2.30
3	Plant height (cm)	189.66	91.33	271.33	130.34	2426.98**	222.96	7.87	30.45	10.56
4	Panicle length (cm)	18.96	13.50	27.75	7.24	16.74**	2.29	7.98	3.09	1.07
5	Panicle breadth (cm)	6.05	3.17	8.50	2.01	1.51**	0.44	10.99	1.82	0.47
6	Panicle weight (g)	45.87	20.00	81.00	652.16	247.39**	93.14	21.04	19.68	6.82
7	Grain yield per plant(g)	30.42	11.67	58.00	68.05	191.80**	57.77	24.99	15.50	5.37
8	100-seed weight (g)	3.62	2.24	4.52	0.17	0.34**	0.07	7.49	0.55	0.19
9	Panicle Harvest Index (%)	65.35	30.60	85.30	306.60	194.87**	23.46	7.41	9.88	3.42
10	Fodder yield per plant (g)	36.61	14.81	69.70	458.74	213.81**	61.72	21.5	16.02	5.55
11	Harvest Index (%)	36.41	14.79	58.37	102.70	150.95**	23.78	13.4	9.94	3.44
12	Grain number per plant (no.)	848.81	286.65	1724.14	29751	164561**	46157	25.3	438.17	151.91
13	Seed set percentage (%)	90.83	60.50	99.233	14.27	112.20**	32.04	6.23	11.54	4.00
14	Pollen viability (%)	97.37	91.76	100.00	7.10	6.25**	2.22	1.53	3.04	1.05

Note: *significance at 5% probability level and ** significance at 1% probability level

High values of PCV and GCV were obtained for GYPP, FYPP, GNPP and HI. This indicated that these traits contributed markedly to the total variability. This also suggests that there is a greater scope for improvement of these traits by direct selection among the genotypes or involving selected lines as parents in hybridization. The results are in accordance with the results obtained by Swamy *et al.* (2018) for GYPP and FYPP, and Chavan *et al.* (2010) for HI.

All the characters except SPAD-PM showed moderate to high estimates of broad sense heritability. Similar results on moderate to high heritability estimates were also observed for PH, PL and DFF by Swamy *et al.* (2018). High heritability estimates were reported for the character PL (Sharma *et al.*, 2006 and Warkad *et al.*, 2008), for 100-SW (Ranjith *et al.*, 2017), for DFF (Arunkumar, 2013 and Khandelwal *et al.*, 2015) and for HI (Godhbarle *et al.*, 2010). Heritability values only indicate the magnitude of quantitative character inheritance, whereas heritability coupled with high genetic advance as per cent of mean is useful in formulating the selection procedure to be used. In the current study, high heritability coupled with high GA as per cent of mean was observed for PH, PL, PHI and HI. Thus, the results indicate that these traits are predominantly under the control of additive gene action and hence these characters can be improved by selection. Similar observations were recorded by Swamy *et al.* (2018) for PH and PL and Godhbarle *et al.* (2010) for HI, PL and PH.

The genetic diversity of 32 sorghum genotypes was investigated using Mahalanobis' (1936) D^2 statistic, and the genotypes were clustered using Tocher's method. In

the current study, four clusters were formed, with Cluster I having the most genotypes (28), followed by Cluster II having two genotypes (296B & AKR 150). Clusters III and IV were solitary, with BJMS 1B and RLT-9 as the sole genotypes, respectively (**Table 2**). Among 14 quantitative traits studied, the highest contribution towards the divergence was by GNPP (18.8%), followed by GYPP (14%) and the lowest being PHI (0.8%) (**Fig. 2**). The average intra (diagonal) and inter cluster (off diagonal) D^2 values are presented in the **Table 2**. The maximum inter cluster distance was noticed between cluster III and cluster IV (609.69) followed by cluster II and cluster IV (418.82) and cluster I and cluster III (373.63). The maximum intra cluster distance was noticed in cluster I (104.79) with 28 genotypes in it. B and R lines have not clustered separately, indicating a lack of diversity between the two populations.

In Principal Component Analysis (PCA), the goal is to reduce the dimensionality of a dataset by transforming the original variables into a smaller set of uncorrelated variables called principal components. These components capture the maximum variability in the data. After performing PCA, each principal component is associated with an eigenvalue. The eigenvalue represents the amount of variance that is captured by that principal component (Jolliffe and Cadima, 2016). The sum of Eigen values equals the number of variables used and the first component is expected to retain the most information. In the present study PCA condensed the 14 quantitative traits into five major principal components which accounted for 81.50 % of the total variation (**Table 3**). The results are in accordance with the findings of Subramanian *et al.* (2019) and the first five principal component axis recorded

Table 2. Distribution of 32 B and R lines of *rabi* sorghum into different clusters and their average intra and inter cluster distances (D2)

S. No.	Clusters	Genotypes	Cluster I	Cluster II	Cluster III	Cluster IV
1	Cluster I	BLT-I-2, BLT-I-3, RLT-19-08, M31-2B, ICSR 13039, CSV14RB, BLT-2020, RLT-19-15, M35-1, RS585, BRJ62, SbABM, RLT2004, BLT-I-1, RLT-19-17, RLT2013, ICSR13042, RLT2036, RS29, 13B, BJMS3B, 104B, 401B, R354, BJMS2B, BLT-2010, ICSR13043, C43	104.79			
2	Cluster II	296B, AKR150	227.87	75.03		
3	Cluster III	BJMS 1B	373.63	184.70	0.00	
4	Cluster IV	RLT-9	182.93	418.82	609.69	0.00

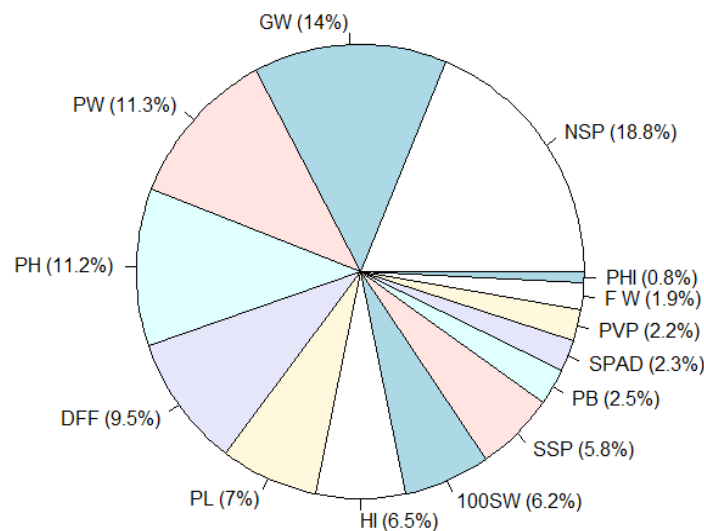


Fig. 2 Per cent contribution of yield and its component traits towards divergence of 32 hybrid parents (B and R lines) in *rabi* Sorghum

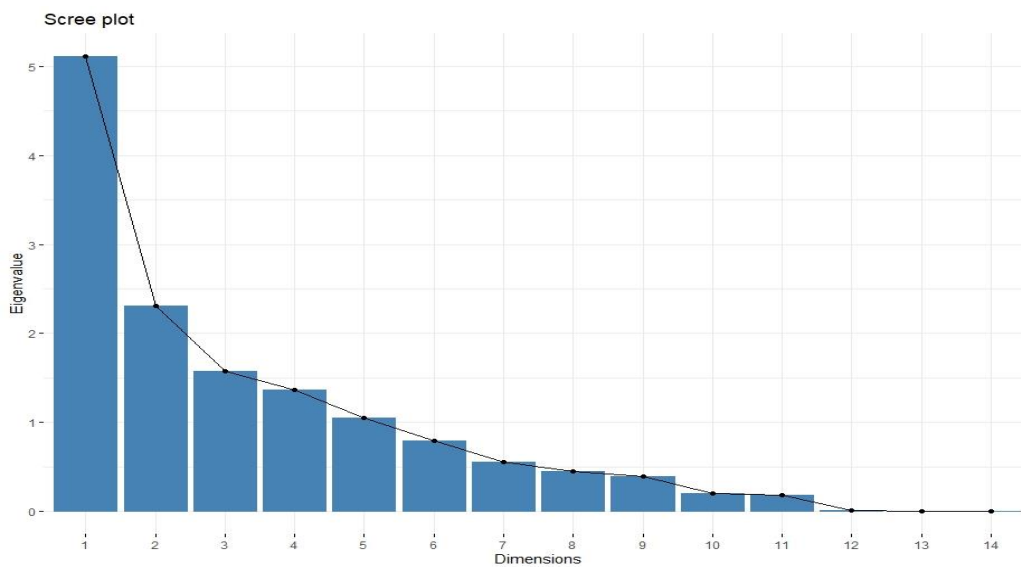
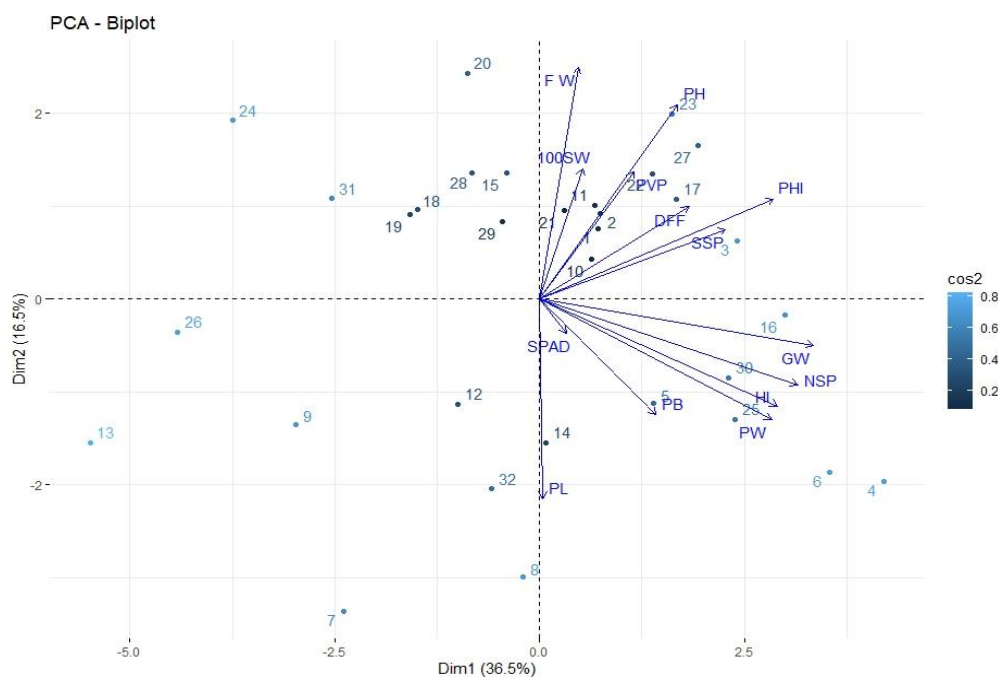


Fig. 3. Scree plot for Eigen values and principal components

Table 3. Principal component analysis for different morphological traits recorded in B and R lines of *rabi* sorghum

	PC1	PC2	PC3	PC4	PC5
Days to 50% flowering	0.232	-0.195	-0.471	0.025	-0.049
SPAD@ physiological maturity	0.041	0.069	0.230	-0.089	0.871
Plant height (cm)	0.217	-0.395	0.153	0.165	-0.136
Panicle length (cm)	0.004	0.407	-0.238	0.416	0.243
Panicle breadth (cm)	0.182	0.240	0.281	0.480	-0.114
Panicle weight (g)	0.362	0.248	-0.108	0.229	-0.002
100 seed weight (g)	0.068	-0.264	0.558	0.317	0.047
Panicle Harvest Index (%)	0.366	-0.203	0.195	-0.198	-0.063
Fodder yield per plant (g)	0.060	-0.475	-0.224	0.432	0.138
Harvest Index (%)	0.372	0.221	0.189	-0.248	-0.116
Grain number per plant (no.)	0.403	0.177	-0.172	-0.059	-0.022
Seed set percentage (%)	0.291	-0.143	0.009	-0.336	0.196
Pollen viability (%)	0.149	-0.263	-0.301	0.019	0.266
Grain yield per plant(g)	0.428	0.096	0.003	0.060	-0.017
Eigenvalue	5.11	2.31	1.57	1.36	1.05
Percentage of variance	36.52	16.50	11.23	9.73	7.52
Cumulative percentage of variance	36.52	53.02	64.25	73.97	81.50

**Fig. 4. PCA – Biplot showing distribution of genotypes across first two components**

eigenvalues greater than one. PC1, PC2, PC3, PC4, and PC5 were responsible for 36.52, 16.50, 11.23, 9.73, and 7.52 % of total variability, respectively. Individual loadings are commonly used to identify the characters that had the greatest influence on the PCA value (Eigen vectors). In the individual loadings, first component is positively influenced by GYPP, GNPP, HI, PHI and PW.

The distribution of genotypes and the characters is depicted in the biplot of PC1 and PC2 in **Fig 4**. The right top quadrants consisted of the genotypes with related to FYPP, 100-seed weight, PH, pollen viability, Days to 50% flowering and seed set percentage and right bottom quadrant comprised the genotypes related with the GYPP, GNPP, HI, PW and PB forming another group.

The genotypes remained scattered in all four quadrants, showing genetic variability in quantitative traits studied. The distance between the locations of any two genotypes on the score plot is directly proportional to the degree of difference/ similarity between them in terms of the yield and yield components.

Traits such as plant height, panicle length, panicle harvest index, and harvest index are predominantly under the control of additive gene action, making these characters suitable for improvement through selection. Principal Component Analysis condensed the 14 quantitative traits into five major principal components, which accounted for 81.50% of the total variation. Cluster analysis divided the 32 genotypes into four groups, with grain number per plant being the major contributor to divergence. B and R lines have not clustered separately, indicating a lack of diversity between the two populations, which suggests a need to diversify these lines to enhance the potential for developing superior hybrids. Genotypes belonging to clusters III and IV, which have the maximum inter-cluster distance, can be used as parents in developing hybrids after testing their combining ability.

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