Plant Archives Vol. 25, No. 1, 2025 pp. 2503-2506 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.1.361

CHARACTER ASSOCIATION AND VARIABILITY STUDIES IN SEGREGATING POPULATION OF *MALDANDI* MALE STERILE CYTOPLASM OF SORGHUM

S. Keerthana[1]* and B.D. Biradar[2]

[1]Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India.
[2]Director of research, University of Agricultural Sciences, Dharwad, Karnataka, India.
*Corresponding author E-mail : keerthanasekar60@gmail.com

(Date of Receiving-12-01-2025; Date of Acceptance-27-03-2025)

ABSTRACT

Sorghum is one of the main staple food crops for the world's poor and food insecure people in the semi-arid tropics of Africa and Asia. Hybrid breeding in sorghum is a successful story in *kharif* sorghum but not to *rabi* sorghum because of the non-suitability of A_1 cytoplasm to *rabi* sorghum.So the present study was made to have a knowledge about the variability and association among the yield and yield attributing traits in the F_2 population made in the background of A_4 cytoplasm M35-1 and DSMR 8 a reported restorer of A_4 *maldandi* cytoplasm. From the variability studies it was found that characters majority of the characters under the evaluation were additive in nature with increased heritability showing little influence of environment on characters studied. By Association analysis it is found that most of the yield attributing characters were found to have positive correlation with yield. Thus, Selection of suitable characters by association and variability studies will yield good outcome in the future breeding programme.

Key words : Sorghum, A_4 cytoplasm, Correlation, Male sterility, *Rabi*, Variability.

Introduction

Sorghum is one of the main food crops for the world's poor and food insecure people in the semi-arid tropics of Africa and Asia. It is an one of the important source of feed, fodder and bio-fuel apart from food. Sorghum (*Sorghum bicolor* L. Moench, 2n=2x=20) comes fifth after wheat, maize, rice and barley globally in terms area and production. In 2021-22, USDA had estimated the world area under sorghum cultivation was 41.97 million hectares and production of 65.21 million tons. The same for the India was estimated to be 4.80 million hectares and 4.60 million tonnes respectively. In India, sorghum is grown in two seasons, *kharif* and *rabi*. The area and production trends of the two seasons are different. Area under *kharif* actually accounted for 62% of the total area under sorghum during 1972–73 declined to 45% by 2020, while the area under *rabi* sorghum increased from 37% (1972-73) to 54% (2020) during the same period. However, the share of *kharif* sorghum production in total production declined less drastically from 70% of total production in 1972–73 to 60% in 2020 because of higher productivity in *kharif* sorghum than that of *rabi*. A similar breakthrough in *rabi* sorghum has not been achieved since the *rabi* crop is cultivated on reserved soil moisture from the rain availability of the *kharif* season and released hybrids were not very successful. The main problem with hybrid seed production is non-availability of proper male sterile cytoplasm. However, sorghum grain produced during *rabi* is highly demanded for human intake as the grains been produced in the *rabi* sorghum cultivars are found to be with high quality. So the present study aims to have a clear cut understanding about the variability and association of various yield attributing traits among the F_2 segregating material derived from the reported restorer of A_4- *maldandi* cytoplasm of sorghum. This could also help to identify the range of transgressive seggregant available in the F_2 seggregating population along with the nature of the yield attributing traits confering restoration.

Materials and Methods

In the present study, F_2 population produced from the cross between DSMR 8 a mutant line from BRJ67 was crossed with the male sterile line M31-2A which is known to have A_4 cytoplasm and it is forwarded until F_2 generation. DSMR 8 was identified as a staple restorer for of A_4 cytoplasm (Swamy *et al.*, 2018) and thus the present experimental material is amenable to find the cytoplasmic and restoration effect of A_4 cytoplasm. An F_2 population of the cross M35-1 and DSMR-8 with a sample size of 400 were maintained along with 5 checks in the augmented design and evaluated for yield and yield related traits.The routine crop protection measure along with agronomic practices were followed during the cropping period.The Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were calculated by the method given by Burton (1952). association studies including correlation analysis was done by the procedure given by Hanson *et al.* (1956) and path analysis was also carried out by following the procedure stated by Dewey and Lu (1959) using the R software.

Fig. 1 : Fertile and sterile panicles in F_2 population.

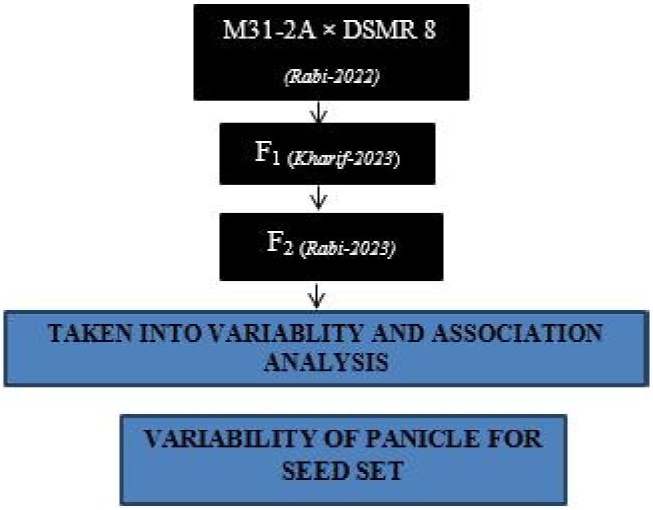

Fig. 2 : Schematic representation of production of F_2 population from the cross between M31-2a and DSMR 8.

Results and Discussion

Variability is one of the important prerequisites for any breeding programme. The reason for this is the response of selection is directly proportional to the extent of the available variation in the population. In this context since though the population is a segregating population, it is evaluated for the variation and shown to have significant variation (Table 1) for all the traits and further analysis was undertaken.

In the variability studies, there was negligible difference between the PCV and GCV as deciphered in Table 2 which implies there in no variation of the genotype and the observed phenotype and ultimately stating that there was no influence of environment, which is a highly desirable aim of basic plant breeding(Reddy *et al.*, 2024). Phenological traits such as plant height and number of leaves per plant showed moderate PCV and GCV .For characters expect the former a high level of PCV and GCV was observed which is stating that these character will respond easily to the selection pressure than compared to the studied phenological traits (Tilaye, 2024). So thus in the population majority of the yield related character simple selection procedures will be sufficient for the improvement of the desired traits. This is also supported by the observed heritability and genetic advance.

An increased magnitude of heritability and genetic advance shows that traits are influenced by additive gene action (Hamidou *et al.*, 2018) and the degree of dominance is less that is tend to be additive in nature, so that the observed value is reliable and phenotypic selection is worthful. This type of trend is shown by all the yield attributing traits that was taken under study (Kumar *et al.*, 2018). But the phenological traits expressed a moderate magnitude of heritability but though there was an higher magnitude of high genetic advance which means to imply that these characters are also governed by additive gene effects but the moderate heritability is observed because of the fact of increased influence of environment over the genotypes studied (BN *et al.*, 2024).

Correlation analysis

The correlation coefficients of various character is showed in the Fig- 4. Single plant yield had been seen to have a significant positive correlation with number of leaves, panicle width and seed set percentage. Panicle length had showed non-significant positive correlation with

Table 1 : Descriptive statistics for variation in F_2 population.

Trait	Mean	Std. Deviation	Range		CV (%)
			Min	Max	
Plant height	212.19	32.8	99.2	300	0.9
Number of Leaves	12.74	2.02	4.9	17.1	5.71
Panicle length	15.34	26.05	3.46	513.96	2.29
Panicle width	6.76	5.98	1.87	72.03	6.73
Panicle weight	81.62	38.28	0.2	206.6	2.28
Seed Set percentage	85.48	23.09	0	99.7	2.01
Single Plant yield	60.72	38.15	0	180.28	12.74

Table 2 : Genetic variability parameters of the yield and yield attributing characters.

Trait	GCV	Category	PCV	Category	ECV	Heritability	Category	GA	GAM	Category
PH	15.29	Medium	15.32	Medium	0.91	99.65	High	66.81	31.49	High
NL	14.81	Medium	15.86	Medium	5.69	87.14	High	3.63	28.52	High
PL	170.82	High	170.84	High	2.31	99.98	High	54.05	352.37	High
PW	88.9	High	89.15	High	6.73	99.43	High	12.35	182.27	High
PWE	46.81	High	46.86	High	2.32	99.76	High	78.72	96.45	High
SS	27.09	High	27.16	High	2.02	99.45	High	47.63	55.73	High
SPY	57.26	High	61.83	High	23.32	85.77	High	66.43	709.41	High

single plant yield (Swamy *et al.*, 2018). Meanwhile seed set percentage showed positive correlation with number of leaves and panicle width and non-significant positive correlation with single plant yield. Panicle weight had showed positive correlation with number of leaves, panicle width (Subhashini *et al.*, 2019), seed set percentage and single plant yield. A non-significant positive correlation was found with panicle length and plant height (Nirosh *et al.*, 2021). For the panicle weight all the traits had showed non-significant positive correlation. It is also noted that panicle length and panicle width have shown a strong positive correlation among themselves (Mofokeng *et al.*, 2019). Along with that plant height had showed positive significant correlation with number of leaves and panicle length and other traits had showed non-significant correlation (Mofokeng *et al.*, 2019). From this it could be inferred that yield related traits like panicle length, width and weight were correlated to single plant yield and seed set percentage in one or the other way and improvement of the character will ultimately increase the yield (Subhashini *et al.*, 2019).

Path analysis

When there is no just one character is important and there are chances that there could be varied level of importance to each character, here could be two kinds of situation. One is kind selection for those character for improving the yield. And other case could be based on the selection index as like multiple trait based selection. The disadvantage of correlation analysis is that the correlation coefficient is not a simple independent entity but it is actually a complex entity. So here comes the role of path analysis where we could split the correlation coefficient into direct effects and indirect effects. For the various direct and indirect effects are shown in the Table 4. In the present study single plant yield is the dependent character and all others were independent characters.

From the path analysis the maximum positive effect towards the yield was given by panicle width followed by seed set percentage. Thus the selection for these two character could impact the yield positively. Negative direct effect was given by plant height. Thus the increased plant height could impact the yield negatively which is shown evidently by the correlation and path analysis. Along with that all the indirect effect given by the trait plant height was found to be negative and confirming our above inference since all the studied traits are related to yield. For the trait panicle length the maximum indirect effect on yield was made by the trait panicle width (Rao *et al.*, 2010). Same trend of result was obtained for the trait panicle width too. For the trait panicle weight the maximum indirect effect for the dependent variable yield was made by seed set percentage, followed by panicle width and number of green leaves per plant. The trait seed set percentage

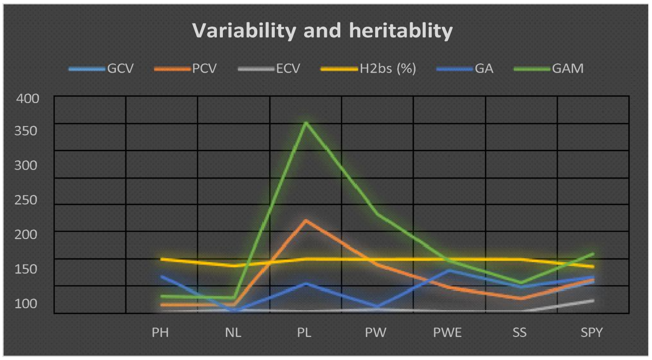

Fig. 3 : Graphical representation of various genetic variability parameters.

Table 3 : Direct and indirect effects of various characters towards single plant yield.

	PH	NL	PL	PW	PWE	SS
PH	**-0.0314**	0.0001	0.0003	0.0005	0.0866	0.0035
NL	-0.0161	**0.0001**	0.0002	0.0006	0.2864	0.0131
PL	-0.0036	0	**0.0024**	0.0027	0.0402	0.0022
PW	-0.0028	0	0.0011	**0.0055**	0.2177	0.0138
PWE	-0.0029	0	0.0001	0.0013	**0.9304**	0.0436
SS	-0.0013	0	0.0001	0.0009	0.4716	**0.0859**
r value	0.0595	0.2843	0.0439	0.2353	0.9724	0.5572

Residual effect: 0.21

Character abbreviation: PH- Plant Height, **NL-** Number of Leaves per plant, **PL-** Panicle Length, **PW-** Panicle Width, **PWE-** Panicle Weight, **SS-** Seed Set percentage

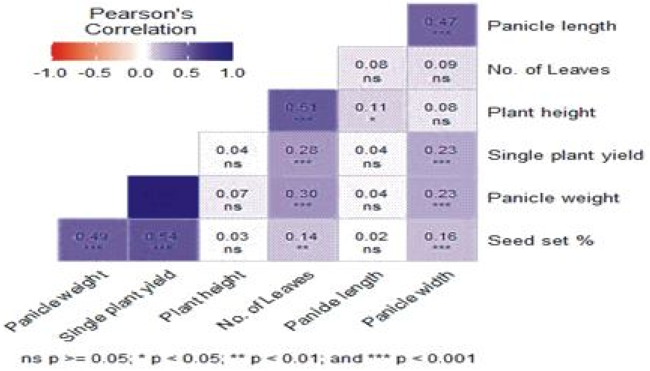

Fig. 4 : Correlation analysis for yield and yield attributing traits.

itself is a representative of single plant yield had found to be indirectly influenced positively by the trait panicle weight and others too. So that by doing path analysis it was found that expect for the plant height all the traits were positively governing the yield and selection for these character will give ample selection response and ultimately we will get an increased single plant yield. The residual effect which actually means the character which we not included that actually determines the yield was found to be 20 percent which inferred the reliability of characters taken for study.

Conclusion

As hybrid breeding in sorghum relies on sterile cytoplasm all the hybrids available till date are based on A_1 cytoplasm. This increase the risk of uniformity in cytoplasm of the hybrids and spread of epidemic as like in maize T cytoplasm. So we are in the urgent situation to have an alternate cytoplasm for hybrid breeding in sorghum not only to overcome the above risk but also to have good preference among the farmer to extensify the revenue by having *rabi* season cropping. So this variability and association studies carried out in the background of A_4 cytoplasm with its proper restorer will definitely give an suitable breeding population and along with that we could gain insights to improve particular traits affecting yield and also to get the transgressive segregants.

References

BN, C., Darshitha S.R., HB M., Harinikumar K.M. and CV B. (2024). Genetic Variability Studies in Sweet Sorghum (*Sorghum bicolor* l.) Genotypes for Sugar and Biomass Related Traits. *J. Adv. Biol. Biotechnol.*, **27(4)**, 206-216.

Hamidou, M., Souley A.K.M., Kapran I., Souleymane O., Danquah E.Y., Ofori K., Gracen V. and Ba M.N. (2018). Genetic variability and its implications on early generation sorghum lines selection for yield, yield contributing traits, and resistance to sorghum midge. *Int. J. Agron.*, **2018**.

Kumar, S., Chauhan M.P., Tomar A. and Kasana R.K. (2018). Coefficient of variation (GCV & PCV), heritability and genetic advance analysis for yield contributing characters in rice (*Oryza sativa* L.). *J. Pharmacog. Phytochem.*, **7(3)**, 2161-2164.

Mofokeng, M.A., Shimelis H., Laing M. and Shargie N. (2019). Genetic variability, heritability and genetic gain for quantitative traits in South African sorghum genotypes. *Australian J. Crop Sci.*, **13(1)**, 1-10.

Nirosh, P.V., Yuvaraja A., Thangaraj K. and Menaka C. (2021). Genetic variability and association studies in segregating generation of red sorghum (*Sorghum bicolor* (L.) *Moench*) population. *Elect. J. Plant Breed.*, **12(2)**, 521-524.

Rao, P.P., Basavaraj G., Ahmed W. and Bhagavatula S. (2010). An analysis of availability and utilization of sorghum grain in India. *SAT eJournal/ ejournal.icrisat.org,* 8.

Reddy, K.R.A.K. and Pitha C.C. (2024). Exploring Genetic Variability, Path Analysis and Divergence in Sorghum (Sorghum bicolor (L.) Moench). *J. Exp. Agricult. Int.*, **46(8)**, 49-62.

Subhashini, S. and Selvi B. (2019). Association and variability studies in F_2 population of sorghum (*Sorghum bicolor* (L.) *Moench*). *Elect. J. Plant Breed.*, **10(2)**, 483-489.

Swamy, N., Biradar B.D., Sajjanar G.M., Ashwathama V.H., Sajjan A.S. and Biradar A.P. (2018). Genetic variability and correlation studies for productivity traits in *Rabi* sorghum [*Sorghum bicolor* (L.) *Moench*]. *J. Pharmacog. Phytochem.*, **7(6)**, 1785-1788.

Tilaye, A. (2024). Genetic Variability and Association of Traits among Sorghum Genotypes [*Sorghum bicolor* (L.) Moench] under Drought Stress Area.