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Research Article

Genetic variability and multivariate analyses in coloured sorghum landraces (*Sorghum bicolor* (L.) Moench) of Tamil Nadu

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Abstract
Sorghum (*Sorghum bicolor* [L.]Moench) is a versatile crop grown in more than 100 countries in tropics and semi-arid regions for food, fodder, fuel and fiber. Red sorghum is noted for its rich phenolic content and specifically 3-deoxyanthocyanin content that lacks hydroxyl group at C-3 position. A total of 80 sorghum landraces collected from various sources from Tamil Nadu were evaluated during *Kharif,* 2019 to record morphological diversity present in the accessions. The 12 quantitative traits were recorded stage wise following IIMR DUS descriptor. The quantitative data collected from 80 sorghum landraces were statistically analyzed by variability study and association study. The high PCV and GCV were recorded for height upto flag leaf, flower length, panicle emergence, total height, panicle length, panicle branch length, panicle neck length, thousand grain weight and single plant yield. The moderate level of GCV and PCV was recorded for leaf length and leaf width. The trait stem diameter showed high PCV and moderate GCV. The variability study indicated that more variations were found in the population which facilitates efficient selection. The grain yield was positively related with leaf width and thousand grain weight. The yield was negatively influenced by height upto flag leaf, flower length, total height, panicle length, panicle neck length and panicle emergence. The results of correlation analysis revealed that the selection for high yielding landraces can be carried out phenotypically by selecting landraces with high grain weight, early panicle emergence, lesser height upto flag leaf, reduced neck length, reduced flower length and more leaf width to develop a desired high yielding sorghum variety.

Keywords
Sorghum landraces, variability study, correlation

INTRODUCTION

Sorghum (*Sorghum bicolor* [L.]Moench) is the fifth most important panicoid millet crop grown in nearly 100 countries in the world (Hariprasanna and Patil, 2015). The versatile sorghum crop which is used for food, fodder, fuel and fibre is grown predominantly in Asian and African countries and act as a staple food for millions of people in tropical and semi-arid regions. Sorghum cultivation in India covers an area of 4.96 Million hectares with average productivity of 967.7 Kg/ha and production of 4.8 Million tonnes (USDA, 2019).

Sorghum is nutritionally good and comparable with other cereals and so it is indicated as “nutritious grain” (Aruna*et al*.2020). Sorghum is also rich in secondary metabolites which made it a climate resilient crop that can overcome varies biotic and abiotic stresses. Red sorghum is good in phenolic content and contains a special pigment called 3- deoxyanthocyanin which lacks a hydroxyl group in the third carbon position. The pigment has high potential to be used as food colourant because it is more stable even under high temperature and alkaline pH. Sorghum

is also rich in antioxidant activity, dietary fibre and can supply gluten free protein. As a whole, if sorghum is included in regular diet as like our ancestors it is possible to eliminate many chronic diseases and also an important problem, malnutrition in developing and under developed countries.

India being its secondary center of origin it is rich in diversity of sorghum (Vavilov, 1951). The available natural variations are the good source of desirable traits and resistant genes to facilitate crop important. The crop has to be improved in yield, nutrition and biochemical aspects. The variability study was conducted in plant material to estimate phenotypic and genetic diversity available in the accessions. Association study give a brief detailed note regarding the relationship between the traits observed and also helps to figure out the trait that contribute positively towards improved yield. This study was conducted with sorghum landraces collected from various parts of Tamil Nadu. Landraces provide more variation and also well adapted to local conditions. The genetic variability and association study for quantitative traits in landraces is an initial step in crop improvement programme.

MATERIALS AND METHODS

The plant material used in the study consists of 80 sorghum landraces which includes red sorghum, white sorghum, yellow sorghum and a released variety as check. The landraces collected from various parts of Tamil Nadu were assimilated from Dr. Ramiah Gene Bank, Tamil Nadu Agriculture University, Coimbatore, Tamil Nadu; Regional Research Station, Paiyur; Agricultural Research Station, Kovilpatti; AnbilDharmalingam Agricultural College and Research Institute, Thiruchirapalli and local collections from Namakkal and Madurai districts. The details related to landraces used in the study are provided in **table 1**. The 79 sorghum landraces and a check (PYR 2) was sown during *Kharif,* 2019 in an experimental design Randomised Block Design (RBD) with two replications at Agricultural College and Research institute, Madurai. The plants are grown well by following recommended agronomic practices. The observation was taken from five plants of each accession at appropriate stages.

The various quantitative traits observed were Height upto flag leaf (HFL), Flower length with pedicle (FL), Time of Panicle emergence (PE), Total Plant height (TH), Stem diameter (SD), Leaf blade length (LL), Leaf blade width (LW), Panicle length without peduncle (PL), Panicle branch length (PBL), Panicle neck length (PNL), Thousand grains weight (TGW) and Single plant yield (SPY).

Table 1.Sources of collection and grain color of sorghum landraces used in the study

S.No	Accessions	Source	Grain Colour
1.	PYR (RS)16.01, PYR (RS)16.02, PYR (RS)16.04, PYR (RS)16.05, PYR (RS)16.06, PYR (RS)16.07, PYR (RS)16.09, PGR (RS)108, PYR (RS)168, TNAUR00402457, TNAUR00402482, TNAUR00402488, TNAUR00402493, TNAUR00402520, TNAUR00402519, TNAUR00402504, TNAUR00402508, TNAUR00404267, TNAUR00404269, TNAUR00404266(SMALL), TNAUR00404266(BOLD), TNAUR00404416, TNAUR00404418	RRS, Paiyur	Red sorghum
2.	TNAUR00402443, TNAUR00402648, TNAUR00402657, TNAUR00404263, TNAUR00404270, TNAUR00404294	Dr.Ramiah Gene Bank, TNAU, Coimbatore	Red sorghum
3.	Venbarour local 1, Muthiyampalayam local 1, Muthiyampalayam local 2, Muthiyampalayam local 3, Muthiyampalayam local 4, Muthiyampalayam local 5, Muthiyampalayam local 6, Veppanthattai local 1, Kottathurlocal 1, Kottathur local 3, Kottathur local 4, Kottathur local 6 (small), Kottathur local 6(bold), Venkalam local 1, Ammapatti local 1, Ammapatti local 3, Ammapatti local 4, Ammapatti local 5, Ammapatti local 6, Sorathur local 1, Kalingamudayanpattilocal 2, Vengatesapuram local 1, Vengatesapuram local 2, Nochiyam local 1, Nochiyam local 2, Visvakudi local 1, Visvakudilocal 2, Keezhapuliyur local 1, Keezhakunnempatti local 1	ADAC & RI, Trichy	Red sorghum
	Chiddayankottai local 1, Kottathur local 5, Ammapatti local 2, Kalikampatti local 1, Settiyapatti local 1, Narupatti local 1, Anumandhanayarkottai L-1	ADAC & RI, Trichy	White sorghum
	Kalingamudayanpatti local 1	ADAC & RI, Trichy	Yellow sorghum
4.	Namakkal, Mappillaiminukkucholam, Sivapuirungucholam, Sivappumappillaiminukku, Usalampatti local	Local collections	Red sorghum
5.	Dummaickenpatti, Papainaickenpatti red sorghum, T.Kallupatti, Villvamarathupatti red, Nainakaram, Ottudanpatti red, Alangarapuram, Duraisamipuram	ARS, Kovilpatti	Red sorghum
	Tenkasi, Thottilovenpatti	ARS, Kovilpatti	White sorghum
6.	PYR 2	RRS, Paiyur (check)	Red sorghum

The Analysis of Variance (ANOVA) was conducted to evaluate the components of variance. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were assessed by adopting the procedure suggested by Burton, 1952. The PCV and GCV estimates were categorised as high (>20%), medium (10-20%) and low (<10%) (Sivasubramanian and Madhavamenon, 1973).Heritability an important factor to estimate selection response was calculated based on Lush, 1940 suggestion and genetic advance as percent of mean was calculated (Johnson *et al*. 1955). The correlation study was conducted to establish relationship between the variables that aids in selection process by using the formula suggested by Falconer, 1960. The Pearson correlation study was conducted using R software packages.

RESULT AND DISCUSSION

The variability present in the materials has to be evaluated to facilitate effective selection process. The phenotypic and genotypic coefficient calculated for 12 quantitative traits were listed in **table 2**. The high GCV and PCV value was observed for plant height upto flag leaf, flower length with pedicle, time of panicle emergence (Subramanian *et al*. 2019), total height (Naoura *et al*. 2019; Subramanian *et al*. 2019), panicle length without peduncle (Karadi and Kajjidoni, 2019; Naoura *et al.* 2019), panicle branch length, panicle neck length (Naoura *et al*. 2019), thousand grains weight (Mofokeng *et al*.2019) and single plant yield (Swamy *et al*. 2018; Subramanian *et al*. 2019). Hence, this shows that the variability observed for these traits were high and there is a good scope for selection in these traits which gives further improvement in the characters. The moderate level of GCV and PCV was recorded for leaf length (Subramanian *et al*. 2019) and leaf width (Singh *et al*. 2018). The variation available for leaf length and width was comparatively less to enable effective selection process for these traits. The trait stem diameter showed high PCV and moderate GCV (Shamini and Selvi, 2018). The PCV is greater than GCV in the character stem diameter this indicates the influence of the environmental on the trait was more. Whereas in other traits the difference between PCV and GCV is comparable and this could be concluded as expression of these traits are not much influenced by environmental factors.

Table 2. GeneticVariability parameters in sorghum landraces

S.No	Traits	Mean	PCV%	GCV%	H%	GA	GAM%
1.	Height upto flag leaf	256.74	30.61	30.60	99.92	161.77	63.01
2.	Flower length with pedicle	20.43	38.59	37.31	93.44	15.18	74.29
3.	Time of Panicle emergence	72.11	24.65	24.48	98.70	36.13	50.11
4.	Total height	294.45	30.03	29.99	99.74	181.71	61.71
5.	Stem diameter	1.95	23.52	19.48	68.61	0.65	33.24
6.	Leaf length	59.60	14.71	13.80	87.95	15.89	26.66
7.	Leaf width	6.09	19.37	16.81	75.32	1.83	30.05
8.	Panicle length without peduncle	20.06	41.88	39.50	88.96	15.40	76.75
9.	Panicle branch length	6.21	60.89	58.18	91.29	7.11	114.51
10.	Panicle neck length	16.29	41.88	39.50	88.96	12.50	76.75
11.	Thousand grains weight	17.78	30.51	30.13	97.54	10.90	61.30
12.	Single plant yield	13.05	39.60	39.54	99.68	10.61	81.31

PCV – Phenotypic Coefficient of Variation, **GCV**- Genotypic Coefficient of Variation, **H**- Heritability, **GA**- Genetic Advance, **GAM**- Genetic Advance Mean

The response of the population towards selection was measured as heritability in quantitative genetics. Heritability in broad sense is defined as “the proportion of phenotypic variance that is attributable to an effect for the whole genotype, comprising the sum of additive, dominance and epistasis effects (Falconer, 1960). The improvement in selected lines over the initial population is determined as genetic advance under selection. The high heritability and genetic advance was recorded in almost all recorded traits this shows that the selection will be effective based on these characters.

The correlation coefficient between traits was tabulated in **table 3** and pictorially represented in **fig 1.** The trait plant height upto base of flag leaf showed positive significant correlation with flower length (r=0.60), total height (r=0.99), stem diameter (r=0.52), panicle length (r=0.63), panicle branch length (r=0.37), panicle neck length (r=0.59), panicle emergence (r=0.73) and negatively association with single plant yield (r=-0.19). The trait is negatively associated with single plant yield which explains that the genotypes with less height upto flag leaf are good yielders.

The length of flower is positively correlated with total height (r=0.66), stem diameter (r=0.29), leaf length (r=0.36), panicle length (r=0.88), branch length (r=0.66), emergence (r=0.48), neck length (r=0.68) and negatively related to single plant yield. The total height was positively related with stem diameter (r=0.51), panicle length (r=0.69), panicle branch length (r=0.43), panicle neck length (r=0.65) and panicle emergence (r=0.72) and negatively associated with yield. Both the characters, length of flower and total height were negatively influencing the

yield. Hence, the genotypes with less height and flower length need to be selected for yield improvement.

The stem diameter showed positive association with leaf length (r=0.28), leaf width (0.39), panicle length (r=0.34), panicle branch length (r=0.28), panicle neck length (r=0.25) and panicle emergence (r=0.29). The leaf length showed significant positive correlation with leaf width (r=0.69), panicle length (r=0.36) and panicle branch length (r=0.34). The width of leaf was positively correlated with grain weight (r=0.25) and single plant yield (r=0.28) but negatively associated with panicle neck length (-0.21). The width of the leaf positively influences the thousand grain weight and the single plant yield. This relationship shows that genotypes with broader leaf blade promote yield.

Table 3. Correlation coefficient of biometrical traits observed in sorghum landraces

	PHF	FL	TH	SD	LL	LW	PL	PBL	PNL	GW	PE	SPY
PHF	**1.00**	0.60*	0.99*	0.52*	0.02	0.01	0.63*	0.37*	0.59*	-0.19	0.73*	-0.19
FL		**1.00**	0.66*	0.29*	0.36*	0.12	0.88*	0.66*	0.68*	-0.08	0.48*	-0.07
TH			**1.00**	0.51*	0.05	0.00	0.69*	0.43*	0.65*	-0.20	0.72*	-0.19
SD				**1.00**	0.28*	0.39*	0.34*	0.28*	0.25*	0.19	0.29*	0.02
LL					**1.00**	0.69*	0.36*	0.34*	0.00	0.09	0.03	0.14
LW						**1.00**	0.14	0.20	-0.21	0.25*	-0.07	0.28*
PL							1.00	0.82*	0.50*	-0.13	0.51*	-0.06
PBL								**1.00**	0.25*	-0.12	0.36*	0.05
PNL									**1.00**	-0.11	0.26*	-0.14
GW										**1.00**	-0.32*	0.72*
PE											**1.00**	-0.22*
SPY												1.00

* Significant at 5% level

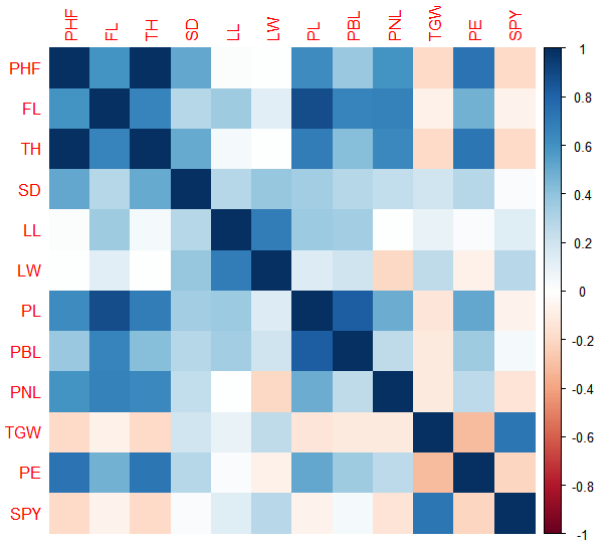

Fig. 1. Pictorial representation of correlation coefficient

The panicle length was positively related to panicle branch length (r=0.82), panicle neck length (r=0.50) and panicle emergence (r=0.51). The neck length showed significant positive association with panicle emergence (r=0.26). The panicle length and panicle neck length negatively influenced the yield. The panicle with more length indicates the loose panicle with less grain and also more neck length was observed in genotypes with open panicle. Hence, genotypes with less neck length and low panicle length coupled with compact type panicle have more number of grains and increase the yield per plant. The panicle branch length showed positive significant correlation with panicle neck length (r=0.25) and panicle emergence (r=0.36).The grain weight was positively related to single plant yield (r=0.72) (Ranjith*et al*. 2017) and negatively associated with panicle emergence (r=-0.32). The panicle emergence is negatively associated with single plant yield (r=-0.22). The relationship among grain weight, panicle emergence and single plant yield explains that the plant yield is highly influenced by both panicle emergence and grain weight. The grain weight is directly proportional to yield and shoed that plant with bold seed automatically gives more yield. The plants with early panicle emergence need to be selected because both are inversely related.

The similar results for some traits were also reported by Subalakhshmi *et al*. 2019; Subhashini and Selvi, 2019 and Akatwijuka *et al*. 2019. The variability present in accessions is the efficient source to improve crop and variability study of the quantitative traits is an efficient statistical tool to evaluate the variation. The association study gives a detailed explanation about the direction of selection to develop a high yielding variety. The plants with medium height and lesser neck length, lesser flower length, high seed weight and increased leaf width with early emergence of panicle will contribute positively to the yield of the plant.

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