Original Research Article

Genetic variability studies for yield and yield contributing traits in *rabi* sorghum (*Sorghum bicolor* L. Moench) in relation to drought tolerance

Abstract

Genetic variability studies were useful for effective selection in a crop species. Presence of desirable variation and the amount of that variation which is heritable is the primary requirement of any breeding program for the crop improvement. Therefore any breeding program for crop improvement depends majorly on the knowledge pertaining to genetic variability, heritability and genetic advance. The genetic variability study was carried out for yield and yield contributing traits in thirty-seven genotypes of *rabi* sorghum with three checks namely M 35-1, Phule Suchitra and CSV-22-R at Sorghum Research Station, V.N.M.K.V., Parbhani during *rabi* 2019. A randomized block design was used with three replications and these treatments were evaluated and data pertaining to eleven traits were recorded with the objective to estimate the genetic variability for the quantitative traits. This investigation revealed presence of highly significant differences among the genotypes indicating presence of large amount of variability in all the eleven characters studied. The study indicated presence of higher estimates of phenotypic coefficient of variation (PCV) for all the traits when compared to genotypic coefficient of variation (GCV) and these estimates are of lower magnitude. Among the forty genotypes studied VJV 107, VJV 106, PEC 30, RSV 1921, RSV 1945 and RSV 1984 were considered as the superior genotypes as these recorded better performance. Higher estimates of GCV and PCV were recorded for the traits; days to 50 per cent flowering, plant height, panicle length, panicle width, fodder yield per plant, biological yield per plant, harvest index and grain yield per plant indicating selection for higher values of these traits of sorghum would be effective. Whereas high heritability coupled with moderate to high genetic advance was observed for traits like plant height, fodder yield per plant and total biomass per plant.

Keywords: Genetic variability, heritability, PCV, GCV, genetic advance.

1. Introduction

Sorghum (*Sorghum bicolor* L. Moench) is one of the important cereal crop in the world occupying fifth position after maize, rice, wheat and barley (FAOSTAT, 2017). Sorghum is used as whole grain or processed into flour, it is gluten free and have essential nutrients (proteins, vitamins and minerals) and nutraceuticals (phenolics, antioxidants and cholesterol lowering waxes) (Assefa *et al*., 2018). It is the staple food in the human diet especially for poor and most food insecure people living in semi-arid tropics (Tonapi *et al*., 2011). Rabi sorghum occupies large area mainly in the states of Maharashtra, Karnataka and Andhra Pradesh with an average productivity of 819 kg/ha (Low). It is an important component of dry land economy irrespective of its low productivity and its area is consistent over many years. Biotic and abiotic stresses are the reasons for low productivity (Bhat & Rao, 2003). Drought is the major abiotic stress limiting crop growth. Water availability to the crop is becoming very essential to meet the production needs as the climate is changing frequently. *Sorghum bicolor* is one of C_4 cereal and mainly due to its morphological and anatomical characteristics such as thick leaf wax, deep root system and physiological responses such as osmotic adjustment, stay green, quiescence it is highly suited for the drought environment (Fracasso *et al*., 2016). This crop can grow in high temperature, high light intensity and low water availability and it is highly efficient in fixing carbon dioxide due to its C_4 photosynthetic pathway (Sasaki & Antonio, 2009). Improving the crop is a key to ensure food security to the increasing population as it is a staple food in the world (Kadam & Fakrudin, 2017). Growth and yield reduction occurs due to water stress in this crop even though it is considered as drought tolerant crop. In drought related studies, identification of the traits (especially morphological and physiological) related to drought stress given higher importance (Jirali *et al*., 2007). Sorghum is affected by water stress at both pre- and post-flowering stages. *Rabi* sorghum is highly affected due to post-flowering drought and it shows highly variable and low productivity. Even though sorghum is highly valued due to its good grain quality (Kebede *et al*, 2001). For reducing the risk due to post-flowering drought superior genotypes are required. This in turn requires the identification of traits (cost effective and easily measurable) related to terminal drought tolerance (Talwar *et al*., 2010). For successful planning and executing of the breeding programme, knowledge regarding the genetic variability is very essential. For stabilizing the production of the crop growing under drought stress during post monsoon especially *rabi* sorghum, identification of the superior traits is essential. In order to increase the yield and drought tolerance among the genotypes identification of the essential traits, hybridization among these divergent sources and finally selection from the segregating generations is to be done (Mitra, 2001). Among the various sorghum genotypes, variation due to drought tolerance was identified and some of the better adopted genotypes were also identified (Jirali *et al*., 2007). The present study was undertaken with objective to estimate the genetic variability for the quantitative traits.

2. Methodology

Experimental material for the proposed work consists of 37 drought tolerant sorghum genotypes received from IIMR, Hyderabad along with three checks namely, **M-35-1, CSV 22R and Phule Suchitra.** These genotypes were evaluated using randomized block design with three replications during *rabi* 2019. The data pertaining to seedling vigour (1-5 scale), days to 50% flowering, plant height (cm), panicle length(cm), panicle width(cm), days to physiological maturity, 100-seed weight (g), fodder yield per plant (g), grain yield per plant (g), total biomass (g/plant) and harvest index (%) were recorded and used for analysis of variance (Panse & Sukhatme, 1958).

Further statistical analysis was carried out using mean values (Table 2) for all the eleven traits under consideration.

3. Results and discussion

Current investigation was carried out to estimate several genetic parameters like estimation of variability i.e., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance (GA) and genetic advance as percentage of mean. Combined ANOVA of the current investigation is furnished in Table 1.0, for the forty genotypes. The data showed presence of highly significant differences among the genotypes, indicating presence of large amount of variability in all the eleven characters studied. These results are in agreement with Sanchez *et al.* (2002), who reported existence of significant differences among the treatments for the plant height and Amanullah *et al*. (2007), and Techale *et al* (2014), who reported existence of significant differences among the treatments for the traits plant height and leaf area. Gebregergs *et al*. (2020) recorded significant differences for the traits; days to flowering, days to maturity, plant height, panicle length, total biomass, harvest index and grain yield.

In the current investigation wide range of variability exhibited by various yield and yield contributing traits which includes plant height (136.23 to 205.00 cm), days to physiological maturity (106.67 to 119.00), days to 50 percent flowering (65.54 to 78.00 %), total biomass per plant (57.82 to 116.3 g), fodder yield per plant (37.93 to 74.15 g), harvest index (23.83 to 39.61 %), grain yield per plant (17.25 to 41.80 g), panicle length (11.17 to 18.06 cm), panicle width (3.80 to 5.73 cm), 100 seed weight (2.21 to 3.56 g) and seedling vigour (1.33 to 3.67). These results are in agreement with Veerabhadiran & kennedy (2001), who reported existence of wide range of variability for various yield contributing traits like 100 seed weight, grain yield per plant and days to 50 per cent flowering and Gebregergs *et al*. (2020), who recorded wide range of variability for various traits like plant height, total biomass, harvest index and grain yield.

Genotypic and phenotypic variance

Current investigation exhibited slightly higher phenotypic variance when compared to genotypic variance and these differences are of lower magnitude. These results are presented in Table 3. Higher values of genotypic and phenotypic variances recorded for the traits days to 50 per cent flowering, plant height, panicle length, panicle width, fodder yield per plant, biological yield per plant, harvest index and grain yield per plant. Similar results were reported by Tariq *et al*. (2012), for plant height and fodder yield; days to 50% flowering, plant height, leaf area and green fodder yield (Singh *et al.* 2019); plant height, total biomass, harvest index and grain yield (Gebregergs *et al*. 2020).

Genotypic and phenotypic coefficient of variation

Current study indicated presence of higher estimates of phenotypic coefficient of variation for all the traits when compared to genotypic coefficient of variation and these estimates are of lower magnitude. These results are presented in Table 3. Moderate to higher estimates of phenotypic and genotypic coefficient of variation observed for traits plant height, panicle length, panicle width, panicle weight, fodder yield per plant, biological yield per plant, 100 seed weight, harvest index and grain yield per plant. Similar results recorded by Veerabadhiran and Kennedy (2001), Date (2002), Kumar and Sahib (2003), Arunkumar *et al*. (2004), Ali *et al*. (2009b), Kusalkar *et al.* (2009), Arunkumar (2013), Chittapur and Biradar (2015), Tesfamichael *et al*. (2015), Dhutmal *et al.* (2015), Khandelwal *et al.* (2015), El-salam & Hovny (2018), Singh *et al.* (2019), Gebregergs and Mekbib (2020).

Heritability and Genetic Advance

Total heritable portion of variation cannot be indicated only by genotypic coefficient of variation. Effectiveness of the selection based on the phenotypic performance is indicated by the presence of high heritability but it does not indicate the genetic gain under selection. Thus it is necessary to estimate the genetic gain under selection i.e., genetic advance. High heritability alone does not indicate the selection is effective; heritability estimates coupled with genetic advance are more useful in predicting the effectiveness of the selection. Selection is effective when there is high heritability coupled with high genetic advance as it indicates the presence of additive gene action whereas high heritability coupled with low genetic advance indicates presence of non-additive gene action thereby selection is ineffective.

In current investigation heritability varied from 64.65 to 96.58 and genetic advance varied from 0.63 to 57.3. High heritability coupled with moderate to high genetic advance is observed for traits like plant height, fodder yield per plant and total biomass per plant which indicates presence of additive gene action and selection for these traits is effective. These results are in agreement with Ambekar *et al.* (2000), Date (2002), Kumar & Sahib (2003), Tariq *et al*. (2012) and Chittapur & Biradar (2015), El-Salam & Hovny (2018), Singh *et al.* (2019) and Gebregergs *et al*. (2020).

High heritability coupled with low genetic advance was observed for traits like days to flower initiation, days to 50 per cent flowering, days to physiological maturity, panicle length, panicle width, 100 seed weight, harvest index and grain yield per plant which indicates presence of non-additive gene action and selection for these traits is ineffective. These results are in agreement with Dhutmal *et al*. (2015). Finally, it is evident that in *rabi* sorghum for the improvement of grain yield all the estimates of genetic parameters i.e., genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance should have higher values.

Table 1: Analysis of Variance for eleven characters of rabi sorghum

Sr. No.	Sources of variation	Degrees of freedom	Seedling vigor	Days to 50 percent flowering	Days to physiological maturity	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	Fodder yield per plant (g)	Total biomass per plant (g)	Harvest index (%)	100-seed weight (g)	Grain yield per plant (g)
1	**Replication**	2	0.408	1.825	0.133	1.468	2.584	0.005	4.507	32.69	1.573	0.041	9.76
2	**Treatment**	39	1.878**	10.17**	42.509**	512.508**	5.082**	0.7706**	246.224**	520.553**	43.227**	0.379**	77.856**
3	**Error**	78	0.545	0.269	0.56	0.417	1.273	0.037	0.998	17.826	1.492	0.051	5.863

**Significant at 1 percent level.

Table 2: The Mean performances of eleven characters studied in *rabi* sorghum

Sr.No.	Genotypes	Seedling vigour	Days to 50 percent flowering	Days to physiological maturity	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	Fodder yield per plant (g)	Total biomass per plant (g)	Harvest index (%)	100-seed weight (g)	Grain yield per plant (g)
1	**RSV 1837**	2.33	76	117.33	180.29	15.7	3.87	61	88	30.37	3.15	27.01
2	**RSV 1921**	1.33	66	119	176.82	14.7	3.89	58.17	83.53	30.5	2.89	25.48
3	**RSV 1945**	3	71.73	106.67	205.22	15.47	5.3	71.13	101.3	29.87	3.32	30.25
4	**RSV 1984**	3	71.33	117	194.67	14.87	4.67	64.3	89.43	28	2.89	25.06
5	**RSV 1988**	3.33	77.33	109.33	177.19	15.47	4.79	63.17	91.63	35.83	2.85	30.2
6	**RSV 2124**	2.67	74.43	119	176.78	15.97	5.07	69.57	100	30.8	3.11	30.8
7	**RSV 2197**	2.67	74.63	118.33	189.98	15.9	4.76	63.4	87.97	30.5	3.05	27.81
8	**RSV 2209**	3.67	75	118	189.78	16.13	4.73	74.03	107.53	31.63	3.17	33.25
9	**RSV 2234**	3	74.53	118.33	161.78	17.17	4.43	57.97	95.53	25.2	2.83	24.1
10	**RSV 2252**	3.67	73.33	118.33	177.22	14.37	4.47	48.47	74.9	33.67	3.32	26.8
11	**VJV 106**	3.33	72.5	119	200.67	16.67	5.6	70.33	96.83	38.03	3.34	38.5
12	**VJV 107**	3	76	117.33	190.12	12.57	5.73	72.47	116.3	39.61	3.45	41.8
13	**VJV 108**	3.33	74.67	106.67	181.87	17.13	4.69	63.27	99.33	26.63	2.87	26.3
14	**VJV 109**	2.33	75.13	119	176.22	13.8	4.57	57.3	84.79	27.63	2.79	24.58
15	**VJV 110**	3	76.7	118	182.56	15.37	4.66	60.63	93.49	28.23	3.12	26.41
16	**VJV 111**	3	75.07	106.67	180.66	12.97	4.2	57.03	75.91	24.4	2.21	18.51
17	**VJV 112**	3.33	73.73	117.67	183.44	16.13	4.85	63.23	88.5	28.67	2.9	25.4
18	**VJV 113**	3.33	76.63	118	185.33	13.8	4.77	55.63	81.8	24.97	2.88	20.4
19	**VJV 114**	3.33	74.27	118	186.22	14.63	4.27	59.53	87.2	26.3	3.02	23.54
20	**VJV 115**	3.67	77.07	117.67	165.11	14.53	4.86	54.27	74.83	29.23	2.87	23.14
21	**CRS 69**	2	75.67	118.33	177.67	14.23	4.5	53.14	70.13	27.7	2.56	20.36
22	**CRS 70**	2.67	74.67	118.33	171.11	12.9	3.97	46.4	66.9	30.73	2.85	20.5
23	**CRS 71**	3	78	118.33	136.22	15.2	4.67	66.2	87.6	27.7	2.98	25.46
24	**CRS 72**	3.33	73.77	110.67	138.78	13.87	4.8	45.8	80.53	33.57	2.82	25.42
25	**CRS 73**	3.33	72.33	118	139.45	11.4	4.1	49.07	71.68	27.97	2.91	22.35
26	**CRS 74**	3.33	73.07	117.67	162.11	13.8	4.37	56.25	80.83	28.37	3.28	24.58
27	**EP 85**	3	74	109.67	180.56	16.67	3.83	65.4	92.33	38.73	3.41	31.4
28	**EP 89**	2.33	76.67	117	180.89	15.33	4.69	63.45	92.53	28.93	3.1	27.41
29	**EP 94**	3.33	70	115.33	178.22	11.17	4.44	58.4	91.58	27.63	3.23	25.62
30	**EP 98**	2.33	73.97	116.67	166.67	12.93	5.73	37.93	58.96	29.97	2.54	21.15
31	**PEC 15**	3.33	74.26	116.67	176.89	16	5.63	63.5	98.61	23.83	2.43	23.51
32	**PEC 23**	2.67	76.31	118	184.22	15.2	5.07	40.57	57.82	28.17	2.84	17.25
33	**PEC 30**	1.33	75.33	117.33	165.56	18.07	5.73	64.5	91.24	29.03	2.89	26.41
34	**PVRL16-2**	2.67	78	106.33	175.67	16.67	5.43	74.15	104.65	29.23	3.44	30.5
35	**PVR 16-3**	3.67	76.67	119	155	13.6	4.8	45.89	65.32	23.9	2.3	20.1
36	**PVR 947**	3.67	77	117.67	174.89	13.67	4.17	57.9	83.34	26.47	2.06	22.54
37	**PVR 950**	3	73.07	117.33	183.22	12	3.8	59.64	85.93	34.37	3.27	29.62
38	**M 35-1 (C)**	3.33	74.33	116.67	169.33	12.4	4.13	69.87	99.27	28.73	3.48	28.46
39	**CSV 22R (C)**	2.67	75	118	181.78	14.37	5.2	72.03	106.3	32.57	3.56	34.15
40	**Phule Suchitra (C)**	3	75	118.33	176.55	15.2	4.5	67.93	95.6	31.77	3.47	30.4
	Mean	2.81	74.58	115.86	177.11	15.08	4.65	60.07	87.5	29.74	2.99	26.41
	SE	0.43	0.3	0.43	0.37	0.65	0.11	0.58	2.44	0.71	0.13	1.4
	CD at 5%	1.2	0.84	1.22	1.05	1.83	0.32	1.62	6.86	1.99	0.37	3.94

Table 3 Genetic Variability Parameters for twenty characters studied in *rabi* sorghum

Sr.No.	Characters	Range		Mean	σ2(g) (Genotypic variance)	σ2(p) (Phenotypic variance)	GCV(%)	PCV(%)	h2 b.s. (%)	GA	GA as % of mean
		Minimum	Maximum								
1	**Seedling vigour**	1.33	3.67	2.8	0.44	0.63	23.74	28.18	70.98	1.16	41.2
2	**Days to 50 percent flowering**	65.54	78	74.54	12.84	14.42	4.89	4.92	92.64	6.89	8.94
3	**Days to physiological maturity**	106.7	119	117.7	9.12	10.24	3.59	3.82	92.14	6.21	6.06
4	**Plant height (cm)**	136.2	205	177	702.54	726.84	16.24	17.86	91.18	57.3	38.42
5	**Panicle length (cm)**	11.17	18.06	15.07	1.45	1.71	8	8.67	85.26	2.29	15.22
6	**Panicle width (cm)**	3.8	5.73	4.66	0.15	0.24	8.41	10.46	64.65	0.65	16.94
7	**Fodder yield per plant (g)**	37.93	74.15	60.07	79.02	81.99	14.8	15.07	96.38	18	29.93
8	**Total biomass per plant (g)**	57.82	116.3	87.49	167.58	173.52	14.79	15.05	96.58	26.2	29.95
9	**Harvest index (%)**	23.83	39.61	29.65	12.47	14.15	11.91	12.68	88.17	6.83	23.03
10	**100-seed weight (g)**	2.21	3.56	2.98	0.11	0.13	11.08	11.91	86.45	0.63	21.22
11	**Grain yield per plant (g)**	17.25	41.8	26.41	24	25.95	18.55	19.29	92.47	9.7	36.74

4. Conclusion:

This research project revealed presence of large amount of scope for a breeder in selecting superior genotypes for yield improvement in rabi sorghum after studying character association as this study recorded presence of large amount of variation for various yield and yield contributing traits. Generally, the traits which exhibit higher values for genotypic coefficient of variation, phenotypic coefficient of variation, high heritability coupled with high amount of genetic advance and significant and positive correlation with aspects related to yield and drought tolerance are used for identification of superior genotypes for drought tolerance. Among all the genotypes and checks VJV 107, VJV 106, PEC 30, RSV 1921, RSV 1945 and RSV 1984 recorded better performance as compared to all the checks and genotypes, in terms of yield as well as drought tolerance aspects. Hence, these genotypes can be used for drought tolerance aspects and play a major role in breeding for abiotic stress tolerance i.e. for drought as well as advanced to next generation.

References:

1 FAOSTAT., 2017. Food and Agriculture Organization of the United Nations Database of agricultural production. *FAO Statistical Databases*. [accessed 2017 November 3]

2 Assefa, S., Shimelis, H., Mwadzingeni, L., and Laing, M., 2018. Agro-morphological characterisation and selection of sorghum landraces. **68**(7), 585–595.

3 Tonapi, V. A., Patil, J., Rao, B. D., Elangovan, M., Bhat, B. V., and Rao, K. R., 2011. Vision 2030 Sorghum. *Directorate of Sorghum Research, Hyderabad, Andhra Pradesh, India*, 38.

4 Bhat, P., & Rao, S. S., 2003. Early-maturing postrainy (*rabi*) season sorghum elite lines with enhanced drought tolerance. *November 2014*, 1–6.

5 Fracasso, A., Trindade, L. M., &Amaducci, S., 2016. Drought stress tolerance strategies revealed by RNA-Seq in two sorghum genotypes with contrasting WUE. 1–19.

6 Sasaki, T., & Antonio, B. A., 2009. Sorghum in sequence. 457(January).

7 Kadam, S. R., &Fakrudin, B., 2017. Marker assisted pyramiding of root volume QTLs to improve drought tolerance in rabi sorghum. September.

8 Jirali, D. I., Biradar, B., & Rao, S. S., 2007. Evaluation of Rabi Sorghum Germplasm(*Sorghum bicolor*L .Moench). June.

9 Kebede, H., Subudhi, P. K., Rosenow, D. T. and Nguyen, H. T., 2001. Quantitative trait loci influencing drought tolerance in grain sorghum (*Sorghum bicolor* L. Moench).*Theor. Appl. Genet.*, **103**:266-276.

10 Talwar, H., Kumari, A., and Rao, S. S., 2010. Strategies to improve drought tolerance in fiab sorghum for predicted. May 2014.

11 Mitra, J., 2001. Genetics and genetic improvement of drought resistance in crop plants. *Current Sci.*,**80**:758-763.

12 Panse, V. G. and Sukhatme, P. V., 1985. Statistical methods for agricultural workers.*ICAR, New Delhi, India*.

13 Ali, M. A., Niaz, S., Abbas, A., Sabir, W. and Jabran, K., 2009b. Genetic diversity and assessment of drought tolerant sorghum landraces based on morpho-physiological traits at different growth stages. *PI. Omics J*., **2**(5):214-227.

14 Amanullah, Khan, A. A., Nawab, K., Khan, A. and Islam, B., 2007. Growth characters and fogger production potential of sorghum varieties under irrigated conditions. *Sarahad J. Agric*., **23**(2):265-268.

15 Ambekar, S. S., Gayakwad, D. S., Khapre, P. R. and Borikar, S. T., 2000. Genetic variability, character association and path coefficient studies in selected germplasm lines of *rabi*sorghum. Paper presented in VIII VasantraoNaik Memorial National Agriculture Seminar on Sorghum under different agro-ecological systems and its industrial utilization, March 1-2, 2000 at College of Agriculture, Nagpur.

16 Arunkumar, B., 2013. Genetic variability, character association and path analysis studies in sorghum (*Sorghum bicolor* L. Moench). *Int. J. Life Sci*., **8**(4): 1485-1488.

17 Arunkumar, B., Biradar, B. D. and Salimath, P. M., 2004. Genetic variability and character association studies in *rabi* sorghum. *Karnataka J. Agric. Sci*., **17**(3):471-475.

18 Chittapur, R. and Biradar, B. D., 2015. Association studies between quantitative and qualitative traits in rabi sorghum. *Indian J. Agric. Res*., **49**(5):468-471.

19 Date, D. M., 2002. Genetic variability and character association studies in selected segregating progenies of *rabi* sorghum (*Sorghum bicolor* L. Moench). M.Sc. (Agri.) Thesis, Marathwada Agric. Univ. Parbhani (India).

20 Dhutmal, R. R., Kalpande, H. V. and More, A. W., 2015a. Genetic variability and heritability studies in *rabi* sorghum drought tolerant genotypes. *Ann. Pl. Soil Res*., **17**(4): 391-394.

21 El-salam, R. M. A., and Hovny, M. R. A., 2018. Variability , heritability , genetic advance and interrelationships for agronomic and yield traits of sorghum B-lines under different environments. **1**(1), 1–13.

22 Gebregergs, G., Mekbib, F., & Moral, M. T., 2020. Estimation of genetic variability, heritability, and genetic advance in advanced lines for grain yield and yield components of sorghum (*Sorghum bicolor* (L.) Moench) at Humera, Western Tigray, Ethiopia. *Cogent Food & Agriculture*, ***6***(1), 1–9.

23 Khandelwal, V., Shulda, M., Jodha, B. S., Nathawat, V. S. and Dashora, S. K., 2015. Genetic parameters and character association in sorghum (*Sorghum bicolor* L. Moench). *Indian J. Sci. Tech*., **9**(22).

24 Kumar, N. H. and Sahib, K. H., 2003. Genetic studies and correlation of biomass related character in forage sorghum under abiotic stress conditions. *J. Res. ANGRAU*, **31**(3):35-39.

25 Kusalkar, D. V., Kachole, U. G., Nirmal, S. V. and Chaudhary, S. B., 2009. Genetic variability analysis in *rabi* sorghum Germplasm. *Int. J. Agric. Sci*., **5**(1):87-89.

26 Sanchez, A., Subudhi, C., Rosenow, D. T. and Nguyen, H. T., 2002. Mapping QTLs associated with drought resistance in sorghum (*Sorghum bicolor* L. Moench). *PI Molecular Biol*, **48**:713-726.

27 Singh, S. K., Gangwar, L. K., & Chaudhary, M. (2019). *Studies on character association and path analysis in forage sorghum*. *7*(5), 2939–2942.

28 Tariq, A. S., Akram, Z., Shabbir, G., Gulffaz, M., Khan, K. S., Iqbal, M. S. and Mahmood, T., 2012. Character association and inheritance studies of different sorghum genotypes for fodder yield and quality under irrigated and rainfed conditions. *African J. Biotechnol*, **11**(38): 9189-9195.

29 Techale, B., Tamene, Y. and Ferede, T., 2014. Response of wild type sorghum (*Sorghum bicolor*L. Moench) accessions to pre-flowering drought stress. *African J. Agric. Res*., **9**(41): 3077-3081.

30 Tesfamichael, A., Githiri, S. M., Kasili, R., Woldeamlak, A. and Nyende, A.B., 2015. Genetic variation among sorghum (*Sorghum bicolor* L. Moench) landraces from Eritrea under post-flowering drought stress condition. *American J. Pl. Sci*, **6**:1410-1424.

31 Veerabadhiran, P. and Kennedy, V. J. F., 2001. Correlation and path analysis studies in selected Germplasm of sorghum. *Madras Agric. J.,***88**(4/6): 309-310.