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Research Article

Genetic Variability Studies on Charcoal Rot Resistance and Fodder Quality Parameters in Minicore Collection of Sorghum (*Sorghum bicolor* (L.) Moench) during *Rabi* Season

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ABSTRACT

Genetic variability, heritability, genetic advance and genetic advance over mean were carried out for charcoal rot component traits, fodder quality traits, yield and their component traits in 236 minicore accessions of sorghum (Sorghum bicolor (L) Moench) during rabi season of 2016-17 at the Main Agricultural Research Station, Dharwad. High PCV and GCV were observed for grain yield per plant (g), plant height (cm), panicle length (cm), number of primaries per panicle, disease parameters, brix percentage, stem thickness (cm), chlorophyll content at flag leaf and maturity stage and fodder yield per plot (kg). All the traits showed a narrow difference between PCV and GCV, indicating that observed variability has been primarily due to genotypic differences with the least influence of environment. High heritability coupled with genetic advance over mean was observed for plant height, disease component traits, panicle length, number of primaries per panicle, panicle weight, 100-seed weight, panicle width, brix percentage, stem girth, chlorophyll content at flag leaf and maturity stage, fodder yield per plot and grain yield per plant, there by indicating that selection would be effective in improvement of these characters as they are controlled by additive genes.

Key words: *Sorghum, fodder, charcoal rot, heritability, genetic advance*

INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] ($2n = 2x = 20$, family Poaceae) is an important grain and fodder crop. It is the fifth most important cereal crop world-wide after wheat, maize, rice and barley. Charcoal rot is caused by the fungus *Macrophomina phaseolina* which is a major disease in the *rabi* sorghum-growing areas causing yield loss ranging from 23% to 64%. It is particularly severe on high-yielding varieties which mature late and quite frequently subjected to moisture stress during the post-flowering period. Incidentally these varieties are also poor in fodder quality. Hence breeding for charcoal rot resistance becomes important in this crop. To achieve any plant breeding objective the existence of genetic variability in the crop is most important.

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Accordingly, the present investigation was aimed to study various parameters of genetic variability for charcoal rot resistance, fodder quality traits, grain yield and their component traits in minicore accessions.

MATERIAL AND METHODS

The experiment was carried out at Botany garden, Department of Genetics and Plant Breeding, Main Agricultural Research Station, University of Agricultural Sciences, Dharwad during *rabi* 2016-17. It involves 236 sorghum minicore accessions and four checks. **E**xperiment was laid out in Randomized Complete Block Design (RCBD) and sowing was done during second week of October (*rabi* season of 2016-17). The trial was laid out with a spacing of 45 X 15 cm and other recommended packages of practices were followed to raise a good crop. To create epiphytotic conditions for charcoal rot incidence, tooth pick method[5] was employed. *Macrophomina phaseolina* was cultured on tooth picks using honey peptone medium as described by Rao *et al.*[16]. In tooth pick method, individual plants were inoculated with *Macrophomina phaseolina* after 15 days of flowering of genotype.

The observations were recorded on disease parameters *viz.*, spreading of fungus, number of internodes crossed by fungus, per cent lodging, per cent incidence disease, days to 50 per cent flowering, days to maturity, plant height, panicle length, panicle width, 100-seed weight, number of primaries per panicle, panicle weight, chlorophyll content at flag leaf stage, chlorophyll content at maturity stage, stem girth, brix per cent at maturity, number of leaves per plant, fodder yield per plot and grain yield per plant were recorded on five randomly selected plants leaving border plants of each row.

Statistical analysis

Analysis of variance was carried out following the standard procedures. The various genetic parameters *viz.*, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (Broad sense), expected genetic advance and genetic advance as per cent of mean (GAM) were calculated as suggested by Burton[4], Hanson *et.al.*[9]and Johnson *et.al*[11]respectively.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating the existence of considerable magnitude of genetic variability (Table 1). The estimate of genetic variability parameters indicated wide range of variations for all the characters studied (Table 2). Relative magnitude of PCV was greater than corresponding GCV for all characters studied, which indicated the effects of environmental factors in expression of morphological characters. All the traits showed a narrow difference between PCV and GCV, indicating that observed variability has been primarily due to genotypic differences with the least influence of environment.

High values of GCV and PCV were found for the traits such as length of spread by *Macrophomina phaseolina,* per cent lodging, per cent disease incidence, number of internodes crossed by fungus, plant height, panicle length, panicle width, 100-seed weight, panicle weight, number of primaries per panicle, stem girth, chlorophyll content at maturity, brix percentage, fodder yield per plot and grain yield per plant which indicated variation for these characters and their contribution towards total genetic variability. The disease parameters of charcoal rot resistance like length of infection and per cent lodging, which have not been studied widely so far, were found to be similar to the report of Patil[14]. As there is greater correspondence between phenotypic and genotypic variability, the selection based on phenotypic differences alone is expected to be effective in improvement of these traits.

However, moderate values of PCV and GCV observed for traits such as, chlorophyll content at flag leaf stage and number of leaves per plant and indicated that these characters are amenable for improvement. In case of numbers of leaves per plant, the results in the present investigation were in agreement with studies of Kukadia *et al.*[12]. A wide range of variation was observed for brix per cent. A similar results noticed by

Jadhav *et al.*[10]. Low estimates of PCV and GCV were recorded for days to 50 per cent flowering and days to maturity in minicore accessions indicating low variability for these traits. Similar observations were noticed by Bheemashankar[1] and Sunil and Sajjanar[18].

Among minicore accessions, high values of PCV and GCV were obtained for grain yield per plant and fodder yield per plot which indicates presence of high degree of variability and low environmental influences on the expression of these characters and hence, these characters can be relied upon simple selection. Similar results were reported by Mukuru[13]and Biradar *et al.*[3]. However, the coefficient of variation indicated only the extent of variability existed for different characters and did not indicate heritable portion of a character.

The heritability estimates indicate the effectiveness of the character in phenotypic selection. Heritability and genetic advance as percent of mean together were more useful for predicting the resultant effect of selected genotypes than heritability alone. In the present study, high heritability coupled with high genetic advance over mean was observed for the traits *viz.*, plant height, length of spread of infection by fungus, number of internodes crossed by fungus, per cent lodging, per cent disease incidence, panicle length, number of primaries per panicle, panicle weight, 100 seed weight, panicle width, chlorophyll content at maturity, stem girth, brix per cent, number of leaves per plant, fodder yield per plant and grain yield per plant. This reveals that these characters would respond to the selection as these are more likely to be controlled by additive gene effects. Similar results for the traits, plant height, 100 seed weight and grain yield per plant were observed earlier by Biradar *et al.*[2].

Girish *et al.*[6] reported high heritability along with high genetic advance over mean for length of spread of fungus, per cent lodging, number of internodes crossed by fungus and seed yield. Moderate heritability was observed for the traits *viz.*, stem girth, days to maturity and fodder yield per plot. These observations are in agreement with earlier studies reported by Halalli *et al.*[8].

High heritability coupled with moderate genetic advance for days to 50 per cent flowering and chlorophyll content at flag leaf stage indicate that these traits are more likely controlled by both additive and non-additive gene actions. These results are in line with earlier results of Sunil and Sajjanar[18]. The high heritability coupled with low genetic advance for days to maturity indicate that this trait was more likely controlled by non-additive gene action and high genotype and environment (G×E) interactions. Warkad *et al.*[17] reported similar trend for this trait.

Table 1: Mean sum of squares of sorghum minicore accessions for charcoal rot, fodder quality, grain yield and their component traits

Components	Replications	Genotypes	Error	S. Em. ±	C. D. at 5 %	C. D. at 1 %	C. V. (%)
Degrees of freedom	1	236	236	-	-	-	-
Lodging percentage	63.87	1810.3*	20.94	3.220	9.010	11.80	16.22
Spread of fungus (cm)	4.480	1992.8*	3.910	1.390	3.890	5.130	5.290
Number of internodes crossed	1.400	4.72*	0.160	0.280	0.790	1.040	17.67
Percent incidence	274.9	1698.3*	120.5	7.740	21.63	28.50	16.66
Days to 50 % flowering	222.8	122.13*	28.07	3.730	10.43	13.75	7.340
Days to maturity	236.3	207.84*	68.56	5.840	16.31	21.50	6.200
Plant height (cm)	393.2	3199.86*	216.15	10.37	28.96	38.17	7.640
Panicle length (cm)	10.06	77.75*	9.740	2.200	6.140	8.100	14.62
100 seed weight (g)	0.550	1.180*	0.140	0.270	0.760	1.000	11.78
Number of primaries per panicle	35.65	314.06*	13.48	2.590	7.230	9.530	8.290
Panicle width (cm)	1.850	7.070*	0.560	0.530	1.480	1.950	10.64
Panicle weight (g)	25.00	989.9*	13.94	2.630	7.350	9.690	7.620
Chlorophyll content at flag leaf stage	41.97	86.10*	16.48	2.860	7.990	10.54	7.670
Chlorophyll content at maturity stage	38.37	317.39*	13.10	2.550	7.130	9.390	13.80
Stem girth (cm)	0.090	0.190*	0.030	0.120	0.350	0.460	13.49
Brix % at maturity	3.360	63.03*	1.500	0.860	2.410	3.180	12.59
Number of leaves per plant	1.020	4.450*	0.750	0.610	1.710	2.260	11.54
Fodder yield per plot (kg)	0.008	0.170*	0.003	0.040	0.110	0.140	13.65
Grain yield per plant (g)	21.45	671.8*	32.16	4.000	11.17	14.72	14.79

Table 2: Estimates of genetic variability parameters in sorghum minicore accessions for charcoal rot, fodder quality, yield and their component traits.

Traits	Range		Grand Mean	PCV (%)	GCV (%)	Heritability (%)	Genetic advance	GA as % of mean
	Minimum	Maximum						
Spread of fungus (cm)	0.000	138.0	37.39	84.50	84.33	99.61	65.10	173.4
Number of internodes crossed	0.000	7.040	2.26	68.90	66.59	93.42	3.020	132.6
Per cent lodging	0.000	100.0	28.35	106.7	105.50	97.71	61.22	214.8
Per cent incidence	0.000	100.0	63.74	47.30	44.06	86.74	53.70	84.53
Days to 50 % flowering	54.50	98.00	72.10	12.01	9.51	62.62	11.16	15.50
Days to maturity	110.0	158.0	133.5	8.80	6.25	50.39	11.51	9.14
Plant height (cm)	87.60	328.1	192.3	21.49	20.09	87.34	74.29	38.67
Panicle length (cm)	6.400	51.00	21.33	31.00	27.33	77.74	10.63	49.64
100 seed weight (g)	1.450	5.71	3.27	24.89	21.92	77.59	1.29	39.78
Number of primaries per panicle	19.00	87.75	44.27	28.90	27.69	91.76	23.99	54.64
Panicle width (cm)	2.320	14.00	7.07	27.63	25.50	85.17	3.004	48.48
Panicle weight (g)	10.10	154.8	48.97	45.74	45.10	97.22	44.93	91.61
Chlorophyll content at flag leaf stage	35.01	61.19	50.82	13.53	11.14	67.86	10.04	18.91
Chlorophyll content at maturity stage	5.880	57.90	26.21	49.03	47.05	92.07	24.48	93.00
Stem girth (cm)	0.500	2.430	1.32	25.41	21.54	71.82	0.407	37.60
Brix per cent at maturity	0.200	28.00	9.73	58.37	56.99	95.34	11.22	114.6
Number of leaves per plant	3.830	13.00	7.54	21.38	18.00	70.78	2.363	31.22
Fodder yield per plot (kg)	0.100	1.530	0.42	69.88	68.53	96.18	0.564	138.5
Grain yield per plant (g)	8.400	132.4	38.34	48.99	46.71	90.89	35.07	91.73

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