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Genetic variability, heritability and genetic gain for quantitative traits in South African sorghum genotypes

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Abstract

Sorghum is one of the most important cereal crops grown in the world for human consumption, animal feed and bio-energy. The objective of the study was to estimate the genetic variability, heritability and genetic gain of some agro-physiological traits of 98 sorghum accessions in South Africa. The studies were conducted at Makhathini in KwaZulu-Natal and Burgershall in Mpumalanga provinces. The experiments were laid out in an alpha lattice design replicated twice. The plant height, panicle length, panicle width and panicle exsertion, rachis number, panicle weight, thousand seed weight, and grain yield per panicle were recorded. The data were subjected to analysis of variance using generalised linear model and means were separated using Duncan Multiple Range Test. Coefficients of variation were also determined. There were significant differences among the traits measured. Plant height was significant and positively associated with panicle length (r =0.139), panicle width (r = 0.127) and panicle weight (r = 0.1457). Panicle exsertion was highly significant and negatively correlated with all other traits except with plant height. The Principal Component analysis revealed three most important PCs contributing a total variation of 92.36%. The PC1, PC2, and PC3 contributed 42.53, 34.65 and 15.18%, respectively. Low, medium and high estimates of broad sense heritability were found in different plant characters under study. Highest heritability estimates were found in plant height, thousand seed weight, panicle length and rachis number. Values of genetic advance ranged between 0.39 to 17655.04 and the genetic gain (of the mean percent) ranged from 3.27 to 372.52. Greater magnitude of broad sense heritability coupled with higher genetic advance in traits studied provided the evidence that these were under the control of additive genetic effects indicating that selection in the germplasm should lead to a fast improvement of the traits.

Keywords: genetic variability, genetic gain, grain yield, heritability, sorghum.

Abbreviations: PH_Plant height (cm), PE_Panicle exsertion (cm), PL_Panicle length (cm), PW_Panicle width (cm) PT_Panicle weight (g), RN_Rachis number, SW_Grain yield /panicle (g), TSW_Thousand seed weight (g), Var_Variety.

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is one of the most important grain crops grown worldwide, with Nigeria, Sudan, Ethiopia, Burkina Faso and Niger leading in terms of production in Africa. In South Africa, the Free State and Mpumalanga provinces are the largest producers. Sorghum is also produced in other provinces such as Limpopo, North West, Gauteng, KwaZulu-Natal, and Northern Cape. In total, South Africa produced 27475 metric tonnes in an area of 54930 hectares in 2014 (FAO, 2016) with the Free State Province being the highest producer. This crop thrives well in tropics and sub-tropics where other crops such as maize and wheat fail. It remains the subsistence crop for small-scale farmers.

Apart from its contribution to food security, sorghum is broadly adapted and can be grown in a wide range of environments. One of its strongest traits is its great adaptability to tropical and subtropical areas of the world where water availability and soil conditions are marginal for other grain crops such as maize (ICRISAT, 2009). It can be produced in a wide variety of soil types, but yields are typically highest in deep, well drained soils with good fertility. It also appears to have a high capacity for osmotic adjustment to stress to maintain turgor pressure in cells (Nguyen et al., 1997), while some sorghum varieties possess “stay-green” trait that enable them to continue to photosynthesize post-flowering, during drought (Jordan et al., 2012). Because of these abilities to survive in harsh conditions it is a vital crop for household food security for many rural communities in marginal agro-ecologies, such as in the dry regions of South Africa, Botswana and Namibia.

Cultivar development is, however, firstly based on the exploitation of genetic variability of the genotypes with the traits of interest (Makanda et al., 2009). Quantitative traits are highly influenced by environmental conditions, and progress of improvement through breeding in such characters is primarily conditioned by the magnitude and nature of variation and interrelationship among them. Progress in any crop improvement venture depends mainly on the magnitude of genetic variability and heritability present in the source material. The observed variability is a combined estimate of genetic and environmental causes, of which only the former is heritable. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance and the change in mean value between generations (Shukla et al., 2006). Genetic advance explains the degree of gain obtained in a character under a particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection. It also indicates the presence of additive genes in the trait and further suggest reliable crop improvement through selection of such traits.

Knowledge of patterns of diversity of genetic material is of great importance and is key component in crop improvement and breeding (Warburton et al., 2008). The extent of variability is measured by genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) which provides information about relative amount of variation in different characters. Continuous improvement of sorghum is imperative for the increased competition for the crop. This can be achieved through effective selection of suitable parent materials of significant genetic variability. A success in crop breeding is depend on the isolation of genetically superior genotypes based on the amount of variability present in the material. Therefore, information on genetic variability existing in a group of populations of sorghum are essential. The progress of selection is more important in any crop improvement and this progress is depended on the existence of genetic variability for yield and yield contributing characters and their heritability (Allard, 2000). Heritability in conjunction with genetic advance has a greater role to play in determining the effectiveness of selection of a character. Hence, an attempt was made to estimate genetic variability, heritability and genetic advance in the available germplasm of sorghum. The objective of the study was to show the variability, heritability and genetic gain of some agro-morphological traits in sorghum accessions collected from various provinces of South Africa.

Results and Discussion

Analysis of variance of the agro-morphological traits

The data of the eight quantitative traits was analysed using linear mixed models. Highly significant ($P \leq 0.001$) differences were observed for all traits measured in both locations except for panicle length at Burgershall which was significant at $P \leq 0.05$ (Table 2). The R^2 ranged from 0.4 for PAL to 0.9 for PEX at Burgershall and to 0.9 GYP at Makhathini. The traits included early flowering, short plant height, medium panicle exsertion and medium sized seeds. Shegro et al. (2013) further reported highly significant differences among the quantitative traits in sorghum accessions under study and the qualitative diversity index values ranged from 31% for panicle shape and compactness to 84% of the glume color. Lekgari and Dweikat (2014) reported genetic diversity based on plant height, days to anthesis and moisture content in sweet sorghum.

Table 3 summarises the mean squares of sites, genotypes and genotype by site interaction from a combined analysis of variance. The two sites showed significant differences ($P \leq 0.001$) in all of the quantitative traits measured. Highly significant differences ($P \leq 0.001$) were also observed among the genotypes for panicle length, rachis number, thousand seed weight and grain yield per panicle. Furthermore, genotype effects were significantly different ($P \leq 0.05$) for panicle weight. Grain yield, plant height, panicle width, and panicle exsertion were non-significant. On the other hand, highly significant differences were observed for the genotype by site interaction on panicle length, rachis number, and thousand seed weight. The significant differences in genotype by environment could be attributed to the different reaction of the genotypes to sites or due to differences between the sites.

Means, heritability, genetic gain and advance of the agro-morphological traits

Heritability is the percentage of phenotypic variance that is attributed to genetic variance. In the present study heritability, was high for the traits plant height (90.1%), thousand seed weight (80.9%), intermediate for panicle length (62.7%), rachis number (64.2%), and low for the other traits (Table 4). High heritability indicates that the environmental influence is minimal on characters. Any of the characters can, therefore, be used for selection. The comparatively lower heritability for grain yield of sorghum, in this study, may be due to the fact that yield is a low heritable character which is controlled by many genes (Maarten et al., 2003). The heritability estimates for different characters depend upon the genetic makeup of the breeding materials under investigation. Therefore, knowledge about these values in genotypes in which breeders are interested is of great significance. High heritability estimates indicate that the selection for these characters will be effective, being less influenced by environmental effects (Maniee et al., 2009). Heritability estimates have been found to be useful in indicating the relative value of selection based on phenotypic expression of different characters.

Character means ranged from 9.63 to 71.27 with mean squares ranging between 17.7 and 31.0 and the environmental mean squares ranged from 12.8 to 2786 (Table 3). The phenotypic variance ranged between 5.9 for panicle width to 1033.3 for plant height. The genotypic variance raged between 1.6 (panicle width) to 199.7 (grain yield per panicle). The environmental variance was between 4.3 (panicle width) and 928.6 (plant height). The PCV ranged between 23.4 and70.0, while the GCV values ranged between 14.4 and 34.7. The genetic advance ranged between 2.55 and 17655.04. The high PCV and GCV were observed for panicle weight. Among these characters the difference between PCV and GCV was the maximum for grain yield and grain yield per panicle. The PCV and GCV values, however, had small differences. These results are in conformity with the results of Geleta et al. (2005) for grain yield per plant, and Kishore and Singh (2005) for fodder yield per plant. Also, Narkhede et al. (2000) reported similar results for panicle length and breadth.

The genetic gain with the percent mean ranged from 3.27 to 372.52 (Table 4). The most important function of heritability

Table 1. List of names of the sorghum accessions used in the study.

Serial number	Accession name	Place of collection/ Origin	Serial number	Accession name	Place of collection/ origin
1	5405	North-West	54	5281	KwaZulu-Natal
2	5333	North-West	55	4547	KwaZulu-Natal
3	5464	North-West	56	5097	KwaZulu-Natal
4	5436	North-West	57	5245	KwaZulu-Natal
5	5454	North-West	58	4952	Free State
6	5430	North-West	59	4909	Free State
7	5393	North-West	60	4905	Free State
8	5337	North-West	61	4891	Free State
9	2167	Eastern Cape	62	Motlerane	ARC
10	3416	Eastern Cape	63	Mammopane	ARC
11	3414	Eastern Cape	64	Macia-SA	ARC
12	3262	Eastern Cape	65	M153	ARC
13	3319	Eastern Cape	66	05 Potch-151	ARC
14	2922	Eastern Cape	67	Maseka-a-swere	ARC
15	3364	Eastern Cape	68	Mammolokwane	ARC
16	3403	Eastern Cape	69	05- Potch-138	ARC
17	2975	Eastern Cape	70	M48	ARC
18	3184	Eastern Cape	71	05 Potch-115	ARC
19	2934	Eastern Cape	72	05 Potch-167	ARC
20	2985	Eastern Cape	73	Manthate	ARC
21	3217	Eastern Cape	74	AS 82	ACCI
22	4276	Mpumalanga	75	AS13	ACCI
23	5476	Mpumalanga	76	AS 1	ACCI
24	4265	Mpumalanga	78	AS 4	ACCI
25	4052	Mpumalanga	79	AS 18	ACCI
26	2055	Mpumalanga	80	AS 19	ACCI
27	5518	Mpumalanga	81	AS 17	ACCI
28	4259	Mpumalanga	82	AS 16	ACCI
29	5502	Mpumalanga	83	AS 11	ACCI
30	5541	Mpumalanga	84	AS 6	ACCI
31	1990	Mpumalanga	85	AS 1 M_2 Ctrl	ACCI
32	4277	Mpumalanga	86	AS 16 M2 Ctrl	ACCI
33	2048	Mpumalanga	87	AS 21	ACCI
34	4161	Mpumalanga	88	AS 8	ACCI
35	1450	Limpopo	89	4942	Free state
36	4312	Limpopo	90	4403	Limpopo
37	1948	Limpopo	91	3281	Eastern Cape
38	1390	Limpopo	92	3439	Eastern Cape
39	5258	KwaZulu-Natal	93	3281	Eastern Cape
40	AS66	ACCI	94	5542	Mpumalanga
41	1413	Limpopo	95	1417	Limpopo
42	1394	Limpopo	96	AS1ems	ACCI
43	1481	Limpopo	97	4442	Limpopo
44	4303	Limpopo	98	4052	Mpumalanga
45	5088	KwaZulu-Natal			
46	5287	KwaZulu-Natal			
47	5233	KwaZulu-Natal			
48	5237	KwaZulu-Natal			
49	4722	KwaZulu-Natal			
50	5246	KwaZulu-Natal			
51	4606	KwaZulu-Natal			
52	4531	KwaZulu-Natal			
53	5274	KwaZulu-Natal			

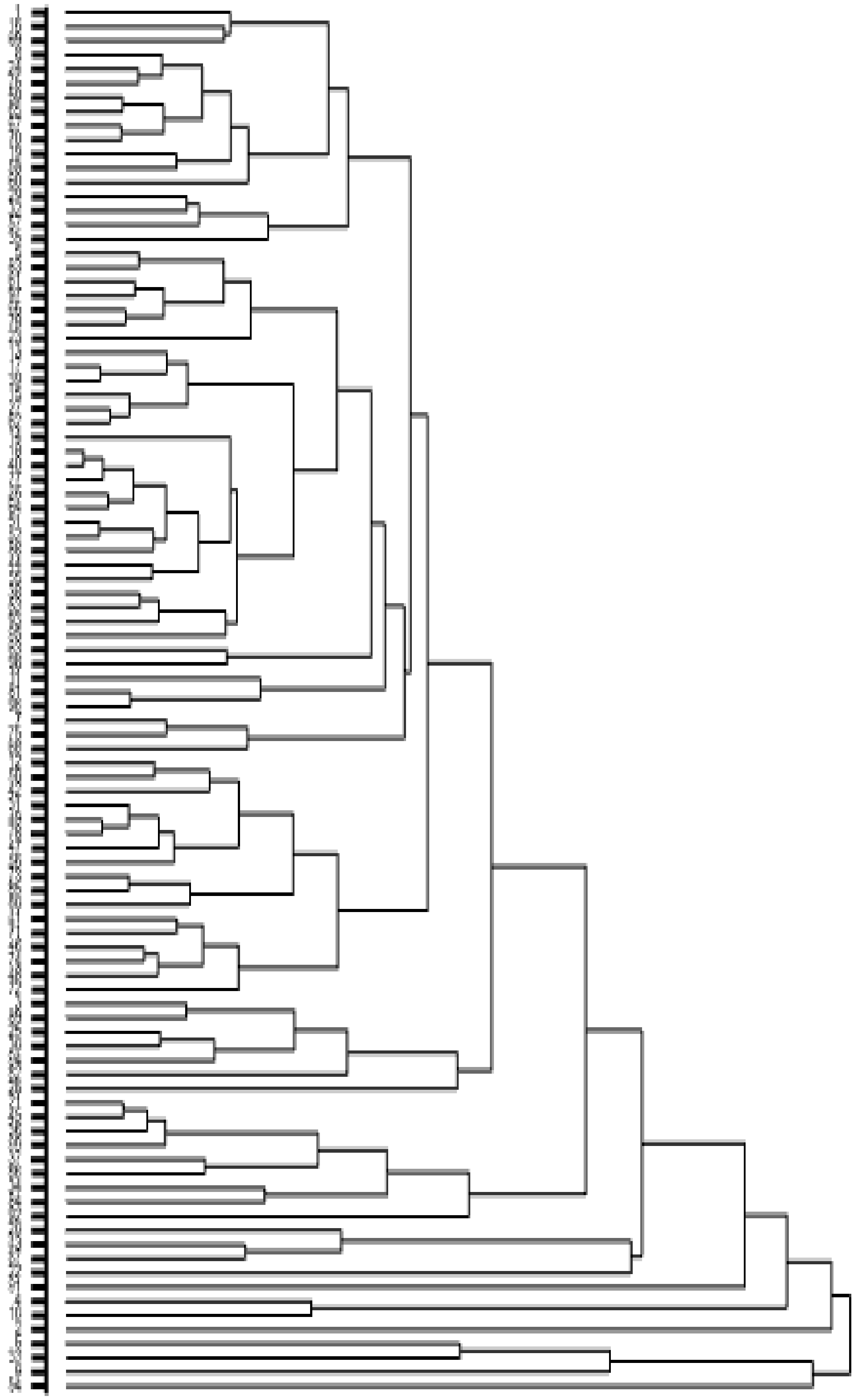

Fig 1. Dendrogram revealing genetic relatedness among 98 sorghum accessions.

Table 2. Mean values of eight quantitative traits in 98 sorghum accessions evaluated at Makhathini and Burgershall, South Africa

Var	Makhathini								Burgershall							
	PH	PL	PW	PE	RN	PT	SW	TW	PH	PL	PW	PE	RN	PT	SW	TW
1	126.7	11.67	7.00	12.00	22.33	24.01	65.70	23.67	126.97	16.00	15.63	31.67	37.00	44.10	149.30	26.33
2	183.00	13.00	15.00	19.33	34.00	37.81	114.70	27.67	111.48	17.07	5.60	21.67	58.00	46.17	78.20	28.00
3	127.00	17.83	15.00	33.00	25.5	55.01	72.50	38.00	83.23	21.67	4.93	33.33	38.33	65.10	61.30	38.00
4	156.00	22.67	15.67	15.00	25.33	23.01	1.50	28.10	98.89	15.8	6.20	10.67	57.33	47.83	190.70	28.00
5	117.00	17.33	17.00	68.33	33.00	42.67	64.00	35.00	148.11	15.00	3.73	25.00	26.00	15.00	66.70	34.67
6	110.4	15.67	16.00	10.33	30.00	129.67	78.30	34.02	72.17	19.00	3.90	27.00	38.00	13.90	75.00	33.00
7	133.7	14.67	14.93	34.4	23.33	135.67	112.70	36.34	78.78	13.07	2.96	35.00	36.00	7.63	44.90	41.33
8	184.7	17.00	15.67	35.75	18.00	95.01	114.00	35.00	94.61	17.00	3.40	32.67	35.5	22.25	70.00	38.00
9	167.7	15.00	13.67	16.67	26.67	77.67	83.30	31.00	102.8	14.8	3.88	24.17	41.17	36.33	141.60	31.33
10	181.7	18.33	16.00	31.33	34.00	10.27	84.70	28.00	68.01	17.87	4.53	27.33	67.33	40.67	116.50	28.00
11	120.00	14.00	13.33	31.67	27.00	60.01	128.70	37.67	132.93	17.00	5.05	27.67	35.33	30.30	121.70	38.00
12	155.7	10.00	14.00	12.00	23.33	83.34	93.00	27.67	133.59	14.53	3.93	33.33	24.67	27.00	127.30	28.00
13	227.00	19.33	15.33	11.33	30.33	63.67	152.00	28.34	79.29	17.2	5.33	33.00	35.00	11.17	79.30	28.00
14	182.00	15.33	16.00	15.67	21.00	31.34	41.70	34.69	99.55	16.65	3.40	36.00	32.33	30.51	136.50	35.00
15	140.00	18.33	17.33	12.33	19.67	77.34	143.30	31.00	85.76	18.73	3.13	36.67	24.67	18.67	43.00	31.33
16	111.3	12.67	16.33	30.00	30.00	67.01	36.30	28.00	87.07	13.99	4.23	36.00	58.33	37.83	74.60	28.00
17	154.00	18.67	15.67	25.67	24.33	24.34	69.50	35.89	87.41	15.36	3.67	29.67	33.5	50.17	80.80	36.33
18	131.00	18.00	17.00	35.33	33.00	50.26	23.50	32.69	81.1	10.84	3.00	33.00	30.00	59.07	75.30	33.00
19	146.3	15.33	15.33	33.67	20.00	23.01	72.30	37..23	81.1	18.00	3.60	28.67	37.5	84.67	102.80	38.00
20	30.00	14.67	16.33	36.33	28.00	33.34	26.30	42.98	84.77	16.57	5.10	40.00	47.00	43.00	132.70	43.00
21	148.6	16.33	15.67	31.33	14.67	44.01	173.50	27.67	100.22	19.33	6.40	25.00	54.00	23.17	135.10	28.00
22	24.7	15.00	17.67	16.67	22.33	20.67	62.00	27.54	122.45	15.78	12.70	35.67	24.67	27.17	30.30	28.00
23	84.7	17.33	13.00	28.67	14.00	92.51	31.50	31.00	105.98	45.6	3.82	34.67	30.33	13.43	119.70	31.33
24	155.1	14.67	17.00	16.33	26.67	77.01	141.30	34.34	95.06	19.4	5.13	24.33	24.67	15.67	78.80	34.67
25	158.3	12.67	15.67	10.67	14.00	17.01	127.00	32.00	81.63	19.8	5.80	34.33	41.33	43.50	162.70	31.33
26	123.3	11.67	15.00	13.00	12.67	15.17	122.00	31.34	77.75	15.33	5.60	33.67	42.33	58.83	217.30	31.33
27	134.3	23.33	16.33	15.33	34.00	39.67	120.30	32.34	125.26	16.46	3.40	30.00	27.5	10.27	39.20	32.00
28	164.5	16.67	15.33	9.33	14.67	45.34	122.70	34.00	101.49	17.13	3.93	31.33	21.33	32.50	53.30	34.67
29	118.3	13.67	13.33	17.33	30.00	79.34	153.00	31.67	104.77	12.2	3.33	20.00	35.00	24.83	85.30	31.33
30	163.3	13.67	15.00	15.33	26.00	14.01	141.00	37.50	83.79	15.6	5.33	23.67	43.67	23.25	102.80	38.00
31	181.7	15.33	15.67	15.67	26.00	80.67	154.00	34.34	80.69	14.4	4.33	24.33	37.00	15.50	57.20	38.67
32	173.00	15.00	15.00	13.33	24.5	15.01	162.50	32.50	72.77	13.6	4.60	34.00	35.5	38.25	86.00	33.00
33	147.7	12.00	14.00	32.67	28.5	87.34	76.00	34.00	91.94	16.23	4.94	30.35	37.62	30.16	102.80	34.13
34	126.7	14.67	15.33	12.33	43.00	20.67	47.00	39.67	99.00	23.77	6.37	22.00	45.33	32.97	177.30	41.1
35	46.00	16.67	16.67	8.33	33.17	123.14	128.00	42.90	104.75	13.13	4.10	37.00	34.00	11.25	156.00	43.00
36	178.00	21.00	14.33	34.33	44.00	14.67	161.70	44.34	100.51	16.82	15.35	25.00	42.33	5.67	87.80	44.67
37	53.00	11.00	15.00	31.67	27.00	59.67	155.00	27.67	96.19	24.00	6.40	27.00	74.00	34.00	78.90	28.00
38	105.6	13.33	15.33	12.33	34.67	49.67	127.00	31.34	94.32	14.00	4.67	25.00	27.00	66.50	108.00	31.33
39	192.00	23.33	15.67	33.33	35.00	35.34	41.70	38.34	74.38	16.42	4.56	35.67	22.33	25.83	87.00	39.67
40	111.2	14.67	16.33	19.33	37.33	13.34	136.80	31.00	86.38	14.73	3.33	33.67	31.00	43.50	46.80	31.33
41	140.3	26.00	13.67	32.33	31.67	42.67	180.30	26.67	79.5	18.13	5.60	25.00	50.00	37.00	83.30	28.00
42	115.7	16.00	15.00	35.33	19.67	93.67	78.00	34.67	107.76	15.6	4.33	27.67	49.00	17.67	94.00	34.67
43	48.00	12.33	16.00	10.67	24.33	77.67	167.70	40.00	112.71	11.47	3.09	40.33	25.00	14.83	74.60	40.33
44	70.00	17.67	16.33	30.33	32.67	23.34	32.70	31.34	130.41	15.73	4.13	20.00	41.00	17.00	183.90	31.33
45	111.7	22.33	15.00	32.67	37.67	90.01	92.00	40.34	118.61	14.53	4.93	34.33	43.67	32.50	167.00	41.33
46	66.00	16.67	16.33	6.00	40.33	47.67	147.70	34.34	127.35	21.67	4.87	35.67	41.33	44.83	49.10	34.67
47	210.5	14.67	14.00	8.67	32.33	25.34	149.30	32.34	79.04	17.93	6.53	34.33	33.00	34.67	119.30	31.33
48	132.00	12.67	15.33	32.00	38.33	40.34	41.70	29.00	118.39	15.07	6.67	39.33	40.5	15.33	130.00	28.00
49	146.1	27.67	12.5	34.00	29.67	32.01	55.00	31.67	98.54	16.06	5.66	34.00	36.33	14.17	157.30	31.33
50	251.7	14.67	15.00	22.00	26.00	82.34	166.70	28.34	83.11	16.2	5.07	31.33	52.5	27.50	73.30	28.00
51	229.3	16.67	17.33	34.33	32.00	66.67	66.70	28.00	90.15	13.73	3.53	23.00	22.33	27.17	98.20	28.00
52	151.7	15.33	14.00	15.33	25.67	52.01	40.70	31.34	99.77	14.95	4.37	23.67	33.33	44.33	100.30	31.33
53	107.7	16.00	15.33	21.33	17.00	27.67	48.30	31.00	76.09	17.6	4.67	39.00	25.00	18.10	121.00	31.33

54	144.3	12.67	16.33	14.33	31.33	59.67	117.00	37.34	110.93	16.2	4.33	20.00	41.67	25.17	162.80	38.00
55	207.2	13.67	17.00	32.00	31.67	23.34	42.50	38.31	86.64	16.8	6.20	36.00	35.67	13.20	79.30	38.00
56	138.3	16.00	15.33	35.00	32.67	50.67	148.80	38.46	117.01	14.27	4.00	27.00	47.67	27.83	147.30	38.00
57	151.00	12.33	16.33	11.33	43.33	91.34	180.00	34.34	115.95	14.8	3.73	35.67	37.00	35.47	61.70	34.67
58	155.4	22.00	16.67	18.67	21.67	78.67	154.70	41.34	96.57	17.13	3.63	35.67	24.67	39.53	73.30	41.33
59	142.00	14.67	15.00	26.67	22.33	66.67	32.70	31.34	114.43	16.55	3.38	36.00	39.00	22.80	99.50	31.33
60	89.3	18.33	14.67	24.33	26.83	75.01	130.20	34.67	115.73	17.26	3.32	32.67	30.33	24.67	73.20	34.67
61	63.00	14.00	17.67	14.33	22.33	45.01	35.70	34.67	106.92	15.93	4.73	34.00	41.33	37.17	92.00	34.67
62	72.3	17.67	17.33	13.67	23.33	79.34	89.30	28.00	67.89	17.8	5.13	2.69	23.00	8.67	68.70	28.15
63	160.00	15.67	15.00	13.67	39.33	46.34	42.30	21.34	100.01	13.41	3.83	26.33	45.33	13.00	51.00	31.33
64	159.3	15.00	14.33	30.00	21.67	44.67	130.30	10.34	74.42	15.27	4.20	25.67	36.33	29.50	90.00	10.33
65	136.7	18.00	15.67	33.00	23.00	54.34	149.30	38.34	86.78	15.2	3.47	39.00	31.33	25.00	71.70	38.00
66	37.00	21.33	14.67	35.33	14.67	57.67	180.40	38.34	80.5	12.01	3.10	36.67	35.00	12.00	71.40	38.00
67	204.3	20.00	14.67	32.67	27.33	29.34	68.70	28.34	115.53	11.68	3.00	30.00	38.67	45.50	143.70	28.00
68	141.3	7.72	14.00	16.67	55.00	126.01	136.00	34.67	80.13	11.72	2.83	30.00	21.67	33.83	79.70	34.67
69	130.5	14.00	4.00	8.67	15.67	119.01	85.70	36.34	83.47	15.67	3.68	30.00	36.17	67.25	137.00	36.33
70	177.9	17.00	15.67	19.33	28.67	64.67	84.40	28.07	103.91	13.97	4.11	30.00	26.67	58.33	138.90	28.00
71	72.00	15.33	13.67	14.33	30.33	28.34	163.70	41.00	117.88	24.00	5.60	30.33	42.5	27.33	109.30	41.33
72	80.00	23.67	15.67	22.33	30.67	23.34	111.00	31.00	73.45	15.76	13.45	36.67	53.33	27.75	176.30	31.33
73	87.8	13.00	15.67	35.33	41.00	37.51	121.00	28.00	128.66	14.09	4.25	32.67	37.62	14.00	71.10	28.00
74	110.5	14.67	15.67	13.67	23.67	39.01	12.30	18.87	160.9	19.9	5.23	35.00	57.33	14.42	168.00	18.90
75	115.00	15.67	14.00	13.67	25.33	28.67	117.70	34.67	83.67	13.44	3.38	30.67	34.67	25.33	89.80	34.67
76	175.00	14.67	13.67	14.33	29.67	84.51	159.00	31.37	78.93	15.73	4.20	33.00	31.00	30.33	83.70	31.33
77	79.7	14.67	15.33	17.00	22.67	77.51	50.70	33.34	121.6	15.15	3.88	27.67	35.33	6.17	129.70	33.26
78	115.6	15.00	14.33	11.00	33.67	78.67	138.70	33.00	79.07	13.39	4.54	36.00	34.17	28.83	90.20	33.15
79	35.3	10.00	14.67	27.00	15.67	99.01	50.30	37.67	80.75	14.1	4.00	33.00	30.00	58.43	132.00	38.00
80	36.7	9.33	16.33	33.33	33.00	57.01	74.70	41.34	128.39	16.12	5.57	34.67	56.00	35.25	93.50	41.33
81	43.7	8.00	8.33	23.33	30.67	11.51	113.80	38.00	95.86	12.67	4.40	25.33	37.00	45.50	176.00	38.00
82	247.00	21.00	16.67	26.00	38.33	66.67	131.00	33.07	96.19	17.53	3.87	35.00	26.00	30.17	85.70	33.26
83	52.2	11.00	15.33	35.33	34.00	16.34	59.20	32.54	108.79	16.37	5.53	33.00	36.33	17.75	78.70	32.5
84	166.00	16.33	14.67	14.67	38.67	12.01	102.30	34.00	131.4	20.5	6.83	31.67	37.62	20.00	102.80	34.13
85	34.7	16.67	3.33	31.33	31.00	59.01	73.00	33.67	91.43	14.07	13.93	30.00	50.00	36.83	174.70	33.00
86	181.3	15.67	16.00	17.00	33.00	34.67	39.00	31.34	110.03	15.03	3.57	24.67	53.67	11.50	154.30	31.33
87	18.3	6.67	16.33	18.00	28.00	20.17	74.70	37.00	90.21	11.88	3.93	20.00	42.67	56.00	120.00	37.59
88	259.3	12.33	10.67	23.67	33.00	14.01	135.30	31.67	98.13	15.2	4.87	38.67	24.67	14.50	60.00	31.33
89	137.00	16.00	15.67	15.67	33.33	41.84	55.00	44.67	118.3	17.93	4.50	35.33	33.33	33.83	151.00	44.67
90	249.7	23.33	17.00	25.00	25.00	10.67	135.00	38.34	99.18	18.87	5.10	39.00	47.67	63.33	78.30	38.00
91	92.4	15.03	16.67	32.67	27.93	6.27	38.50	43.23	89.62	14.27	4.23	32.33	35.33	22.67	90.00	43.26
92	236.3	13.00	13.67	16.67	36.33	16.01	23.00	34.34	110.4	15.93	4.43	20.00	35.67	20.67	72.70	34.67
93	58.7	16.67	14.67	8.00	16.00	53.67	156.30	48.00	113.97	18.12	5.00	33.00	31.33	16.50	83.30	48.00
94	170.7	16.67	13.67	15.67	14.67	30.34	165.70	34.31	131.17	10.73	4.47	23.67	35.33	59.17	99.70	34.67
95	44.7	7.00	15.67	17.00	11.00	63.34	123.00	28.34	110.23	17.47	4.87	20.00	32.33	16.60	90.00	28.15
96	53.7	12.33	15.33	34.33	23.67	56.01	180.00	41.34	75.19	14.67	3.33	38.33	41.33	12.17	91.80	41.33
97	56.7	14.67	13.33	12.67	31.00	113.67	82.70	33.00	69.48	9.86	3.35	30.00	31.00	22.67	83.10	33.00
98	78.2	14.45	14.33	27.33	29.69	79.82	108.60	41.81	94.41	13.33	4.47	30.00	35.33	16.67	65.30	41.33
CV (%)	18.7	19.9	14.2	19.5	30.3	27.8	20.3	17.5	11.2	37.3	36.2	8.6	14.5	39.7	18.5	15.8
SE	24.2	3.12	2.12	4.37	8.47	14.59	20.15	5.58	11.109	6.06	1.79	2.61	5.47	11.98	18.97	5.39
LSD (5%)	43.58	5.61	3.82	7.88	15.24	26.27	36.28	8.85	17.891	9.76	2.88	4.2	8.82	19.29	30.55	8.69
R^2	0.89	0.7	0.64	0.89	0.58	0.87	0.9	0.65	0.82	0.41	0.73	0.9	0.84	0.74	0.87	0.57
F pr.	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001	0.043	<.001	<.001	<.001	<.001	<.001	<.001

Table 3. Combined analysis of variance of eight quantitative traits in two locations, Makhathini and Burgershall.

Source of variation	DF	PH	PL	PW	PE	RN	PT	SW	TW
Site	1	819.01**	15.43**	807.07**	366.65**	248.24**	316.54**	247.28**	6585.49**
Genotype	97	109.59	281.43**	111.4	119.55	283.41**	139.54*	123.75	171.26**
Gen*Site	95	96.99	177.13**	97.45	117.79	206.83**	116.01	103.01	158.78**
Residual		2786	12.33	12.97	60.17	73.97	692.2	2082	20.99

Table 4. Estimates of genetic parameters of eight quantitative traits in 98 sorghum accessions.

Trait	Mean	MS_G	MS_E	V_p	δ^2_p	δ^2_g	δ^2_e	PCV	GCV	H^2	GA	GG%
PL	14.59	35.18	13.12	3.42	11.70	7.33	4.37	23.44	27.48	62.65	2.55	39.98
PE	9.63	17.70	12.77	2.43	5.90	1.64	4.26	25.22	13.31	27.85	0.85	8.33
PT	27.44	1106.80	835.40	19.21	368.93	90.47	278.47	70.00	34.66	24.52	59.95	30.82
PH	71.27	3100.00	2786.00	32.15	1033.33	104.67	928.67	45.10	14.35	90.13	62.98	0.90
RN	30.61	206.68	74.08	8.30	68.89	44.20	24.69	27.12	21.72	64.16	639.62	21.33
SW	48.36	2703.00	2104.00	30.02	901.00	199.67	701.33	62.07	29.22	22.16	17655.04	372.52
TW	16.46	103.28	19.76	5.87	34.43	27.84	6.59	35.65	32.06	80.87	52.69	3.27
PW	30.22	857.00	585.20	16.90	285.67	90.60	195.07	55.93	31.50	31.72	6765.50	228.46

Table 5. Correlations among eight quantitative traits in sorghum.

	PE	PH	PL	PW	RN	SW	TW	PT
PE	-							
PH	0.102**	-						
PL	-0.1563***	0.139**	-					
PW	0.5279***	0.127**	-0.2501***	-				
RN	-0.3216***	-0.0123	0.2299***	-0.3538***	-			
SW	-0.207***	0.064	0.0661	-0.2489***	0.1911***	-		
TW	-0.6474***	-0.1872***	0.2087***	-0.7337***	0.4664***	0.2974***	-	
PT	0.472***	0.1457**	-0.0931*	0.4443***	-0.1986***	0.0568	-0.5***	-

** = Significant at 0.01 probability level; *** = highly significant at 0.001 probability level

Table 6. Principal Component factor loadings of the agro-morphological traits.

Trait	PC1	PC2	PC3
PE	-0.01774	0.04281	0.12967
PH	0.38763	0.89888	-0.20158
PL	0.00633	0.00575	-0.01861
PW	-0.01193	0.02558	0.06078
RN	0.02900	-0.02449	-0.07175
SW	0.89837	-0.40712	-0.10211
TW	0.03565	-0.08804	-0.17870
PT	0.08370	0.09695	0.61773
Eigen values	2426494	1976803	865875
Percent variation	42.53	34.65	15.18
Cumulative variation	77.18	57.71	49.83

in genetic studies of quantitative characters is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value. Characters with high heritability can easily be fixed with simple selection resulting in quick progress. However, it has been accentuated that heritability alone has no practical importance without genetic advance (Najeeb et al., 2009). Genetic advance shows the degree of gain obtained in a character under a particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection. Johnson et al. (1955) reported that heritability values along with estimates of genetic gain were more useful than heritability alone in predicting the effect of selection. High heritability estimates associated with high genetic advance as per-cent mean (GG) were obtained in the characters viz., thousand seed weight, which indicated that selection for these characters would be more effective because they showed high heritability and genetic advance (as percent of mean). High heritability values followed by high genetic advance indicated the presence of additive gene action (Johnson et al., 1955; Kashif et al., 2003). High genetic advance coupled with high heritability estimates offers the most suitable condition for selection. It also indicates the presence of additive genes in the trait and further suggest reliable crop improvement through selection of such traits. Estimates of heritability with genetic advance are more reliable and meaningful than individual consideration of the parameters (Nwangburuka et al., 2012).

Correlations among the agronomic traits

Panicle exsertion was highly significant and well correlated with all other traits but significant for plant height (Table 5). Plant height was negatively correlated with panicle length, rachis number and thousand seed weight, and positively correlated with panicle width, plant height and panicle weight. Plant height was highly significant and negatively correlated with thousand seed weight but not significant with rachis number and grain yield. It was further significant and positively associated with panicle length, panicle width and panicle weight. Panicle length was highly significant and positively correlated with rachis number and thousand seed weight, negatively associated panicle width and weight per panicle. Panicle width was highly significant and negatively associated with all the traits but positively associated with panicle width. Rachis number was highly significant and positively correlated with grain yield and thousand seed weight but negatively associated with weight per panicle. Grain yield was positively correlated with thousand seed weight and positively but insignificant with weight per panicle. Thousand seed weight was highly significant and negatively correlated with weight per panicle.

It is important for breeders to consider the association among the pairs of the yield related traits; hence correlation studies are essential for assessing the association between them. In this study, there were significant correlations observed among the yield related traits. Information on significant correlation among the characters is important for initiation of breeding programmes as it gives a chance for selection of genotypes with desirable traits concurrently. Various studies reported correlations among yield and yield components in their crop of interest. In sorghum, Tesso et al. (2011) reported significant positive correlation between leaf traits and yield components excluding thousand seed weight and panicle length. Nabin et al. (2013) also observed significant correlations among the fodder yield per plant with thousand grain weight and plant height. El-Din et al. (2012) reported a positive and highly significant correlation between number of grain per head and grain yield and positive significant correlation between panicle length and grain yield. Moreover, non-significant negative correlation was observed between panicle width and grain yield per panicle. Jankovic et al. (2012) also reported the presence of very strong to almost complete, statistically very significant positive correlations among the morphological productive indicators per species. The positive correlations among these traits suggested that the characters are important and good indicators for indirect selection of high yielding genotypes.

Principal component analysis

The Principal Component analysis revealed three most important PCs contributing a total variation of 92.36% (Table 6). The PC1, PC2, and PC3 contributed 42.53, 34.65 and 15.18%, respectively. The most contributing traits to the total variation in PC1 were seed weight, plant height and panicle weight; in PC2 were plant height and seed weight; and PC3 were panicle weight, weight per panicle and panicle exertion. Application of PCA tool and multivariate statistical analysis also provide useful means to estimate morphological diversity within and between germplasm collections (Adugna, 2014).

Clustering

The accessions are clustered into three major groups (Figure 1). These groups are also subdivided into subgroups. Accession 54, 9 23 and 6 are clustered together hence are closely related to one another. Accession 10 is distantly related with the other accessions. In the second cluster, accessions 4, and 10 were closely related whereas the rest of the accessions formed about 12 sub-sub clusters. The most diverse accessions were 1, 60, 54, 2, 28 and 14. The genetic relatedness is useful for selection of parental lines for hybridization in crop improvement. The diversity observed among the sorghum genotypes could be useful in improvement of sorghum for various traits. Updhyaya et al. (2010) reported variation on the qualitative and quantitative traits and identified specific traits as new sources in sorghum germplasm. Rao et al (1996) found a considerable diversity for all characters studied among over four thousand sorghum accessions. Dosso-Aminon et al. (2015) also reported a vast genetic diversity among 142 landraces collected in Northern Benin using agronomic traits.

Materials and Methods

Plant material, trial design and management

Ninety-eight sorghum accessions obtained from the Agricultural Research Council, African Centre for Crop Improvement and Department of Agriculture, Forestry and Fisheries, South Africa were used in the study (Table 1). The accessions were planted in two locations, Makhathini in KwaZulu-Natal and Burgershall in Mpumalanga during the 2011/12 growing season. The experiments were laid in an alpha lattice design replicated twice. The experimental plot size was a row of 3 m long with inter-row and intra-row spacing of 0.75 m and 0.25 m, respectively, at both sites. Cultural practices for optimum sorghum growing conditions were applied. The Lime Ammonium Nitrate was top-dressed at 45 days after planting. Insect pests aphids and stem borer were controlled by cobalt and stalkborer shaker, respectively. The trials were irrigated using a sprinkler irrigation system and kept weed free during the growing period.

Data collection and analysis

The traits measured and associated abbreviations are shown in Table 1. Five randomly selected plants in the inner row were measured for quantitative traits. Plant height was measured from the ground to the tip of the panicle at maturity (cm); panicle length was measured from the lower panicle branch to the tip of the panicle at maturity (cm); panicle width was measured as width of panicle in natural position at the widest part (cm); grain weight was measured by weighing 1000 grains at 12% moisture content; grain yield per panicle measured as weight of grain per panicle (g); panicle weight was recorded before threshing averaging five panicles per plot. Rachis number measured as number of rachis per panicle. Panicle exsertion was measured as length of peduncle from flag leaf to the base of inflorescence (cm) as 1= < 2 cm, Slightly exerted; 2 = 2-10 cm, Exserted; 3 = >10, Well exerted; 4 = Peduncle recurved.

The data were subjected to analysis of variance using generalised linear model in GenStat 17.0, and significant means were separated using Duncan Multiple Range Test. The phenotypic and genotypic variances were estimated according Burton and de Vane (1953) and these components of variance (δ^2_p, δ^2_e, δ^2_g) were used for the estimation of coefficients of variation (PCV, GCV) as described by Singh and Chaudhary (1977) as follows:

$$\text{PCV} = \frac{\sqrt{ó2P}}{x} x\ 100 \quad \text{and GCV} = \frac{ó2g}{x} x\ 100$$

Where PCV is phenotypic coefficient of variation, GCV is genotypic coefficient of variation, $\delta^2 p$ and $\delta^2 g$ are phenotypic and genotypic variances, respectively. Heritability and expected genetic advance (K=2.06 at 5% selection intensity) were computed for each character based on the formula developed by Allard (1960). GA is expected genetic advance and μ is population mean.

Heritability = $\delta_2 g$ / $\delta_2 p$
Expected genetic advance = K.δ^2_p /μ; and Genetic advance as percentage of mean = GA/μ x 100.

Conclusion

The results obtained in the present study revealed the existence of wide variability for the traits measured among the sorghum genotypes, indicating that selection should lead to a fast genetic improvement of the traits. High heritability was obtained for some traits but may not always be associated with large genetic advance. Since high heritability does not always indicate a high genetic gain, heritability is recommended to be considered in association with genetic advance to predict the effect of selecting superior crop varieties.

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