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Nutritive Value and Fodder Potential of Different Sorghum (Sorghum bicolor L. Moench) Cultivars

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ABSTRACT

Keywords

Sorghum, Forage yield, Fodder quality, Genetic
diversity,
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standards.
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14 June 2017 Available Online: 10 August 2017 The current work was focused on evaluating 24 sorghum accessions for fodder yield potential and nutritional quality during summer 2015 in the Department of Forage Crops, TNAU, Coimbatore. Plant samples were collected at 50% flowering stage and evaluated for nine fodder yield and 13 forage quality parameters. Grounded samples were used for assessing the fodder quality. The variety K 3 showed superiority for green fodder yield per plant with 1452.40g followed by TKSV 1050 (1409.47g) and the accession TKSV 1126 was exceptionally better in quality with high nutrition and less in fibre portions. Variability analysis observed that phenotypic selection of traits *viz.*, number of leaves per plant, ether extract, dry fodder and green fodder yield per plant would be effective for fodder improvement. Genetic diversity analysis leads to the formation of five clusters. Cluster V had accessions with high yield potential and quality and Cluster II was confined with accessions having better forage quality. Furthermore, the accession TKSV 1126 obtained 'A1' grade (AFIA standards) with high nutritional quality; less fibre; better digestibility and metabolisable energy and could well be used as a donor in improving the nutritional content of sorghum varieties, which is lacking in the present-day cultivars.

Introduction

A large segment of the rural population comprising approximately 40 million people have 2-3 cattle and 5-6 sheep per family providing 30-40% of income for livelihood.

As the projected demand for fodder in India in 2020 is expected to be 855 MT of green fodder, 526 MT of dry fodder and 56 MT of concentrate feed (Dikshit and Birthal, 2010), as against the present demand of 666 MT of green fodder and 138 MT of dry crop residues, there is a need to emphasize for increased fodder production so that we could provide more support to livestock industry in the country.

Sorghum (*Sorghum bicolor* L. Moench), the fifth most important cereal crop, is a gifted genus of the tropical regions that provide food, feed, stover (dry straw) and fuel to millions of poor farmer families and their livestock. It plays an important role as a major grain cum fodder crop. Sorghum crop provides excellent forage in dry land areas. Sorghum has four desirable qualities *viz.*, high dry matter yield; light use; water use and nitrogen use efficiency. It is nutritious, juicy, palatable and well-liked by the cattle and can withstand high temperature and minimal soil moisture.

Forage quality is an important selection criterion in fodders especially so in fodder sorghum because the performance of dairy animals not alone depends on availability of fodder but on the continuous availability of quality forage in adequate amount. Therefore, the critical limitation on profitable animal production in developing countries is the insufficient availability of quality forage (Sarwar et al., 2002). Forage yield in quantity alone cannot measure the feeding value of the crops. So, the quality value of forages like palatability and nutritional value of forage must be determined for measuring the feed value. Protein content and digestibility of fodder are two important components for quality in fodder sorghum. Improving the nutritive value of forage sorghum for productive ruminants shall be achieved by increasing dry matter digestibility and the lignin content. reducing Such improvements can be accomplished through genetic breeding and selection, choosing the optimal stage for harvest and improving growth factors (Carmi et al., 2006). In this perspective, an effort has been made in the present investigation to explore the nutritive value and fodder potential of sorghum accessions to identify high biomass, nutrient rich quality fodder which is the need of the hour.

Materials and Methods

Twenty-four sorghum germplasm accessions viz., TKSV 1126, TKSV 1166, TKSV 1050, TKFS 1161, TKFS 11107, TKSV 1133, TKSV 1182, TKSV 1127, TNS 623, TKFS 1051, TKSV 1123, TKSV 1046, TKSV 1171, TKFS 1049, TKSV 1115, TKSV 1130, TKFS 11111, TKFS 1198, K 11, K 3, IS 18758, IS 18551, SPV 2123 and TAM 428 were used evaluating their fodder yield potential and nutritional quality. The accessions were raised in two replications along with the local check CO (FS) 29 in two rows of 4m length per replication with a spacing of 45cm x 15cm using randomized block design. All the recommended agronomic practices were followed during the entire crop period.

Observations recorded

Five plants were randomly selected and evaluated for fodder yield potential at days to 50 per cent flowering. The observations were recorded on plant height (PLH), stem girth (STG), number of tillers per plant (NOT), number of leaves per plant (NOL), leaf length (LEL), leaf breadth (LEB), leaf stem ratio (LSR), green fodder yield per plant (GFY) and dry fodder yield per plant (DFY).

For quality assessment plant samples were collected during panicle initiation and were chopped, air dried and finally oven dried at 60°C for two days. The oven dried samples were ground and sieved using different sieve sizes and utilized for the estimation of crude protein content (CPC), crude fibre content (CFC), crude ash content (CAC), ADF (Acid detergent Fibre), NDF (Neutral detergent fibre) and ether extract (EET). The traits nonfibre carbohydrates (NFC), nitrogen free extract (NFE), total digestible nutrients (TDN), digestible dry matter (DDM), dry matter intake (DMI), relative forage quality (RFO) and metabolisable energy (MER) were derived using various equations (Appendix 1).

Grading systems *viz.*, AFIA (Australian Fodder Industry Association) standards for cereal hay (AFIA, 2004) and the Southeastern forage quality categorization system (Dennis, 2011) was used to grade the accessions for their nutritional quality.

Statistical analysis

Phenotypic and genotypic components of traits were worked out based on the formula given by Goulden (1952). Heritability in broad sense and genetic advance as per cent of means were worked out as per Allard (1960)and Johnson et al., (1955)Genotypic respectively. correlation coefficients were computed from the mean of traits over replications for all the characters keeping MER as the dependent variable by using formula given by Weber and Moorthy Correlation coefficients (1952). were compared against table r values at (n-2) degrees of freedom at the probability levels of 0.05 and 0.01 to test their significance (Panse and Sukhatme, 1961).

Diversity analysis was carried out to study clustering pattern of the accessions. Data of nine fodder yield and 13 quality parameters were subjected for multivariate hierarchical cluster analysis. Similarity matrix was generated using the SIMINT programme of NTSYS-pc software version 2.02i (Rohlf, 2005). Similarity coefficients were used for cluster analysis and dendrogram was constructed by UPGMA method (Sneath and Sokal, 1973).

Results and Discussion

The analysis of variance for the fodder yield traits and quality parameters showed significantly high differences among the genotypes for all the characters. This indicated the existence of abundant variability among the accessions studied.

Per se performance

Plant height is an important growth parameter which influences fodder quantity, quality and mostly shows relative vigour of the crop. Long slender fine stems are often preferred by animals than short thick stems as they affect palatability of the forage. K 3 which observed the highest mean of 346.10cm for PLH did not differ significantly with K 11 (324.10cm) and TKFS 1049 (321.90cm). Correspondingly the tallest genotype K 3 recorded high GFY (1452.40g) and DFY (262.30g) but was significantly on par with TKSV 1050 (1409.5g and 213.35g). It is evident from the results that if there has been higher GFY, there would be higher DFY (Table 1). The results obtained were in parallel with Yousef *et al.*, (2009), Simili *et al.*, (2010) and Palta and Karadavut, (2011).

Green leaves contribute much to the forage quality. The accession TKFS 1198 observed high mean performance for the traits NOL (13.60), LEL (92.90cm) and LSR (0.26). Tall plants produce more number of leaves and vice-versa. This was obvious from our results. Accession K 11, with a mean PLH of 324.10cm registered high NOL of 12.80, while the genotype TKSV 1046 which recorded a low mean PLH (136.80cm) obtained a low mean NOL of 9.20. Similar significant differences among sorghum cultivars were also reported by Naeem et al., (2002) and Nabi et al., (2006).

Crude protein content is of utmost importance as it largely determines the palatability and digestibility of forage crops. The genotype TKSV 1171 recorded highest CPC (12.78%) but was on par with the genotypes TKSV 1182, TKSV 1126, TKFS 1161, TKSV 1166 and TKFS 11111 with mean CPC of 12.43, 11.94, 11.73, 10.61 and 10.47%, respectively. The difference among genotypes may be due to relative contribution of leaves to total biomass and concentration of protein in dry fodder (Table 2). The significant differences in crude protein content among various sorghum genotypes have also been reported by Filho et al., (2004), Nabi et al., (2006) and Tauqir et al., (2009). Conversely, in the

present study the genotype TKSV 1171 which showed high CPC obtained low LSR. Therefore, this genotype could be improved through hybridization programmes to increase the leaf count and simultaneously the leafstem ratio which would reflect on achieving more protein content.

Fat content (EET) was high in TKSV 1133 (4.49%) and was statistically on par with TKFS 1161 (4.14%) and TKSV 1126 (4.13%). The high level of fat observed here would be beneficial to the feed industry, because fat is a major source of energy. Inversely, higher fat content could decrease the palatability of the diet by coating the fibre which would also affect the digestibility of the feed (John, 2005). The genotypes TKSV 1133, TKFS 1161 and TKSV 1126 recorded high fat content and also exhibited high significance for digestibility and dry matter intake. The accession, TKSV 1126 which recorded high DDM (66.31%), DMI (2.18%) and MER (11.41 MJ ME/kg DM) would be a donor desirable for use in quality improvement programme to obtain high fat with better palatability content and digestibility.

Presence of high level of fibre portions in the fodder material adversely affects the forage quality. Higher the fibre content lower is the digestibility and moreover, fibre portion increases with the age of the plant. The genotype TKSV 1127 exhibited high mean CFC of 30.10% whereas IS 18551 and TKSV 1126 recorded low mean CFC of 18.75 and 19.75%, respectively. Acid detergent fibre was minimum in TKSV 1126 (29.00%) and maximum in three genotypes viz., TKSV 1127 (41.00%), TKFS 1049 (41.00%) and TKFS 1198 (41.00%). Neutral detergent fibre ranged from 55.00 (TKSV 1126) and 72.00 (SPV 2123) per cent. Similar reports by Marsalis et al., (2010), Machado et al., (2011), Barba et al., (2012) and Matos et al.,

(2014) supported our findings. Lower the ADF, the feed is highly digestible (*i.e.*, of high quality) and lower NDF leads to higher intakes (John, 2005). Considering the above facts, the genotype TKSV 1126 was identified as good quality forage (high nutrient content; palatability; digestibility and intake rate) owing to reduced fibre portions.

Non-fibre carbohydrates (starch, sugar and pectin) are the non-cell wall carbohydrates which are digested faster than structural carbohydrates and fused instantly by the microbes in the rumen. Highest mean for this trait was exhibited by TNS 623 (24.34%). Higher the proportion of NFC more will be the nutritive value. Conversely, in our findings, TNS 623 recorded low mean CPC of 6.90% though having higher intake and digestibility rates.

Digestibility (DDM) and Energy (MER) are closely linked to vegetative stage. Young leaves have higher DDM and MER levels. The energy that is absorbed by the cow after the loss of some gross energy is known as Metabolisable Energy (MER). It is the energy used for maintenance of body systems, activity, milk production, pregnancy and weight gain, higher the value, better the quality of the feed. Furthermore, the digestibility rate and the energy synthesized declines sharply once heading starts. The accession TKSV 1126 recorded the highest mean for DDM of 66.31%, while the genotype TNS 623 observed high mean MER of 11.97%. Our results were in accordance with the findings reported by Mizubuti et al., (2002) and Barba et al., (2012).

Overall, the accession K 3 expressed high fodder potential owing to high significant mean performance for most of the yield traits *viz.*, PLH, NOT, GFY and DFY. On the quality front, the accession TKSV 1126 was exceptional in nutritional value with high protein and low fibre portions leading to high digestibility and intake rates combined with high metabolisable energy.

Variability parameters

The estimates of PCV were greater than their corresponding GCV for all the fodder yield and quality parameters (Table 3) denoting environmental factors influencing their expression to some degree or the other 2015). Broad (Ghorade *et* al., sense heritability ranged from 33.34 (LEB) to 99.91 per cent (NOL) for fodder yield traits and 78.92 (CFC) and 99.40 per cent (EET) among the quality parameters. High heritability was observed for all the fodder yield and quality traits indicating that these characters would respond positively to selection because of their broad sense heritability except leaf width (33.34%) which showed a moderate estimate of heritability. Fodder yield traits viz., NOT, DFY, GFY, PLH, LSR and NOL and quality parameters such as EET, NFC, CPC and CAC exhibited high expected genetic advance per cent over mean.

High GCV, heritability and genetic advance as per cent of mean was recorded by NOL, EET, DFY and GFY which indicates that these characters are controlled by additive gene action and phenotypic selection for these characters would be effective for fodder improvement.

Correlation analysis

Knowledge of association between yield and its component traits and among the component parameters themselves can improve the efficiency of selection in plant breeding. When there is positive association of major yield characters and its components, breeding would be very effective. But when these characters are negatively associated, it would be difficult to exercise simultaneous selection for them in developing a variety (Nemati *et al.*, 2009).

Correlation analysis among the fodder yield and quality parameters with MER as the dependent variable observed the traits GFY and DMY having positive significant association (Appendix 2) with PLH, NOT, CFC, ADF and NDF and between themselves. Leaf length showed positive and highly significant association with NFC, NFE and TDN. ADF obtained a perfect negative correlation for DDM. Another significant association was observed between NDF and DMI. The quality improving traits (NFC, NFE, TDN, DDM, DMI, RFQ and MER) observed significant positive association within themselves.

The traits PLH, NOT, NOL and LSR were positively and significantly associated with GFY and DFY. When the number of leaves is many, there will be a greater surface area for photosynthesis; greater photosynthesis can translate into more photosynthates, ultimately resulting in increased fodder yield (Alhassan *et al.*, 2008). This is evident from our results (Appendix 2). It is also noticed that the characters that exhibited positive associations with fodder yield have also showed positive associations among themselves.

The traits representing fibre portions viz., CFC, ADF and NDF had a strong positive significant association within themselves. Correlation among the above three traits were very high. It was also noticed that the trait CFC showed negative and highly significant association with NFC, NFE, TDN, DDM, DMI, RFQ and MER. Likewise, ADF observed significant negative associations with CPC, NFC, DMI and RFQ, while it showed a perfect negative relationship with DDM inferring that high ADF causes poor digestibility (John, 2005). Similarly, NDF observed significant negative highly

association with DMI deducing that high NDF leads to poor intake rates (John, 2005). This indicated that when fibre content is high, the nutrient content will be low; digestibility and palatability will be poor, ultimately resulting in poor intake due to poor forage quality. Moreover, the presence of higher portion of structural carbohydrates (Pectin, cellulose, hemicellulose, lignin and silica) in the forage will seriously affect the digestibility of the fodder.

Non-fibre carbohydrates had positive and significant association with LEL, NFE, TDN, DDM, DMI, RFQ and MER evidencing that when the fibre content is very low in the feed there is higher palatability, intake and digestibility, eventually resulting in higher metabolisable energy and superior forage quality.

The trait TDN, which encompasses the digestible crude protein, crude fat, crude fibre and nitrogen free extract observed positive and a perfect correlation with MER signifying the need of nutrients for obtaining higher energy. Hence, genotypes that deliver high energy can be alternatively selected using TDN and *vice-versa*.

Our data also revealed some interesting associations such as GFY showing positive significant association with CFC, DDM, DMI, RFQ and significant negative correlation with CPC and LSR. These associations infer that stem weight might have contributed to a higher ratio to the overall GFY. Therefore, resulting in lower quality fodder as stems contribute majority of the fibre portions.

Genetic diversity

As suggested by Rohlf (2005), the accessions were grouped into different clusters based on the coefficient values. The accessions were grouped into five clusters at the coefficient of 0.15 (Fig. 1). Among the clusters, cluster I was the largest comprising seven accessions followed by cluster IV with six accessions. Cluster V formed the smallest group with three accessions.

Discernible variations were observed among the formed clusters. Based on the cluster mean (Table 4), cluster V observed high cluster mean for PLH (311.63cm), LEL (88.07cm), GFY (1254.92g), DFY (200.82g), (17.09%), NFE (54.96%), NFC TDN (70.35%) and MER (11.12 MJ/kg DM), whereas cluster II exhibited high mean for most of the quality parameters such as high CPC (9.90%), EET (2.99%), CAC (11.25%), DDM (62.22%), DMI (2.01%) and RFQ (113.62). The accessions viz., TKSV 1050, K 11 and TKFS 1049 which formed cluster V and the accessions, TKFS 1161, TKSV 1171, TNS 623 and TKSV 1046 could be utilized in back crossing programmes as donors for transferring traits of interest.

Grading for quality estimates

Fodder quality represents the ability of the cow to digest and utilize the nutrient components present in the source. Higher the amount and digestibility of nutrients; more will be the fodder quality. Fodder with high quality and digestibility contains lowest amount of structural carbohydrates (cellulose, hemicellulose) and lignin. The accessions were graded as per AFIA standards and Southeastern forage quality categorization system (Table 5). Based on AFIA standards, the accession TKSV 1126 gained the highest grade of 'A1', while four accessions viz., TKSV 1127, TKFS 1049, SPV 2123 and TAM 428 attained the lowest grade of 'C3'. On the basis of AFIA standards, TKSV 1126 exhibited superior quality (A1 grade). The high relative fodder quality value signifies its superior quality and that it can be utilized for improving the quality attributes.

Accessions	PLH	STG	NOT	NOL	LEB	LEL	LSR	GFY	DFY
TKSV 1126	200.8	1.5	1.0	9.4	8.8	76.3	0.2	566.6	79.2
TKSV 1166	176.8	1.6	1.0	9.8	9.2	77.9	0.2	516.7	76.2
TKSV 1050	288.9	1.7	4.2	10.4	9.9	89.0	0.2	1409.5	213.4
TKFS 1161	168.1	1.7	1.0	9.6	9.0	75.1	0.2	358.8	51.7
K 11	324.10	1.50	2.60	12.80	7.90	87.10	0.20	1131.50	210.77
TKFS 11107	296.70	1.52	1.60	13.00	9.38	84.40	0.20	887.10	122.45
TKSV 1133	170.00	1.88	1.00	10.00	8.92	81.10	0.26	583.37	110.77
TKSV 1182	175.60	1.92	1.00	9.80	8.92	66.00	0.24	691.53	68.74
TKSV 1127	229.60	1.68	1.00	12.20	9.06	71.90	0.24	744.40	112.45
TNS 623	209.00	1.64	1.00	10.40	9.44	86.20	0.24	575.27	100.69
TKFS 1051	287.90	1.70	3.40	13.40	8.22	70.20	0.17	1117.07	204.92
TKSV 1123	197.60	2.26	1.00	11.60	9.36	82.30	0.22	858.80	128.35
TKSV 1046	136.80	1.86	1.00	9.20	8.50	75.40	0.19	437.67	63.67
TKSV 1171	217.70	2.28	1.00	9.80	9.54	70.50	0.20	443.63	51.19
TKFS 1049	321.90	1.70	2.60	10.80	8.04	88.10	0.15	1223.80	178.35
К 3	346.10	1.72	3.60	11.20	9.02	80.10	0.20	1452.40	262.30
TKSV 1115	198.40	2.24	1.00	12.20	8.92	78.50	0.21	777.40	111.65
TKSV 1130	197.10	1.96	1.00	12.60	9.36	77.30	0.24	725.23	89.22
TKFS 11111	279.40	2.18	2.00	9.80	9.52	82.70	0.12	1137.90	222.58
TKFS 1198	288.90	1.82	1.80	13.60	8.04	92.90	0.26	850.90	167.55
SPV 2123	239.20	1.62	1.00	12.80	9.62	73.40	0.17	1194.33	176.55
IS 18758	187.00	2.00	1.00	12.40	9.32	80.80	0.28	699.47	105.13
IS 18551	255.80	1.96	1.00	10.80	10.24	88.20	0.20	733.60	87.76
TAM 428	210.00	1.94	2.20	12.20	9.40	85.10	0.23	768.10	160.75
Grand mean	233.48	1.83	1.63	11.24	9.07	80.02	0.21	828.54	131.51
SEd	10.61	0.11	0.02	0.55	0.45	2.99	0.02	51.07	7.84
CD (0.05)	21.08	0.23	0.04	1.08	0.88	5.93	0.03	101.44	15.56
CV %	7.19	9.91	1.76	7.67	7.77	5.90	11.57	9.75	9.42

Table.1 Mean performance of 24 sorghum accessions for fodder yield traits

Accessions	CFC	CPC	EET	CAC	ADF	NDF	NFC	NFE	TDN	DDM	DMI	RFQ	MER
TKSV 1126	19.8	11.9	4.1	10.0	29.0	55.0	18.9	54.2	71.9	66.3	2.2	127.5	11.4
TKSV 1166	22.1	10.6	3.4	10.0	33.0	58.0	18.0	53.9	70.6	63.2	2.1	118.8	11.2
TKSV 1050	25.0	9.9	3.1	10.0	36.0	62.0	15.0	52.0	68.8	60.9	1.9	108.3	10.8
TKFS 1161	22.1	11.7	4.1	11.0	33.0	59.0	14.1	51.0	69.4	63.2	2.0	114.8	11.0
K 11	24.45	8.72	3.79	9.00	34.00	59.00	19.49	54.04	71.10	62.41	2.03	117.57	11.26
TKFS 11107	26.40	8.40	2.74	9.00	39.00	70.00	9.86	53.46	69.39	58.52	1.71	96.71	10.95
TKSV 1133	21.60	9.52	4.49	9.00	32.00	59.00	17.99	55.39	73.00	63.97	2.03	120.71	11.61
TKSV 1182	24.50	12.43	3.77	9.00	35.00	63.00	11.81	50.31	69.11	61.64	1.90	107.02	10.89
TKSV 1127	30.10	7.14	3.07	11.00	41.00	70.00	8.79	48.69	65.80	56.96	1.71	91.71	10.28
TNS 623	21.60	6.90	3.77	8.00	33.00	57.00	24.34	59.74	74.94	63.19	2.11	128.27	11.97
TKFS 1051	28.00	8.30	3.42	14.00	39.00	66.00	8.29	46.29	64.01	58.52	1.82	94.61	9.95
TKSV 1123	25.45	9.73	3.08	10.00	37.00	65.00	12.19	51.74	68.58	60.08	1.85	102.94	10.80
TKSV 1046	21.60	8.19	1.33	13.00	34.00	56.00	21.48	55.88	68.34	62.41	2.14	119.06	10.75
TKSV 1171	23.55	12.78	2.73	13.00	37.00	69.00	2.50	47.95	65.30	60.08	1.74	92.33	10.19
TKFS 1049	24.00	6.86	1.33	9.00	41.00	66.00	16.81	58.81	71.14	56.96	1.82	105.16	11.27
К 3	25.50	7.95	1.68	10.00	37.00	70.00	10.38	54.88	68.78	60.08	1.71	95.86	10.83
TKSV 1115	24.00	9.98	1.68	10.00	35.00	61.00	17.35	54.35	68.74	61.64	1.97	109.94	10.83
TKSV 1130	22.55	9.45	1.68	11.00	31.00	56.00	21.87	55.32	69.08	64.75	2.14	120.35	10.89
TKFS 11111	24.95	10.47	0.63	10.00	30.00	60.00	18.90	53.95	67.30	65.53	2.00	109.43	10.56
TKFS 1198	24.00	9.10	1.68	7.00	41.00	62.00	20.22	58.22	72.01	56.96	1.94	113.32	11.43
SPV 2123	23.05	7.84	1.68	10.00	40.00	72.00	8.48	57.43	70.52	57.74	1.67	95.55	11.16
IS 18758	21.60	8.30	1.68	13.00	35.00	65.00	12.03	55.43	68.46	61.64	1.85	102.76	10.78
IS 18551	18.75	9.84	2.38	12.00	33.00	58.00	17.79	57.04	70.91	63.19	2.07	119.27	11.23
TAM 428	22.55	7.77	0.63	9.00	40.00	63.00	19.60	60.05	71.30	57.74	1.90	110.42	11.30
Grand mean	23.63	9.33	2.58	10.29	35.63	62.54	15.26	54.17	69.52	61.15	1.93	109.27	10.97
SEd	1.04	0.53	0.07	0.62	1.27	1.81	1.94	1.28	0.92	1.00	0.06	3.81	0.17
CD (0.05)	2.09	1.07	0.15	1.25	2.56	3.65	3.90	2.58	1.85	2.01	0.11	7.66	0.34
CV %	5.38	7.01	3.46	7.36	4.38	3.55	15.57	2.89	1.62	200	3.61	4.27	1.90

Table.2 Mean performance of 24 sorghum accessions for quality parameters



Fig.1 Dendrogram for sorghum accessions derived by UPGMA from the dissimilarity matrix

		Ra	nge	Phenotypic	Genotypic		Expected	
Traits	Grand mean	Minimum	Maximum	coefficient of variation (%)	coefficient of variation (%)	Heritability (%)	genetic advance % of mean	
PLH	233.5	136.8	346.1	25.6	24.6	92.1	48.6	
STG	1.8	1.5	2.3	15.7	12.2	60.2	19.5	
NOT	1.6	1.0	4.2	60.0	60.0	99.9	123.5	
NOL	11.2	9.2	13.6	14.4	12.1	71.4	21.1	
LEB	9.1	7.9	10.2	9.5	5.5	33.3	6.5	
LEL	80.0	66.0	92.9	10.1	8.2	65.9	13.7	
LSR	0.2	0.1	0.3	20.1	16.5	66.9	27.7	
GFY	828.6	358.8	1452.4	38.1	36.8	93.5	73.4	
DFY	131.5	51.2	262.3	46.7	45.7	95.9	92.3	
CFC	23.6	18.8	30.1	11.5	10.1	78.9	18.4	
СРС	9.3	6.9	12.8	19.1	17.8	86.5	34.0	
EET	2.6	0.6	4.5	44.8	44.6	99.4	91.7	
CAC	10.3	7.0	14.0	17.6	16.0	82.6	30.0	
ADF	35.6	29.0	41.0	10.7	9.8	83.3	18.4	
NDF	62.5	55.0	72.0	8.6	7.9	83.1	14.8	
NFC	15.3	2.5	24.3	37.5	34.1	82.8	63.9	
NFE	54.2	46.3	60.1	7.0	6.4	83.1	12.1	
TDN	69.5	64.0	74.9	3.8	3.4	81.6	6.3	
DDM	61.2	57.0	66.3	4.8	4.4	82.5	8.2	
DMI	1.9	1.7	2.2	8.6	7.8	82.2	14.5	
RFQ	109.3	91.7	128.3	10.7	9.8	84.0	18.5	
MER	11.0	10.0	12.0	4.4	4.0	81.5	7.4	

Table.3 Mean, range and variability parameters for the fodder yield and quality traits

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Troite		С	luster mean		
Traits	Ι	II	III	IV	V
PLH	208.16	182.90	290.35	219.73	311.63
STG	1.81	1.87	1.76	1.97	1.64
NOT	1.17	1.00	2.05	1.53	3.13
NOL	11.34	9.75	11.70	11.77	11.33
LEB	9.34	9.13	9.39	8.73	8.60
LEL	79.64	76.80	80.15	78.50	88.07
LSR	0.24	0.21	0.17	0.23	0.19
GFY	679.16	453.84	1167.93	813.18	1254.92
DFY	101.53	66.81	195.97	132.00	200.82
CFC	22.49	22.21	24.98	24.59	24.47
СРС	9.29	9.90	8.67	9.84	8.51
ЕЕТ	2.43	2.99	1.68	3.02	2.73
CAC	10.86	11.25	9.75	9.83	9.33
ADF	34.57	34.25	36.50	36.50	37.00
NDF	60.71	60.25	68.00	62.67	62.33
NFC	16.71	15.61	11.91	14.64	17.09
NFE	54.94	53.65	54.93	52.72	54.96
TDN	69.72	69.51	69.00	69.24	70.35
DDM	61.97	62.22	60.47	60.47	60.08
DMI	1.99	2.01	1.77	1.92	1.93
RFQ	112.97	113.62	99.39	108.09	110.34
MER	11.01	10.97	10.88	10.92	11.12
Cluster entries	TKSV 1126 TKSV 1166 TKSV 1130 TKSV 1127 IS 18758, TAM 428 IS 18551	TKFS 1161 TKSV 1171 TNS 623 TKSV 1046	TKFS 11107 K 3 TKFS 11111 SPV 2123	TKSV 1133 TKSV 1123 TKSV 1115 TKSV 1182 TKFS 1051 TKFS 1198	TKSV 1050 K 11 TKFS 1049

Table.4 Cluster mean for various fodder yield and quality traits and entries forming various clusters

Accession No.	AFIA grade	RFQ Category
TKSV 1126	A1	Good
TKSV 1166	B1	Good
TKSV 1050	B2	Fair
TKFS 1161	B1	Good
K 11	B2	Good
TKFS 11107	C2	Fair
TKSV 1133	B2	Good
TKSV 1182	B1	Fair
TKSV 1127	C3	Fair
TNS 623	B3	Good
TKFS 1051	C2	Fair
TKSV 1123	B2	Fair
TKSV 1046	B2	Good
TKSV 1171	B1	Fair
TKFS 1049	C3	Fair
К 3	B3	Fair
TKSV 1115	B2	Fair
TKSV 1130	B2	Good
TKFS 11111	B1	Fair
TKFS 1198	C2	Good
SPV 2123	C3	Fair
IS 18758	B2	Fair
IS 18551	B2	Good
TAM 428	C3	Good

Table.5 AFIA grade and RFQ category of the accessions

On the basis of Southeastern forage quality categorization systems, none of the accessions fell under the group premium with a RFQ value above 140. However, 11 accessions were categorized as good quality forage with the accession TNS 623 having the highest RFQ value of 128.27 followed by TKSV 1126 (127.5). Thirteen accessions fell in the fair quality category with TKSV 1127 recording the lowest RFQ value of 91.71.

In conclusion, under the light of present study, the superiority of K 3 and TKSV 1050 for fresh and dry fodder yield over the local check CO (FS) 29 suggests their adoption for general cultivation. Moreover, the genotype TKSV 1126 which ranked top with its dry matter having the best nutritional value, high intake and digestibility rates could be used for quality improvement to transfer desirable traits to high yielding genotypes through back crossing programme. Hybridization could be attempted between lines having high yield potential and nutritional quality to develop genotypes possessing rich nutritional fodder which is the demand of the present era.

Abbreviations

PLH-Plant height, STG-Stem girth, NOT-Number of tillers per plant, NOL-Number of leaves per plant, LEL-Leaf length, LEB-Leaf breadth, LSR-Leaf-stem ratio, GFY-Green fodder yield per plant, DFY-Dry fodder yield per plant.

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Appendix.1 Trait descriptor list

S. No.	Character	Trait code	Method	Unit/ Measurement
1.	Plant height	PLH	Main stalk - measured from ground level to tip of the panicle	cm
2.	Stem girth	STG	Diameter or width of the 4 th internode from top	cm
3.	Number of tillers per plant	NOT	Total number of tillers in each plant sample	-
4.	Number of leaves per plant	NOL	Total number of leaves in each plant sample	-
5.	Leaf breadth	LEB	Width of the 3 rd leaf blade from top at its widest point	cm
6.	Leaf length	LEL	Length of the 3 rd leaf from top, from base to tip	cm
7.	Leaf-stem ratio	LSR	Ratio of leaf weight to stem weight	-
8.	Green fodder yield per plant	GFY	Average weight of the plant	g
9.	Dry fodder yield per plant	DFY	Average weight of the plant under moisture free basis	g
10.	Crude fibre content	CFC	AOAC, 1990	%
11.	Crude protein content	CPC	AOAC, 1995	%
12.	Ether extract	EET	AOAC, 1980	%
13.	Crude ash content	CAC	Ash of animal feed, 942.05 (AOAC, 1990)	%
14.	Acid detergent fibre	ADF	Van Soest et al., 1991	%
15.	Neutral detergent fibre	NDF	Van Soest and Goering, 1990 and Mertens, 1992	%
16.	Non-fibre carbohydrates	NFC	Weblink - Nutrition and feed terms	%
17.	Nitrogen free extract	NFE	Weblink - Nutrition and feed terms	%
18.	Total digestible nutrients	TDN	John Moran, 2005	%
19.	Digestible dry matter	DDM	Moore and Undersander, 2002b	%
20.	Dry matter intake	DMI	Moore and Undersander, 2002b	%
21.	Relative forage quality	RFQ	Moore and Undersander, 2002a,b	-
22.	Metabolisable energy	MER	John Moran, 2005	MJ ME/Kg DM

Appendix.2 Genotypic correlation coefficient for the various traits under study

1	P L H	S T G	N O T	N O L	L E B	L E L	L S R	G F Y	D F Y	C F C	CP C	E E T	C A C	A DF	N D F	NF C	NF E	T D N	D D M	D MI	RF Q	M E R
P L H	1.0 00	- 0.3 03	0.7 59* *	0.4 34 *	0.2 10	0.4 67 *	0.4 32*	0.8 36* *	0.8 21* *	0.4 41 *	- 0.35 7*	0.2 20	0.23 5	0.40 8*	0.4 29*	0.17 2	0.04 4	- 0.07 8	- 0.40 8*	- 0.43 5*	- 0.37 4*	- 0.07 9
S T G		1.0 00	- 0.2 62	0.1 09	0.3 13	0.1 01	- 0.0 19	- 0.1 82	- 0.1 79	0.0 57	0.33 4	- 0.3 89*	0.26 5	- 0.10 1	0.0 05	- 0.11 0	- 0.11 9	- 0.34 8*	0.10 2	- 0.02 9	0.15 1	- 0.34 7*
N O T			1.0 00	0.2 14	- 0.2 18	0.3 31	0.3 27	0.8 08* *	0.8 32* *	0.4 18 *	0.27 5	0.1 45	0.05 7	0.30 7	0.2 44	- 0.09 5	0.08 7	0.19 1	0.30 7	0.26 5	- 0.27 9	0.19 3

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N O L		1.0 00	0.2 14	0.2 11	0.1 16	0.4 03*	0.4 16*	0.4 41 *	- 0.51 8**	0.2 72	- 0.09 2	0.58 2**	0.4 37*	0.16 2	0.06 9	0.12 6	- 0.58 2**	- 0.44 1*	- 0.39 8*	0.12 5
L E B			1.0 00	- 0.0 05	0.0 55	0.0 85	0.2 00	0.2 46	0.19 2	- 0.0 98	0.16 7	0.22 0	0.0 74	0.16 2	0.03 3	0.03 0	0.22 0	- 0.05 9	- 0.05 9	0.02 7
L E L				1.0 00	0.0 49	0.3 32	0.4 02*	0.2 08	0.37 2*	- 0.2 46	0.52 3**	0.07 3	0.2 07	0.53 2**	0.64 7**	0.56 4**	0.07 3	0.19 3	0.33 7	0.56 4**
L S R					1.0 00	0.4 31*	- 0.4 01*	0.2 06	0.04 4	0.3 23	- 0.18 4	- 0.06 5	- 0.1 95	0.15 9	0.10 6	0.32 5	0.06 5	0.18 9	0.27 0	0.32 5
G F Y						1.0 00	0.9 32* *	0.4 69 *	0.40 3*	- 0.3 24	- 0.18 9	0.37 6*	0.4 54*	0.17 3	0.05 8	0.13 6	- 0.37 6*	- 0.46 1*	0.42 3*	0.13 6
D F Y							1.0 00	0.4 57 *	- 0.45 5*	- 0.3 37	- 0.24 0	0.33 7	0.3 60*	- 0.04 9	0.11 9	- 0.07 9	- 0.33 7	- 0.37 3*	- 0.33 0	- 0.08 0
C F C								1.0 00	- 0.27 2	- 0.0 24	0.00 4	0.58 2**	0.6 41* *	- 0.51 7**	- 0.56 1**	- 0.61 1**	- 0.58 2**	- 0.65 6**	- 0.72 7**	- 0.61 3**
C P C									1.00 0	0.3 66*	0.13 4	- 0.50 6**	0.2 87	0.16 5	- 0.46 5**	0.17 3	0.50 6**	0.27 7	0.16 2	0.17 2
E E T										1.0 00	0.06 3	- 0.30 1	- 0.2 17	- 0.10 4	- 0.44 7*	0.16 4	0.30 1	0.21 9	0.24 7	0.16 3
C A C											1.00 0	0.10 2	0.0 86	- 0.42 7*	- 0.52 0**	- 0.71 9**	0.10 2	- 0.07 5	- 0.30 7	- 0.71 8**
A D F												1.00 0	0.7 81* *	- 0.48 2**	0.02 1	0.23 0	- 1.00 0**	- 0.79 1**	- 0.70 9**	0.23 0
N D F													1.0 00	- 0.83 6**	- 0.28 1	- 0.45 3*	- 0.78 1**	- 0.99 8**	- 0.94 7**	- 0.45 3*
N F C														1.00 0	0.67 3**	0.67 6**	0.48 2**	0.83 3**	0.88 9**	0.67 5**
N F E															1.00 0	0.79 5**	0.02 1	0.29 0	0.49 5**	0.79 6**
T D N																1.00 0	0.23 0	0.46 0*	0.71 0**	1.00 0**
D D M																	1.00 0	0.79 0**	0.70 9**	0.23 0
D M I																		1.00 0	0.95 1**	0.46 0*
R F Q																			1.00 0	0.70 9**
M E R																				1.00 0