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Research Article

Processing of Specific Sorghum Genotypes for Semolina Recovery and their Nutrient Composition

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Abstract: Today's agriculture programme demands production of designer foods which is beneficial both to producers and consumer. Agriculture requires transformation from subsistence farming to consumer demand oriented one with good market and income generation approach. Sorghum with its diverse end uses is one such food which can play significant role and be profitable to farmers. In the present study, 60 sorghum genotypes were evaluated over two seasons to identify genotypes suitable for semolina recovery, endosperm texture efficiency and proximate composition. Semolina recovery, percent starch and percent protein had significant ($p \leq 0.0001$) association with white, brown and red sorghum genotypes. Semolina recovery ranged from 36.17% to 66.55%, whereas starch ranged from 52% to 66.25% and protein ranged from 7.3% to 12.35%. Similarly nonsignificant deference was observed with endosperm texture in brown and red sorghum genotypes and ranged from 25% to 100%. Mean ± standard deviation (SD) values were calculated for white, red, and brown sorghum genotypes. In this study, the information given and the genotype identified will help in enhancing the demand for sorghum as a beneficial industrial crop.

Keywords: Sorghum, Starch content, Protein content, Semolina, Endosperm texture.

INTRODUCTION

Sorghum stands for staple food in semi-arid regions worldwide. Most of the countries produced sorghum grain from *kharif* season (rainy season) can be polished with pearling machine and used for traditional food products like cakes, bread and biscuits. In India, most of the sorghum produced is consumed as *roti* or *chapatti* (unleavened flat bread) [1]. On the other hand, the sorghum that is harvested in the *rabi (*post-rainy season) is of superior quality and used only for food. Sorghum is commonly called as *jowar* or great millet and also considered as coarse grain due to the presence of outer fibrous bran of seeds. Sorghum is rich in leucine but poor in lycine.

In India, sorghum production is 1.85 million tons during 2019-2020 [2]. High yielding varieties and hybrids has been improved with agronomic traits that resulted in excess production. [3]. Sorghum constitutes a source of minerals, proteins and calories so that about 700 million people are nourished by sorghum and sorghum protein is superior compared to wheat in protein digestibility and biological value. Millets, sorghum and pulses are used as staple grains for house hold consumption [4].

Grain sorghum can also be processed to develop different end products such as flours, semolina, alcoholic beverages, pet foods and packaging materials [5]. Sorghum grain with hard endosperm texture is more suited for the semolina (*rava*) preparation and determines the milling quality and quantity of end product [6]. Sorghum processed food products are emerging for human consumption such as flakes, vermicelli, pasta etc [7].

Sorghum is available in three colours as red, white and brown, recently red variety has been developed for food use [8]. Sorghum is a gluten free grain and it has good source of nutrients such as fibre, micronutrients, antioxidant phenolics and cholesterol-lowering waxes [9]. Sorghum products usually have a shelf-life of over one year. A few important sorghum products are sun dried *papad*, *badi* and *kurdigai.* These can be available through marketing channels and those are used similar to rice products. If the technology for specific industrial end uses are developed, sorghum could be in abundant demand in the future [10].

Semolina is easy to prepare and consume and they make most popular food products of sorghum, dedicated grain proximate compositional evaluation programs for improved grain quality towards specific

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end product, without compromising for yield form the basis of link between farm products and industry.

In the present study, we have generated information on end-product specific genotypes by studying i) the relative contribution of genotypes and ii) understanding the relationship between associated grain quality traits and yield, and iii) identifying the potential genotypes that can be used in the proximate analysis programs aimed at development of genotypes suitable for high semolina recovery and endosperm texture efficiency.

MATERIAL AND METHODS

Plant Material

The grains of 60 sorghum (Sorghum bicolor (L.) Moench) genotypes were used in this study including the germplasm lines, improved lines, parental hybrids and cultivated lines, belonging to different races from different countries. Out of 60 genotypes, 36 were white-grained, 17 had red grains and 7 had brown grains (Table-1). The material includes some major sorghum varieties ('CSV 13', 'CSV 15') and one check (C-43) was used for nutritional properties. The list of the genotypes included in the present study are provided in (Table-1). These genotypes were sown in randomized complete block design (RCBD) with two replications, each with two rows of 5 m length for two consecutive years (2012-2013) during rainy and post-rainy seasons at Indian Institute of Millet Research, Rajendranagar, Hyderabad, India. The colour of the grain was recorded visually based on the colour of pericarp. The crop was harvested at the panicle (ear head) maturity stage. Panicles were threshed for grain and 200 g grain was used for experimental purpose. Whole grain was stored at 4 $^{\circ}$C for further analysis.

Chemicals

AR grade solvents and Millipore distilled water (Merck-Millipore, Synergy, UV plus) were used in the analysis. The chemicals phenol, sulphuric acid, sodium acetate, ethanol, glucose, salicylate, ammonium chloride were purchased from Sisco Research Laboratories, Mumbai, India. Amyloglucosidasge was purchased from Sigma-Aldrich, U.S.A. All the chemicals were of analytical grade.

Table-1: List of the genotypes included in the study

S. No	Genotype name	Group	Colour of grain
1	27B (1), 296B (2), 463B (3), 7B (4), AKMS 14B (5), IMS 9B (15)	Female parents of Released hybrids	White grain
2	AKR 150 (6), AKR 354 (7), C 43 (8), I 12 (14), RS 627 (20), RS 673 (21)	Male parents of Released hybrids	White grain
3	CSV 13, (9), CSV 15 (10)	Released cultivars	White grain
4	IC345194 (11), IC305903 (12), IC305923 (13), IS 33648 (17), IS 40751 (18), IS 18035 (38)	Germplasm lines	White grain
5	SPV 1258 (22), SPV 1293 (23), SPV 1471 (24), SPV 1606 (25), SPV 1616 (26), SPV 1731 (27), SPV 1732 (28), SPV 1733 (29), SPV 1734 (30), SPV 1750 (31), SPV 1760 (32), SPV 1775 (33), SPV 459 (34), SPV 462 (35), SPV 711 (36), SPV 933 (37),	Improved lines from All India Co-ordinated Research Program on Sorghum (AICRP-Sorghum	White grain
6	IS 31681 (16), IS 4372 (19), IS 1212 (39), IS 1206 (40), IS 12735 (41), IS 16151 (42), IS 20298 (43), IS 20743 (44), IS 23514 (45), IS 2389 (46), IS 28141 (47), IS 28313 (48), IS 29241 (49), IS 29950 (50), IS 30533 (51), IS 3158 (52), IS 4060 (53)	Germplasm lines	Red grain
7	IS 12697 (54), IS 20697 (55), IS 23992 (56), IS 24462 (57), IS 30466 (58), IS 30508 (59), IS 715 (60)	Germplasm lines	Brown grain

Grain yield and milling traits

Semolina recovery (SER)

200g of sorghum grain from each genotype in each replication was taken then cleaned and was kept in oven at 40 $^{\circ}$C for 30 min to equilibrate moisture content in the grain samples. Then the grain was milled in the grinding machine (Natraj domestic flour mill, India), using sieve number 3 with pore size of 700 µm. Semolina (*rava*) was obtained after grinding and was weighed. The percentage of semolina was calculated using the initial weight of grain (200 g). From the ground sample, the semolina was subjected to purification and separated by using different sieves. Biochemical analysis of semolina was done for percent starch and percent protein using standard methods [9].

Endosperm texture (ENT)

Endosperm texture was analysed by visual assessment on ten sorghum grains in each plant according to the DUS guidelines of sorghum [11]. Initially the sorghum seeds were soaked for 1 hour and were sectioned longitudinally and visual observation was done on percentage of vitreous (corneous) endosperm. The data was recorded as 25% vitreous, 50% vitreous, 75% vitreous and >90% vitreous. Data

was recorded on ten plants in each genotype and average values were used for further analysis.

Grain biochemical quality traits

Starch content (%)

Starch content was estimated by using method Southgate [12] with some modifications. Defatted sorghum flour (75 mg) was taken and it was autoclaved for 90 min at 19 lbs pressure. The content was hydrolysed using the enzyme amyloglucosidase (25 mg contains 5.75 units/mg) and 2M sodium acetate buffer was added. The hydrolysed sugars were estimated after diluting the extract with Millipore distilled water by phenol-sulphuric acid method [13] and the absorbance was read at 490 nm in a UV-Spectrophotometer (Schimadzu, Japan). Percent starch content was calculated by using 0.9 as conversion factor for sugars.

Protein content (%)

Total protein content was estimated by using colorimetric determination of total Kjeldhal nitrogen using salicylate [14]. Defatted grain sorghum flour (100 mg) accurately weighed (Mettler balance, Austria) into digestion tube with concentrated sulphuric acid and the mixture was digested for one hour at 425 $^{\circ}$C in digestor (Gerhardt, Germany). Sample was converted to ammonia (Kjeldhal nitrogen) and absorbance was read at 685 nm. Ammonium chloride was used as a reference standard with a concentration range of 1-20µg /ml (nitrogen). The amount of protein was calculated by multiplying the amount of nitrogen obtained with a factor 6.25 (N X 6.25).

STATISTICAL ANALYSES

All replication wise data are presented as mean ± standard deviation (SD). The significant difference was calculated using one way ANOVA, and the P value was set at *P ≤ 0.05, **P ≤ 0.01, ***P ≤ 0.001, ****P ≤ 0.0001.

RESULT AND DISCUSSION

Proximate composition of sorghum genotypes are given in the table [15]. The starch content showed significant (p≤0.0001) difference between white, red and brown sorghum genotypes. Highest starch content was seen in the genotype C-43 (66.25%) compared to red sorghum genotype IS 30533 (63.3%) and brown sorghum genotype IS 715 (62.85%). Starch content of white sorghum genotype ranged from 52% in RS 673 to 66.25% in C-43 and red sorghum genotype ranged from 57.55% in IS 4060 to 63.3% in IS 30533 whereas in brown sorghum genotype, it ranged from 56.55% in IS20697 to 62.85% in IS 715 genotype (Table-2). Among white, red and brown sorghum genotypes, lowest starch content was recorded as 52% in the white sorghum genotype RS 673. Similarly mean ± standard deviation (SD) values was calculated for starch content in white, red, and brown sorghum genotypes as 60.2%, 60.5% and 59.3% (Table-2). Significant progress is observed in the sorghum genetics since nineties. Physical and biochemical grain quality constitution have been studied [16, 17]. Starch is the main component in all the cereals, [18] and it was reported that the proximate composition of starch content in the sorghum-wheat flour biscuits ranged from 63.32% to 70.65%, the variation is due to type of cultivar and difference in the process variables. According to [19] the starch and fiber content of pure sorghum cookies were 73.73% and 2.24% respectively.

The protein content showed significant (p≤0.001) difference between white, red and brown sorghum genotypes. The protein content in sorghum grain ranged from 7.3% to 12.35%, and IS 12706 red sorghum genotype gave a significantly higher level of protein content 12.35% par with the white sorghum genotype IC345194 which showed protein content 12.25%, whereas low level of protein content was recorded as 7.3% in the brown sorghum genotype IS30508. Similarly mean ± standard deviation (SD) values was calculated for protein content in white, red, and brown sorghum genotypes as 9.9%, 9.3% and10.3% respectively (Table-2). Protein content in sorghum ranged from 9.6% to 14% and it was reported that crude protein in sorghum ranged from 9.14% to 13% [20-22]. Semolina recovery showed significant (p≤0.0001) difference between white, brown and red, brown sorghum genotypes, whereas non-significant difference was observed between white and red sorghum genotypes for semolina recovery. The range observed was 36.17% to 66.55% over the season with the genotype SPV933 white sorghum genotype expressing high recovery (66.55%). In the red sorghum genotypes, the semolina recovery ranged from 44.20% (IS12735) to 59.48% (IS23514), whereas in the brown sorghum genotypes, it ranged as 38.35% (IS23992) to 50.29% (IS20697) respectively. Similarly, low level of semolina recovery was recorded as 36.17% in the white sorghum genotype AKMS14B. For semolina recovery in white, red and brown sorghum genotypes, mean ± standard deviation (SD) values were calculated as 48.47%, 45.10% and 48.48% respectively (Table-2). Semolina from sorghum grain is the good source of calcium, iron, phosphorus, potassium and other minor elements [10, 23]. Semolina is the coarse part of the grain which is used in different food preparations. Genotypes suitable for semolina can also be used for making further sorghum products. [24] Reported that vitreous (corneous) endosperm expands while floury endosperm remains intact and genotype with corneous (hard) endosperm is more suitable for semolina preparation [1].

Endosperm texture among the genotypes had variation from 25% to 100% vitreousness. Genotypes with 100% vitreousness are considered as best genotypes. 27B, IC305923, IS33648, IS4372, SPV1750 and IS30533 white and red sorghum genotypes had shown 100% vitreousness. Endosperm texture showed

significant ($p \leq 0.0001$) difference between white vs. red and white vs. brown sorghum genotypes, whereas non-significant difference was observed between red vs. brown sorghum genotypes. Mean ± standard deviation (SD) values was calculated for endosperm texture in white, red and brown sorghum genotypes as 56.5%, 44.6%, 49.1% respectively (Table- 2).

Table-2: Grouping of the sorghum genotypes and mean performance

Genotype	Traits	Performance of the genotype for the trait			Best five genotypes
Red sorghum	Recovery (%)	**Mean**	**Min**	**Max**	
IS31681, IS4372, IS1212, IS1206, IS12735, IS16151, IS20298, IS20743, IS23514, IS2389, IS28141, IS28313, IS29241, IS29950, IS30533, IS3158, IS4060	Semolina	45.1	44.2	59.4	IS23514, IS29950, IS29241, IS28313, IS4060
	Starch content	60.5	57.55	63.3	IS30533,IS16151, IS23514, IS28141, IS29950
	Protein content	9.3	9	12.35	IS12706, IS4060, IS1212, IS28313, IS29950
	Endosperm texture	44.6	25	100	IS30503, IS20743, IS2389, IS28313,IS1212
White sorghum	Recovery (%)				
27B, 296B, 463B, 7B, AKMS14B, IMS 9B, AKR150, AKR354, C 43, I12, RS627, RS673,CSV13,CSV15, IC345194, IC305903, IC305923, IS33648, IS40751, IS18035, SPV1258 , SPV1293, SPV1471, SPV1606, SPV1616, SPV1731, SPV1732, SPV1733, SPV1734, SPV1750, SPV1760, SPV1775, SPV459, SPV462, SPV711, SPV933,	Semolina	48.4	36.1	66.5	SPV933, SPV1616, SPV1471, I12, CSV13
	Starch content	60.2	52	66.25	C-43, IMS9B, AKR150, 463B, IC305903
	Protein content	9.9	8	12.25	IC345194, IMS9B, SPV1258, SPV1750, SPV1731
	Endosperm texture	56.5	25	100	27B, IC305923, IS33648, IS4372, SPV1750
Brown sorghum	Recovery (%)				
IS12697, IS20697, IS23992, IS24462, IS 30466, IS30508, IS715	Semolina	48.4	38.5	50.2	IS20697, IS12697, IS30466, IS24462, IS715
	Starch content	59.3	56.55	62.8	IS715, IS23992, IS24462, IS30466, IS12697
	Protein content	10.38	7.3	11.25	IS23992,IS30466,IS715, IS20697,IS24462
	Endosperm texture	49.1	25	75	IS12697, IS24462, IS30508, IS23992, IS715

CONCLUSION

The sorghum genotypes evaluated in this study exhibited considerable proximate variability, semolina recovery and endosperm texture. Higher genotypic variability was observed for many of the traits studied. It would be possible to utilize the variation identified in sorghum improvement programs aimed at development of cultivars with high semolina recovery and proximate composition without compromising on productivity. The identified best sorghum genotypes will play a major role in enhancing the demand for sorghum as a beneficial industrial crop. With the availability of end product specific genotypes, farmers are benefitted with premium price and supply of superior quality raw material. Farming of identity-preserved-genotypes satisfies the demand and supply chain of industries.

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