



Nutritional composition of sorghum [*sorghum bicolor* (L.) Moench] genotypes cultivated without and with water stress



Valéria A.Vieira Queiroz ^{a,*}, Camila Santana da Silva ^b, Cícero Bezerra de Menezes ^a, Robert Eugene Schaffert ^a, Flávia F. Mendes Guimarães ^a, Lauro José M. Guimarães ^a, Paulo Evaristo de Oliveira Guimarães ^a, Flávio Dessaune Tardin ^a

^a Brazilian Agricultural Research Corporation – Embrapa, Embrapa Maize & Sorghum, Rodovia MG 424, km 65, Sete Lagoas, Minas Gerais CEP 35701-970, Brazil

^b Centro Universitário de Sete Lagoas – UNIFEMM, Av. Castelo Branco, 2465, Sete Lagoas, MG CEP: 35701-242, Brazil

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ABSTRACT

The carbohydrates, proteins, lipids, fibers (Neutral Detergent Fiber – NDF) and ash contents of 100 sorghum genotypes were evaluated and superior materials for each nutrient were identified. The genotypes were grown in environments without (WoWS) and with post-flowering water stress (WthWS). Tocher analysis grouped data into 9 clusters showing great variability for the nutritional characteristics, which were not influenced by race or place of origin. The carbohydrates, proteins, lipids, fibers and ash contents had, respectively, the following variations: 55.2–75.2%; 8.6–18.9%; 1.7–4.9%; 9.3–25.2% and 1.1–2.4%, in both environments. The best results were identified in the genotypes BR007B, SC59 and SC1033 for carbohydrates, SC325, SC320 and SC124 for proteins, SC35, N268B and Lian Tang Ai for lipids, SC673, SC467 and (SN142) REDBINE SA386-60 (ASA N98) for fiber and SC224, SC566, SC467 and SC1356 for ash. The carbohydrate, protein and ash contents were lower and the fiber was higher in samples grown in the environment with water stress. Lipids were not affected by the water stress. The genotypes listed above have great potential to develop cultivars with high nutritional value, especially to arid and semi-arid regions and may contribute to food security.

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1. Introduction

Information on the nutritional composition and other components present in fresh and processed foods are necessary for program development in various areas, such as nutrition, health,

education, agriculture, industry and food commerce (Giuntini et al., 2006). Knowledge of the chemical composition of foods is essential to estimate nutrient intake adequacy and nutritional status and health of individuals, as well as being essential for the calculation of diets, especially in the daily practice of nutrition and health professionals (Queiroz et al., 2009).

According to Giuntini et al. (2006), since the 1960s, the Food and Agriculture Organization of the United Nations (FAO) has been proposing new guidelines and criteria for the area of food composition, one of the initiatives being the promotion of sustainable use of biodiversity. According to FAO, the vast knowledge of food composition information of different cultivars of different regions and countries is important to ensure the conservation and sustainable use of biodiversity in human nutrition and food safety programs and all quality information on food composition must be used and disseminated.

Furthermore, the knowledge of variation in nutrient concentration of different groups of genotypes is important to support plant breeding programs to develop grain cultivars with high

Abbreviations: WthWS, with water stress; WoWS, without water stress; FAO, Food and Agriculture Organization of the United Nations; GxE, genotype versus environment; Embrapa, Brazilian Agricultural Research Corporation; IGD, Institute of Genome Development; NPK, nitrogen, phosphorus and potassium formula; USDA, United States Department of Agriculture; NDF, Neutral Detergent Fiber; AOCS, American Oil Chemists' Society; AOAC, Association of Official Analytical Chemists; ANOVA, Analyzes of variances; ICRISAT, International Crops Research Institute for the Semi-Arid-Tropics.

* Corresponding author. Rodovia MG 424, km 65, Sete Lagoas, Minas Gerais CEP 35701-970, Brazil.

E-mail addresses: valeria.vieira@embrapa.br (V.A.Vieira Queiroz), camilasilvasant@yahoo.com.br (C.S. da Silva), cicero.menezes@embrapa.br (C.B. de Menezes), robert.schaffert@embrapa.br (R.E. Schaffert), flaviafmenandes@yahoo.com.br (F.F.M. Guimarães), lauro.guimaraes@embrapa.br (L.J.M. Guimarães), paulo.guimaraes@embrapa.br (P.E.O. Guimarães), flavio.tardin@embrapa.br (F.D. Tardin).

nutrient value. Traditional plant breeding involves recombination and selection of genotypes with different genetic background (active genebanks, core collections and association panels) and depends on exploiting natural variation (Teixeira et al., 2013). However, according to Ray et al. (2008) the seed composition is affected by environmental factors, especially during the seed-filling period, so, the selection for high nutritional content should be preceded by analyses for genotype \times environment interaction (G \times E).

In this context, plants exposed to some kind of stress may show a wide range of complex and variable responses that are dependent on the inherent sensitivity of the particular genotype to stress (Cramer et al., 2011). According Thitisaksakul et al. (2012), water stress during grain development may cause reduction in starch content due to alterations in enzyme activity responsible for starch biosynthesis.

Sorghum [*Sorghum bicolor* (L.) Moench] and some millets have the greatest drought tolerance among all cereals, so, they are important crops in arid regions. Consequently, sorghum has been used as a staple food by millions of people, mainly in Africa and Asia, supplying about 70% of the daily caloric intake and has an important role in food security of these populations (Dicko et al., 2006).

Sorghum is grown mainly for animal feed in Brazil, and its consumption as a human food has not been explored. However, recently, there is considerable interest in sorghum for food because of its phytochemical content, nutritional potential and the possibility of use in gluten-free products (Awika and Rooney, 2004; Paiva et al., 2015; Taylor et al., 2014). Embrapa (Brazilian Agricultural Research Corporation) Maize & Sorghum has a large collection of sorghum accessions (more than 7000) that have not been characterized for these food quality characteristics; consequently, there is great potential to be explored for use in human nutrition. Furthermore, the effect of water stress on the nutritional profile of these genotypes has not been investigated.

The objective of this study was to evaluate the nutritional composition of 100 sorghum genotypes grown in with and without water stress environments and to identify superior genotypes to develop cultivars with high nutritional quality for food.

2. Material and methods

Seeds of 100 diverse sorghum genotypes (Table 1), from the IGD (Institute of Genome Development) sorghum association panel with high genetic variability were used in this study. Trials were planted at the Embrapa Maize and Sorghum research station, located in Nova Porteirinha, MG, in June 2010. The genotypes were grown in two environments: without water stress (WoWS, Environment 1) and with post-flowering water stress (WthWS, Environment 2) in order to evaluate water stress on the nutritional composition of sorghum grain. The experimental plots consisted of two rows 3 m long, spaced 0.50 m between rows. The planting fertilization consisted of the application of 300 kg ha⁻¹ of the NPK (nitrogen, phosphorus and potassium) formula 08-28-16. Twenty five days after planting, 150 kg ha⁻¹ of urea was applied. Supplemental water was applied by sprinkler irrigation for 2 h once a week. In the WoWS environment, the irrigation remained until the grain filling phase and in the WthWS irrigation was suspended about 50 days after planting, at the boot stage, that is just prior to the emergence of the panicle where the panicle is extended into flag leaf sheath. The harvest of the trials took place in October 2010. After harvesting, the seeds were transported to Embrapa Maize and Sorghum in Sete Lagoas, Minas Gerais, where the panicles were threshed and the grain was stored in a cold chamber at 10 °C until analysis.

2.1. Pericarp color, origin and race of the genotypes

The pericarp color of the genotypes was determined visually and the origin and race (Table 1) was based on Casa et al. (2008); USDA (2013); Morris et al. (2013) e Sukumaran et al. (2012).

2.2. Nutritional composition of the 100 sorghum genotypes

The seeds were milled in a Marconi cyclone mill, to a particle size of 0.5 mm and the seed samples were packaged in polyethylene bottles until analyzed, at the Centesimal Composition Laboratory at Embrapa Maize and Sorghum between April and May 2012. Neutral Detergent Fiber (NDF) was analyzed using a 0.5 g of sample with a Tecnal EQ LCC 08 fiber analyzer using the Ankom system with filter bags (ANKOM, 2006). The lipids were determined in a 1 g of sample using an XT10 Ankom Fat extractor, following the AOCS Protocol (2004). From the quantification of total nitrogen, protein content was determined by the Dumas method (Wiles et al., 1998) in 0.25 g of sample using an FP-528 Leco Nitrogen Analyzer and the results were multiplied by the factor 6.25. The ash content was determined in a 2 g of sample, according to the AOAC Method (2000) with calcination of the organic matter in a Q 318 D 24 Quimis muffle at 600 °C for 2 h. The carbohydrate concentration of the samples was determined by the difference between the total in the sample (100%) and the content of proteins, lipids, fibers and ash. All results were expressed on a dry matter basis, which was determined by the gravimetric method in a 2 g sample, using a forced-air oven at 105 °C for 6 h.

2.3. Grains per 100 g

One hundred grams of each genotype were weight and the number of grains was counted.

2.4. Statistical analyzes

Analyzes of variances (ANOVA) were performed for the levels of carbohydrates, proteins, fibers, lipids and ash, with two replications, and grains per 100 g with three replications, considering a completely randomized design. Skott–Knott test was used to compare the treatment averages. The genetic variability in 100 sorghum genotypes for the nutrients in each environment (with and without water stress) was assessed by Tocher's clustering technique based on the Mahalanobis distance. Pearson correlation coefficients were obtained between all traits and the significance of the correlation estimates were assessed by t-test. These statistical analyzes were performed using the statistical software GENES VS 2009 7.0 (Cruz, 2006).

The average carbohydrate, protein, lipid and ash levels of each genotype were plotted on scatterplots, the WoWS environment averages were plotted on the y-axis, and the WthWS environment averages were plotted on the x-axis as proposed by Guimarães et al. (2009).

3. Results and discussion

Based on the analysis of variance there were significant differences ($p < 0.01$) for the genotype nutritional composition and the environment source of variation (Supplementary Table 1). Tocher analysis grouped data into 9 clusters for both environments, showing great variability for the characteristics evaluated. In the first two groups, the concentration of genotypes was 75% for the environment without stress (WoWS) and 80% for the WthWS. The other groups were less expressive, being made up of a few genotypes. There was no grouping's relationship with race or place of

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