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PHENOTYPIC VARIABILITY AND CORRELATION ESTIMATES FOR TRAITS OF BURKINA FASO' SWEET GRAIN SORGHUM GENOTYPES

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ABSTRACT

Sweet grain sorghum [*Sorghum bicolor* (L.) Moench] is a neglected crop mainly grown for its sweet grains in the pasty form. Although its taste is the main character of interest, knowledge of protein related content of the grain, especially when linked to its value for infant porridge appears equally important. The objective of this study was to evaluate the status of crude protein content of pasty grains and to determine genetic correlations between morphological and biochemical traits among sweet grain of sorghum genotypes in Burkina Faso. Eight sweet grain sorghum cultivars (BTO2, BZI1, KBZ4, PBO5, PGO3, SBR7, SPI2, STO4) were evaluated through 13 morphological and two biochemical variables. Crude protein content of these genotypes was also compared with the composition of two controls of sweet stalk sorghum (ETS) and ordinary grain sorghum or common sorghum (EBS). The analysis of variance revealed variability within sweet grain sorghum accessions, mainly on the biochemical traits (crude protein and water content) and two morphological traits (peduncle and panicle lengths), which discriminated significantly in the thresholds of 1 and 5%, respectively. In addition, sweet grain sorghum had low crude protein content compared to other types of sorghum, except, two genotypes of sweet grain sorghum (BZI1 and STO4) which recorded higher protein content compared to the common sorghum. An important and negative correlation was noted between sowing-flowering cycle and protein content.

Key Words: Crude protein, *Sorghum bicolor,* sweet stalk sorghum

RÉSUMÉ

Le sorgho grains sucrés [*Sorghum bicolor* (L.) Moench] est une culture négligée produite essentiellement pour ses grains sucrés au stade pâteux. Bien que la saveur sucrée du grain soit le principal caractère d'intérêt, une connaissance de la teneur en protéines totales du grain au stade pâteux pourrait favoriser son utilisation pour implémenter les bouillies infantiles et contribuer à sa meilleure valorisation. La présente étude vise donc à déterminer la teneur en protéines totales des grains au stade pâteux du sorgho grains sucrés et établir les corrélations génétiques entre les caractères morphologiques et biochimiques. Ainsi, huit génotypes de sorgho grains sucrés (BTO2, BZI1, KBZ4, PBO5, PGO3, SBR7, SPI2, STO4) ont été évalués à l'aide de 13 caractères morphologiques et deux caractères biochimiques. La teneur en protéines totales de ces génotypes a été ensuite comparée à celle de deux témoins dont un sorgho à tige sucrée (ETS) et un sorgho ordinaire (ESB). L'analyse de variance a révélé une variabilité au sein des cultivars de sorgho grains sucrés observée surtout au niveau des traits biochimiques (teneur en protéines totales des graines et teneur en eau des graines) et de deux traits morphologiques (longueur du pédoncule et longueur de la panicule) qui ont significativement discriminé les accessions aux seuils de 1 et 5%, respectivement. De plus, le sorgho grains sucrés a présenté une faible teneur en protéines totales comparativement aux autres types de sorgho à l'exception de deux génotypes (BZI1 et STO4) qui ont montré une teneur en protéines plus élevée que le sorgho ordinaire. Une forte corrélation significative et négative a été également notée entre le cycle semis-floraison et la teneur en protéines totales.

Mots Clés: Protéines totales, *Sorghum bicolor,* sorgho à tige sucrée

INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] is the sixth most grown cereal crops in the world. It is a major staple food and fodder crop in tropical and semi-tropical Africa (Dogett, 1988; Zhao *et al.,* 2019). Sweet grain sorghum, the genetic resources of which are less valued, is particularly neglected. As such, information on national production and the extent of its cultivation are scarcely available in the national agricultural statistics.

Sweet grain sorghum is mainly cultivated for its grains which are consumed in pasty form. It is generally harvested before the main food crops, and therefore, constitutes a food of choice in rural areas during the period preceding the harvest of other cereals (Nebié *et al.,* 2012). Its sweet grains in pasty form are eaten directly; while its leaves and stems are exploited for fodder or domestic fuelwood (Sawadogo *et al.,* 2014a; Tiendrebeogo *et al.,* 2018; 2020). Moreover, the sale of panicles harvested at the pasty grains stage generates income for producers and retailers (Sawadogo *et al.,* 2017). Compared to common grain sorghum and sweet stalk sorghum, sweet grain sorghum is a minor crop in regions like West Africa; a factor that seriously threatens the preservation of its genetic resources (Sawadogo, 2015).

Most previous studies on sweet grain sorghum focused on its genetic diversity using agromorphological markers (Nebié *et al.,* 2012; Sawadogo *et al.,* 2014a, 2014b) and microsatellite markers (Sawadogo *et al.,* 2018). Other research efforts have identified mainly sugars responsible for the sweet taste (Sawadogo *et al.,* 2017) and genotypes with high grain yield and of high forage potential (Tiendrebéogo *et al.,* 2018); as well as determine the response of dual-use genotypes to mineral fertilisation (Tiendrebéogo *et al.,* 2020). Outputs from such studies highlight the existence of diversity within this sorghum, the predominance of the main race *caudatum* and the intermediate *caudatum-guinea* and the possibility of their improvement by direct selection (Sawadogo, 2015). They also attributed the sweet taste of grain at the pasty

stage to mainly fructose (Sawadogo *et al.,* 2017). However, no study has addressed the nutritional value of the grain in terms of protein content of grains, despite its important physiological roles. The objective of this study was to evaluate the status of crude protein content of pasty grains and to determine genetic correlations between morphological and biochemical traits among sweet grain of sorghum genotypes in Burkina Faso.

MATERIALS AND METHODS

Experimental site. The trial was conducted in the fields of the experimental site of the "Institut Supérieur des Sciences et Technologies Agricoles (ISSTA)" at Boulbi, a southern suburban area of Ouagadougou in Burkina Faso. The site is located at 12°13'35.3''N Latitude and 1°31'24.2''E Longitude. The experimental plots were established on a clay-sandy to sandy texture soil. The study was conducted during the rainy season of May-October 2015.

Plant materials. Eight sweet grain sorghum cultivars (Table 1) sampled from the Biosciences Laboratory of Joseph KI-ZERBO University germplasm, collected between 2008 - 2012 from four important production zones of sorghum in Burkina Faso, were used for this study. These sweet grain sorghum genotypes were selected so as to integrate the main botanical races and the different climatic zones of origin (Sawadogo, 2015). Two genotypes, including sweet stalk sorghum and common grain sorghum were added as controls, especially for crude protein content analysis.

Experimental design. The experiment was laid out in a Fisher block design, with three replications. Each replication included 12 lines of 6 m long each for each genotype. The distance between replications was 2 m, while the row spacing and spacing between plants were, respectively, 0.8 and 0.4 m. Each genotype was sown on one line per replication. To minimise edge effects, two additional lines of fills were planted around each replication.

Biochemical analyses. Water content was determined by the method of AOAC 925:10 (Horwitz, 2000), whereby 20 g of grains from the main panicle of each assessed sweet grain sorghum genotype, were collected at the pasty stage and placed in petri dishes. Sample-containing dishes were oven dried for 48

TABLE 1. Agroclimatic zone and botanical race of the sweet grain sorghum genotypes assessed in Burkina Faso

Type of sorghum	Genotypes	Climatic zone	Botanical race
Sweet grain sorghum	BTO2	North Sudanese	*Caudatum*
	BZI1	South Sudanese	*Caudatum-guinea*
	KBZ4	South Sudanese	*Caudatum*
	PBO5	Sub Sahelian	*Caudatum-guinea*
	PGO3	Sub Sahelian	*Caudatum*
	SBR7	South Sudanese	*Caudatum*
	SPI2	SubSahelian	*Caudatum-guinea*
	STO4	South Sudanese	*Caudatum*
Sweet stalk sorghum	ETS	Sub-sahelian	*Bicolor*
Common grain sorghum	EBS	Sub-sahelian	*Guinea*

hours at 75 °C. The dried samples were cooled in a desiccator at room temperature and reweighted. Water content (GWC) was obtained gravimetrically by applying the following formula:

$$GWC\ (\%) = \frac{Pf - Ps}{Pf} * 100$$

Where:

Pf = weight of fresh seeds, and Ps = weight of dry seeds.

Crude protein determination of the eight sweet grain sorghum genotypes and two controls was performed by the Kjeldahl method AOAC 925:10 (Horwitz, 2000). It consisted of digestion of organic nitrogen into ammonium and then determining it by acidimetry. A quantity of 0.2 g of sorghum flour from the sample to be analysed, a Kjeltabsck tablet (3.5 g of potassium sulfate K_2SO_4, 4 g of copper sulfate $CuSO_4$, $5H_2O$), 10 ml of concentrated sulfuric acid and a few drops of hydrogen peroxide were successively introduced into a Kjeldahl flask. The digestion was done for 4 hours at 400 °C. A blank was treated accordingly, , except that the sample was replaced with distilled water. Each sample was assayed in triplicates. Crude protein content (GPC) was calculated according to the following formula:

$$GPC\ (\%) = \frac{(Ve - Vb) \times N \times 14{,}01 \times F}{PE}$$

Where:

Ve = drop of burette of the sample (ml), Vb = drop of white burette (ml), N = normality of the acid used for the titration, PE = sample test (g), F = 6.25, conversion factor F (coefficient based on a nitrogen content of 16.8 percent for the main processed sorghum protein, glutelin), and 14.01 = molar mass of nitrogen.

Plant variables measured. Fifteen quantitative variables, including 13 phenological and morphological variables measured directly in the field and the two biochemical traits, grain crude protein content (GPC) and grain water content (WPC) determined by laboratory analysis were collected.

The phenological and morphological traits included days to flowering (NDF); while leaf length (LEL), leaf width (LEW), internode length (INL), number of internodes (NIN), peduncle length (PDL), plant height (PHT), stem diameter (SDI; at 0.3 m from plant base), panicle length (PAL), panicle width (PAW), weight of the main panicle (PWT), and weight of grains of the main panicle (PGW) were collected during the pasty stage of grain. At maturity, only one hundred grain weight (HGW) trait was determined on dry grain. The pasty stage of panicles is shown in Figure 1.

Statistical analysis. The data collected were analysed using the Statistica software Version 6. A one-way analysis of variance was carried out to verify significance differences between sweet grain sorghum cultivars for all variables. The coefficient of variation was determined to evaluate the level of variation of the mean observed between cultivars for all variables. In addition, means separation test of Newman-Keuls at the 5% threshold was performed to determine the significance of the means differences between sweet grain sorghum genotypes for the discriminating characters. The same test was used to compare the crude protein content of sweet grain sorghum genotypes to the controls (common sorghum and sweet grain sorghum). Pearson's R coefficient was also carried out to measure correlations between variables.

RESULTS

Variation of characters. The results of analysis of variance for the 15 quantitative traits are presented in Table 2. Peduncle length

Figure 1. Sweet grain sorghum panicles at the pasty grain stage. (a) Beginning pasty stage, (b) Intermediary pasty stage, (c) End pasty stage.

TABLE 2. Results of analysis of variance of quantitative variables of sweet sorghum genotypes

Type of traits	Genotypes	Minimum	Maximum	Mean	CV (%)	F
Agromorphological traits	NDF (days)	66	73	71.46	2.30	2.05ns
	PHT (cm)	203.3	338.67	278.12	10.94	0.68ns
	SDI (cm)	2.32	2.96	2.82	4.30	1.37ns
	LEW (cm)	7.93	15.4	10.39	19.12	0.48ns
	LEL (cm)	60.33	88.83	78.27	8.88	1.88ns
	INL (cm)	21.33	25.17	23.53	4.34	1.53ns
	NIN	10.67	13.67	12.49	5.53	1.83ns
	PDL (cm)	33.87	56.57	49.20	11.11	**2.85***
	PAL (cm)	29.67	39.93	32.73	7.41	**4.07***
	PAW (cm)	9.57	15.77	13.05	13.16	0.37ns
	PWT (g)	111.6	248.23	173.19	25.48	1.27ns
	PGW (g)	88.13	207.77	149.96	26.02	1.10ns
	HGW (g)	1.7	4.6	2.67	22.84	0.69ns
Biochemical traits	GPC (%)	10.92	13.99	12.49	5.85	**7.43****
	GWC (%)	32	56	45.17	14.91	**8.76****

R^2 = Coefficient of determination; CV = Coefficient of variation; F = Fisher' value; significant: *P < 0.05; **P < 0.01; ns = not significant; NDF = Number of days to flowering; PHT = Plant height; SDI = Stem diameter; LEW = Leaf width; LEL = Leaf length; INL = Internodes length; NIN = Number of internodes; PDL = Peduncle length; PAL = Panicle length; PAW = Panicle width; PWT = Weight of the main panicle; PGW = Weight of grains of the main panicle; HGW = Hundred grain weight; GPC = Grain protein content; GWC= Grain water content

(PDL) and panicle length (PAL) were significantly different (P<0.05) among the sweet grain sorghum genotypes, but the others phenological and morphological traits were not significant difference for the eight genotypes. The length of peduncle varied from 33.87 to 56.57 cm, and, the length of main panicle ranged from 29.67 to 39.93 cm.

The accessions had a relatively short sowing-flowering cycle, varying from 66 to 73 days. For grain composition, crude protein content and water content significantly

discriminated (P<0.01) the sweet grain sorghum genotypes. The pasty grain had crude protein content ranging from 10.92 to 13.99%, with a water content varying from 32 to 56%.

Sweet grain sorghum genotypes. The results of means separation test using discriminating traits (Table 3) revealed that genotype SBR7 had the greatest length of peduncle (54.92 cm) and water content (57.67%). Genotype PBO5 had the longest panicles (36.54 cm) and BZI1 genotype the highest crude protein content (13.55). BTO2 genotype displayed the lowest values of these parameters, with 40.40 cm for the length of peduncle, 30.31 cm for the length of panicle, 35% for grain water content and 11.79% for crude protein content.

Crude protein content. Results revealed that sweet grain sorghum genotypes had lower protein content than sweet stalk sorghum (Table 4). In addition, six sweet grain sorghum genotypes had a lower protein content than the ordinary grain sorghum. Only BZI1 and STO4 genotypes had protein content higher than common sorghum.

Correlation analysis. The Pearson correlation test revealed 15 significant correlations between traits (Table 5). Grain protein content (GPC) was negatively correlated with number of days to flowering (r = -0.742; P<0.05); while grain water content (GWC) was positively related with peduncle length (r = 0.78; P<0.05). The number of internodes (NIN) was negatively related with panicle width (r = 0.91; P<0.01), main panicle weight (r = 0.958; P<0.01) and weight of grains of main panicle (r = 0.94; P<0.01).

Stem diameter (SDI) was positively correlated with leaf length (r = 0.94; P<0.01), panicle width (r = 0.88; P<0.01) and main panicle weight (r = 0.70; P<0.05). Panicle width positively related with main panicle weight (r = 0.84; P<0.01), and weight of grains of the main panicle (r = 0.81; P<0.05). Leaf length (LEL) was positively linked to internode length (r = 0.71; P<0.05) and main panicle width (r = 0.86; P<0.01). However, the internode length (INL) and peduncle length were negatively related to leaf width (r = 0.72; P<0.05) and weight of the main panicle (r = 0.71; P<0.05). The weight of the main panicle (PWT) was positively correlated with the weight of grains of the main panicle (r = 0.98; P<0.01).

DISCUSSION

Sweet grain sorghum accessions in Burkina Faso. Morphological variability was observed within grain sorghum accessions only on two traits (Table 2). This difference could be explained by the small size of the sample (8) compared to other studies which used larger accessions samples (Sawadogo *et al.,* 2014a, b; Tiendrebéogo *et al.,* 2018). On the other

TABLE 3. Results of Neman Keuls means separation test of the four discriminating traits for sweet sorghum

Genotype	SBR7	SPI2	PGO3	BZI1	STO4	KBZ4	PBO5	BTO2
PDL (cm)	54.92^{a}	52.20^{ab}	51.07^{ab}	50.20^{ab}	48.89^{ab}	48.28^{ab}	47.63^{ab}	40.40^{b}
PAL (cm)	36.36^{ab}	30.81^{b}	31.87^{ab}	32.23^{ab}	34.17^{ab}	33.92^{ab}	36.54^{a}	30.31^{b}
GPC (%)	12.83^{abc}	12.38^{bc}	11.80^{c}	13.55^{a}	13.26^{ab}	11.95^{c}	12.36^{bc}	11.79^{c}
GWC (%)	57.67^{a}	47^{a}	48.67^{a}	46.67^{a}	45.33^{a}	36.33^{b}	49.67^{a}	35^{b}

PDL= Peduncle length; PAL = Panicle length; GPC = Grain protein content; GWC = Grain water content; a, b, c = the values followed by the same letters are not significantly different at the threshold of 5%

TABLE 4. Mean values of total protein content of genotypes of sweet grain sorghum and controls among accessions

Genotypes	Crude protein (%)	Standard deviation
ETS (Sweet stalk sorghum)	17.480[a]	0.433
BZI1	13.549[b]	0.431
STO4	13.264[bc]	0.252
ESB (Common sorghum)	13.255[bc]	0.249
SBR7	12.833[bcd]	0.253
SPI2	12.375[cd]	0.503
PBO5	12.363[cd]	0.243
KBZ4	11.950[d]	0.259
PGO3	11.797[d]	0.014
BTO2	11.791[d]	0.867

ETS and ESB are controls; a. b. c, d = the values followed by the same letters within a column are not significantly different at the threshold of 5%

hand, the differences could be due to the criteria of selection of accessions based mainly on morphological traits (botanical race), which could have allowed the selection of genotypes, genetically close on the quantitative agro-morphological characters.

The precocity of the sowing-flowering cycle (66 -73 days) would confirm their exploitation welding food by farmers (Sawadogo, 2015). This precocity of the cycle would constitute a selective advantage in so far as we are witnessing increasingly a shortening of the rainy season and a general drop in rainfall over the years (Nebié *et al.,* 2012).

The variability of the material for protein and the water contents (Table 2) of the grains could be justified by not taking these traits into account when selecting the genotypes. As all genotypes were evaluated in same environment, this variability would, therefore, be essentially genetic. For the water content, the value obtained (32-56%) was similar to that of Ogbonna *et al.* (2004) of 35 to 40%, and Tiendrebéogo *et al.* (2018) of 26.72 to 52.44%, but significantly different from those reported by Tasie and Gebreyes (2020) on ordinary sorghum; which ranged between 9.661 to 12.937%. The high water content observed may be linked to the specificity of this sorghum. Indeed, this sorghum is harvested at the pasty grain stage, during which the water content is still high.

The protein content of sweet grain sorghum grains, which varied from 11.79 to 13.55%, was similar to values reported on ordinary grain sorghum by Dicko *et al.* (2006) of 7 to 15%, Johnson *et al.* (2010) of 3.25 to 14.53%, Chung *et al.* (2011) of 11.25 to 13.42%, Badigannavar *et al.* (2016) of 10.30 to 14.90% and Tasie and Gebreyes (2020) of 8.20 to 16.48%. However, it had weak protein content compared to sweet stalk sorghum (17%) genotypes. The protein content difference between sorghum types may be attributed mainly to the genetic difference (Deosthale *et al.,* 1972). In general, sweet grain sorghum genotypes were less rich in protein than the two others types of sorghum.

The positive correlations observed between panicle width, weight of the main panicle, and weight of the grains of the main panicle would suggest improvement of one of these traits leads to that of others traits. That could

TABLE 5. Pearson's phenotypic correlation coefficient of 15 quantitative traits of sweet and common sorghum genotypes of Burkina Faso

Traits	NDF	PHT	SDI	LEW	LEL	INL	NIN	PDL	HGW	PAL	PAW	PWT	PGW	GPC
NDF	1.000													
PHT	-0.104	1.000												
SDI	0.063	-0.071	1.000											
LEW	-0.334	-0.217	0.075	1.000										
LEL	0.024	0.102	**0.940****	-0.199	1.000									
INL	0.114	0.248	0.448	**-0.727***	**0.710***	1.000								
NIN	0.360	-0.150	-0.706	-0.256	-0.610	-0.071	1.000							
PDL	-0.137	-0.097	-0.601	-0.636	-0.361	0.317	0.617	1.000						
HGW	-0.260	-0.296	0.412	-0.180	0.461	0.292	-0.190	0.092	1.000					
PAL	-0.314	0.171	0.200	-0.326	0.256	0.192	-0.659	0.062	0.105	1.000				
PAW	-0.282	0.099	**0.882****	0.077	**0.861****	0.418	**-0.910****	-0.502	0.335	0.525	1.000			
PWT	-0.192	0.292	**0.709***	0.223	0.613	0.060	**-0.958****	**-0.712***	0.088	0.612	**0.849****	1.000		
PGW	-0.287	0.343	0.624	0.175	0.556	0.062	**-0.948****	-0.609	0.076	0.700	**0.817***	**0.986****	1.000	
GPC	**-0.742***	-0.209	-0.305	0.238	-0.278	-0.113	-0.056	0.401	-0.117	0.195	0.029	-0.173	-0.096	1.000
GWC	-0.185	-0.369	-0.377	-0.515	-0.237	0.198	0.292	**0.785***	0.382	0.241	-0.227	-0.488	-0.434	0.441

NDF = Number of days to flowering, PHT = Plant height, SDI = Stem diameter, LEW = Leaf width, LEL = Leaf length, INL = Internodes length, NIN = Number of internodes, PDL = Peduncle length, PAL = Panicle length, PAW = Panicle width, PWT = Weight of the main panicle, PGW = Weight of grains of the main panicle, HGW = Hundred grain weight, GPC = Grain protein content, GWC = Grain water content, $R^{2:}$ = Coefficient of determination, Significance at *P < 0,05; **P < 0,01

facilitate their genetic improvement. Also, panicle width was positively related by stem diameter and leaf length. Previous studies of Tiendrebéogo *et al.* (2018) on sweet grain sorghum from Burkina Faso and Naoura *et al.* (2019) on dry-season sorghum from Chad, also reported similar results between these variables. Indeed, genotypes with large panicles have large stems and long leaves, which would promote good photosynthetic activity and good nutrition of plants.

On the other hand, the negative correlations recorded would show a reduction of panicle width, weight of the main panicle, and weight of the grains of the main panicle with the increase in the number of internodes. Tiendrebéogo *et al.* (2018) contrastingly noted a positive correlation between these characters. Our results could be explained by greater mobilisation of the substances synthesised during photosynthesis in vegetative growth. This is also confirmed by the negative correlation recorded between the sowing-flowering cycle and the protein content, which could limit in selection, the possibilities of improving the grains protein content with an extension of the cycle.

CONCLUSION

The study highlights low variability in the genotypes evaluated for most of the agromorphological traits. However, protein and water contents of the grains significantly discriminate the accessions. In addition, a negative correlation between the sowing-flowering cycle and the protein content was observed. Although sweet grain sorghum is less rich in protein than sweet stalk sorghum, some genotypes like BZI1 and STO4 have protein contents similar to ordinary sorghum. A more in-depth study of the amino acid composition of these two genotypes could make it possible to complete the results of this study.

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