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 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, SP12, 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 également été 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
Variability and correlation estimates for traits of sorghum 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 Bouli, 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 hours. The water content was calculated as: water content (%) = (weight of wet sample - weight of dry sample) / weight of wet sample x 100.

| 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      | Sub Sahelian      | 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:

\[
\text{GWC} (%) = \frac{P_f - P_s}{P_f} \times 100
\]

Where:

\(P_f\) = weight of fresh seeds, and \(P_s\) = 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 Kjeltabck tablet (3.5 g of potassium sulfate \(K_2SO_4\), 4 g of copper sulfate \(CuSO_4 \cdot 5H_2O\), 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:

\[
\text{GPC} (%) = \frac{(V_e - V_b) \times N \times 14.01 \times F}{PE}
\]

Where:

\(V_e\) = drop of burette of the sample (ml), \(V_b\) = 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 (HG) 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
Variability and correlation estimates for traits of sorghum 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 varied among the genotypes. The results are presented in Table 2.

**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   | 5.30  | 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** |       |

R² = Coefficient of determination; CV = Coefficient of variation; F = Fisher’s 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.
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)  | $54.92^{ab}$ | $52.20^{ab}$ | $51.07^{ab}$ | $50.20^{ab}$ | $48.89^{ab}$ | $48.28^{ab}$ | $47.63^{ab}$ | $40.40^{a}$ |
| PAL(cm)  | $36.36^{ab}$ | $30.81^{a}$ | $31.87^{a}$ | $32.23^{b}$ | $34.17^{b}$ | $33.92^{b}$ | $36.54^{a}$ | $30.31^{b}$ |
| GPC(%)   | $12.83^{bc}$ | $12.38^{bc}$ | $11.80^{a}$ | $13.55^{a}$ | $13.26^{b}$ | $11.95^{c}$ | $12.36^{bc}$ | $11.79^{c}$ |
| GWC(%)   | $57.67^{a}$ | $47^{a}$ | $48.67^{a}$ | $46.67^{a}$ | $45.33^{a}$ | $36.33^{a}$ | $49.67^{a}$ | $35^{a}$ |

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%
Variability and correlation estimates for traits of sorghum

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 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).

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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 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<sup>a</sup> | 0.433              |
| BZI1                  | 13.549<sup>b</sup> | 0.431              |
| STO4                  | 13.264<sup>c</sup> | 0.252              |
| ESB (Common sorghum)  | 13.255<sup>bc</sup> | 0.249              |
| SBR7                  | 12.833<sup>bcd</sup> | 0.253              |
| SPI2                  | 12.375<sup>d</sup>  | 0.503              |
| PBO5                  | 12.363<sup>d</sup>  | 0.243              |
| KBZ4                  | 11.950<sup>i</sup>  | 0.259              |
| PGO3                  | 11.797<sup>l</sup>  | 0.014              |
| BTO2                  | 11.791<sup>i</sup>  | 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%.
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, R² = 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 BZII 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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**REFERENCES**

Badigannavar, A., Girish, G., Ramachandra, N, V. and Ganapathi, T.R. 2016. Genotypic variation for seed protein and mineral content among post-rainy season-grown sorghum genotypes. *The Crop Journal* 4(1): 61–67. https://doi.org/10.1016/j.cj.2015.07.002

Chung, I.M., Kim, E.H., Yeo, M.A., Kim, S.J., Seo, M.C. and Moon, H.I. 2011. Antidiabetic effects of three Korean sorghum phenolic extracts in normal and streptozotocin-induced diabetic rats. *Food Research International* 44(1):127–132. https://doi.org/10.1016/j.foodres.2010.10.05

Deosthale, Y., Nagarajan, V. and Rao, K.V. 1972. Some factors influencing the nutrient composition of sorghum grain. *Indian Journal of Agricultural Sciences* 42:100–108.

Dicko M. H., Gruppen H., Traoré A. S., Voragen A. G. and Van Berkel W. J. 2006. Sorghum grain as human food in Africa: relevance of content of starch and amylase activities. *African Journal of Biotechnology* 5(5):384–395. http://www.academicjournals.org/AJB
Doggett, H. 1988. Sorghum. 2nd Ed. Longman Scientific and Technical, New York, NY. 512pp.

Naoura, G., Sawadogo, N., Atchozou, E.A., Emendack, Y., Hassan, M.A., Reoungal, D., Amos, D.N., Djirabay, N., Tabo, R. and Laza, H. 2019. Assessment of agromorphological variability of dry-season sorghum cultivars in Chad as novel sources of drought tolerance. *Scientific Reports* 9 : 19581, 12p. | https://doi.org/10.1038/s41598-019-56192-6

Horwitz, W. 2000. *Official Methods of Analysis of AOAC International* 17th Edition. *Journal of the Association of Official Analytical Chemists*, Gaithersburg, MD, USA.

Johnson, W.B., Ratnayake, W.S., Jackson, D.S., Lee, K.M., Herrman, T.J., Bean, S.R. and Mason, S.C. 2010. Factors affecting the alkaline cooking performance of selected corn and sorghum hybrids. *Cereal Chemistry* 87(6): 524-53. https://doi.org/10.1094/CCHEM-06-10-0087

Kondombo, C.P., Barro, A., Kaboré, B., and Bazier, J.M. 2016. On-Farm diversity of sorghum [*Sorghum bicolor* (L.) Moench] and risks of varietal erosion in four regions of Burkina Faso. *International Journal of Biodiversity Conservation* 8(8):171-179. https://doi.org/10.5897/IJBC2016.0966

Nebié, B., Gapili, N., Traore, R.E., Nanema, K.R., Bationo-Kando, P., Nebie, B., Sawadogo, M. and Zongo, J.D. 2012. Diversité phénotypique des sorghos à grains sucrés du centre nord du Burkina Faso. *Sciences et Techniques, Sciences Naturelles et Agronomie* 32(1 et 2):73-84.

Ogbonna, A.C., Obi, S.K.C. and Okolo, B.N. 2004. Optimization of proteolytic activities in malting sorghum. *Process Biochemistry* 39(6):711-716. https://doi.org/10.1016/S0032-9592(03)00181-X

Sawadogo, N., Nebié, B., Kiebré, M., Bationo-Kando, P., Nanema, K.R., Traoré, R.E., Gapili, N., Sawadogo, M. and Zongo, J.D. 2014a. Caractérisation agromorphologique des sorghos à grains sucrés (*Sorghum bicolor* (L.) Moench) du Burkina Faso. *International Journal of Biological and Chemical Science* 8(5):2183-2197. doi: 10.4314/ijbcs.v8i5.22

Sawadogo, N., Nanema, K.R., Bationo, P., Traore, R.E., Nebie, B., Tiama, D., Sawadogo, M. and Zongo, J.D. 2014b. Évaluation de la diversité génétique des sorghos à grains sucrés (*Sorghum bicolor* (L.) Moench) du Nord du Burkina Faso. *Journal of Applied Biosciences* 84(1): 7654-7664. doi: 10.4314/jab.v84i1.3

Sawadogo, N. 2015. Diversité génétique des sorghos à grains sucrés [*Sorghum bicolor* (L.) Moench] du Burkina Faso. Thèse de Doctorat., Université de Ouagadougou, 194pp.

Sawadogo, N., Ouedraogo, M.H., Traore, R.E., Nanema, K.R., Kiebre, Z., Batio-Kando, P., Nebie, B., Sawadogo, M. and Zongo, J.D. 2017. Effect of Agromorphological diversity and botanical race on biochemical composition in sweet grains sorghum [*Sorghum bicolor* (L.) Moench] of Burkina Faso. *Journal of BioScience and Biotechnology* 6(1):263-269. .uni-plovdiv.bg

Tasie, M.M. and Gebreyes, B.G. 2020. Characterization of nutritional, antinutritional, and mineral contents of thirty-five sorghum varieties grown in Ethiopia. *International Journal of Food Science* 2020:11p. Article ID 8243617, https://doi.org/10.1155/2020/8243617

Tiendrebeogo, J., Sawadogo, N., Kiebre, M., Kabore, B., Bationo/Kando, P., Kiendrebeogo, T., Ouedraogo, M.H. and
Sawadogo, M. 2018. Evaluation comparative de la production de grains et du fourrage de sorgho à grains sucrés du Burkina Faso. SPECIAL SIST 2017 SNA2_agrono27i: 261-271.

Tiendrebeogo, J., Sawadogo N., Kiendrebeogo, T., Kiebre, Z., Sawadogo, B., Kiebre, M., Zerbo, A., Nanema, K.R. and Sawadogo, M. 2020. Réponse agromorphologique de 14 génotypes de sorgho grains sucrés du Burkina Faso à la fertilisation minérale. *Journal of Applied Biosciences* 145:14880-14891. https://doi.org/10.35759/JABs.v145.3

Zhao, Z.Y., Che, P., Glassman, K. and Albertsen, M. 2019. Nutritionally enhanced sorghum for the arid and semiarid tropical areas of Africa. Zhao, Z.Y. and Dahlberg, J. (Eds.), vol. 1931 of Methods in Molecular Biology, Humana Press, New York, NY, USA. https://doi.org/10.1007/978-1-4939-9039-9_14