Chapter

Assessment of Genetic Variability of Three Types of Sorghum Cultivated in Burkina Faso Using Morphoagronomic Quantitative Traits and Brix

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Abstract

In Burkina Faso, three types of sorghum are mainly grown. Despite their genetic proximity revealed by molecular markers, the identification of distinctive agro-morphological traits between sweet grain sorghum, sweet sorghum and grain sorghum could contribute to better management of their genetic resources. Thus, 42 genotypes consisting of the three sorghum types were evaluated in a three replicate Fisher incomplete block design using 20 quantitative traits. The results showed a high variability of traits within each sorghum type and a greater closeness between sweet grain sorghum and sweet stalk sorghum. In addition, nine traits clearly discriminated sweet grain sorghum from the other sorghum types. Sweet grain sorghum expressed the highest values of the sowing-heading cycle, leaf sheath length, stem diameter, productive tillers, and panicle width and the lowest values of mean heading-flowering difference, 100-grain weight, and Brix. Moreover, the 'sorghum type' factor is less preponderant than the 'genotype factor' in expressing the variability of all traits. Therefore, the 42 genotypes are organized into three genetic groups independently of the sorghum- type factor, where the group I contains all sweet grain sorghum genotypes and three sweet stalk sorghum genotypes. These results could be exploited in sorghum breeding programs.

Keywords: sorghum, agro-morphological variability, genetic relationship, Brix, Burkina Faso

1. Introduction

Burkina Faso is a Sahelian country whose socioeconomic development is mainly based on agriculture [1]. The agricultural sector employs about 80% of the total population and is the country's main provider of food resources [2]. However, agricultural production is affected by climatic hazards such as irregular rainfall and shortened rainy seasons, resulting in huge yield losses and permanent food insecurity [3]. To cope with these climatic constraints, crop diversification appears to be the most appropriate solution for resilient agriculture.

In Sahelian countries such as Niger, Mali, Senegal, and Burkina Faso, cereals are the staple food of the population [4]. Sorghum [*Sorghum bicolor* (L.) Moench] is the most important crop. Moreover, it is the main food crop for millions of people and excellent fodder for animals in semiarid and arid tropical areas [5]. Sorghum is the fifth most important cereal crop in the world and the third most important in Africa after maize and rice in terms of production volume and area sown [6].

In Burkina Faso, sorghum is the second most important cereal crop after maize, with an estimated total production of 1,839,570 tonnes, including 1,425,103 tonnes of white sorghum and 414,467 tonnes of red sorghum [7]. However, these statistics do not highlight all types of sorghum produced. Indeed, several types of sorghum with varied but little known potential are grown in Burkina Faso and maintained by farmers [8–10]. These include grain sorghum, sweet grain sorghum, sweet sorghum, and dyer sorghum [11]. These sorghums are mainly exploited for human consumption for their grains or the sweet juice from their stems, for animal feed for their straw, and for dyeing for their strongly anthocyanated leaf sheaths [11]. The dynamic management of this diversity by farmers allows for evolutionary adjustment to a heterogeneous environment, but also to meet diversified use needs [12]. Most previous studies focusing on genetic diversity within each sorghum type have reported the existence of genetic diversity within grain sorghum [12–14], sweet grain sorghum [10], and sweet sorghum [11]. In addition, grain sorghum and sweet sorghum have been the subject of several scientific works. However, work on sweet grain sorghum is relatively recent [9, 10, 15, 16]. Therefore, information on the distinctive agro-morphological traits of this sorghum compared with other cultivated sorghums remains scarce. This could constitute a constraint to the rational exploitation of the potential of this genetic resource in breeding programs. To date, few studies on the genetic relationships between sweet grain sorghum and other sorghum types grown in Burkina Faso have been carried out using nuclear and chloroplast molecular markers. Although the results obtained showed genetic proximity between these sorghum types [17, 18], the evaluation of these sorghums under identical cropping conditions could help identify agro-morphological and biochemical traits specific to sweet grain sorghum that could be exploited in sorghum improvement programs. Thus, the present study aims to compare the quantitative agro-morphological and biochemical characteristics of sweet grain sorghum with grain sorghum and sweet sorghum grown in Burkina Faso. In particular, the aim is to (i) determine the agro-morphological and biochemical traits of sweet grain sorghum that are similar to those of other cultivated sorghums, (ii) identify the distinctive traits, and (iii) evaluate the effect of the factors "genotype" and "sorghum type" on the variability of the three types of sorghum grown in Burkina Faso.

2. Material and method

2.1 Plant material

The plant material consisted of 42 sorghum genotypes including 22 sweet grain sorghum, 10 sweet sorghum, and 10-grain sorghum (common sorghum). The seeds of sweet grain sorghum and sweet sorghum came from the germplasm of the Laboratoire Biosciences of Université Joseph KI-ZERBO. The seeds of grain sorghum were obtained from the "Institut de L'Environment et de Recherche Agricole (INERA)," "Kamboinsé," Burkina Faso.

2.2 Experimental site

The agro-morphological evaluation took place under rainfed conditions in 2020 at the experimental station of the "Institut du Développement Rural (IDR)" in "Gampéla." The locality is located in the northern Sudanese climatic zone with geographical coordinates of 12°25' North latitude and 1°21' West longitude. The soil is very heterogeneous, deep, of low chemical fertility, and predominantly sandy loam texture [19]. During the trial from July to October, the average monthly temperature ranged between 26 and 28°C for a cumulative rainfall of 769 mm.

2.3 Experimental design

The experimental setup was an incomplete Fisher block with three replications, each subdivided into three sub-blocks. Each sub-block consisted of 14 lines and 11 patches per line with 0.8 m row spacing and 0.4 m inter-patches. Each replication had 42 lines with one line per genotype and two borderlines. The distances between replications and sub-blocks were respectively 2 and 1 m for a total area of 504 m^2.

2.4 Cultivation techniques

The field was plowed with a tractor and leveled before sowing on July 18, 2020. In the course of the trial, a wedding with one plant per stake was carried out 15 days after sowing, followed by two weedings on the 18th and 35th day after sowing respectively. Ridging was then carried out toward the end of the vegetative development of the plants in order to counteract the lodging caused by the high winds. NPK fertilizer (14–23-14) was applied at each weeding at a rate of 50 kg/ha, and urea was applied at the time of weeding at a rate of 50 kg/ha.

2.5 Data collection

A total of 20 quantitative traits, of which 19 were agro-morphological and one (01) biochemical, were determined by measurement or counting. These traits are related to phenology, vegetative organ characteristics, yield parameters, and soluble sugar content (Brix).

2.5.1 Phenology-related traits

Four variables have been determined. These are the sowing-emergence cycle, the sowing-heading cycle, the sowing-flowering cycle, and the heading-flowering difference.

2.5.2 Vegetative-organs-related traits and the soluble sugar content of the stem (Brix)

The leaf characteristics were the number of leaves per plant, the length of the third leaf under the panicle, the width of the third leaf under the panicle, the length of the leaf sheath, and the separation, which corresponds to the half-distance between the base of the blade of the third leaf and the fifth leaf under the panicle. On the stem, the length of the internode, the number of internodes, the diameter of the main stem, and the number of vegetative tillers were determined. The height of the plant at maturity (HPL) was also measured. The soluble sugar content of the stem (Brix) was determined at the hard grain stage using a portable digital refractometer (ATAGO PAL-α) with an accuracy of ±0.2% on the two central internodes located in the middle of the stem.

2.5.3 Yield-related traits

Five traits were measured. These are the number of productive tillers per plant, the length of the peduncle, the weight of 100 grains, and the length and width of the panicle.

2.6 Data analysis

Data processing and analysis were carried out with the Excel 2016 spreadsheet and Xlstat 2016 software. An analysis of variance coupled with a Newman–Keuls test of the separation of means at the 5% threshold was carried out in order to evaluate the variability of the material studied and to determine on the one hand the variables that discriminate the types of sorghum and on the other hand the effects of the factors "genotype" and "type of sorghum" on the expression of the characters through the coefficient of determination (R^2). A principal component analysis (PCA) was also carried out to highlight the variables that characterize each type of sorghum. A hierarchical ascending classification (HAC) was finally carried out according to the genotypes, using the majority of the quantitative characters in order to observe the grouping of the genotypes. The groups obtained were finally characterized by discriminant factor analysis (DFA).

3. Results

3.1 Comparison of sweet grain sorghum with other cultivated sorghums based on phenology-related traits

The results recorded in **Table 1** showed an absence of significant differences between sweet grain sorghum and the two other types of sorghum grown in Burkina for the number of days to emergence and the sowing-flowering cycle. On the other hand, the two other characteristics significantly discriminated grain sorghum from

Traits	Sweet grain sorghum	Grain sorghum	Sweet sorghum
Sowing-emergence cycle (days)	3.206 a	3.0331 a	3.100 a
Sowing-heading cycle (days)	72.810 b	70.467 a	69.800 a
Sowing-flowering cycle (days)	73.920 a	74.300 a	72.801 a
Heading-flowering difference (days)	1.111 a	3.834 c	3.000 b

a, b, c: values followed by the same letters are not significantly different at the 5% threshold.

Table 1.
Results of the Newman–Keuls mean separation test of phenological traits according to sorghum type.

the two other sorghum types. Indeed, it has a longer sowing-flowering cycle and a shorter mean time to flowering (1 day) than sweet sorghum (3 days) and grain sorghum (4 days).

3.2 Comparison of sweet grain sorghum with other cultivated sorghums based on vegetative traits and soluble sugar content of the stem

The analysis of the results in **Table 2** reveals that of the 10 agro-morphological traits, only the number of leaves and the number of internodes did not significantly discriminate the three types of sorghum studied. A significant difference was observed between sweet grain sorghum and the other two sorghums in terms of leaf sheath length and stem diameter. Indeed, sweet grain sorghum was clearly distinguished from the other two types of sorghum by longer leaf sheaths and larger stem diameter. However, it has similar characteristics to grain sorghum in terms of leaf size and sweet sorghum in terms of vegetative shoot production, separation, internode length, and plant height.

As for the soluble sugar content (Brix), a significant variation according to the type of sorghum was observed. Sweet grain sorghum expressed a Brix value (12.32%) significantly lower than grain sorghum (13.98%) and sweet sorghum (18.89%).

Traits	Sweet grain sorghum	Grain sorghum	Sweet sorghum
Vegetative tillers	1.532 b	0.667 a	1.442 b
Leaves number	12.040 a	12.575 a	11.867 a
Leaf length (cm)	68.809 a	68.376 a	73.199 b
Leaf width (cm)	9.570 b	9.405 b	8.075 a
Leaf sheath length (cm)	21.742 b	20.121 a	19.867 a
Separation (cm)	21.310 b	13.869 a	20.745 b
Internodes number	11.492 a	11.608 a	10.783 a
Internodes length (cm)	21.518 b	14.421 a	20.704 b
Stem diameter (cm)	2.1218 b	2.0350 ab	1.9350 a
Plant height (cm)	263.508 b	199.116 a	259.801 b
Brix (%)	12.324 a	13.975 b	18.885 c

a, b, c: values followed by the same letters are not significantly different at the 5% threshold.

Table 2.
Results of the Newman–Keuls mean separation test of vegetative traits and Brix according to sorghum type.

Traits	Sweet grain sorghum	Grain sorghum	Sweet sorghum
Productive tillers	0.155 b	0.017 a	0.092 ab
Peduncle length (cm)	50.789 ab	45.413 a	54.093 b
Panicle width (cm)	10.807 c	9.573 b	8.492 a
Panicle length (cm)	28.158 a	32.891 b	27.972 a
100-grain weight (g)	2.438 a	2.629 b	2.695 b

a, b, c: values followed by the same letters are not significantly different at the 5% threshold.

Table 3.
Results of the Newman–Keuls mean separation test of yield and Brix parameters according to sorghum type.

3.3 Comparison of sweet grain sorghum with other cultivated sorghums based on yield-related traits

All yield-related traits significantly discriminated all cultivated sorghum types (**Table 3**) but panicle length showed no significant difference between sweet grain and sweet sorghum. Sweet grain sorghum is clearly distinguished from the other two types of sorghum by an intermediate peduncle length, wider panicles, lighter grains, and a higher number of productive tillers.

3.4 Effect of "genotype" factor and "sorghum type" factor on trait expression

The results recorded in **Table 4** showed variability of the material at the level of most of the characters except for the number of productive tillers. The comparative analysis of the coefficients of determination (R^2) revealed a preponderance of the genotype factor in the expression of all the characteristics, explained by higher values (>50%) except for the production of productive tillers (36%). However, the influence of the "sorghum type" factor was quite important in the expression of heading-flowering difference (54%), Brix (44%), panicle width (37%), and plant height (31%).

3.5 Description of sorghum types grown

The results of the principal component analysis (PCA) indicate that the first two axes contribute 100% of the total variance (**Figure 1**). Thus, the projection in the ½ plane in the biplot of the variables and the sorghum type factor shows that axis 1 with an inertia rate of 55.06% negatively associated with the variables' sowing-flowering cycle, the number of internodes, leaf width, stem diameter, and panicle width and positively the variables leaf length and Brix. Axis 2, which explains 44.94% of the total variability, is positively associated with the variables panicle length, mean heading-flowering distance, and 100-grain weight. They are opposite to the variables plant height, vegetative tillering, and productive tillering. The biplot shows that sweet sorghum positively related to axis 1 is characterized by long leaves and a high Brix value. Grain sorghum positively associated with axis 2 is opposite to sweet grain sorghum. Sweet grain sorghum is characterized by a short panicle, a short difference between flowering and heading, taller plants, and a large number of vegetative and productive tillers. Grain sorghum is characterized by a long panicle, a long average time between flowering and heading, shorter plants, and a smaller number of vegetative

Factors	**Genotype**		**Sorghum type**	
Traits	**Pr > F**	**R^2**	**R^2**	**Pr > F**
Sowing-emergence cycle	0.010	0.50	0.05	0.070
Sowing-heading cycle	< 0.0001	0.70	0.10	0.003
Sowing-flowering cycle	< 0.0001	0.71	0.02	0.378
Heading-flowering difference	< 0.0001	0.83	0.54	< 0.0001
Vegetative tillers	< 0.0001	0.60	0.19	< 0.0001
Leaves number	< 0.0001	0.72	0.03	0.221
Leaf length	< 0.0001	0.66	0.09	0.004
Leaf width	< 0.0001	0.82	0.22	< 0.0001
Leaf sheath length	0.000	0.59	0.11	0.002
Separation	< 0.0001	0.93	0.31	< 0.0001
Internodes number	< 0.0001	0.74	0.03	0.140
Internodes length	< 0.0001	0.88	0.28	< 0.0001
Stem diameter	< 0.0001	0.68	0.10	0.002
Plant height	< 0.0001	0.87	0.31	< 0.0001
Brix	< 0.0001	0.75	0.44	< 0.0001
Productive tillers	0.459	0.36	0.06	0.026
Peduncle length	< 0.0001	0.96	0.8	0.009
Panicle width	< 0.0001	0.65	0.37	< 0.0001
Panicle length	< 0.0001	0.88	0.18	< 0.0001
100-grain weight	< 0.0001	0.61	0.11	0.001

F: Fisher value, Pr; probability, R^2: coefficient of determination.

Table 4.
Effects of genotype and sorghum type factors on the expression of the studied traits.

and productive tillers. Moreover, the analysis of Euclidean distances (**Table 5**) revealed greater proximity between sweet grain sorghum and sweet sorghum (11.025). The greatest distance was recorded between sweet grain sorghum and grain sorghum (65.771).

3.6 Organization of the diversity of sorghum grown in Burkina Faso

The dendrogram (**Figure 2**) derived from the hierarchical ascending classification (HAC), based on the Euclidean distances between individuals, divides the sorghum genotypes into three groups with one truncation at inertia level 100 (truncation 1) independently of the sorghum types. Thus, group I consists of all sweet grain sorghum genotypes and three sweet sorghum genotypes. Group II is composed of five sweet sorghum genotypes and two-grain sorghum genotypes. Group III consists of seven-grain sorghum genotypes and two sweet sorghum genotypes. In addition, a subdivision of group I genotypes into sweet grain sorghum and sweet sorghum is observed at truncation level 50 (truncation 2) conforming sweet grain sorghum is

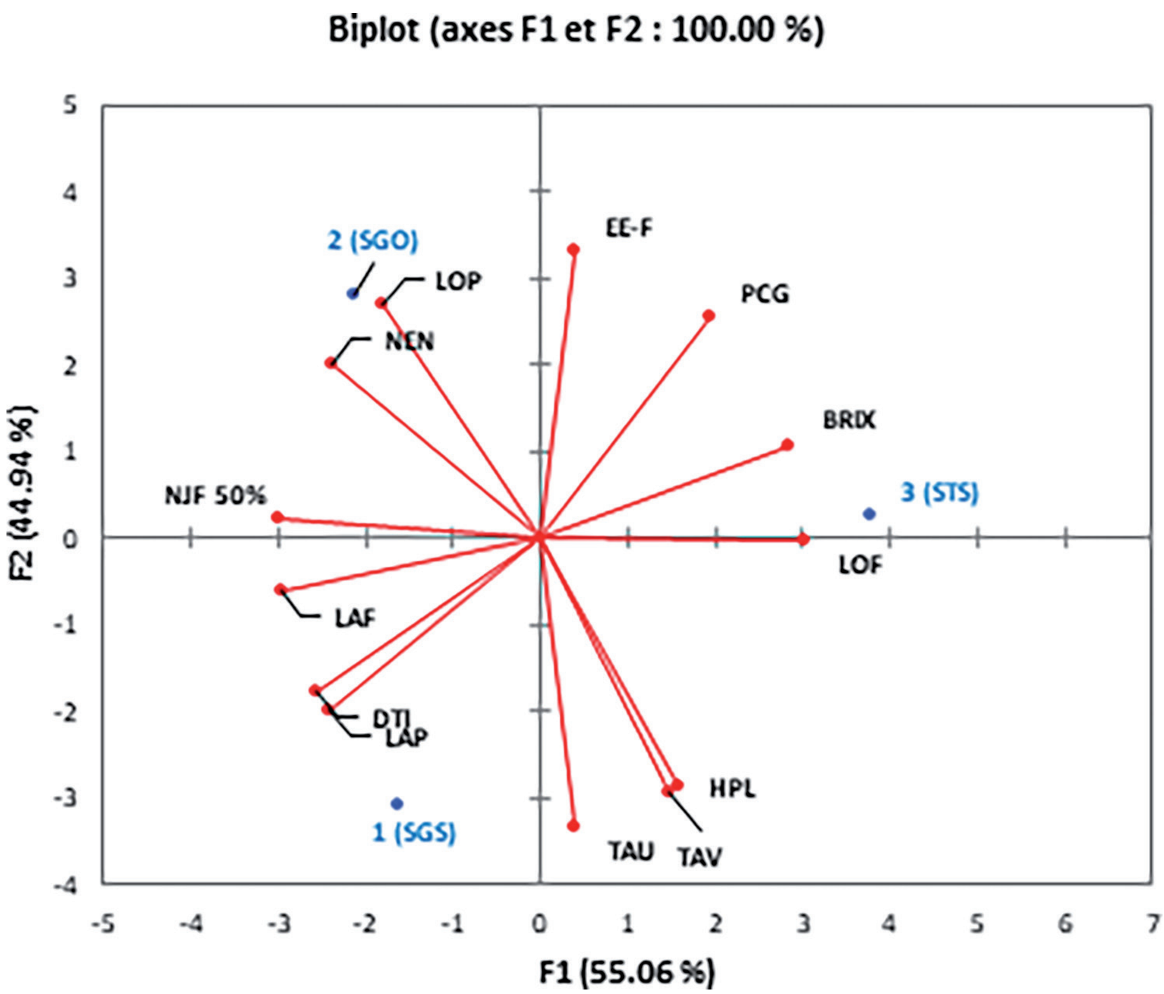

Figure 1.
Projection of variables and sorghum types in the ½ plane of the principal component analysis. Legend: STS: sweet sorghum, SGO: Grain sorghum, SGS: Sweet grain sorghum, NJF: Sowing – flowering cycle, EE-F: Difference flowering - earing, TAV: Vegetative tillers, LAF: Leaf width, LOF: Leaf length, NEN: Internodes number, DTI: Stem diameter, HPL: Plant height, TAU: Productive tillers, LAP: Panicle width, LOP: Peduncle length, PCG: 100-grain weight.

	Sweet grain sorghum	Grain sorghum	Sweet sorghum
Grain sorghum	65.771	0	
Sweet sorghum	11.025	62.676	0

Table 5.
Matrix of Euclidean distance between sorghum types.

more homogeneous. Sweet sorghum is the most heterogeneous as its genotypes are distributed in all three groups.

3.7 Characterization of the sorghum groups obtained

The characterization of the groups obtained from AHC by discriminant factor analysis (DFA) is shown in **Figure 3**. Group I, which includes all sweet grain sorghum genotypes and three sweet sorghum genotypes, is characterized by wider stalks and panicles and a greater number of productive tillers. Group II, which is mainly made up of sweet sorghum genotypes, is characterized by taller plants, longer internodes and

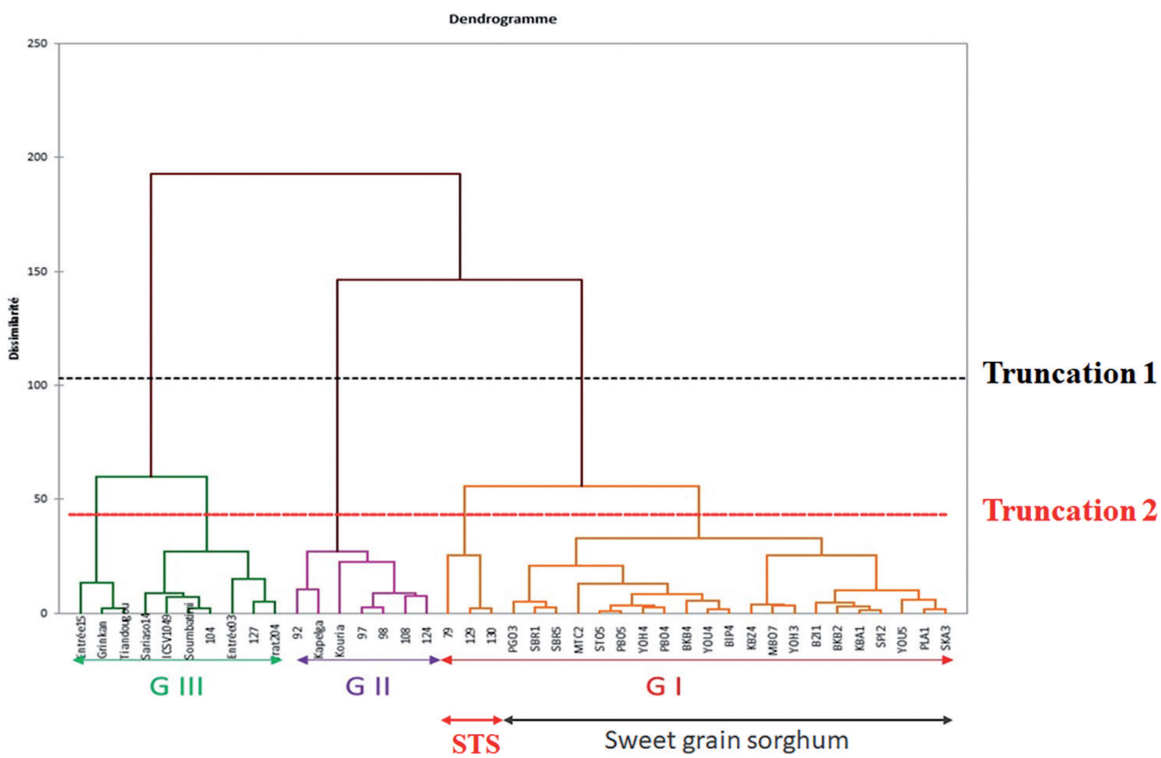

Figure 2.
Dendrogram of the hierarchical ascending classification of the genotypes of the three types of sorghum grown in Burkina Faso. Legend: STS: sweet sorghum.

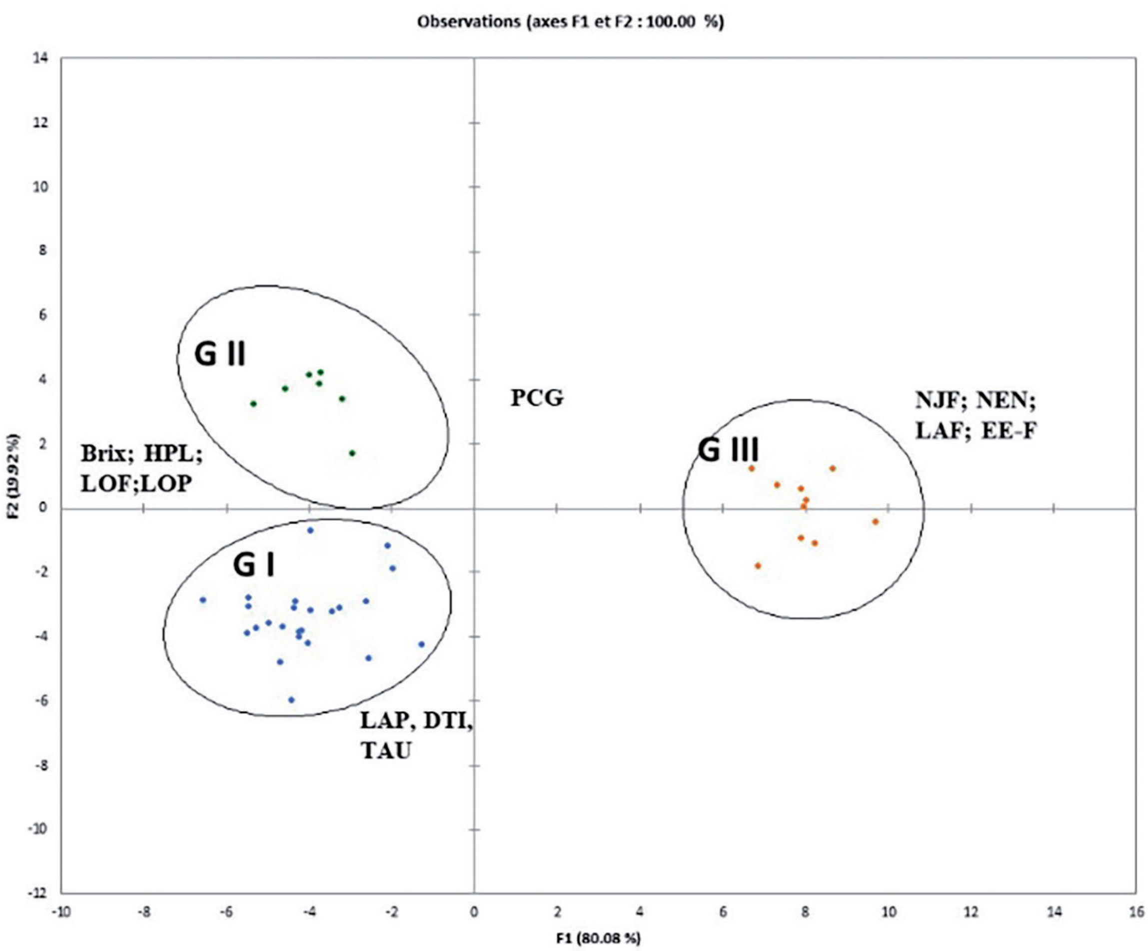

Figure 3.
Position of groups from the bottom-up classification in discriminant factor analysis (DFA).

panicles, and a higher Brix value. Group III, which is predominantly grain sorghum, contains genotypes with a longer sowing-flowering cycle, a longer mean time between flowering and heading, a higher number of internodes, and wider leaves.

4. Discussion

The absence of significant differences between the three types of sorghum grown in Burkina Faso in terms of the characters, sowing-emergence cycle, sowing-flowering cycle, number of internodes, and number of leaves, coupled with the low influence of the "sorghum type" factor in the expression of the characters, could testify to the genetic proximity between the three types of sorghum grown. This is confirmed by the organization of genotypes into agro-morphological groups independently of the "sorghum type" factor in the hierarchical ascending classification. Similar results are reported by [18] and [17] on these sorghum types using molecular markers. Indeed, the three sorghum types generally coexist in combination in traditional production systems. A gene flow could exist between them insofar as sorghum, although it is preferentially self-pollinated, has an outcrossing rate that can vary from 7–40% [20, 21]. The genetic proximity between these sorghums could confirm that they belong to the same species [17]. Therefore, the only determining factor in their differentiation would be the genotype, hence the high values of coefficients of determination recorded in the study with this factor. However, the smaller gap between heading and flowering observed in sweet grain sorghum and its preferential harvesting at the doughy grain stage could explain its earliness compared with the two types of sorghum grown. In addition, the duration of the sowing-flowering cycle of all three types of sorghum studied is lower than the results reported by [22] on sweet sorghum (76 days), by [23] on sweet grain sorghum (91 days), and by [24] on grain sorghum (79 days). This difference could be explained by the late establishment of the trial. Flowering was early and clustered for the genotypes of the three sorghum types studied. These results could be explained by the sensitivity of these sorghums to photoperiod variation as reported by several previous studies [24–26].

Seven of the 15 characteristics related to vegetative organs and yield, as well as the Brix, made it possible to clearly discriminate sweet grain sorghum from grain sorghum and sweet sorghum. Indeed, sweet grain sorghum is characterized by a more robust and less sweet stem emitting more productive tillers, longer leaf sheaths, a wider panicle supported by an intermediate-sized peduncle, and carrying lighter grains. This is confirmed by principal component analysis, which revealed an association between this sorghum and these variables. Similar results on panicle width and grain weight of sweet grain sorghum and Brix are reported in previous studies [10, 17]. The weak grain weight of sweet grain sorghum could be explained by its asymmetric shape and mealy consistency in contrast to the other two types, which have elliptical and glassier grains. In addition, the weakly stem Brix value of sweet grain sorghum compared with sweet sorghum and grain sorghum could be related to a difference in the accumulation organs. Sweet grain sorghum would accumulate its sugars a lot in the grains as the stem. Moreover, some sweet grain sorghum and grain sorghum genotypes expressed higher Brix values than some sweet sorghum genotypes. This suggests that Brix is a trait more influenced by genotype than sorghum type, which is a simple classification criterion. Similar results were reported by [27] on grain sorghum under mineral fertilization conditions and [22] on sweet sorghum (8.88–21.83%). The Brix would be a polygenic trait with epistatic interactions and additive effects [28–30] unlike the sweet taste of the grain, which is controlled by a single biallelic gene [31, 32].

Finally, several results obtained revealed greater genetic proximity between grain sorghum and sweet stem sorghum. Indeed, among the variables discriminating the types of sorghum, similar characteristics were recorded between sweet grain sorghum and sweet sorghum in five variables (number of vegetative tillers, separation, internode length, plant height, panicle length). However, only two of these variables, i.e., leaf length and width, bring sweet grain sorghum closer to grain sorghum. This is confirmed on the one hand by the Euclidean distances, which showed a smaller distance between sweet sorghums and on the other hand by the results of the hierarchical classification where a composite group consisting of all sweet grain sorghum genotypes and three sweet sorghum genotypes was obtained. [18] also showed that sweet sorghums (sweet sorghum, sweet grain sorghum) are genetically more closely related (Fst = −0.0558) to grain sorghum [17], however, showed greater proximity between sweet grain sorghum and grain sorghum using molecular markers. This difference in molecular and phenotypic proximity could be explained by the generally polygenic determinism of the traits taken into account in the estimation of phenotypic distance, which can lead to convergence phenomena [33]. According to [34], lines with the same value for a quantitative trait may have different alleles for each of the loci involved. The effect of environmental factors on phenotype expression could also explain this difference in molecular and phenotypic distances.

Finally, the fact that all sweet grain sorghum genotypes belong to the same agromorphological group could indicate a greater homogeneity of this type of sorghum compared with the other two types [17] also reported low diversity within this sorghum type compared with the other two sorghum types.

5. Conclusion

The study revealed a weak influence of the factor "type of sorghum" in the expression of all the characters. Nine characters, including two related to phenology, six to vegetative organs and yield, and Brix, allowed us to distinguish sweet grain sorghum from sweet sorghum and grain sorghum. Sweet grain sorghum is characterized by a robust, low-sugar stem, longer leaf sheaths, a broad panicle, and lighter grains. The study shows also that sweet sorghums are genetically similar to grain sorghum. These results could contribute to better management of sorghum genetic resources in Burkina Faso through their use in the national sorghum breeding program. Indeed, crosses could be made between these different types of cultivated sorghum to create single, three-way or double hybrids containing sweet grains and sweet stems. These hybrids could then be evaluated in multi-location trials in contrasting environments to select genotypes by environment. Marker-assisted selection could also be used to identify drought-tolerant genotypes of interest. Furthermore, the analysis of the nutritional composition of the grains of these genotypes of interest, in particular their profile in essential amino acids (lysine), vitamins, and sugars, could be the basis for their exploitation in the food industry for the manufacture of infant porridges and biscuits.

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Conflicts of interest

The authors declare that they have no conflicts of interest regarding the publication of this paper.

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Data availability

The data supporting the findings of this study are available on request from the corresponding author.

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