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Evaluation of medium maturity group of soybean (*Glycine max* L. Merr) for agronomic performance and adaptation in Sudanian zone of Burkina Faso

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Soybean is an economically important crop that provides oil and high-quality protein. In Burkina Faso, soybean is one of the promising crops identified in the framework of the strategy for the development of agricultural sectors. However, very few improved varieties have been developed. The identification of newly improved varieties with high agronomic potential and adapted to the climatic conditions will strengthen soybean production in the country. The objective of this study was to evaluate the agronomic performance of 24 soybean genotypes at the Farako-Bâ Research Station in the Sudanian zone of Burkina Faso. The experimental design was an alpha lattice arranged in a 50 cm × 5 cm with 3 replications. The results of this research revealed significant differences ($p < 0.05$) among genotypes with reference to days to flowering, days to maturity, number of nodules, plant height, pod clearance, number of pods, pod shattering, hundred seed weight and number of nodes. Nodules score and diameter, number of branches and grain yield were non-significant. Based on agronomical traits, three genotype groups were clustered. Clusters 1 consisted of the high grain yield groups with the genotypes TGX2017-5E (2083.33 kg/ha), TGX1993-4FN (1666.67 kg/ha), TGX2017-6E (1666.67 kg/ha) and TGX2016-4E (1583.33 kg/ha), being the highest yielding.

Key words: Soybean, agronomic performance, adaptation, genetic variability, Burkina Faso.

INTRODUCTION

Soybean (*Glycine max* L. Merr) is one of the world's most important cultivated crops grown for use as food and feed. It was known to be grown on over 120 million hectares around the world in 2017 (FAOSTAT, 2019). The world soybean production increased by 3.79% annually from 2000 to 2020 and reached an average

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annual production of 361 million tons in 2020. Soybean is a good source of protein for human and animal nutrition and as a biofuel feedstock (Delele, 2021). It consists of more than 36% proteins, 30% carbohydrates, and excellent amounts of dietary fiber, vitamins, and minerals (Chuwang et al., 2018). The soybean grain accounts for 57% of the world's oilseed production, which makes it the most important crop for producing edible oil (USDA, 2001; SOYSTATS, 2011). Soybean oil has many uses including its use in the industry as fuel additive (Schori and Charles, 2003). The introduction of soybean in West Africa was an initiative of Agricultural Research but its cultivation has remained underdeveloped despite the efforts and the progress made by the research teams (Picasso et al., 1984). In Burkina Faso, soybeans were chosen in 2006 by the government as a strategic crop with an estimated annual production of 51.708 tons (DGPER, 2020). Soybean is used essentially in food and feed and contributes to strengthening the resilience of poor households to food insecurity (Pimentel et al., 2005). Indeed, soybean cultivation in Burkina Faso is less rigorous than corn and cotton; however, it requires well-drained soils, optimal production temperatures between 25 and 33°C and seasonal rainfall ranging from 500 to 800 mm (Sia, 2016). Several regions of the country with high potential for soybean production have been identified: the regions of Hauts Bassins, Boucle de Mouhoun, Cascades, Centre East, East and Southeast (Bila et al., 2009). These regions constitute a real potentiality for the promotion of soybeans for achieving food security. Despite the strengths of this crop as a cultural precedent, the soybean sector is still being structured in Burkina Faso. The first seed imports were American varieties and those developed by IITA. Since the inception of soybean improvement in 1974, IITA has played a leading role in developing tropical high-yielding soybean varieties and improved agronomic technologies (Khojely et al., 2018). This has contributed to the promotion of high-yielding soybean varieties, suitable for processing and marketing needs and suitable for smallholder farmers in sub-Saharan Africa (Siamabele, 2021). Despite its great potential, soybean production is influenced by climatic and agronomic factors, pests and nutrient availability in the soil (Aduloju et al., 2009). Abiotic stresses including drought, flooding, lodging, frost and nutrient deficiency in the soil make up the major abiotic constraints (Mannan, 2014). Other constraints (biotic in nature) including stresses caused by diverse pathogens (bacteria, fungi and virus), pests (nematodes) and weeds form the second major production constrains of soybean. All these multiple constraints have detrimental effects on soybean growth and development and can result in significant yield losses in soybean (Kim et al., 2016). Although, new soybean accessions tolerant to pod dehiscence and resistant to diseases such as soybean rust, a bacterial pustule, have been developed by the International Institute of Tropical Agriculture (IITA), Burkina Faso have very few improved varieties. Currently, the most used and widespread are G196 and G197. Increasing soybean production to meet the required quantities can best be achieved through an increase in yield per unit area, which can partly be achieved by the cultivation of high-yielding improved varieties. Consequently, the introduction and careful selection of newly improved soybean genotypes in breeding programs may provide the necessary genetic variability for the development and the adaptation of cultivars to biotic and abiotic stresses (Boni, 2015). This study aims to assess yield performance and adaptability of 21 newly developed soybean genotypes in Burkina Faso.

MATERIALS AND METHODS

Plant and experimental site

The planting material consisted of 21 newly developed soybean genotypes obtained from IITA (Abuja, Nigeria) and three soybean varieties (G175, G196 and G197) already used in Burkina Faso breeding program (Table 1). The field study was conducted during the 2020 raining season at the Farako-Bâ Research Station in Burkina Faso. The genotypes were planted on 20 June 2020 at a rate of 1 seed per 5 cm per planting (20 plants/m) with a sowing density of 50×5 cm flat. Weed control was done manually on the 15 and 45th day after sowing.

Experimental design

The experimental design is an alpha lattice of 3 replicates separated from each other by 2 m. Each replication consists of 24 entries distributed in 4 blocks, each consisting of 6 varieties. The blocks are separated from each other by 80 cm. The elementary plot is represented by 4 rows of 4 m with 50 cm of row spacing, that is, a gross area of 0.5 m×4 m×4 (8 m^2). The useful plot consists of the two central lines, that is, an area of 4 m^2. The plant harvest was done when 95% pods reach maturity.

Data collection

The agronomical and morphological growth parameters (Table 2); 50% flowering, 50 and 95% pod maturity, number of nodes, plant height, pod clearance, number of branches, number of pods per plant, nodulation (number of nodules per plant, nodule diameter, nodule distribution on root system), shattering, hundred seed weight, plant yield, potential yield and grain yield were recorded. The soybean rust, one of the major diseases and bacteria pustule, frogeye disease and soybean mosaic virus have been evaluated at R3 and R6 stages.

Data analysis

Analysis of variance (ANOVA) was performed using XLSTAT version 2016 on all quantitative variables. All treatment means were compared using the Least Significant Difference (LSD) at 5% level of significance. A correlation analysis between agromorphological parameters was also carried out. In order to structure the soybean lines from IITA and Burkina Faso, the principal component analysis

Table 1. List of soybean genotypes belonged to the medium (intermediate) maturity group used in this study.

Ord_Id	Name of lines	Genetic nature	Origin	Seed coat color	Maturity group
1	TGX2025-6E	Line	IITA	Yellow	Medium
2	TGX2009-16F	Line	IITA	Yellow	Medium
3	TGX2017-5E	Line	IITA	Yellow	Medium
4	TGX2025-9E	Line	IITA	Yellow	Medium
5	TGX2016-3E	Line	IITA	Yellow	Medium
6	TGX2011-6F	Line	IITA	Yellow	Medium
7	TGX1987-14F	Line	IITA	Yellow	Medium
8	TGX2017-6E	Line	IITA	Yellow	Medium
9	TGX2025-10E	Line	IITA	Yellow	Medium
10	TGX2015-1E	Line	IITA	Yellow	Medium
11	TGX2025-14E	Line	IITA	Yellow	Medium
12	TGX2008-4F	Line	IITA	Yellow	Medium
13	TGX1989-19F	Line	IITA	Yellow	Medium
14	TGX2022-4E	Line	IITA	Yellow	Medium
15	TGX1993-4FN	Line	IITA	Yellow	Medium
16	TGX2010-11F	Line	IITA	Yellow	Medium
17	TGX2020-1E	Line	IITA	Yellow	Medium
18	TGX2019-1E	Line	IITA	Yellow	Medium
19	TGX2016-4E	Line	IITA	Yellow	Medium
20	TGX2027-1E	Line	IITA	Yellow	Medium
21	TGX2023-3E	Line	IITA	Yellow	Medium
22	G175 (check-1)	Line	INERA	Yellow	Early
23	G196 (check-2)	Line	INERA	Yellow	Undetermined
24	G197 (check-3)	Line	INERA	Yellow	Undetermined

and Cluster analysis was performed with R software using average linkage.

RESULTS AND DISCUSSION

Variability for days to flowering and days to maturity

Analysis of variance between soybean genotypes was highly significant (P < 0.001) for days to flowering (50% flowering) and days to maturity (Table 3).

Flowering days ranged from 45 (G175) to 58 days (TGX1993-4FN, TGX2011-6F, TGX2022-4E and TGX2023-3E). From the 24 genotypes, 15 showed values below the average for the days to flowering (51 days), including two controls (G175 and G197). These findings suggested different genetic backgrounds among the 24 soybean genotypes studied for days to flowering. Baig et al. (2018) also claimed that different plant genotypes have significant impact on days to flowering.

Maturity days ranged from 78 to 106 days and 99 to 119 days for 50 and 95% maturity, respectively. For the 50% maturity, 11 genotypes presented values below the average (98 days). The control genotype G175 with 78 days for days to 50% maturity confirmed its precocity (group 00). It is followed by the genotypes TGX2008-4F (89 days) and TGX2025-14E (91 days). Concerning days to 95% maturity the genotypes TGX1989-19F and TGX2008-4F were the first to reach their physiological maturity around 99 days. They were followed by genotypes TGX2010-11F and TGX2025-14F (101 days). These results agreed with Zorome (2017) and Singh and Shrestha (2019) who found similar variations.

Variability in soybean plant nodulation

Analysis of variance conducted for the soybean genotypes showed significant difference for the number of nodules (P < 0.001). However, no significant differences were observed for nodule diameter and score. The nodules number ranged from 1 to 33 with an average of 11 nodules per plant.

Among the 24 soybean genotypes, 8 nodulated more efficiently (above average) and the best were genotypes TGX2023-3E (with 33 nodules), TGX1987-14F (26 nodules) and TGX2011-6F (18 nodules). The numbers of nodules per plant in this study are lower than the nodulation norm for soybean, which is in the order of 30 to 50 nodules/plant (IRAD/CNSPG, 2006). The low

Table 2. List of some traits and their measurements (IITA).

Traits	Abbreviation	Measurement	Unit
Days to flowering	50 % Flo.	More than 50% flowering in the plot	DD/MM/YY (day)
Days to maturity	50% Mat.	More than 50% maturity in the plot	DD/MM/YY (day)
Plant height	pH	Height of the plant from the base of the main stem to the top on 10 central plants of the elementary plot	cm
Number of branches	Nb_Bra	Count the number of branches on 10 randomly selected plants in each net plot	Number
Pod clearance	Pod_Cle	Height from the base of the main stem to the node of the first pod formed on 10 central plants of the elementary plot	cm
Number of pod per plant	Nb_Pod	The number of pods per plant on 10 central plants of the elementary plot	Pod
Nodulation (distribution of nodules on the root system)	Nod_Sco	Nodulation was recorded at 50% days to flowerings from 5 randomly selected plants at both ends of the plot after the net yield plot 1 = no nodules, 2 = a few nodules, 3 = half the roots have nodules, 4 = more than half the roots have nodules, 5 = all roots have nodules	score
Grain yield	Grain_Y	Weighing the seeds produced in a net plot and then converted into kg per ha	tg/ha
Pod shattering	Pod_Sha	Two weeks after the harvest date (95% Maturity) of each plot, score shattering at both ends of the plot after the net yield plot was harvested. 1 = no pod shattered, 2 = 25% of pods shattered, 3 = 50% of pods shattered, 4 = 75% of pods shattered, 5 = all plants shattered	Score
Rust (R3 and R6 stages)	Rst	1 = no lesion, 2 = some lesion on some plant, 3 = some lesions on all plants, 4 = severe infection, 5 = severe infection with leaf abscission	Score
Soybean mosaic virus	SMV	1 = no virus symptoms observed, 2 = occasional mild symptoms, 3 = moderate infection, 4 = severe and generalized symptoms 5 = severe with probable loss of performance	Score

number of nodules could be due to the soil texture, nutrient content and low photosynthesis which are important factors in nodule mass or both. The nodules of all the genotypes had interesting diameters that varied from 4 to 7 mm. These nodules belong to the large nodule category (3.5 to 5.0 mm) (Djekoun and Planchon, 1991). The large nodules would indicate high nitrogenase activity in the lines and constitute a real water reserve and would be less affected by drought (Thu et al., 1986).

Variability in plant morphological traits

The results of the analysis of variance showed highly significant differences (p<0.001) among the genotypes for pod clearance and the number of nodes. Genotypes also exhibited significant difference in the mean plant height. Plant height ranged from 60 (G196) to 109 cm (TGX2017-5E) and pod clearance ranged from 9 (G196) to 24 cm (TGX2011-6F). Of the introduced lines, 12 had a mean plant height above the trial average, reflecting their good adaptability to the environment. The mean plant height range observed in the current study agrees satisfactorily with those observed by Njoroge et al. (2015). The genotypes also presented very interesting pod clearance with an average of 15 cm. Among the 24 genotypes evaluated, 19 including control G175 and G197, showed pod clearance greater than those recommended (11 to 12 cm). These genotypes have the advantage of better resistance to *Sclerotinia* rot and facilitate good, mechanized harvesting (TERRE-INOVIA, 2019). Low pod clearance stages may expose them to soil splash from rainfall and thus make them more susceptible to white mold (IRAD/CNSPG, 2006). Greater pod clearance reduces harvest losses especially since the lowest pods usually have the most and largest seeds (Thai et al., 2019).

Yields and yield components performance

Analysis of variance showed significant difference for the number of pods per plant and 100 seed weight. These variations agreed with Zorome (2017). They might be attributed to genetic variability that characterizes soybean genotypes. The number of pods per plant ranged from 29 (TGX2008-4F) to 88 plants (TGX2019-1E) and hundred seed weight ranged from 10 (TGX1989-19F, TGX2023-3E) to 16 g (TGX2009-16F). Hundred seed weight is essential character to optimize the yield and also play important role in adaptation of a cultivar and influence to seed vigor (Morrison and Xue, 2007). There was no statistically significant difference among the genotypes for number of branches and yields. However, grain yield was found very interesting and ranged from 666.67 to 2083.33 kg/ha with an average of 1248 kg/ha. Genotype TGX2017-5E (2083.33 kg/ha) had the highest mean grain yield followed by genotypes TGX1993-4FN (1666.67 kg/ha), TGX2017-6E (1666.67 kg/ha) and TGX2016-4E (1583.33 kg/ha). The early control genotype G175 gave a yield of 1416.67 kg/ha with the potential of producing a yield of 6 t/ha. Among the introduced genotypes, 11 presented mean grain yield higher than the average of the trial (1250 kg/ha).

Pod shattering

Significant difference (p<0.001) was recorded for pod shattering among the 24 soybean genotypes. Pod shattering ranged from 0 to 50% with an average of 12% (Table 3). In this study, 15 genotypes were resistant to shattering (0-10% shattered pod) and 9 genotypes were intermediate (11-70%) according to Bailey et al. (1997) and Mohammed et al. (2014). From the 21 introduced genotypes, 71.43% were resistant to pod shattering. Pod shattering is a serious constraint that causes 34 to 99% seed losses (Katembo, 2018). In tropical areas such as Burkina Faso, delayed harvesting contributes to considerable yield loss, especially on varieties which are susceptible to pod shattering (Krisnawati and Adie, 2017). Pod shattering is affected by different environmental factors such as dry climate, low humidity, high temperature, and rapid temperature changes (Agrawal et al., 2002). Zhang and Boahen (2010) reported that the rate of shattering was faster on non-irrigated soybean than irrigated soybean. Pods position (lower, middle and upper) in soybean plants influences pod-shattering (Krisnawati and Adie, 2017). Pods position at the lower part was more susceptible to pod shattering than those at middle and upper part.

Reaction of soybean genotypes to diseases

Observations were carried out on soybean rust, SMV, bacteria pustule and frogeye leaf spot diseases. Symptoms of rust and soybean mosaic virus were observed in the trial. Almost all the plants of the trial were completely free of bacteria pustule and frogeye leaf spot disease symptoms. Significant difference (p<0.001) was observed for rust (R3 and R6 stages) diseases among the 24 soybean genotypes. However, no significant differences were observed for SMV. Figure 1 shows soybean diseases and scores distribution, the impact of rust disease (R6 stage) and SMV to grains yield. Most genotypes of the trial did not show symptoms of rust (R3 and R6 stage) with a score of 1 (0% disease infection). Only 3 genotypes had a score of 2 (25% of disease symptoms). The results of this research showed that rust disease and SMV with the observed scores did not affect grain yield. In previous researches, rust appears to be a damaging crop disease causing severe yield losses in tropical and subtropical soybean-producing countries (Kolmer et al., 2009). SMV have been reported and can cause yield losses ranging from 8 to 94% (Gui et al.,

Table 3. Mean of the agromorphological parameters of soybean lines.

Genotype	50% F.	50% M.	95% M	Nb_Nod	Nod_Sco	Nod_Dia	pH	Pod_Cle	Nb-pod	Pod_Sha	100 SW	Plt_Y	Grain_Y	Pot_Y	Nb_Nd	Nb_bra
G175 (check 1)	45	78	105	11	2	5	71	12	38	42	13	15	1416.67	6	16	3
G196 (check 2)	56	106	119	3	2	6	60	9	38	50	11	6.87	875	2.75	12	3
G197 (check 3)	49	93	106	11	3	6	83	13	70	25	13	11.97	1250	4.79	16	3
TGX1987-14F	52	103	108	26	3	7	108	21	57	25	13	7.31	1250	2.93	20	3
TGX1989-19F	51	93	99	11	2	4	68	13	34	0	10	11.29	1041.67	4.51	14	2
TGX1993-4FN	58	101	108	16	2	5	107	23	66	8	12	9.74	1666.67	3.89	21	3
TGX2008-4F	47	89	99	10	2	6	71	11	29	0	13	13.06	1250	5.22	13	1
TGX2009-16F	52	96	109	3	2	6	78	16	72	0	16	12.36	1225	4.95	18	3
TGX2010-11F	47	92	101	6	2	6	80	11	52	0	14	9.33	1291.67	3.73	14	2
TGX2011-6F	58	104	112	18	3	7	106	24	77	0	15	7.41	1333.33	2.97	21	4
TGX2015-1E	47	102	110	4	2	6	72	10	64	0	14	6.93	1166.67	2.77	15	3
TGX2016-3E	50	99	105	5	2	5	85	20	46	25	13	11.32	1416.67	4.53	19	3
TGX2016-4E	50	98	105	12	2	4	88	17	57	0	13	10.84	1583.33	4.33	18	3
TGX2017-5E	50	94	103	8	2	5	109	21	63	25	14	11.81	2083.33	4.72	20	4
TGX2017-6E	49	105	113	5	2	6	88	13	66	8	15	12.78	1666.67	5.11	16	3
TGX2019-1E	48	96	103	16	2	5	86	13	88	25	11	5.99	958.33	2.40	21	4
TGX2020-1E	51	100	107	4	2	5	86	18	35	25	12	9.01	1083.33	3.60	16	2
TGX2022-4E	58	111	118	10	2	5	80	12	65	0	14	8.36	1333.33	3.34	16	4
TGX2023-3E	58	101	107	33	3	5	94	21	58	0	10	11.06	1416.67	4.43	21	3
TGX2025-10E	47	105	110	16	3	6	64	9	39	0	13	11.11	1166.67	4.45	15	3
TGX2025-14E	49	91	101	6	2	5	68	14	35	17	13	11.23	1083.33	4.49	13	2
TGX2025-6E	52	98	105	1	2	4	69	12	50	0	14	6.70	666.67	2.68	17	3
TGX2025-9E	54	100	110	9	2	6	99	18	74	8	13	3.89	808.33	1.56	21	3
TGX2027-1E	46	102	108	16	2	6	84	16	51	0	14	6.65	916.67	2.66	20	3
Grand mean	51	98	107	11	2	5	83	15	55	12	13	9.67	1248	3.87	17	3
CV (%)	2	4	4	64.4	24	22.4	20.6	30.8	33.7	55.8	12.6	50.10	37.1	50.1	12.5	31
P value	0.001**	0.001**	0.001**	0.001**	0.153^{NS}	0.359^{NS}	0.014*	0.001**	0.011*	0.001**	0.010*	0.528^{NS}	0.182^{NS}	0.528^{NS}	0.001**	0.087^{NS}

NS: No significant; *: significant; **: highly significant.

2021).

Correlation test

The Pearson correlation matrix at the 5% threshold revealed several correlations between the variables studied (Table 4). Strong positive and significant (*P*≤0.0001) correlations were observed between grain yield and plant height (r = 0.612), grain yield and pod clearance (0.470). Grain yield was positive and significantly correlated to the number of pods (r= 0.255) and the number of nodules (r= 0.245). This means that a higher value of those agro-morphological characters will result in a higher grain yield. Hundred seed weight was positive and significantly correlated with number of pods (r = 0.245), number of branches

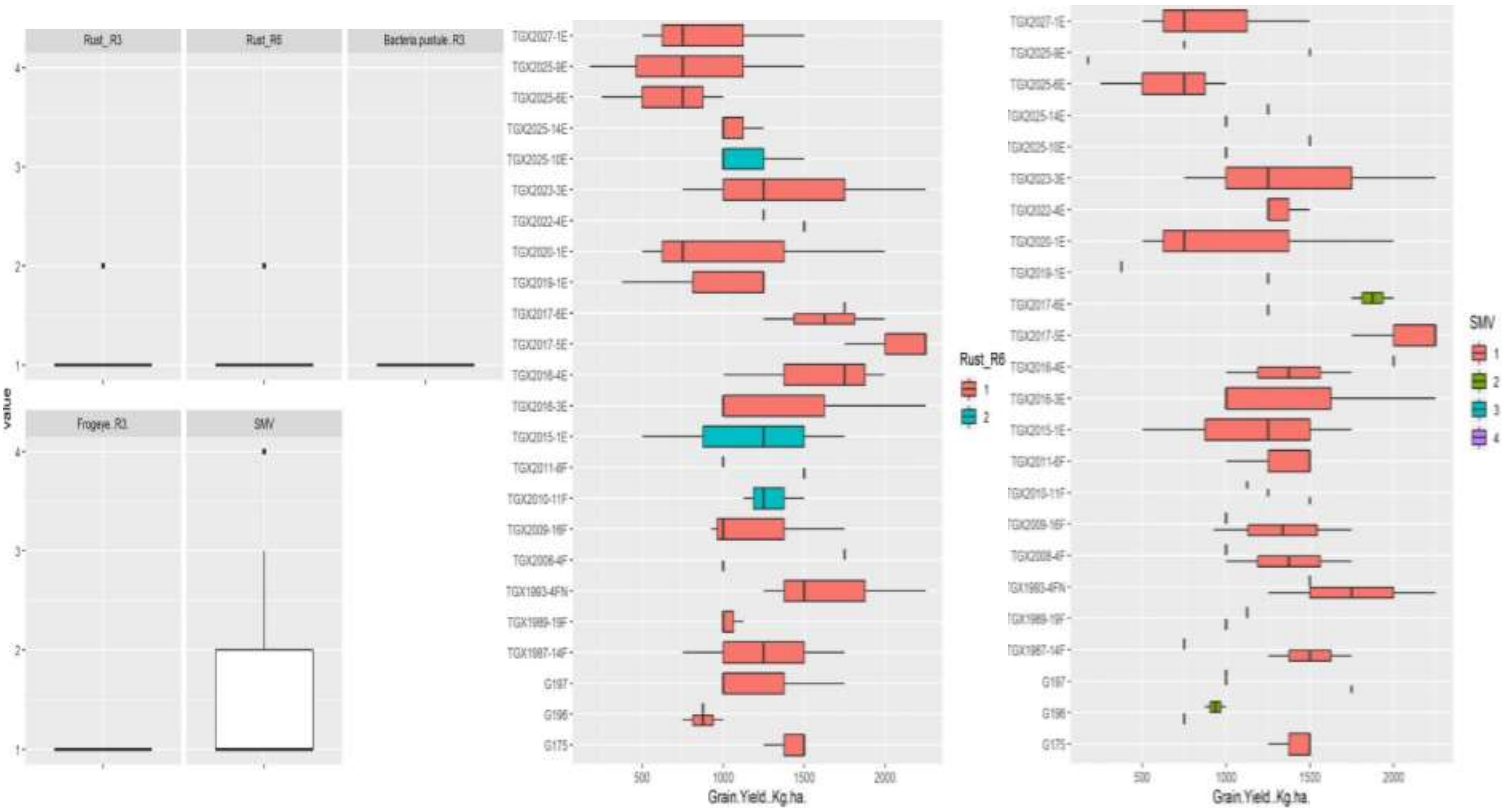

Figure 1. Soybean diseases evaluation; a= soybean diseases and score distribution, b= rust disease (R6 stage) and impact to grain yield, c= SMV and impact to grain yield.

(r= 0.314) and 95% day to maturity(r= 0.269). This result contradicts that of Li et al. (2020) who showed that the hundred seed weight was negatively correlated with numbers of pods and branches. Pod number per plant was found to have a strong, positive and significant (*P*≤0.0001) correlation to number of branches (r= 0.609), number of nodes (r= 0.538) and plant height (r= 0.512). The present research demonstrated that it was beneficial to cultivate high yielding soybeans by choosing higher plant height, pod clearance, more pods, mores nodules, mores nodes of the

Table 4. Correlation test between the agromorphological parameters.

Variable	50 % F.	50% M.	Nb_Nod	Sco_Nod	Nod_Dia	PH	Pod_Cle	Nb_Pod	Pod_Sha	100SW	Plt_Yield	Pot_Yield	Gra Yield	95 % M	Nb_Nd	Nb_Bra
50 % F.	1															
50% M.	0.495***	1														
Nb_Nod	0.218	0.074	1													
Score_Nod	0.230	0.146	0.698***	1												
Nod_Dia	-0.024	0.021	0.255*	0.072	1											
PH	0.307*	0.107	0.421**	0.330*	0.289*	1										
Pod_Cle	0.370**	0.097	0.404**	0.270*	0.170	0.766***	1									
Nb_Pod	0.252*	0.200	0.161	0.197	0.109	0.512***	0.151	1								
Pod_Sha	-0.067	-0.205	-0.119	-0.098	-0.034	0.036	0.038	-0.096	1							
100SW.	-0.119	0.146	-0.069	-0.004	0.192	0.154	0.154	0.245*	-0.236*	1						
Plt_Yield	-0.166	-0.333	0.072	0.068	0.034	0.090	0.112	-0.189	0.122	0.115	1					
Po_ Yield	-0.166	-0.333	0.072	0.068	0.034	0.090	0.112	-0.189	0.122	0.115	1***	1				
Gra Yield	0.062	-0.107	0.245*	0.189	0.194	0.612***	0.470***	0.255*	0.089	0.167	0.609***	0.609***	1			
95 % M.	0.443***	0.626***	-0.028	0.041	0.127	0.076	0.049	0.197	0.171	0.269*	-0.167	-0.167	-0.032	1		
Nb_Nd	0.308*	0.240*	0.405**	0.287*	0.058	0.679***	0.629***	0.538***	-0.034	0.132	-0.163	-0.163	0.186	0.140	1	
Nb_Bra	0.258*	0.362*	0.096	0.127	0.028	0.220	0.080	0.609***	0.040	0.314*	-0.136	-0.136	0.156	0.393**	0.530***	1

*: Significant; **: Highly significant; ***: Very highly significant. Values in bold are different from 0 at significance level alpha=0.05.

main stem and more branches. The associations reveal that hundred seed weight was negatively correlated to pod shattering (r= -0.235). The results of this research followed previous studies conducted by Ngalamu et al. (2013) and Li et al. (2020).

Cluster analysis in soybean genotypes

The cluster analysis resulting from the hierarchical ascending classification (HAC) grouped the genotypes of soybean in three classes (Figure 2). Cluster 1 consisted of 9 genotypes, the most yielded, the highest plant height, the highest pod clearance, the highest pod number, the highest hundred seeds weight, the highest number of nodules, the highest number of nodes and branches (Table 5). Cluster 2 consisted of 5 genotypes and was characterized by the lower yields. Cluster 3 included 10 genotypes with the earliest days to flowering and days to maturity, and acceptable grain yield (1181 kg/ha). The genotypes from this group had the best shattering (9%).

PCA analysis

Principal component analysis (PCA) is usually used in plant breeding to reduce the variables and genotypes of groups to determine the best parameters which explain the variability. Figures 3 to 5 show the results of the principal component analysis performed with the different parameters, their contribution to the genetic variability, variables and genotypes distribution in PCA Biplot. Analysis distinguished two axes that explain 51.6% of the total genetic variability within the soybean genotypes. Yield parameters, plant yield and potential yield are positively correlated to axis 1 (32.5% of the total variability) and contributed to 9% of the total variability (51.6%). Grain yield highly correlated to axis 1 and contributed between 7.5 and 9% to the variability. Yield components such as pod number per plant were highly correlated to axis 2 (19.1% of the total variability) with a contribution to variability of between 5 and 6%. Hundred seeds weight, shattering and nodules diameter contributed very little to the variability, that is, 2% each of the total variability (51.6%). Morphological parameters such as plant height and the number of nodes correlated to axis 2 contributed around 9 and 8%

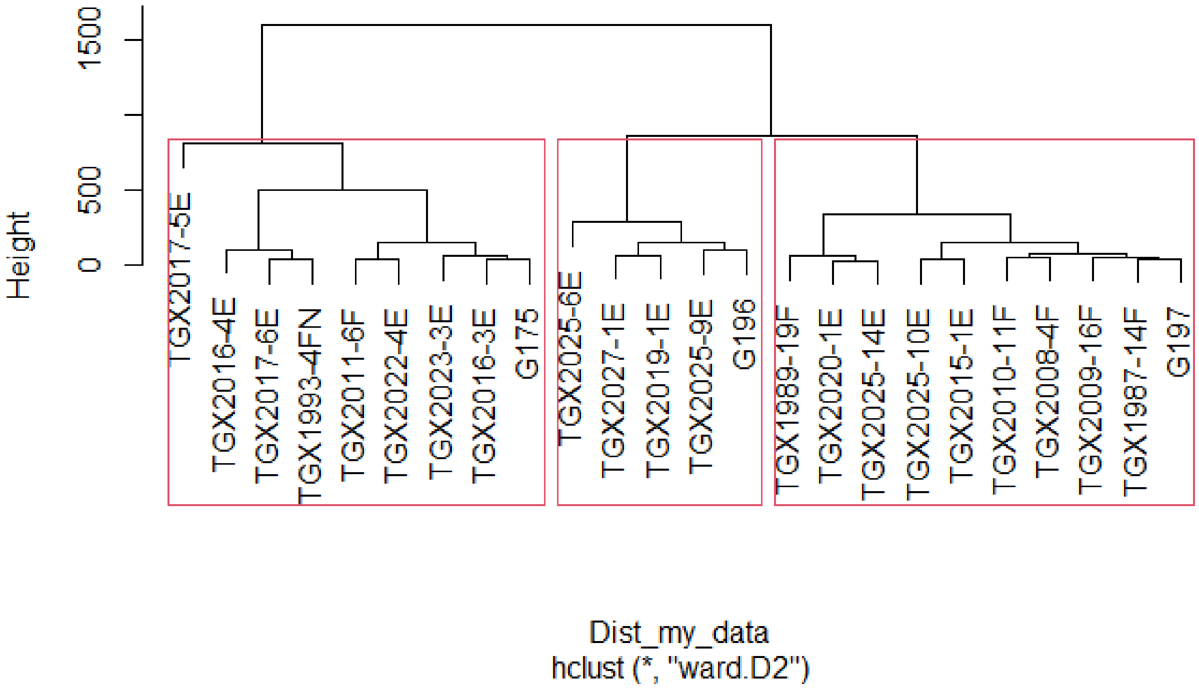

Figure 2. Cluster analysis of twenty-four genotypes of soybean in Soudanian zone of Burkina Faso.

Table 5. Agromorphological traits of soybean genotypes and their clustering.

Variable	**Cluster**		
	C1	**C2**	**C3**
Day to flowering	52	51	49
Day to maturity (50% Mat.)	97	101	96
Day to maturity (95 % Mat.)	106	109	105
Nodule number	11	9	10
Nodule score	2	2	2
Nodule diameter (mm)	5	5	6
Plant height (cm)	100	80	78
Pod clearance (cm)	20	14	14
Pod number/plant	61	60	49
Pod shattering (%)	18	17	9
Hundred seeds weight	14	13	13
Plant yield (g/plant))	11	6	10
Grain yield (kg/ha)	1781	845	1181
Potential yield (t/ha)	4	2	4
Number of nodes of main stem	19	18	15
Number of branches	4	3	2

of the total variability, respectively.

Conclusion

Soybean genotypes evaluated in this study presented an interesting variability and adaptability ability for most of the traits. The introduced genotypes TGX2017-5E, TGX1993-4FN, TGX2017-6E and TGX2016-4E were the most high-yielding (1500-2000 kg/ha). The association study revealed that soybean yield has a positive correlation with plant height, pod clearance, number of

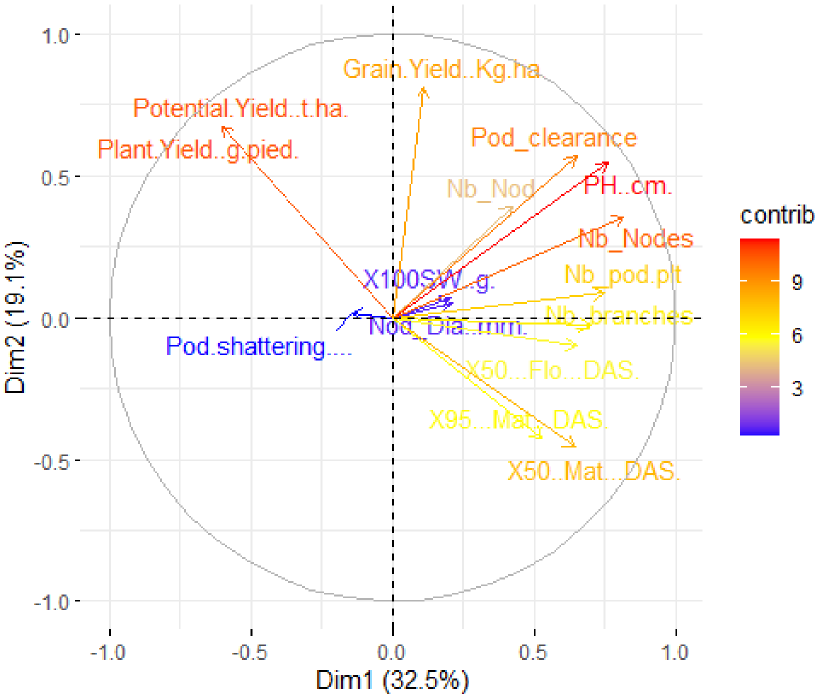

Figure 3. Variables distribution in the PCA design.

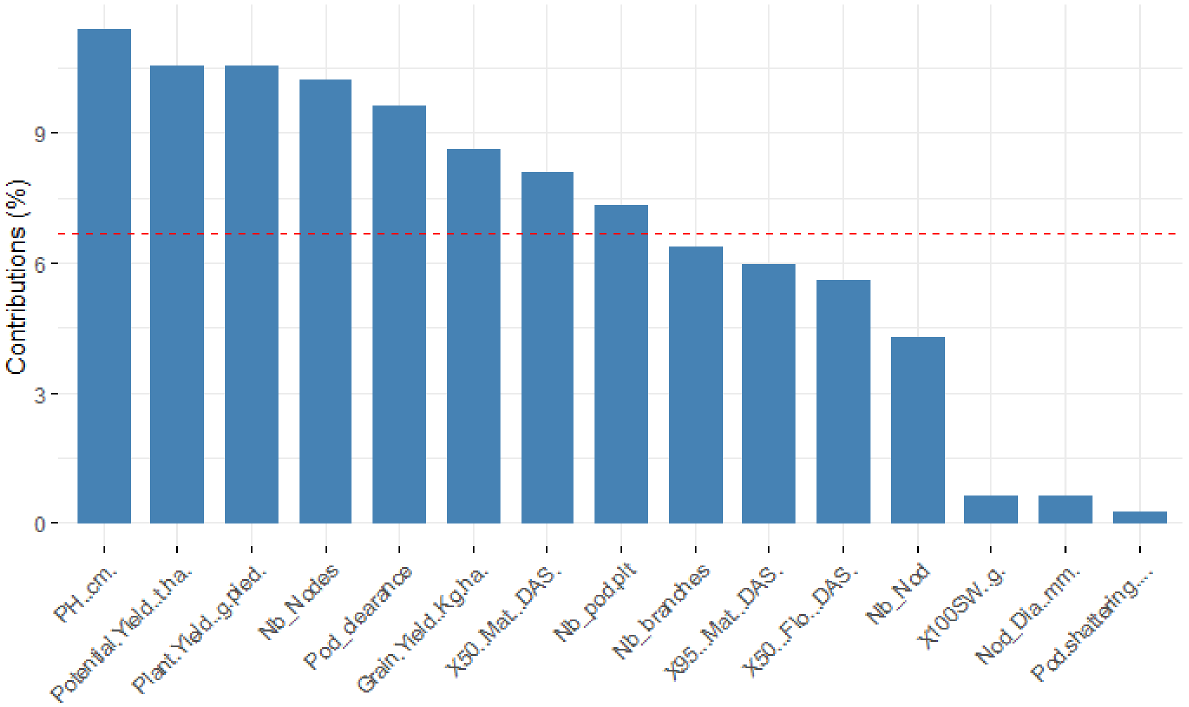

Figure 4. Variables' contribution to the genetic variability among the soybean genotypes.

pods, number of nodules, number of nodes and number of branches. Those yield components could be used as selection criteria in the breeding program to obtain high-yielding soybean cultivars. The soybean disease

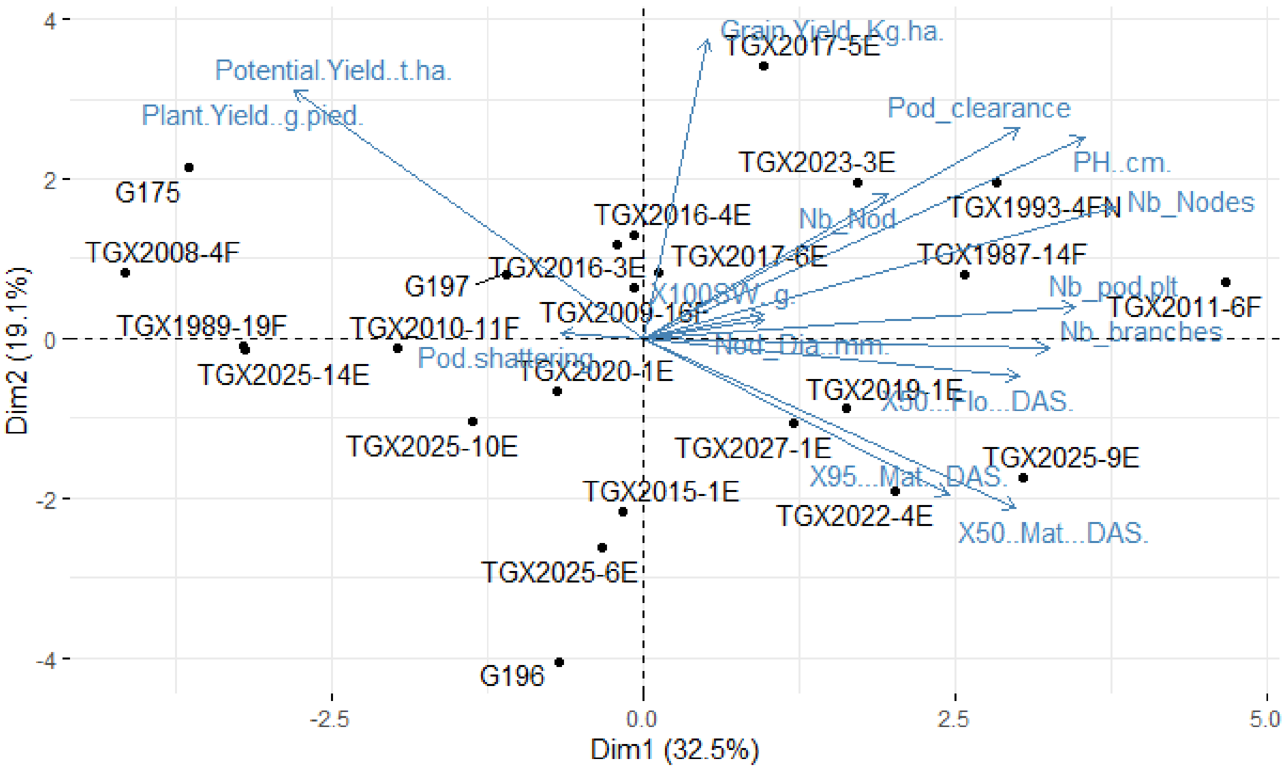

Figure 5. Variables and genotypes distribution in PCA-Biplot.

assessment in this study identified symptoms of rust disease and VMS. Most genotypes showed symptoms with a score of 1. All genotypes were asymptomless for bacterial pustule and frogeye leaf spot disease. Further research could confirm the adaptability of these soybean genotypes in different agro-ecological zones of Burkina Faso and facilitate their adoption by farmers.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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