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Productivity and Stability of Soybean [*Glycine max* (L.) Merrill] Lines in Burkina Faso

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Abstract

The study compared 37 new soybean genotypes and three local controls in two agroecological zones in Burkina Faso using an alpha-lattice design. Analysis of variance (ANOVA), additive main effects and multiplicative interaction (AMMI) analysis, and genotype plus genotype-environment interaction (GGE) biplot analysis revealed highly significant effects of genotype, environment, and genotype-environment interaction, as well as high stability and high yield for five genotypes (TGX2017-6E, TGX1987-14F, TGX1987-10F, TGX2018-5E, and TGX2007-3F). Three lines showed specific adaptation to the wetter southern Sudanian site, and no severe symptoms of rust or mosaic virus were reported. Variety registration could be considered for the most stable genotypes, with Fada N'Gourma as the main trial site.

Keywords

Glycine max, Soybean, Stability, GGE, Burkina Faso

1. Introduction

Soybean [*Glycine max* (L.) Merrill] is the world's most important legume, with a global gross soya harvest estimated to be 398.2 million tons in 2023 [1]. Soybeans are a crucial source of oil, proteins with high nutritional value, carbohydrates, isoflavones, vitamins, and minerals [2]. Soya is widely used in human nutrition and helps improve the resilience of poor households during periods of food insecurity.

Therapeutically, soybean consumption prevents osteoporosis, breast or colon cancer, type 1 diabetes, improves cognitive function, and fights oxidative stress [3]. It is also used as a raw material in the manufacture of various industrial products [4].

In Burkina Faso, legumes are a vital source of nutrients for the population. They have high protein content, 35.76%, 31.04%, 27.29%, and 22.55% respectively for zamnè, soybeans, peanuts, and cowpeas [5]. Soybeans are consumed in various forms, such as milk, cheese, kebabs, yogurt, and other products like fritters, cakes, and cookies [6]. Soya also plays a considerable agronomic role through its capacity for atmospheric nitrogen fixation within the soil, thus constituting an important cultural precedent [7] [8]. With this in mind, soya has been identified as one of the strategic crops within the policy framework to support stakeholders in the development and promotion of agricultural products in Burkina Faso [9].

However, soybean production faces significant challenges, including the low yield of existing varieties, the lack of improved varieties adapted to diverse agroecological zones, and diseases such as soybean rust and viral infections. These biotic and abiotic constraints have led to a steady decline in yields.

The development of new soybean cultivars with good stability, suitable adaptation to climatic conditions, and resistance to bacterial, fungal, and viral diseases is essential for improving soybean productivity. Such advancements would benefit stakeholders across the value chain, including producers, traders, processors, distributors, and consumers.

Genotype × environment interaction (G × E) refers to the variation in a genotype's performance based on the production environment [10]. This interaction significantly affects a genotype's grain yield and poses challenges in drawing reliable conclusions about genotype agronomic performance [11]. Therefore, it is crucial to identify genotypes based on a comprehensive understanding of their interactions with various environments. Explanation of technical term abbreviations is important for comprehension. Data from multilocation trials (MLTs) can serve as a guide for selecting the best genotypes adapted to specific environments [12].

The Biplot GGE method is a reliable technique for analyzing GEI. It is used to identify stable genotypes and optimal production environments [13]. The study aimed to investigate the adaptive potential of selected soybean genotypes. Specifically, the objectives were to:

(i) evaluate the agronomic performance and stability of newly introduced soybean genotypes in comparison to local varieties,

(ii) identify the optimal environment for the different genotypes, and

(iii) identify the primary soybean diseases.

2. Materials and Methods

2.1. Study Sites

The field studies were conducted in two stations of the Institute of Environment and Agricultural Research (INERA) during the 2021 rainy season. These research centers are located in the Hauts Basins (Farako-Ba) and Central-East (Fada N'Gourma) regions of Burkina Faso. These sites were selected because they are areas of widespread soybean cultivation. The cumulative annual rainfall and geographical coordinates are presented in Table 1.

Table 1. Sites, geographical coordinates, and Rainfall.

Study site	**Geographical position**			**Rainfall (mm)**	**T (˚C)**		**Climate**
	Altitude	**Latitude**	**Longitude**		**min**	**max**	
Farako-Ba	417 m	11˚05'25.8" N	04˚19'37.4" O	1145.1	19˚	39˚	Southern sudanian
Fada N'G.	400 m	11˚56'16" N	0˚17'48" E	767.1	18˚	39˚	Northern sudanian

T (˚C): Temperature in degrees Celsius, min: minimum, max: maximum.
Source: Data of INERA Farako-Ba and Fada N'Gourma.

2.2. Plant Material

Table 2. List of soybean genotypes involved in the evaluation.

Number	Lines	Origin	Number	Lines	Origin
1	TGX2025-6E	IITA	21	TGX2010-14F	IITA
2	TGX2009-16F	IITA	22	TGX1835-10E	IITA
3	TGX2017-5E	IITA	23	TGX2027-4E	IITA
4	TGX2016-3E	IITA	24	TGX1988-5F	IITA
5	TGX2011-6F	IITA	25	TGX2023-4E	IITA
6	TGX1987-14F	IITA	26	TGX1987-10F	IITA
7	TGX2017-6E	IITA	27	TGX1951-4F	IITA
8	TGX2025-10E	IITA	28	TGX2025-16E	IITA
9	TGX2015-1E	IITA	29	TGX2027-7E	IITA
10	TGX2025-14E	IITA	30	TGX2004-7F	IITA
11	TGX2008-4F	IITA	31	TGX2009-1F	IITA
12	TGX1989-19F	IITA	32	TGX2023-1E	IITA
13	TGX1993-4FN	IITA	33	TGX2010-5F	IITA
14	TGX2010-11F	IITA	34	TGX2007-3F	IITA
15	TGX2020-1E	IITA	35	TGX2018-5E	IITA
16	TGX2019-1E	IITA	36	TGX2013-2F	IITA
17	TGX2016-4E	IITA	37	TGX2007-1F	IITA
18	TGX2027-1E	IITA	38	G175 (check 1)	INERA
19	TGX2023-3E	IITA	39	G196 (check 2)	INERA
20	TGX2009-14F	IITA	40	G197 (check 3)	INERA

The planting material consisted of 37 newly developed soybean genotypes obtained from the International Institute of Tropical Agriculture (IITA) in Abuja, Nigeria. These genotypes were compared with three control varieties from the Institute of Environment and Agricultural Research (INERA) in Burkina Faso (Table 2).

Table 3. Agromorphological parameters and soybean diseases measured.

Trait	Abbreviations	Descriptions		Unit
Days to 50% flowering	50% Flo	More than 50% of the plants in the plot have flowered		days
Pod clearance (first pod insertion height)	Podc	The height from the base of the main stem to the node of the first pod is measured using a tape measure on 10 central plants within each elementary plot.		cm
Number of pods per plant	Nppp	The number of pods per plant on 10 central plants of the elementary plot.		Pod
Number of branches per plant Number of nodules	Nbpp Nbno	Count the number of branches on 10 randomly selected plants in each net plot. After heavy rain, carefully dig up the soil to unearth 5 plants, counting the nodules on the roots. 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.		Number Number score
100-seed weight	100w	Average weight of 100 grains after drying. For each variety, count and weigh three batches of 100 grains.		g
Grain yield	Yield	Weighing the seeds produced in a net plot and then converting them into kg per ha		kg ha^{-1}
Rust (R3 and R6 stages)	Rust	Disease severity 1 = no lesions, 2 = some lesions on some plants, 3 = some lesions on all plants, 4 = severe infection, 5 = severe infection with leaf abscission	Sporulation level No sporulation <25% of fully sporulating lesions 26 - 50% of fully sporulating lesions 51 - 75% of fully sporulating lesions Fully sporulating lesions	score
Soybean mosaic virus	Smv	Disease severity 1 = leaf healthy 2 = Mosaic symptom 3 = Mosaic symptom with small leaf 4 = Mosaic symptom with small leaf and curly 5 = Mosaic symptom with small leaf, curly, and stunting	Reaction of the plant Very tolerant Moderately tolerant Mildly tolerant Susceptible Very susceptible	score

Source: Miles *et al.* (2006), Bachkar *et al.* (2019).

2.3. Experimental Design and Growth Conditions

Two experimental trials were conducted using an alpha lattice design with three replications. Each replication is consisted of forty elementary plots distributed across five blocks. Each block contained eight soybean genotypes. Randomization was carried out using exhaustive sampling. The blocks were spaced 80 cm apart. The elementary plot is represented by 4 rows of 5 m with 50 cm of row spacing. The plot area was 0.5 m × 5 m × 4 (10 m^2). The net plot consisted of two central lines (5 m^2). Technical terms were explained when first introduced.

The sowing process was carried out manually on July 15, 2021. Three seeds were evenly distributed every 20 cm. This resulted in 15 plants per meter in each 5-meter-long row. Weeding was performed 14 days after sowing, keeping one seedling per package. Fertiliser was applied at 150 kg ha^{-1} NPK 15 days after sowing. Ridging was performed at the onset of flowering, and 50 kg ha^{-1} of urea was applied. The harvest was done at 95% pod maturity.

2.4. Data Collection

Agronomic, morphological, and yield parameters (**Table 3**), including 50% flowering, number of pods, pod clearance, number of branches per plant, number of nodes per plant, 100-seed weight, and grain yield, were recorded. The soybean mosaic virus and soybean rust were evaluated at the R6 stage [14] [15].

2.5. Data Analysis

The data were first subjected to Shapiro-Wilk and Levene tests to verify their normality and homoscedasticity. An analysis of variance was performed to estimate the effects of genotype, environment, and genotype × environment (G × E) interaction on the measured traits at the 1% threshold level using GenStat 12th Edition. GGE biplot analysis was also used to identify stable genotypes that produced high yields in both environments. Analysis of variance across the two locations was conducted for each trait, and the LSD (least significant difference) test was applied to identify groups of genotypes that actually differ from each other. Correlation coefficients were computed to determine the relationships between seed yield and yield components using the R software package version 4.4.0.

3. Results

3.1. Agronomic Performance of Soybean Genotypes

The analysis of variance showed a highly significant difference ($P < 0.01$) among soybean genotypes for days to flowering (50% flowering), pod clearance, number of branches per plant, 100-seed weight, number of nodules, soybean mosaic virus, and soybean rust, except for grain yield (**Table 4**).

Days to 50% flowering ranged from 38 days (G175) to 58 days (G196, TGX1835-10E, TGX2011-6F, and TGX1993-4FN), with an average of 50 days. Among the 40 genotypes, 24 had days to 50% flowering below the average value of 50 days. The average number of nodules per plant ranged from 8 to 24, with an overall average of 14 nodules. Among the 40 genotypes, 15 exhibited higher-than-average nodulation (14 nodules), including one of the control genotypes (G197). The most highly nodulated genotypes were TGX2023-3E (24 nodules), TGX2027-1E (20 nodules), TGX1987-14F (19 nodules), and TGX1951-4F (19 nodules).

A highly significant difference in the height of the first pod insertion was observed among the genotypes. The average height of the first pod insertion across the two sites was 10 cm. TGX1993-4FN (16 cm), TGX2023-3E (16 cm), and TGX2027-7E (15 cm) had the highest first pod insertion heights. The shortest insertion heights were observed in TGX2025-16E, TGX2023-1E (6 cm), and TGX2025-10E (7 cm).

The average number of branches per plant was 5. Twenty-four genotypes were distinguished by having a number of branches per plant greater than or equal to the average of 5 branches.

Table 4. Great mean of trait evaluation across sites.

Genotype	50% Flo	Podc	Nbpp	Nppp	Nbno	100w	Yield	Smv	Rust
G196 (check 2)	58	9	5	92	8	10	1321	1	2
G197 (check 3)	52	12	4	75	14	12	1800	2	1
G175 (check 1)	38	7	3	38	16	13	2138	1	1
TGX1835-10E	56	12	5	60	8	11	2200	1	1
TGX1951-4F	49	10	4	72	19	13	1991	1	1
TGX1987-10F	51	9	4	84	13	14	3081	1	1
TGX1987-14F	53	10	6	82	19	13	3009	1	1
TGX1988-5F	52	10	5	57	14	12	1678	1	1
TGX1989-19F	50	11	4	55	13	12	1891	1	1
TGX1993-4FN	57	16	6	121	13	10	3133	1	1
TGX2004-7F	47	7	5	84	11	12	2649	1	1
TGX2007-1F	50	10	5	58	10	14	2386	1	1
TGX2007-3F	50	11	5	63	16	12	2868	1	1
TGX2008-4F	50	8	4	66	14	12	2396	1	1
TGX2009-14F	48	8	5	87	11	12	1553	1	1
TGX2009-16F	50	6	5	85	11	14	2614	2	2
TGX2009-1F	49	11	5	64	12	10	1688	1	1
TGX2010-11F	48	6	4	85	11	13	2456	1	1
TGX2010-14F	52	7	5	65	8	13	1899	1	1
TGX2010-5F	53	7	5	80	11	18	2074	1	1
TGX2011-6F	56	12	5	93	16	11	1538	1	1
TGX2013-2F	48	9	4	68	9	14	2492	2	1
TGX2015-1E	48	8	4	80	16	11	1892	1	1
TGX2016-3E	53	11	5	71	13	12	1850	1	1
TGX2016-4E	52	12	5	71	15	15	1568	1	1
TGX2017-5E	49	12	5	67	15	10	1355	1	1
TGX2017-6E	48	8	5	91	11	15	3560	1	1
TGX2018-5E	50	11	4	69	18	14	3010	1	1
TGX2019-1E	47	11	4	51	15	12	1626	1	1
TGX2020-1E	54	10	6	98	16	13	2434	1	1
TGX2023-1E	49	6	4	72	13	12	2555	1	1
TGX2023-3E	55	16	5	58	24	10	1845	1	2
TGX2023-4E	48	8	5	89	11	16	3158	1	1

Continued

TGX2025-10E	50	7	5	68	16	12	2086	1	1
TGX2025-14E	52	10	5	46	12	14	2034	1	1
TGX2025-16E	51	6	5	79	13	15	3048	1	1
TGX2025-6E	51	12	4	46	15	15	1689	1	1
TGX2027-1E	49	14	4	52	20	12	1709	1	1
TGX2027-4E	47	9	4	69	12	14	2228	1	1
TGX2027-7E	49	15	3	35	11	14	1782	1	1
Great mean	50	10	5	71	14	13	2207	1	1
CV (%)	3.7	35.3	31.5	22.3	45.2	22.9	54.3	21.2	18.5
P value	0.001**	0.001**	0.001**	0.001**	0.001**	0.001**	0.089 ns	0.001**	0.001**

** indicates a highly significant difference, and ns means not significant.

3.2. Performance of Genotypes Across Environments

The combined analysis of the two sites showed a statistically non-significant difference among genotypes for cumulative yield (**Table 5**). However, a significant difference among the genotypes was observed in each environment for grain yield (**Table 6**). At Farako-Ba, TGX1993-4FN (4805 kg ha^{-1}) achieved the highest yield, while TGX2027-7E (1017 kg ha^{-1}) recorded the lowest. At Fada N'Gourma, the lowest yield was observed with the genotype TGX2011-6F (231 kg ha^{-1}).

Table 5. The means of soybean genotypes and LSD groups of days of flowering, 100-seed weight, number of nodules, and number of branches per plant in Burkina Faso.

Sites	**E1**	**E2**	**E1**	**E2**	**E1**	**E2**	**E1**	**E2**
Genotypes	**50% Flo**	**50% Flo**	**100w**	**100w**	**Nbno**	**Nbno**	**Nbpp**	**Nbpp**
G196 (check 2)	57.33^{a}	58.00^{a}	7.23^{c-e}	13.00^{f-i}	11.88^{a-c}	3.50^{b}	5.44^{b-d}	4.40^{ab}
G197 (check 3)	52.00^{e-g}	52.00^{c-h}	8.06^{b-e}	15.33^{c-f}	14.62^{a-c}	13.50^{ab}	4.98^{b-d}	3.20^{a-e}
G175 (check 1)	38.33^{n}	37.00^{m}	11.54^{a-e}	14.33^{d-h}	18.48^{a-c}	14.00^{ab}	4.47^{cd}	2.20^{c-e}
TGX1835-10E	54.33^{c-e}	58.00^{a}	10.31^{a-e}	12.33^{g-i}	13.16^{a-c}	2.75^{b}	5.11^{b-d}	4.26^{a-d}
TGX1951-4F	48.00^{h-m}	49.33^{f-l}	9.72^{a-e}	15.33^{c-f}	18.55^{a-c}	18.91^{ab}	5.77^{b-d}	2.70^{b-e}
TGX1987-10F	$51.00f^{g-i}$	51.66^{d-i}	13.43^{ab}	14.00^{d-i}	18.69^{a-c}	7.00^{b}	5.72^{b-d}	3.23^{a-e}
TGX1987-14F	53.33^{d-f}	53.00^{b-f}	11.64^{a-e}	14.00^{d-i}	21.66^{a-c}	15.41^{ab}	8.22^{a}	3.40^{a-e}
TGX1988-5F	51.00^{f-i}	52.33^{c-g}	9.74^{a-e}	13.33^{e-i}	24.29^{ab}	4.25^{b}	5.88^{b-d}	3.93^{a-e}
TGX1989-19F	48.33^{g-l}	51.66^{d-i}	9.33^{a-e}	14.66^{d-h}	16.40^{a-c}	10.00^{ab}	4.27^{d}	3.16^{a-e}
TGX1993-4FN	56.33^{a-c}	58.00^{a}	8.03^{b-e}	11.33^{i}	12.61^{a-c}	13.16^{ab}	7.33^{ab}	5.00^{a}
TGX2004-7F	48.00^{h-m}	46.66^{l}	9.64^{a-e}	13.66^{e-i}	17.43^{a-c}	3.91^{b}	7.05^{a-c}	3.06^{a-e}
TGX2007-1F	49.00^{g-l}	50.33^{e-l}	13.02^{a-c}	15.66^{c-f}	14.29^{a-c}	5.00^{b}	5.60^{b-d}	3.90^{a-e}
TGX2007-3F	51.33^{f-h}	49.00^{g-l}	11.27^{a-e}	12.00^{hi}	25.20^{a}	7.58^{b}	5.77^{b-d}	4.93^{a}
TGX2008-4F	48.33^{g-l}	51.00^{d-j}	10.78^{a-e}	13.00^{f-i}	13.55^{a-c}	14.00^{ab}	5.49^{b-d}	3.03^{a-e}

Continued

TGX2009-14F	47.66^{h-m}	47.33^{j-l}	11.20^{a-e}	13.00^{f-i}	18.27^{a-c}	4.00^{b}	6.11^{b-d}	3.60^{a-e}
TGX2009-16F	50.00^{f-k}	50.00^{e-l}	12.87^{a-d}	15.00^{c-g}	13.86^{a-c}	8.58^{ab}	6.05^{b-d}	4.20^{a-e}
TGX2009-1F	49.66^{g-l}	48.00^{i-l}	7.92^{b-e}	12.00^{hi}	15.55^{a-c}	9.00^{ab}	6.27^{a-d}	3.96^{a-e}
TGX2010-11F	47.33^{i-m}	49.33^{f-l}	10.75^{a-e}	14.00^{d-i}	13.57^{a-c}	9.25^{ab}	5.04^{b-d}	3.50^{a-e}
TGX2010-14F	51.33^{f-h}	52.66^{c-g}	13.26^{a-c}	13.00^{f-i}	11.14^{bc}	4.58^{b}	6.44^{a-d}	3.60^{a-e}
TGX2010-5F	51.33^{f-h}	54.66^{b-d}	15.06^{a}	21.00^{a}	12.16^{a-c}	8.91^{ab}	6.05^{b-d}	4.10^{a-e}
TGX2011-6F	57.00^{ab}	54.66^{b-d}	6.94^{de}	16.00^{c-e}	16.27^{a-c}	15.25^{ab}	6.16^{b-d}	3.70^{a-e}
TGX2013-2F	46.66^{k-m}	49.00^{g-l}	11.32^{a-e}	16.00^{c-e}	12.91^{a-c}	5.91^{b}	5.55^{b-d}	2.46^{b-e}
TGX2015-1E	46.00^{lm}	49.33^{f-l}	8.62^{b-e}	14.33^{d-h}	19.02^{a-c}	13.25^{ab}	5.77^{b-d}	3.16^{a-e}
TGX2016-3E	50.66^{f-j}	55.33^{a-c}	9.14^{a-e}	14.00^{d-i}	19.99^{a-c}	6.91^{b}	6.48^{a-d}	3.10^{a-e}
TGX2016-4E	52.00^{e-g}	52.33^{c-g}	11.18^{a-e}	18.66^{b}	16.07^{a-c}	13.00^{ab}	6.05^{b-d}	3.66^{a-e}
TGX2017-5E	49.00^{g-l}	48.33^{h-l}	6.73^{e}	13.33^{e-i}	16.32^{a-c}	12.83^{ab}	5.61^{b-d}	3.93^{a-e}
TGX2017-6E	44.66^{m}	50.66^{e-k}	11.86^{a-e}	17.66^{bc}	10.33^{c}	12.08^{ab}	5.61^{b-d}	4.06^{a-e}
TGX2018-5E	47.66^{h-m}	52.66^{c-g}	13.26^{a-c}	15.33^{c-f}	24.94^{ab}	11.91^{ab}	4.72^{cd}	3.43^{a-e}
TGX2019-1E	47.00^{j-m}	47.00^{kl}	10.01^{a-e}	13.66^{e-i}	15.75^{a-c}	14.41^{ab}	4.83^{b-d}	2.33^{b-e}
TGX2020-1E	50.33^{f-k}	58.33^{a}	8.88^{b-e}	16.33^{c-e}	18.86^{a-c}	14.00^{ab}	6.61^{a-d}	4.90^{a}
TGX2023-1E	48.66^{g-l}	49.66^{e-l}	9.26^{a-e}	15.66^{c-f}	18.36^{a-c}	8.50^{ab}	4.61^{cd}	3.60^{a-e}
TGX2023-3E	54.66^{b-d}	56.00^{ab}	6.47^{e}	14.33^{d-h}	24.72^{ab}	24.00^{a}	5.67^{b-d}	4.33^{a-c}
TGX2023-4E	48.33^{g-l}	46.66^{l}	12.93^{a-d}	18.66^{b}	14.99^{a-c}	7.50^{b}	5.61^{b-d}	4.16^{a-e}
TGX2025-10E	48.66^{g-l}	51.66^{d-i}	10.08^{a-e}	14.66^{d-h}	18.94^{a-c}	13.91^{ab}	6.11^{b-d}	3.73^{a-e}
TGX2025-14E	50.33^{f-k}	52.66^{c-g}	12.11^{a-e}	16.33^{c-e}	13.83^{a-c}	10.83^{ab}	6.05^{b-d}	3.30^{a-e}
TGX2025-16E	49.33^{g-l}	51.66^{d-i}	12.89^{a-d}	16.33^{c-e}	18.44^{a-c}	8.50^{ab}	5.66^{b-d}	3.43^{a-e}
TGX2025-6E	48.33^{g-l}	53.33^{b-e}	13.43^{ab}	16.66^{b-d}	19.44^{a-c}	9.58^{ab}	5.55^{b-d}	2.86^{a-e}
TGX2027-1E	47.33^{i-m}	49.33^{f-l}	9.27^{a-e}	14.33^{d-h}	24.35^{ab}	16.08^{ab}	5.05^{b-d}	2.70^{b-e}
TGX2027-4E	46.66^{k-m}	47.66^{j-l}	12.23^{a-e}	15.33^{c-f}	14.34^{a-c}	10.08^{ab}	5.66^{b-d}	2.06^{e}
TGX2027-7E	50.33^{f-k}	47.66^{j-l}	13.69^{ab}	14.00^{d-i}	15.16^{a-c}	6.91^{ab}	4.50^{cd}	2.10^{de}

E1: Fada N'Gourma, E2: Farako-Bâ. Means in the same column followed by different letter (s) are significantly different at $P < 0.05$.

Table 6. The means of soybean genotypes and LSD groups of several pods, Grain Yield, Rust (R6 stage), and Soybean mosaic virus (Smv) in Burkina Faso.

Sites	**E1**	**E2**	**E1**	**E2**	**E1**	**E2**	**E1**	**E2**
Genotypes	**Nppp**	**Nppp**	**Yield**	**Yield**	**Rust**	**Rust**	**Smv**	**Smv**
G196 (check 2)	95.63^{a-c}	89.23^{bc}	905.84^{bc}	1735.87^{a}	1.33^{a}	2.00^{a}	1.00^{b}	1.00^{b}
G197 (check 3)	90.72^{a-d}	59.46^{bc}	903.95^{bc}	2696.43^{a}	1.00^{b}	1.00^{b}	2.00^{a}	1.00^{b}
G175 (check 1)	38.56^{i}	36.70^{c}	2056.18^{a-c}	2220.2^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX1835-10E	71.70^{a-g}	47.20^{bc}	2011.46^{a-c}	2387.93^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX1951-4F	81.33^{a-g}	63.40^{bc}	2197.04^{a-c}	1784.03^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}

Continued

TGX1987-10F	79.66^{a-g}	87.86^{bc}	3358.74^{ab}	2803.01^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX1987-14F	80.66^{a-g}	82.50^{bc}	3668.36^{a}	2349.44^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX1988-5F	57.53^{e-i}	57.03^{bc}	1571.10^{a-c}	1785.61^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX1989-19F	72.00^{a-g}	37.50^{c}	2050.38^{a-c}	1732.42^{a}	1.33^{a}	1.00^{b}	1.00^{b}	1.00^{b}
TGX1993-4FN	100.16^{a}	142.60^{a}	1412.78^{a-c}	4852.39^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2004-7F	92.56^{a-d}	75.53^{bc}	2638.17^{a-c}	2660.69^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2007-1F	50.56^{g-i}	65.80^{bc}	2657.22^{a-c}	2115.71^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2007-3F	61.33^{d-i}	64.46^{bc}	2465.40^{a-c}	3270.76^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2008-4F	72.16^{a-g}	60.60^{bc}	1854.19^{a-c}	2937.70^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2009-14F	89.66^{a-d}	84.73^{bc}	1755.06^{a-c}	1350.56^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2009-16F	82.03^{a-g}	88.03^{bc}	1907.46^{a-c}	3320.83^{a}	1.00^{b}	2.00^{a}	1.66^{a}	2.00^{a}
TGX2009-1F	62.00^{d-i}	65.23^{bc}	1173.32^{a-c}	2201.69^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2010-11F	82.70^{a-f}	88.16^{bc}	2062.87^{a-c}	2849.49$_{a}$	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2010-14F	68.66^{a-h}	61.86^{bc}	2468.80^{a-c}	1328.30$_{a}$	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2010-5F	80.86^{a-g}	78.96^{bc}	1845.50^{a-c}	2301.58^{a}	1.33^{a}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2011-6F	100.00^{a}	85.93^{bc}	231.11^{c}	2845.30^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2013-2F	76.33^{a-g}	60.13^{bc}	2858.12^{a-c}	2125.92^{a}	1.00^{b}	1.00^{b}	2.00^{a}	1.00^{b}
TGX2015-1E	87.33^{a-e}	72.86^{bc}	1836.41^{a-c}	1948.13^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2016-3E	62.74^{d-i}	80.00^{bc}	1209.36^{a-c}	2491.79^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2016-4E	77.08^{a-g}	63.93^{bc}	751.71^{bc}	2384.70^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2017-5E	68.13^{b-h}	66.03^{bc}	647.47^{bc}	2062.46^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2017-6E	90.66^{a-d}	90.40^{bc}	3780.10^{a}	3339.37^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2018-5E	71.03^{a-g}	67.40^{bc}	2690.91^{a-c}	3329.13^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2019-1E	57.00^{e-i}	44.63^{c}	2029.62^{a-c}	1222.76^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2020-1E	90.50^{a-d}	106.53^{b}	1171.24^{a-c}	3696.30^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2023-1E	71.66^{a-g}	71.90^{bc}	1963.70^{a-c}	3146.36^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2023-3E	64.06^{c-i}	51.90^{bc}	1711.11^{a-c}	1978.42^{a}	1.00^{b}	2.00^{a}	1.00^{b}	1.00^{b}
TGX2023-4E	96.55^{ab}	81.00^{bc}	2126.47^{a-c}	4188.89^{a}	1.33^{a}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2025-10E	64.00^{c-i}	71.43^{bc}	1900.01^{a-c}	2272.34^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2025-14E	51.00^{f-i}	41.83^{c}	1889.63^{a-c}	2177.46^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2025-16E	86.00^{a-e}	71.63^{bc}	2414.04^{a-c}	3681.88^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2025-6E	53.00^{f-i}	39.00^{c}	2235.40^{a-c}	1143.28^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2027-1E	51.16^{f-i}	53.63^{bc}	1736.32^{a-c}	1682.38^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2027-4E	72.66^{a-g}	65.00^{bc}	2228.85^{a-c}	2226.76^{a}	1.33^{a}	1.00^{b}	1.00^{b}	1.00^{b}
TGX2027-7E	41.00^{hi}	29.73^{c}	1972.24^{a-c}	1592.20^{a}	1.00^{b}	1.00^{b}	1.00^{b}	1.00^{b}

Note. Means in the same column followed by different letter (s) are significantly different at $P < 0.05$.

3.3. Yield and Yield Components

The combined analysis of variance showed that the genotype (G), the environment (E), and genotype × environment interaction (GEI) effects were highly significant ($P < 0.01$) for the studied traits (**Table 7**). The contribution to the sum of mean squares of genotype, environment, and G × E varied depending on the trait. Most of the contributions to the total sum of squares were explained by the environment (E), followed by genotype and genotype × environment. For the number of days to 50% flowering, the environment explained 58.71% of the total variation, followed by the genotype (37.07%) and the G × E interaction (4.21%). The contribution to the sum of squares was 1.73% for genotype, 97.57% for environments, and 0.69% for GEI for the 100-seed weight. The contribution to the total sum of the squares expressed by E, G, and G × E was 79.87%, 10.57% and 9.56%, respectively, for grain yield.

Table 7. Combined analysis of variance for 6 traits and the percentage of mean squares for G, E, and G × E.

SV	df	Mean square					
		50% Flo	Nppp	Nbpp	100w	Nbno	Yield
Replication	2	4.879	221.8	13.85	12.02	29.81	401,840
Genotype (G)	39	75.14**	1814.0**	2.42**	18.46**	72.74**	1,960,135**
Env (E)	1	119.01**	1363.5**	294.13**	1038.46**	2647.50**	14,809,916**
G × E	39	8.54**	292.5**	1.09**	7.40**	38.22**	1,772,086**
Error	158	1.58	235.1	0.37	2.14	21.55	1,282,740
Total	239	15.24	506.7	2.17	10.08	43.68	1,522,356
% G		37.07	52.27	0.81	1.73	2.63	10.57
% E		58.71	39.29	98.82	97.57	95.97	79.87
% G × E		4.21	8.42	0.36	0.69	1.38	9.56

50% Flo: days to 50% flowering; Nppp: number of pods per plant; Nbpp: number of branches per plant; 100w: 100-seed weight; Nbno: number of nodules; yield: grain yield (kg ha^{-1}); ** indicates significance at $P < 0.01$ probability level; df = degree of Freedom, G × E = Genotype by environment interaction; SV: sources of variation.

3.4. Reaction of Soybean Genotypes to Diseases

Symptoms of rust and soybean mosaic virus (Smv) were observed in the trials (**Tables 4 and 6**). A highly significant difference ($p < 0.01$) among the 40 genotypes was observed for rust (Stage R6) and Smv diseases. The majority of genotypes showed rust and Smv symptoms with a score of 1 (0% disease infection). TGX2023-3E, TGX2009-16F, and the control (G196) scored 2 (25% rust symptoms), while TGX2013-2F and the control (G197) scored 2 (25% virus symptoms).

3.5. Stability of Environments Using the AMMI Model

Information on stable and unstable environments was provided by the IPCA-1 score. Positive and negative IPCA-1 scores revealed the status of the environments (stable or unstable). Fada N'Gourma had a positive IPCA-1 score and low mean yield in a stable environment. On the contrary, Farako-Bâ had a negative IPCA-1 score and a high mean yield (2456 kg ha^{-1}), above the general mean (2207 kg ha^{-1}), in the unstable environment. The genotypes reacted differently to environmental variation. The AMMI model was used to select the best genotypes for a specific environment. The four best genotypes selected for each environment are presented in Table 8. Table 9 provides the ranking of tested soybean lines from more stable to more unstable. Among the tested genotypes, TGX2017-6E was the highest-yielding and most stable genotype, while TGX2023-4E was high-yielding but unstable across the test environments.

Table 8. Four best genotypes per site.

Env	Mean	IPCA1 score	The first four AMMI-selected genotypes			
			1	2	3	4
E1	1959	48.99	TGX2017-6E	TGX1987-14F	TGX1987-10F	TGX2013-2F
E2	2456	−48.99	TGX1993-4FN	TGX2023-4E	TGX2020-1E	TGX2025-16E

AMMI: Additive Main Effects and Multiplicative Interaction Model, Env.: Environment, Env. Index: Environmental index, E1: Fada N'Gourma, E2: Farako-Bâ.

Table 9. 40 most stable genotypes according to stability superiority measure coefficients.

Genotypes	Cultivar superiority	Means (kg ha^{-1})	Ranking
TGX2017-6E	28,616	3560	1
TGX2023-4E	39,684	3158	2
TGX2025-16E	40,453	3048	3
TGX2018-5E	43,833	3010	4
TGX2007-3F	52,875	2868	5
TGX1987-10F	54,719	3081	6
TGX1993-4FN	70,052	3133	7
TGX2009-16F	73,156	2614	8
TGX2004-7F	76,345	2649	9
TGX2023-1E	77,623	2555	10
TGX1987-14F	78,466	3009	11
TGX2010-11F	87,006	2456	12
TGX2008-4F	92,189	2396	13
TGX2020-1E	101,784	2434	14
TGX2013-2F	103,546	2492	15
TGX2007-1F	109,379	2386	16
TGX1835-10E	115,021	2200	17
TGX2027-4E	116,254	2228	18
G175 (check 1)	123,752	2138	19

Continued

TGX2025-10E	127,392	2086	20
TGX2010-5F	128,116	2074	21
TGX2025-14E	134,114	2034	22
TGX1951-4F	149,011	1991	23
TGX2016-3E	152,264	1851	24
TGX2015-1E	152,658	1892	25
TGX2023-3E	156,756	1845	26
TGX1989-19F	159,078	1891	27
G197 (check 3)	161,505	1800	28
TGX2009-1F	172,769	1688	29
TGX2027-7E	173,716	1782	30
TGX2010-14F	176,735	1899	31
TGX2027-1E	177,825	1709	32
TGX1988-5F	178,561	1678	33
TGX2016-4E	190,759	1568	34
TGX2025-6E	201,795	1689	35
TGX2019-1E	202,981	1626	36
TGX2009-14F	204,546	1553	37
TGX2011-6F	207,797	1538	38
TGX2017-5E	219,964	1355	39
G196 (check 2)	224,677	1321	40

3.6. GGE Biplot Analysis

3.6.1. Agronomic Performance and Genotypic Stability

The GGE biplot is designed to identify the best-performing and stable genotypes (**Figure 1**). The best genotype is the one with a high PC1 score (high mean yield) and a PC2 score close to zero (high stability). PC1 and PC2 represented 54.72% and 45.28%, respectively, of the GGE (genotype and genotype × environment interaction), totaling 100% of the GGE. In the interpretation of GGE biplots, the Average Environment Coordination (AEC) axis allows for the visualization of both the mean performance and the stability of genotypes across multiple environments. An ideal genotype performs well and is stable. In this study, the best-performing genotypes are TGX2017-6E, TGX2018-5E, TGX2007-3F, TGX1987-10F, and TGX1987-14F. They performed above the mean and were close to the ideal genotype, shown in a small circle. Furthermore, comparison of the long projection lines on the AEC axis with low PC2 scores indicates that the genotypes TGX2018-5E, TGX2007-3F, TGX2004-7F, and TGX2008-4F were the most stable, while TGX1993-4FN, TGX2027-1E, TGX2025-6E, TGX2011-6F, TGX2017-5E, and TGX2019-1E were the most unstable due to their high PC2 scores. The genotypes TGX2011-6F, G196, G197, and G175 are undesirable because of their negative PC2 scores and low performance (**Figure 1**).

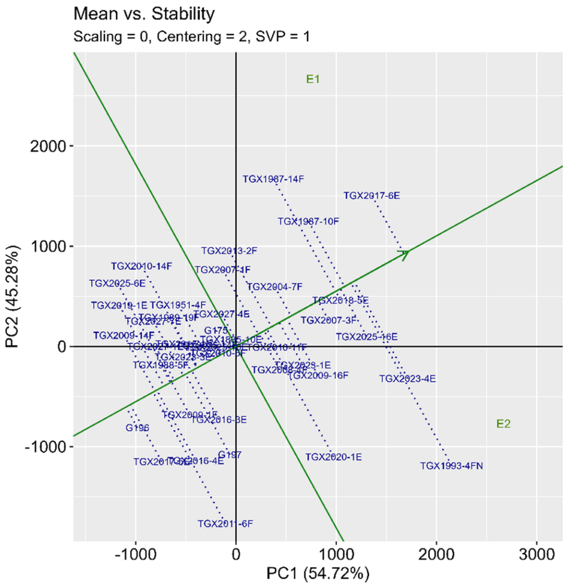

Figure 1. GGE Biplot graph showing the ranking of genotypes according to performance and stability.

3.6.2. Comparison of Genotypes with the "Ideal" Genotype

The GGE biplot based on genotype comparison for grain yield is shown (center of the concentric circle) in **Figure 2**. According to the comparison procedure, genotypes closer to the center performed well, while genotypes further away had low performance. The TGX2017-6E genotype at the center of the circle is the ideal genotype in terms of its performance and stability. Genotypes TGX2018-5E, TGX1987-10F, TGX1987-14F, TGX2007-3F, and TGX2025-16E were the most desirable and stable, whereas genotypes TGX2010-14F, TGX2025-6E, TGX2011-6F, and G196 were the most unstable across both environments.

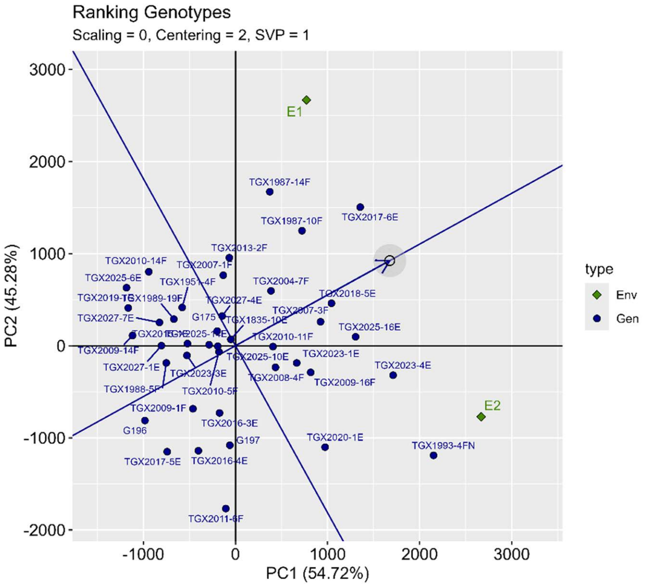

Figure 2. GGE biplot graph showing the comparison of genotypes with the "ideal" genotype.

3.6.3. Comparison of Environments

Similar to the ideal genotype, the ideal environment is located in the first concentric circle (**Figure 3**). The ideal environment is the one at the center of the concentric circles, and it is possible to identify desirable environments based on their proximity to the ideal environment. In this study, Fada N'Gourma is an ideal environment, representative of discriminating genotype performance. Farako-Ba is an unstable environment, with a negative score on the ordinate of AEC.

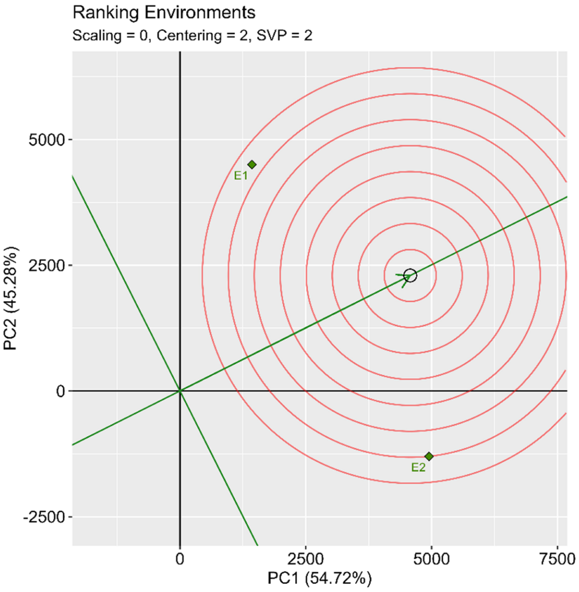

Figure 3. GGE biplot graph showing a comparison of environments with the "ideal" environment.

3.6.4. Identification of Performed Genotypes and Their Environments

The polygon shows the best genotypes and their associated environments (**Figure 4**). The GGE biplot polygon is formed by connecting the genotypes that are farthest from the biplot origin, so that all remaining genotypes are contained within the polygon. The test environments are divided into nine sectors, each containing different genotypes. Seven genotypes are located at the vertices of the polygon: TGX2017-6E, TGX1987-14F, TGX2025-6E, G196, TGX2017-5E, TGX2011-6F, and TGX1993-4FN.

These genotypes are either the best or the worst in one or both environments. The GGE graph identified two distinct soybean-growing environments for grain yield. The first environment comprises the medium-yielding (E1) environment (Fada N'Gourma), with the best genotype TGX2017-6E, followed by TGX1987-14F, TGX1987-10F, TGX2018-5E, and TGX2007-3F. The second highest-yielding environment (E2) corresponds to Farako-Ba, with the best genotype TGX1993-4FN, followed by TGX2020-1E and TGX2023-4E. However, the results also identified certain genotypes that are not linked to any environment. These genotypes are poorly adapted to the two experimental sites (TGX2011-6F, G196, TGX2025-6E, and TGX2017-5E).

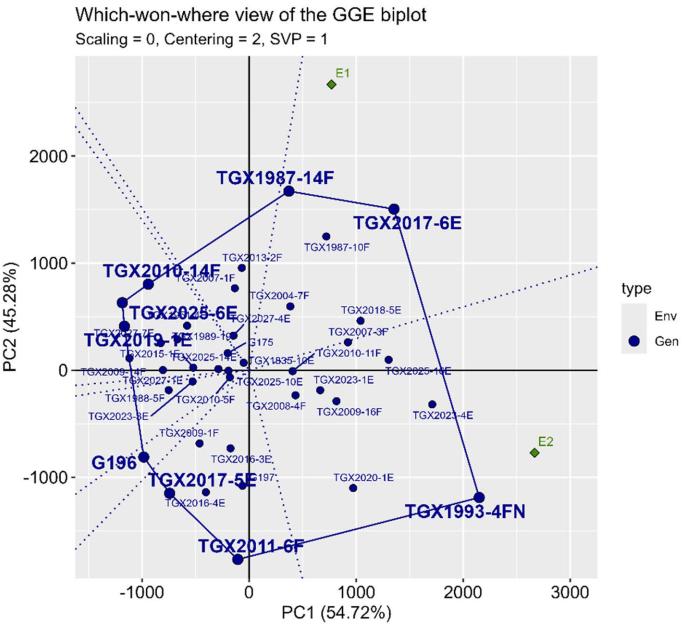

Figure 4. GGE biplot graph showing the performed genotypes in each "Which-won-where" environment.

3.7. Correlation Analysis

Pearson correlation matrix revealed significant correlations among the traits studied (**Table 10**). The number of days to reach 50% flowering (r = 0.00 ^{NS}) and the number of nodules (r = −0.11 ^{NS}) showed no significant relationship with seed yield. However, there was a positive and significant correlation between the number of pods per plant (r = 0.34***), the 100-seed weight (r = 0.30***), and seed yield. The number of branches per plant had a near-zero but significant correlation coefficient (r = −0.00***) with seed yield.

Table 10. Correlation coefficients between seed yield and yield components of soybean genotypes across 2 environments in Burkina Faso.

Traits	Yield (kg ha^{-1})
Number of days to 50% flowering (50% Flo)	0.00 ^{NS}
Number of nodules (Nbno)	−0.11 ^{NS}
Pod clearance (Podc)	−0.18**
Number of branches per plant (Nbpp)	−0.00***
Number of pods per plant (Nppp)	0.34***
100-seed weight (100w)	0.30***

*, **, *** Significant at 0.05, 0.01, and 0.001 levels of probability, respectively, NS = Not significant.

4. Discussion

The analysis of variance showed a highly significant difference ($P < 0.01$) in the number of days to 50% flowering, pod clearance, number of branches per plant, number of pods per plant, 100-seed weight, and grain yield between the studied soybean genotypes. These variations indicate the genetic variability that characterizes soybean genotypes. This result is in agreement with previous studies reported by [16] [17] on soybeans. The combined analysis of variance revealed that the effect of genotype (G), environment (E), and genotype × environment interaction (G × E) on the number of days to 50% flowering, number of pods per plant, number of branches, 100-seed weight, and grain yield was highly significant ($P < 0.01$). The traits studied indicate that soybean genotypes react differently to environments. Moreover, the existence of G × E interaction allows genotypes to be selected for specific environments. The contribution to the total sum of mean squares varies according to the trait under consideration. In fact, in multilocation trials, the greatest proportion of variation in agromorphological traits is due to the environment. These results are consistent with the findings of [18] [19]. Similarly, in the present study, except for the number of pods per plant, the environment explains the high variability of the studied traits. The genotype × environment interaction has little influence on the traits compared to that of the environment and genotype, which explains most of the variation. The contribution to the total sum of mean squares for grain yield is in satisfactory agreement with that observed by [20].

The 100-seed weight, number of branches per plant, and number of pods per plant are important yield parameters. The results for 100-seed weight and number of branches per plant are consistent with those of [16] [20]. The number of branches per plant is therefore an essential criterion for the selection of improved soybean varieties. A greater number of branches leads to more pods per plant, resulting in higher grain yield. This result is in line with the observations of [21]. However, the average number of pods per plant (71 pods) obtained in this study was higher than that recorded in their study. These observed variations may be attributed to genotypic differences or environmental effects. The highly significant mean squares of the environments for different traits indicate that the two environments are different, which is in agreement with recent results reported by [22]. According to the cumulative rainfall data, it is clear that the wettest site is Farako-Ba, while Fada N'Gourma receives the lowest rainfall. Indeed, Farako-Ba, located in the southern Sudan climate zone, is well-watered, whereas Fada N'Gourma, located in the northern Sudanian climatic zone, experiences relatively low rainfall. In addition, the climatic characteristics of the localities (longitude and altitude) indicate diversity within these study sites. Soybean genotypes respond differently to these environments. Furthermore, two main soybean diseases that hamper soybean production in Burkina Faso were observed. The low rust and Smv scores recorded in the majority of genotypes (score 1) indicate that the genotypes do not show symptoms of these diseases. Consequently, these two diseases do not cause any loss of grain yield. These observations perfectly corroborate previous results reported by [16] on soybeans.

GGE biplots can be used to identify the best environments and genotypes. In this study, two distinct environments for grain yield evaluation are displayed. The relationship between environments and the 'which-won-where' model shows that Farako-Ba is different from Fada N'Gourma. The best-performing soybean genotypes in terms of grain yield (kg ha^{-1}) have been identified at two key sites. At Farako-Ba, the highest yields were recorded for TGX1993-4FN (4805), TGX2023-4E (4305), TGX2025-16E (3679), and TGX2020-1E (3205). In Fada N'Gourma, the top-performing genotypes included TGX1987-14F (3987), TGX2017-6E (3700), TGX1987-10F (3223), and TGX2013-2F (2323). These genotypes consistently outperformed the control varieties G196, G197, and G175, which yielded 1842, 2209, and 2005 kg ha^{-1} at Farako-Ba and 936, 824, and 2154 kg ha^{-1} at Fada N'Gourma, respectively.

The differences in agronomic performance between the two sites can be attributed to climatic conditions, with the southern Sudanian zone offering more favorable conditions than the northern Sudanian zone. This highlights the significant role of G × E interactions and environmental factors in genotype performance. The importance of selecting genotypes adapted to specific environments is further emphasized by the significant G × E interactions observed for the traits studied.

Analysis of stability using the IPC-1 scores of the AMMI model reveals distinct environmental characteristics: Fada N'Gourma represents a stable, medium-yielding environment, whereas Farako-Ba is an unstable, high-yielding environment. Stable genotypes, including TGX2017-6E, TGX1987-14F, TGX1987-10F, and TGX2013-2F, performed well in Fada N'Gourma, while TGX1993-4FN, TGX2023-4E, TGX2020-1E, and TGX2025-16E excelled in Farako-Ba.

The GGE biplot analysis provided additional insights into yield, stability, and environmental representativeness. TGX2017-6E, TGX1987-14F, TGX1987-10F, TGX2018-5E, and TGX2007-3F were identified as genotypes with superior yields and stability. Notably, Fada N'Gourma emerged as the most discriminating and representative environment for selecting soybean genotypes. Previous studies, such as [16], identified 18 genotypes with high grain yields in medium maturity groups, including TGX2017-6E (5.11 t ha^{-1}), TGX2017-5E (4.72 t ha^{-1}), and TGX1993-4FN (3.89 t ha^{-1}).

Finally, the 'who wins' biplot highlights genotype preferences for specific environments, reinforcing the value of selecting genotypes adapted to particular localities. The identified genotypes represent promising candidates for targeted adoption in distinct environments.

With regard to the relationships between yield traits, it was particularly interesting to find that the number of pods per plant, 100 seed weights per plant, and the number of branches per plant were correlated with grain yield. The positive, weak, and highly significant association between the number of pods per plant and 100-seed weight revealed the importance of these traits in determining grain yield. The correlation between these two traits and seed yield indicates that they could be used for the indirect selection of high-yielding soybean genotypes. These results are in line with previous reports on associations between seed yield and the number of pods per plant as well as 100-seed weight in soybeans [23] [24].

5. Conclusions and Recommendations

The analysis of variance of the 40 soybean genotypes evaluated at the Farako-Ba and Fada N'Gourma experimental stations showed that these genotypes behaved differently, expressing significant variations for the majority of the characteristics studied. This study highlighted the effect of the G × E interaction through GGE biplot analysis, demonstrating the stability of the genotypes as well as the discriminatory capacity of the two environments for grain yield. GGE biplot analysis identified stable and high-yielding genotypes in both environments. The genotypes TGX2017-6E, TGX1987-14F, TGX1987-10F, TGX2018-5E, and TGX2007-3F, in this sequence, showed the greatest grain yield stability on average across the environments studied, with respective yields of 3560, 3009, 3081, 3010, and 2868 kg ha^{-1}. The three control varieties (G196, G197, and G175) were less efficient and stable, with yields of 1321, 1800, and 2138 kg ha^{-1}, respectively. Thus, depending on the conditions of each environment, the yield components exhibit different behavior. Therefore, this information can be useful in the soybean breeding process using the genotypes in this study. Fada N'Gourma is a discriminating environment and could be recommended as a primary testing center for the evaluation of new soybean genotypes in Burkina Faso.

Data Availability

The data are available from the corresponding author upon reasonable request.

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Conflicts of Interest

The authors declare that they have no conflicts of interest.

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