















Research Article

Evaluation of Early Maturity Group of Soybean (*Glycine max* L. Merr.) for Agronomic Performance and Estimates of Genetic Parameters in Sudanian Zone of Burkina Faso

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Soybean is one of the promising food crops and feeds which contributes significantly to the development of agriculture in Burkina Faso. However, very few improved soybean varieties have been developed in the country. The introduction of new genotypes with high agronomic potential and adapted to the climatic conditions of the Sudanian zone of Burkina Faso will boost soybean production in the region. Twenty-four (24) newly introduced soybean genotypes were evaluated for their agromorphological and adaptation characteristics in the Sudanian zone of Burkina Faso. The variability parameters such as genotypic and phenotypic coefficient of variation, broad sense heritability, and expected genetic advance were estimated for 14 agromorphological characters. The experimental design used in this study was an alpha lattice with 3 replications. Planting was done following a spacing of 50 cm (inter-row) × 5 cm (within row). Analysis of variance revealed significant difference ($P < 0.001$; $P < 0.05$) for all characters studied except the nodule diameter, nodule score, and grain yield. The values of the phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters indicating the influence of environmental factors. The highest GCV and PVC values were found in the number of nodules (70.07% and 77.26%), number of seeds per plant (41.34% and 44.18%), and number of pods per plant (29.27% and 33.50%), respectively. High estimates of heritability coupled with high genetic advance expressed as a percentage of mean were observed for 10 of the 14 traits, suggesting an important expected genetic gain allowing more success in selection.

1. Introduction

Soybean (*Glycine max* L. Merr.) is one of the oldest cultivated crops and the most important oilseed legume in the world [1]. It is the fourth most important crop in the world in terms of area harvested and production [2]. The world soybean production has exploded for 40 years and has experienced an average annual growth much faster than that of

cereals (+5% per year for soybeans, 2% for wheat, and 3% for corn) [3]. Globally, the world soybean production is increasing rapidly from 2011 to 2020 with a growth rate of 37.99% and reached an average annual production of 361 million tons in 2020 [4]. Soybean consists of more than 60% of the world's production of oilseeds, 30% of the world's oil produced and 70% of the oilseed meals produced. Soybean meal is the best vegetable protein source considering

quantity as well as its quality [5]. It consists of more than 36% proteins, 30% carbohydrates, and excellent amounts of dietary fiber, vitamins, and minerals [6]. The introduction of soybean in Burkina Faso (ex Haute Volta) as a cultivated crop began in 1958 and was an initiative of Agricultural Research [7]. During the period of the Revolution from 1983 to 1987, soybean cultivation in Burkina Faso was encouraged as part of a food self-sufficiency strategy. From 2010 to 2012, the government launched a national campaign to promote soybean production in the country. As a strategic crop, soybean is used essentially in food and feed and contributes to strengthening the resilience of poor households to food insecurity [8]. The annual soybean production in Burkina Faso is estimated to be around 51,708 tons. This quantity mainly comes from 8 regions of which 5 have high potential for production (the Center-East, Center-West, Center-South, the East, and Hauts-Bassins) and 3 with medium potential (the South-West, Boucle du Mouhoun, and the Cascades region) [9]. Despite the strengths of this crop, the soybean production sector is still being structured in Burkina Faso. Soybean production is influenced by climatic change, agronomic factors, pests, and nutrient availability in the soil [10]. Abiotic stresses that affected soybean production include drought, flooding, lodging, frost, and nutrient deficiency in the soil [11]. The most prominent among biotic stresses in soybean production include diverse pathogens (bacteria, fungi, and viruses), pests (nematodes), and weeds. All these multiple constraints combined with unfavorable climatic changes cause yield losses and have led to the abandonment of soybean production in certain regions [12]. Furthermore, the soybean varieties vulgarized (G196 and G197) in Burkina Faso have relatively long maturity cycles and do not guarantee a good harvest. Therefore, the development or introduction of improved soybean genotypes carefully selected in breeding programs may provide early maturity genotypes of soybean adapted to the agroecological conditions of the country, which combine good resistance to diseases. The use of these early maturity genotypes could contribute to increasing soybean productivity and guaranteeing a good income for farmers. This study aims to evaluate the yield performance and estimate the genetic parameters of soybean genotypes belonging to the early maturity group in Burkina Faso. These genotypes were developed by the International Institute for Tropical Agriculture (IITA).

2. Materials and Methods

2.1. Plant Material and Experimental Site. The planting material consisted of 22 improved soybean genotypes obtained from IITA (Abuja, Nigeria) and two soybean varieties (G175 and G196) already used in the Burkina Faso breeding programme (Table 1). The seeds of the 22 soybean accessions before being transferred to Burkina Faso were previously treated with an insecticide, Phos-toxin (55% aluminum phosphide) and with a fungicide, Bendaco (Carbendazium 12% + Mancozeb 63% WP). The field study was conducted during the 2020 rainy season at

the Farako-Bâ Research Station in Burkina Faso (Figure 1). The genotypes were planted on 11 July 2020 at a rate of 1 seed per hill with a spacing of 5 cm between hills and 50 cm between rows (20 plants/m²). Weed control was done manually on the 15th and 45th days after sowing.

2.2. Experimental Design. The experimental design used was an alpha lattice with 3 replications separated from each other by 2 m. Each replication consisted of 24 entries distributed in 4 blocks, each consisting of 6 varieties. The blocks were separated from each other by 80 cm. The elementary plot was represented by 4 rows of 4 m with 50 cm of row spacing, that is, a gross area of 0.5 m × 4 m × 3 (6 m²). The net plot consisted of the two central lines, that is, an area of 4 m². Harvesting was done when 95% of pods reached maturity.

2.3. Data Collection. The agronomical and morphological growth parameters; days to 50% flowering (50% Flo), 50 and 95% pod maturity (50% and 95% Mat), number of nodes (Nb_nd), plant height (PH, cm), pod clearance (Pod_cle, cm), number of branches (Nb_bra), number of pods per plant (Nb_pod/plt), pod length (Pod_len), number of seeds per plant (Nb_sd/plt), number of nodules per plant (Nb_nod), nodule diameter (Nod_dia, mm), nodules score (nodule distribution on root system, Nb_sco), pod shattering (Pod_sha, %), hundred seed weight (100 SW, g), and grain yield (Gra_Y, t/ha) were recorded. The soybean rust, one of the major fungi diseases and soybean mosaic virus has been evaluated.

2.4. Data Analysis. An analysis of variance (ANOVA) was performed using GenStat Release 12.1 on all quantitative variables. All treatment means were compared using the Duncan multiple comparisons test at a 5% level of significance. Based on the variance component obtained from the ANOVA and the significance, the genetic parameters were estimated. Thus, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), broad sense heritability (H²), and expected genetic advance (GA) were calculated according to Jalata et al. [13] procedure. The GCV expresses the heritable portion, while the PCV is an expression of both the genetic and environmental effects on the trait. Higher PCV versus GCV indicates a significant contribution of environment and genotypes by environment interaction in the expression of a given trait.

3. Results and Discussion

3.1. Variability of Phenological and Morphological Traits in Soybean Early Maturity Group. Genetic variability is the prerequisites for genetic improvement in any crop breeding program. The analysis of variances between the early soybean maturity group genotypes were highly significant ($P < 0.001$) for most of the phenological and morphological traits except nodule scores and diameters (Table 2).

TABLE 1: List of genotypes belonged to the maturity group of soybean.

Ord_Id	Name of lines	Genetic nature	Origin	Seed cost color	Maturity group
1	TGX2009-14F	Line	IITA	Yellow	Early
2	TGX2025-19E	Line	IITA	Yellow	Early
3	TGX2010-14F	Line	IITA	Yellow	Early
4	TGX1835-10E	Line	IITA	Yellow	Early
5	TGX2027-4E	Line	IITA	Yellow	Early
6	TGX1988-5F	Line	IITA	Yellow	Early
7	TGX2023-4E	Line	IITA	Yellow	Early
8	TGX1987-10F	Line	IITA	Yellow	Early
9	TGX1951-4F	Line	IITA	Yellow	Early
10	TGX2025-16E	Line	IITA	Yellow	Early
11	TGX2027-7E	Line	IITA	Yellow	Early
12	TGX2004-7F	Line	IITA	Yellow	Early
13	TGX2009-1F	Line	IITA	Yellow	Early
14	TGX2023-1E	Line	IITA	Yellow	Early
15	TGX2004-13F	Line	IITA	Yellow	Early
16	TGX1485-1D	Line	IITA	Yellow	Early
17	TGX2010-5F	Line	IITA	Yellow	Early
18	TGX2016-2E	Line	IITA	Yellow	Early
19	TGX2007-3F	Line	IITA	Yellow	Early
20	TGX2018-5E	Line	IITA	Yellow	Early
21	TGX2013-2F	Line	IITA	Yellow	Early
22	TGX2007-1F	Line	IITA	Yellow	Early
23	G175 (check-1)	Line	INERA	Yellow	Early
24	G196 (check-2)	Line	INERA	Yellow	Medium

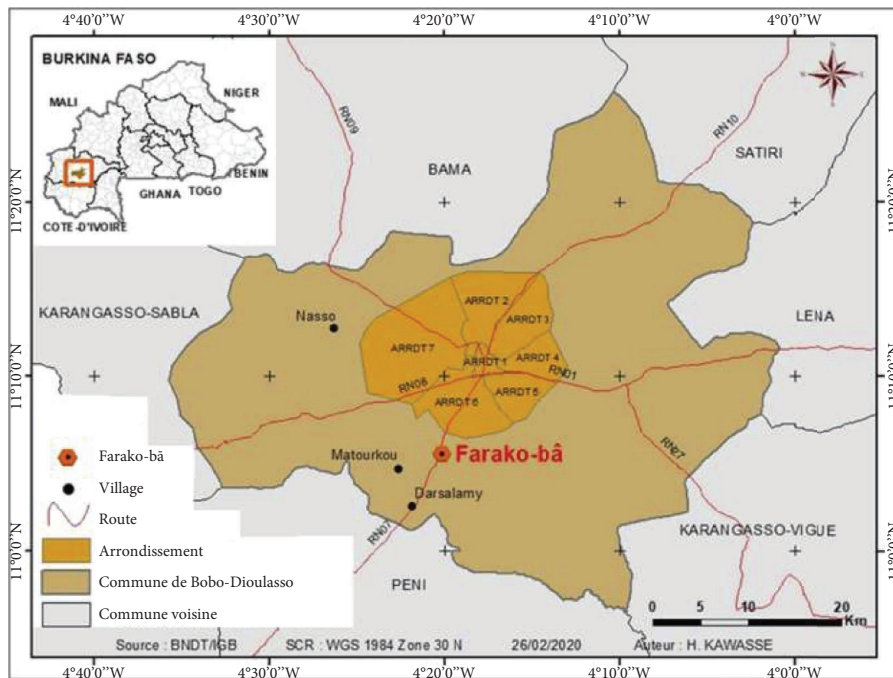


FIGURE 1: Administrative map of DDREA-Ouest/INERA, Farako-Bà locating the experimental site (BNDTAGB, 2020).

3.1.1. *Variability of Phenological Traits.* Days to flowering ranged from 45 (TGX2004-13F) to 58 days (TGX2025-19E, TGX2016-2E, and TGX2009-1F) with an average of 48 days. Results showed that 7 genotypes of soybean were the earliest (45–48 days) and better than the control early genotype G175

(50 days). Compared with previous work, the early maturity check genotype G175 took five 5 days more in the climatic condition of Burkina Faso to reach 50% flowering [14]. This result is suggesting a probable photoperiod sensitivity observed for that genotype. In fact, photo sensitivity has an

TABLE 2: Analyses of variances of phenological and morphological growth parameters.

Variables	Source of variations	d.f.	s.s.	m.s.	v.r.	F pr.
50% Flo (JAS)	Nb_genotype	23	1203.65	52.33	89.71	<0.001**
	Error	48	28	0.58		
50% Mat (JAS)	Nb_genotype	23	6810.54	296.11	247.91	<0.001**
	Error	48	57.33	1.194		
95% Mat (JAS)	Nb_genotype	23	5539.28	240.84	912.65	<0.001**
	Error	48	12.67	0.264		
Nb_nod	Nb_genotype	23	2776.54	120.72	5.63	<0.001**
	Error	48	1029.33	21.44		
Nod_sco (%)	Nb_genotype	23	3.11	0.13	1.39	0.165NS
	Error	48	4.67	0.097		
Nod_dia (mm)	Nb_genotype	23	24.99	1.086	1.00	0.480NS
	Error	48	52	1.083		
PH (cm)	Nb_genotype	23	3992.10	173.57	1.88	<0.033*
	Error	48	4433.59	92.37		
Pod_cle (%)	Nb_genotype	23	1301.66	56.59	5.28	<0.001**
	Error	48	514.29	10.71		
Nb_nd	Nb_genotype	23	349.11	15.18	17.35	<0.001**
	Error	48	42	0.87		

NS: no significant; *: significant at 5%; **: highly significant at 1%; s.s.: sum of squares; d.f.: degree of freedom; m.s.: mean squares; Nb_genotype: number of genotype.

influence on the phenology of soybean plants from different sowing periods [15]. However, the results of this study confirmed previous findings and suggested a genetic background among the 24 soybean genotypes [16]. Days to 50% maturity ranged from 79 (G175, TGX2010-14F) to 110 days for the control genotype G196 (medium maturity group). Eleven (11) genotypes were the earliest and presented values below the average (94 days). Days to 95% maturity ranged from 88 (G175) to 120 days (G196) with an average of 104 days. From the 24 soybean lines, 12 genotypes presented values below the average. The control genotype G175 was the earliest maturing genotype of the group for 50 and 95% maturity. It was followed by the genotypes TGX2018-5E, TGX2016-2E, and TGX2027-7E (94 days each for 95% maturity). The low values of the coefficients of variation, 1.2 and 0.5% for, respectively, days to 50 and 95% maturity indicate low variability for the cropping cycle within the soybean genotypes under this study. However, according to Zhang and Bellaloui [17] maturity dates of soybean varieties within the same maturity group can vary from 10 to 15 days depending on the time of planting and location.

3.1.2. Genetic Variability of Morphological Traits of Early Maturity Group of Soybean. Plant height ranged from 63 cm (TGX2009-14F) to 97 cm (TGX2004-13F), with an average of 75.9 cm. Most of the genotypes of the introduced early maturity group had a mean plant height above the control genotypes (G175 and G196), reflecting their good adaptability to the environment [18]. Pod clearance ranged from 11 (G175) to 29 cm (TGX1835-10E), with an average of 17.42 cm. Most of the genotypes of this study had a good pod clearance, which contributes to reducing harvest losses and facilitate mechanized harvesting [19]. These genotypes have the advantage of better resistance to *Sclerotinia* [20].

However, low pod clearance stages may expose soybean genotypes to soil splash from rainfall and thus make them more susceptible to white mold [21].

3.1.3. Genotypic Variation in Soybean Nodule Number.

The mean number of nodules per plant was found to range from 2 for TGX2007-3F and TGX1835-10E to 28 for TGX1951-4F. The number of nodules per plant in this study was low compared to the average observed in several works (30 to 50 nodules/plant) [21]. Severe environmental conditions such as salt stress, drought stress, acidity, alkalinity, nutrient deficiency, fertilizers, heavy metals, and pesticides contribute to suppressing the growth and symbiotic characteristics of most rhizobia and reducing significantly the number of nodules [22, 23]. A predicted gene family associated with roots has been identified in some legumes crops. The action of this gene family (root-controlled supernodulators) regulates the number of nodules per plant and favors supernodulation [24]. The nodule size of all the genotypes was better and varied from 4 to 7 mm, with an average of 5.24 mm diameter. These nodules belong to the large nodule category (3.5 to 5.0 mm) [25]. The soybean genotypes with large nodules size diameter indicated high nitrogenase activity and constitute a real water reserve, and were less affected during water-deficit stress [26, 27]. Table 3 shows the mean values of phenological and morphological parameters among the twenty-four soybean genotypes.

3.2. Yield Performance and Yield Components. Significant differences ($P < 0.01$, $P < 0.001$) were observed for the number of branches, number of pods per plant, pod length, number of seeds per pod, and pod shattering traits among the soybean genotypes (Table 4). However, no significant differences were observed for grains yield.

TABLE 3: Mean performance of the soybean genotypes for phenological and morphological growth parameters.

Genotypes	50% Flo (DAS)	50% Mat (DAS)	95% Mat (DAS)	Nb_nod	Nod_sco	Nod_dia (mm)	PH (cm)	Pod_cle (cm)	Nb_nd
TGX2004-13F	45	109	116	10	2	5	97	20	18
TGX1951-4F	56	107	117	28	3	5	83	16	16
TGX2023-1E	49	105	111	8	2	5	89	14	16
TGX2007-1F	52	107	117	5	2	5	78	20	17
TGX2013-2F	51	101	111	6	2	5	78	14	15
TGX2010-5F	58	106	111	8	2	7	74	17	14
TGX2023-4E	47	98	107	7	2	6	78	16	13
TGX1987-10F	52	83	96	6	2	6	78	21	14
TGX2018-5E	47	84	93	15	2	6	84	21	19
TGX2025-19E	58	95	106	8	2	5	78	13	16
TGX2025-16E	47	98	108	8	2	6	67	15	13
TGX2007-3F	50	91	99	2	2	5	77	26	18
G175 (check 1)	50	79	88	20	2	5	77	11	15
TGX1835-10E	50	90	99	2	2	5	74	29	19
TGX1988-5F	49	96	105	4	2	5	81	18	17
TGX1485-1D	48	95	105	3	2	4	71	12	14
G196 (check 2)	51	110	120	3	2	5	66	14	13
TGX2016-2E	58	93	100	6	2	5	74	15	15
TGX2009-1F	58	82	93	8	2	5	73	16	17
TGX2027-7E	47	83	93	10	2	5	71	20	13
TGX2027-4E	49	84	97	20	2	5	74	14	13
TGX2004-7F	52	89	99	4	2	5	65	17	12
TGX2009-14F	54	88	99	4	2	5	63	15	12
TGX2010-14F	46	79	94	3	2	6	71	23	13
Grand mean	47.681	93.79	103.528	8.21	2.056	5.24	75.9	17.42	15.11
CV (%)	1.6	1.2	0.5	56.4	15.2	19.9	12.7	18.8	6.2

3.2.1. Variability in Branches Number. Genotypes varied in their ability to produce branches and productive pods per plant. On average, the number of branches per plant ranged from 1 (TGX2004-7F) to 5 (TGX2004-13F) and the number of productive pods per plant ranged from 19 (TGX2007-3F and TGX2010-14F) to 60 (TGX2004-13F). The genotype (TGX2004-13F) was the most prolific in terms of the number of branches and productive pods. It was followed by genotypes TGX2023-1E (3 branches and 52 pods per plant) and TGX2013-2F (3 branches and 42 pods per plant). These results agreed with those of Zoromé [28] who found similar variations in the numbers of branches and pods per plant. Pod length varies from 3.04 in TGX2009-1F to 4.06 cm in TGX2004-13F. Again, the number of seeds per pod was significant and more than 66% of genotypes had a seed number per pod above the average of the trial (2 seeds per pod).

3.2.2. Variability in Hundred Seeds Weight. The hundred seed weight from the trial ranged from 12 (TGX1835-10E, TGX1835-10E, and TGX2009-1F) to 21 g (TGX2010-5F), with an average of 15 g. Hundred seed weight is an essential parameter and contributes to optimizing the yield. It is very important for soybean plant adaptation and influences the seed vigor [29]. The tested genotypes did not differ statistically for grain yield. However, potential grain yield was found to be very interesting and ranged from 0.924 (TGX1988-5F) to 2.681 t/ha (TGX2013-2F). More than 45.83% of genotypes had a mean potential grain yield above the trial average (1.54 t/ha).

3.2.3. Variability of Pod Shattering. The pod shattering in this study was identified in field conditions according to IITA protocol. The mean of pod shattering ranged from 42 to 75%, with an average of 55.56%. Pod shattering is one of the major constraints for soybean because it could considerably reduce grain yield [30]. From this study, 75% of the genotypes were intermediate to pod shattering (11–70% shattered pod), and 25% of the genotypes with 75% shattered pod were susceptible [31, 32]. As a consequence, the management of pod shattering is of great importance for achieving higher productivity and reducing yield losses [33]. Globally, the genotypes of the early maturity group of soybean seem more sensitive to pod shattering than those of the medium maturity group, as shown by the work of [14]. In general, pod shattering is affected by different environmental factors (dry climate, low humidity, high temperature, and rapid temperature changes) and irrigation systems [34, 35]. Table 5 shows the mean values of the yield and yield component parameters.

3.3. Variation of Soybean Genotypes Reaction to Diseases. A major constraint to soybean production is disease. Observations were carried out to identify symptoms of diseases that affected soybean production in Burkina Faso fields. The assessment identified symptoms of rust at stages R3 and R6, frogeye leaf spot, and soybean mosaic virus in the trial.

A significant difference ($P < 0.01$; $P < 0.001$) was observed for rust (R3 and R6 stages) and SMV diseases among the 24 soybean genotypes. However, no significant differences were

TABLE 4: Analyses of variances of yield and yield components.

Variables	Source of variations	d.f.	s.s.	m.s.	v.r.	F pr.
Nb_bra	Nb_genotype	23	41.21	1.79	3.00	<0.001**
	Error	48	28.67	0.60		
Nb_pod/plt	Nb_genotype	23	6969.19	303.01	4.22	<0.001**
	Error	48	3442.60	71.72		
Pod_len (cm)	Nb_genotype	23	2.71	0.12	2.38	0.006*
	Error	48	2.38	0.05		
Nb_sd/pod	Nb_genotype	23	9.21	0.40	2.22	0.010*
	Error	48	8.67	0.18		
Nb_sd/plt	Nb_genotype	23	77799.6	3382.6	8.04	<0.001**
	Error	48	20206.1	421.0		
Pod_sha (%)	Nb_genotype	23	9444.44	410.63	23.65	<0.001**
	Error	48	833.33	17.36		
100 SW (g)	Nb_genotype	23	274.87	11.95	8.96	<0.001**
	Error	48	64.00	1.33		
Gra_Y (t/ha)	Nb_genotype	23	85.98	3.74	1.42	0.153NS
	Error	48	126.67	2.64		

NS: no significant; *: significant at 5%; **: highly significant at 1%; s.s.: sum of squares; d.f.: degree of freedom; m.s.: mean squares; Nb_genotype: number of genotype.

TABLE 5: Mean performance of the soybean genotypes for yield and yield components.

Genotypes	Nb_bra	Nb_pod/ plt	Pod_len (cm)	Nb_sd/ pod	Nb_sd/ plt	Pod_sha (%)	100 SW (g)	Gra_Y (t/ha)
TGX2004-13F	5	60	4.06	3	179.70	75	15	1.755
TGX1951-4F	3	37	3.59	3	155.40	50	16	2.448
TGX2023-1E	3	52	3.70	3	110.50	75	16	1.876
TGX2007-1F	2	28	3.83	3	93.30	75	16	1.687
TGX2013-2F	3	42	3.55	2	93.27	75	16	2.681
TGX2010-5F	3	21	3.70	2	88.67	50	21	1.636
TGX2023-4E	2	26	3.55	2	87.70	50	18	1.687
TGX1987-10F	2	28	3.79	3	78.97	50	14	1.741
TGX2018-5E	2	30	3.85	2	72.07	50	15	1.077
TGX2025-19E	2	36	3.61	3	71.87	75	16	1.116
TGX2025-16E	3	33	3.41	2	71.57	50	16	1.464
TGX2007-3F	3	19	3.82	3	67.20	42	12	1.411
G175 (check 1)	2	33	3.67	3	66.60	50	15	2.092
TGX1835-10E	2	22	3.79	3	63.07	50	12	0.947
TGX1988-5F	2	24	3.69	2	62.20	75	13	0.924
TGX1485-1D	3	36	3.87	3	57.70	50	14	1.433
G196 (check 2)	3	23	3.51	2	57.20	50	13	1.360
TGX2016-2E	2	33	3.55	2	56.37	50	14	1.431
TGX2009-1F	3	32	3.09	2	55.23	50	12	1.767
TGX2027-7E	2	23	3.61	2	54.60	50	14	0.962
TGX2027-4E	2	31	3.41	2	54.40	50	15	1.151
TGX2004-7F	1	21	3.85	2	42.87	42	14	1.729
TGX2009-14F	2	23	3.67	2	41.00	50	13	1.416
TGX2010-14F	2	19	3.57	2	37.87	50	13	1.212
Grand mean	2.458	30	3.7	2	76	55.56	15	1.54
CV (%)	31.4	27.8	6.1	17.3	27.1	7.5	7.9	42.2

observed for frogeye leaf spot disease. Figure 2 shows diseases scores distribution of rust (R3 and R6) and SMV diseases scores. Most genotypes in the trial showed symptoms of rust (R6 stage) and SMV diseases with a score of 2 (25% of these leaves tissues recovered with symptoms). In general, symptoms with a score of 2 affect less grain yields of soybean

genotypes [14]. Several diseases, including soybean rust, frogeye leaf spot, red leaf blotch (*Coniothyrium glycines*), and sudden death syndrome (SDS), have been reported as major soybean diseases in Africa [36]. In the future, soybean diseases may be continuously severe and difficult to manage, especially with the significant changes in the global climate [37].

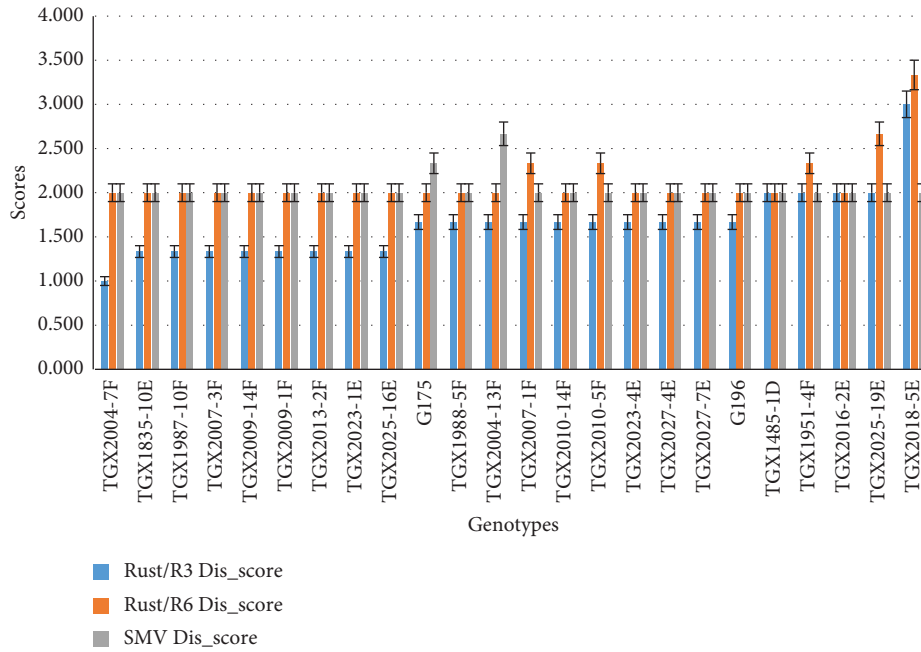


FIGURE 2: Distribution of diseases scores in the 24 soybean genotypes.

TABLE 6: Estimates of variability parameters of soybean genotypes.

S.n	Traits	Min	Max	Mean	GCV	PCV	h^2 (%)	GA	GAM
1	50% Flo (DAS)	38.00	58.00	47.68	8.71	8.76	99.44	8.56	17.94
2	50% Mat (DAS)	79.33	110.00	93.79	10.57	10.59	99.80	20.42	21.78
3	95% Mat (DAS)	88.00	120.00	103.53	8.649	8.655	99.95	18.45	17.82
4	Pod_sha (%)	41.67	75.00	55.56	20.61	21.06	97.86	23.59	42.45
5	Nb_nod	1.667	27.67	8.21	70.07	77.27	90.69	11.85	144.34
6	PH (cm)	63.07	96.50	75.90	6.85	10.02	68.40	10.72	14.12
7	Pod_cle (cm)	11.10	28.80	17.42	22.45	24.93	90.04	8.06	46.25
8	Nb_nd	11.67	19.33	15.11	14.45	14.89	97.07	4.50	29.77
9	Nb_bra	1.333	5	2.46	25.67	31.44	81.65	1.30	52.88
10	Pod_len (cm)	3.087	4.060	3.70	4.08	5.36	76.18	0.31	8.41
11	Nb_pod/plt	18.93	59.90	30.00	29.27	33.50	87.37	18.09	60.29
12	Nb_sd/pod	2.00	3.00	2.00	13.53	18.27	74.09	0.56	27.88
13	Nb_sd/plt	37.87	179.70	76.00	41.34	44.18	93.57	64.72	85.16
14	100 SW (g)	12.00	20.67	15.00	12.54	13.31	94.26	3.88	25.84

3.4. Estimates of Components of Variation (GCV and PCV).

The phenotypic coefficients of variation (PCV) were higher than the genotypic coefficients of variation (GCV) for all the traits in this study (Table 4). Similar results were observed by Zida et al. [38]. The genetic coefficient variance (GCV) was maximum for nodules number per plant followed by the number of seeds per plant (41.34) and the number of branches per plant (25.67). The phenotypic coefficient variance (PCV) ranged from 5.36 to 77.27. It was of higher magnitude for nodules number per plant (77.27), followed by the number of seeds per plant (44.18), and the number of pods per plant (33.50). It was the minimum for pods length (5.36) followed by days de maturity 95% (8.65) and days to flowering (8.76).

The highest difference between GCV and PCV values was observed for plant height (6.85–10.02). Moderate magnitudes of GCV and PCV were observed for the number of seeds per plant (13.53–18.27) followed by pod length (4.08–5.36). Days to 95% maturity showed the lowest difference between GCV and PCV estimates (8.649–8.654). It was followed by days to 50% maturity (10.57–1059) and days to 50% flowering (8.71–8.76). Similar findings were obtained by Baraskar et al. [39].

3.5. Heritability and Genetic Advance of Traits. The estimates of heritability ranged from 68.40% to 99.95% (Table 6). Maximum heritability was observed for days to 95%

maturity (99.95), followed by days to 50% maturity (99.80) and days to 50% flowering (99.44). Minimum heritability was observed for plant height (68.40%), followed by the number of seeds per plant (74.09%), and pod length (76.18%). Except for plant height showed high values for heritability, that is, higher than 70% this indicated that the differences observed among the genotypes are mainly of a genetic nature [40]. Traits whose heritability is higher allow greater success in the selection so that the chance of obtaining superior progenies with selected individuals is higher [41].

Among the characters, 10 of them had both high (>20%) genetic advance as a percentage of the mean and high heritability (>70%). Similar results have been reported by Machado et al. [40] and Drabo et al. [42].

4. Conclusions

Traditionally, genetic diversity in soybean has been based on the differences in morphological and agronomic characters and pedigree information. The findings of this study are very important for breeding programs, but particular soybean genotypes are adapted to specific agroecological regions and the phenotypes are strongly influenced by environmental factors. Soybean genotypes evaluated presented an interesting variability and adaptability for most of the traits. Most of the introduced soybean genotypes such as TGX2013-2F, TGX1951-4F, TGX2023-1E, TGX2004-13F, and TGX1987-10F were the highest yielding (1.7–2 t/ha). The traits evaluated in this study revealed different levels of variability, heritability, and genetic advance among genotypes. The estimate of PCV was higher than the GCV for all the traits, indicating the influence of environmental factors in the expression of the phenotype. Most of the studied traits revealed high heritability, expected genetic advance and genetic advance as percent of means indicating that traits are less influenced by environment in their expression, allowing greater success in the selection. This would guarantee success in selection by increasing the chance of obtaining superior progeny with selected individuals for those traits. The characters with both high heritability and high GAM may be used as selection tools in future breeding programs.

Data Availability

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

Conflicts of Interest

The authors declare that they have no conflicts of interest.

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