



Full Length Article

Heritability, Stability and Path Coefficient Analysis for Grain Yield and Yield Attributing Traits in Rice Varieties under Three Irrigation Regimes in Burkina Faso

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Abstract

Rice is currently grown in Burkina Faso in the context of high climatic variability. However, the expression of genetic potential of a species depends on the environment. The aim of this study was to estimate the genetic parameters of morpho-agronomic traits and evaluate the genetic potential of rice varieties in different environments. Thus, twenty rice varieties were assessed over two consecutive years in a split-plot design with three replications under three water regimes: sprinkler irrigation (E1), drip irrigation (E1) and submersion irrigation (E3). The results showed that variety FKR19 recorded the lowest genotypic superiority index (0.01) and variety FKR42 the highest (0.66). All the traits assessed had higher genotypic variance components than the environmental variance components. Indeed, the average panicle weight, number of grains per panicle and number of full grains per panicle expressed high expected genetic gains relative to the mean (> 40%) associated with high broad-sense heritability values (> 0.85) in environments 1 and 2. In addition, panicle leaf width length had the highest positive direct effect (+ 5.08) on grain yield, whereas grain width had the highest negative direct effect (-1.77) on grain yield. However, this study was based on a few pheno-agromorphological characteristics in a single agro-climatic zone, which is still insufficient. These results could be used in rice improvement programs in Burkina Faso. © 2024 Friends Science Publishers

Keywords: Genetic progress, Environment, *Oryza*, Irrigation, Genetic variability, Path coefficient

Introduction

Rice is one of the main staples and the main irrigated crops in the world (Kruzhilin *et al.* 2017). It is grown across 154 million hectares/year, representing approximately 11% of the world's arable land (Prakash *et al.* 2018). Rice cultivation has spread around the world because of its adaptability to several environments and high yields (Adekoya *et al.* 2014). Today, developing countries account for around 95% of rice production and 85% of rice exports (Prakash *et al.* 2018).

In Burkina Faso, rice is currently grown in a context of high climatic variability, resulting in unstable yields

depending on the cropping system used. In fact, the national average yield of the varieties grown by farmers (2 t/ha) is well below their potential yield, which is estimated to be more than 7 t/ha (Saito *et al.* 2017; Tanaka *et al.* 2017). Like the rest of the Sudano-Sahelian zone, Burkina Faso is subject to the vagaries of climate, and the decline and poor spatio-temporal distribution of rainfall affecting the hydrology of developed areas, making them less efficient. Water scarcity is often the reason why rice is irrigated from its original purpose. Rice is thus replaced by other crops in the dry season and increasingly in the rainy season (Yaméogo *et al.* 2021). The reduction in water availability and the increase in its cost are jeopardizing the traditional

system of transplanted rice cultivation in puddles (Maraseni *et al.* 2018). Given the vulnerability of available water resources and the increased need to increase agricultural production due to an ever-growing population, it is essential to explore the possibilities of improving and stabilizing rice yields under other production systems (Nikiéma *et al.* 2023).

Most of the numerous studies conducted locally on rice have focused on the study of its genetic diversity (Sié 1991; Sié and Dakouo 1998), the identification of varieties tolerant to iron toxicity (Konaté *et al.* 2022) and the performance assessment under a rainfall regime and irrigated rice varieties (Sanou *et al.* 2019; Nikiéma *et al.* 2021; Yaméogo *et al.* 2021).

However, the heritability of morpho-agronomic traits and expression of the genetic potential of rice varieties grown in Burkina Faso in several environments have received very little attention. To stabilize rice production, it is crucial to identify high-yielding varieties adapted to pressure irrigation (Nikiéma *et al.* 2022). Rice grain yield is a complex quantitative trait and an integrated function of some constituent traits (Sharma and Sharma 2007). Thus, knowledge of the quantitative characteristics associated with yield is one of the best ways to improve the production of a plant species such as rice under pressure irrigation. In addition, determining the magnitude of the direct effects of the constituent traits on yield helps to determine the most appropriate traits as selection criteria (Chukwudi *et al.* 2022). Productivity potential, like any trait, can be improved by selection. Higher yields can be obtained by accumulating genes favorable for the trait in the same plant, or by modifying the plant's architecture to enable it to make better use of the resources of the environment (water, soil minerals) in which it grows (Zahour 1992). Thus, the growing area limits of a crop can be extended by modifying some of its morphological or physiological characteristics (Zahour 1992).

The success of genetic improvement programs is based on the knowledge and availability of the species' genetic variability (Temesgen 2021). Assessing genetic variability is therefore a prerequisite for planning an effective breeding program (Rasheed *et al.* 2023). Quantitative genetics has made a major contribution to our knowledge of genetic variability and heritable traits in plants (Wang *et al.* 2020). It plays a fundamental role in varietal selection and genetic improvement.

The current challenge for breeders is to maintain the stability of the agronomic performance of varieties over the years and in the environment. To achieve this level of reliability and precision in varieties, the heritability of traits must be sufficiently well known. It is desirable to evaluate and use the diversity available for crop improvement to meet specific needs in relation to a specific ecosystem. The general objective of this study was to understand the level of expression of the genetic potential of rice varieties under different methods of irrigation. This involves (i) estimating

the genetic parameters of the traits measured, (ii) determining stability indices and (iii) assessing the direct effects of agronomic traits on grain yield.

Materials and Methods

Study site

The experiment was conducted in Bama on the demonstration site of the IRRIFASO company (Fig. 1), located in the northwest of the city of Bobo-Dioulasso, on the national road N°9 Bobo-Faramana on the border with Mali. The experimental site is located at 11°22.3260" North latitude, 4°22.2410" West longitude. The climate is Sudanian, characterized by an alternating dry season from October to April and a five-month rainy season from May to September (Kambou 2019).

Plant material and growing environment

The plant material consists of 20 lowland/irrigated rice varieties from the gene bank of the INERA Farako-Bâ rice and rice-growing program (Table 1). Four of these varieties are Nerica (interspecific varieties) and sixteen are *Oryza sativa* (intra-specific varieties). The interspecific varieties (NERICA) are highly productive compared with the intra-specific varieties (Sié *et al.* 2008). NERICA are the result of an interspecific cross between *Oryza sativa* (L.), a high-yielding Asian rice variety, and *Oryza glaberrima* (Steud), an African rice variety that is less productive but more resistant to the biotic and abiotic stresses of African growing conditions. NERICA hybrids are both productive like their Asian parent and resistant like their African parent (Sié *et al.* 2008). As for the 16 other varieties of rice, they come from the cross *Oryza sativa* x *Oryza sativa*. These varieties were selected on the basis of their yield potential and the extent to which they are used in Burkina Faso. The three environments corresponding to three water regimes were: sprinkler irrigation system (E1), drip irrigation system (E2) and submersion irrigation system.

Trial design and maintenance

The two trials conducted over two consecutive seasons (2020–2021 and 2021–2022) were set up using a split-plot design with three replications, with rice varieties as the main factor and the three water regimes as secondary factors. Direct sowing occurred on December 10, 2020 for the first trial and on December 10, 2021 for the second trial. The seedlings were thinned to one seedling per bunch eight days after emergence. The distances between rows and seed pots were 25 cm each. During ploughing, 5000 kg/ha of organic manure (compost) was applied, based on rice straw. The plants also received a micro dose of NPK fertilizer (14-23-14) at 200 kg/ha 10 days after being sown, using a capsule.

Table 1: Characteristics of the varieties used

Varietal group	Genetic nature	Name
NERICA	Lines	FKR56N, FKR58N, FKR60N, FKR62N
<i>O. sativa</i>	Lines	FKR14, FKR16, FKR18, FKR19, FKR34, FKR42, FKR64, FKR76, FKR78, FKR80, FKR84, IR67, IR841, SAHEL177, SAHEL328, SAHEL329

NERICA: New Rice of Africa

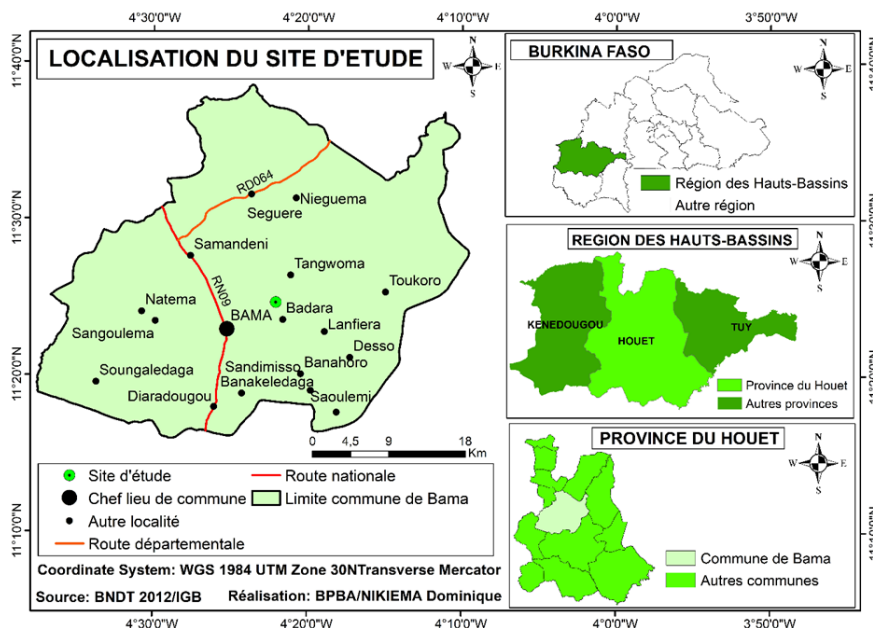


Fig. 1: Location of the Bama study site

Super granular urea was applied 12 days after emergence as a supplement.

Pressure irrigation (sprinkler and drip) was scheduled daily based on the plot size according to the formula of Mariyappillai *et al.* (2022): $V = E_p \times K_p \times K_c \times W_p \times A$: volume of water required (L/d-); E_p : evaporation from the tank (mm/d-); K_p : pan factor (0.8); K_c : crop factor (varies from 0.95 to 1.21 depending on the stage of the rice crop, Dembélé *et al.* (1999)); W_p : wetting percentage (0.5); A : area/plant.

In the control (submerged irrigation), the plot was irrigated 24 h before sowing and after being placed in mud. The plot was irrigated, followed by complete drainage to maintain moisture until emergence. Irrigation continued until the end of the third week (from day 15 to day 25) at a water level of approximately 5 cm, followed by complete drainage from day 25 to day 27 for herbicide application. The plot was irrigated and kept to a strict minimum under slurry for two days before fertilizer application. The water level was raised to approximately 5 cm up to panicle initiation and then to 10 cm up to the pasty stage (15 days after flowering). The plot was drained completely, and irrigation was stopped 15 days after flowering. The water table was monitored using a graduated ruler inserted into a piezometer.

Surface irrigation by submersion consisted of filling the previously created compartments with water. The plot is

divided into rectangular areas surrounded by bunds. The plot is supplied with water from an intake downstream, which discharges the water into the main open canal. This water then flows into secondary and tertiary canals before finally reaching the production plot.

For the sprinkler and drip irrigation systems, the pumping unit is powered by an electric pump powered by solar panels. The pumping unit draws water from the source and pumps it into the distribution network to operate the sprinklers or drippers. PVC (63PE) pipes had been laid underground to carry water at the end of various irrigation systems (Nikiéma *et al.* 2023).

In the sprinkler irrigation system, a flexible plastic hose was connected to the main pipe running to the water source. Sprinklers were installed on the flexible plastic pipe at 10 m intervals and 1 m in height to distribute the water in the form of rain. The capacity of one sprinkler to disperse water is over a radius of 5 m².

In the drip irrigation system, a main pipe (threaded connexion) is connected to the water source to bring the water to the secondary pipes or ramps (25 mm diameter polyethylene pipe), passing through a sieve philtre (to philtre the water before it reaches the drip lines) and a tap. The drippers were placed between the rows of seedlings, and the drip line was placed parallel between the two rows of seedlings and 0.3 m separated from the two drippers on the same line (Nikiéma *et al.* 2023).

Table 2: Parameters recorded

Variables	Description
Cycle (days)	Time elapsed from sowing to 50% flowering (NDF)
Average plant height at harvest (cm)	Measurement taken from the base of the plant to the tip of the highest leaf or panicle using a graduated ruler on six holes per variety and replication in each environment (PLH)
Average number of tillers per hole at maturity	Manual counting of the number of tillers on six holes per variety and per replication in each environment (NTH)
Average number of panicles per hole	The average number of panicles per hole was obtained by manually counting the number of panicles in six holes per variety and replication in each environment (NPH)
Average width of panicle leaf (cm)	Measurement was carried out on the last leaf before the panicle in six holes per variety and replication in each environment. In each plot, measurements were taken on five leaves and three measurements were taken on each leaf (PWI)
Average panicle leaf length (cm)	Measurement was carried out on the last leaf before the panicle in six holes per variety and per replication in each environment. In each plot, measurements were taken on five leaves (PLL)
Average panicle weight (g)	Determination from the average of a sample of six panicles per variety and per replication in each environment and weighed individually (PAW)
Number of total spikelets per panicle	The number of spikelets was determined by counting all spikelets (filled and unfilled) from six randomly selected panicles of 06 sample plants per variety in each plot and averaged (NSP)
Number of filled grains per panicle	The number of grains was determined by counting only filled grains from six randomly selected panicles of 06 sample plants in each plot and averaged (NFG)
Thousand grains weight (g)	Weighed using a 1/10 precision balance. 1000 full grains from each repetition in each environment were taken using the grain counter (TGW)
Grain yield (t/ha)	Yield per hectare (ha) was obtained for each variety in each environment according to the following formula: $GYI = \frac{PWS(kg)}{NS(m^2)} \times 10000 (m^2)$

GYI: Grain yield; PWS: Product weight of yield squares; NS: number of squares

Data collection

Data were collected on characteristics related to phenology, organ measurements and grain yield. The various characteristics measured and their methods of determination are listed in Table 2.

Additional parameters such as grain length (GRL), grains width (GRW), panicle length (PAL), straw yield (SYI) and harvest induce (HIN) have been collected in order to assess their contribution to grain yield.

Data analysis

Statistical analyses of variance were performed using SAS version 9.1 software. Each combination of years and irrigation system constituted a trial environment. In the combined analyses of variance, trial environments, replications, year, genotype \times environment \times year interactions and all other sources of variation were considered as random effects, whereas genotypes were considered as fixed effects. The individual and combined components of the analysis of variance were deduced to estimate the stability and genetic parameters of the measured traits. The various genetic parameters were calculated using the formulas presented in Table 3. According to Singh (2001), heritability in the broad sense is high or very high if its value is equal to or greater than 80%, moderate between 40 and 80% and low if its value is less than 40%. Phenotypic and genotypic coefficients of variation above 20% were considered high, those between 10 and 20% moderate, and those below 10% low (Deshmukh *et al.* 1986). R software version 4.1.1 was used to analyze the sequential regression and estimate the contribution (path coefficient) of agronomic traits to grain

yield. According to Lenka and Mishra (1973), the path coefficient is very high if its value is greater than 1, high between 0.3 and 1, moderate between 0.2 and 0.29, low between 0.1 and 0.19 and negligible between 0.00 and 0.09 in the case of rice.

Results

Mean and range of trait performance among rice varieties for the 2020–2021 season

The agronomic performance results for the various parameters measured or calculated in the three growing environments are summarized in Table 4. The analysis of variance revealed significant differences in each environment for all the traits studied, except the number of days 50% of flowering and the number of tillers per hole at maturity in environment (submersion irrigation). The coefficients of variation for environment 1 (sprinkler irrigation) ranged from 0.79 to 7.90% for the days to 50% flowering and grain yield, respectively. Grain yield varied from 2.60 to 5.85 t/ha. Grain yield varied from 2.60 to 5.85 t/ha. In environment 2 (drip irrigation), panicle weight, number of total spikelets per panicle, number of filled grains per panicle and grain yield recorded a coefficient of variation greater than 10%. In environment 3, only the width of the panicle leaf and the number of tillers per hole had coefficients of variation greater than 10%.

Mean and range of performance characteristics among rice varieties for the 2021–2022 season

There was a highly significant difference ($P = 0.0001$) between the varieties for all traits in the three environments (Table 5). The coefficient of variation ranged from 2.55 to

Table 3: Estimated genetic and stability parameters

Formula	Meaning	References
$Y_i = \sum Y_{ij}/N$	Genotypic mean	(Lin and Binns 1988; Annicchiarico 2002)
$V_{env} = \sum (Y_{ij} - Y_i)^2/N - 1$	Environmental variance	
$P_i = \sum (Y_{ij} - M_j)/2N$	Index of genotypic superiority	
$CV(\%) = 100(\sqrt{V_E}/Y_i)$	Coefficient of variation	
$\sigma_g^2 = (MS_g - MS_e)/r$	Genotypic variance	(Burton and DeVane 1953; Johnson <i>et al.</i> 1955; Allard 1960)
$\sigma_p^2 = MS_g / r$	Phenotypic variance	
$\sigma_g^2 = MS_g - (MS_{GE} + MS_{GY} - MS_{GEY})/REY$	Genotypic variance	
$\sigma_{GEY}^2 = (MS_{GEY} - MS_e)/r$	Variance of interaction between G, E and Y	
$\sigma_p^2 = \sigma_g^2 + \sigma_{GE}^2/E + \sigma_{GY}^2/Y + \sigma_{GEY}^2/YE + \sigma_e^2/REY$	Phenotypic variance	
$H_{BS}^2 = \sigma_g^2 / \sigma_p^2$	Heritability in the broad sense	
$GCV(\%) = (\sqrt{\sigma_g^2} / \bar{X}) \times 100$	Coefficient of genotypic variation	
$PCV(\%) = (\sqrt{\sigma_p^2} / \bar{X}) \times 100$	Coefficient of phenotypic variation	
$GA = H_{BS}^2 \times \sqrt{\sigma_p^2} \times I$	Expected genetic gain	
$GAM(\%) = (GA / \bar{X}) \times 100$	Expected genetic gain relative to the mean	

I: selection intensity - 2.06%; Y_{ij}: yield of genotype i in environment j; N: number of test environments; M_j: best yield in environment j; MS_g: mean square of the genotypes; MS_e: mean square of the error; \bar{X} : Grand mean of the characters under study; Y_i: Genotypic mean; MS_{GEY}: Mean squares of interaction (G*Y*E); E: Number of environments; r: number of replications, Y: year

Table 4: Performance of agronomic parameters in each environment for the 2020–2021 campaign

Source	NDF (days)	PLH (cm)	PLW (cm)	PLL (cm)	NTH	NPH	PAW (g)	NGP	NFG	TGW (g)	GYI (t/ha)
Environment 1											
Min	105	69.88	18	1.02	16	11	1.24	74	53	16.29	2.60
Max	120	114.06	36	1.58	47	32	4.33	190	167	25.89	5.85
CV	0.79	1.06	4.10	2.86	6.02	4.57	6.14	4.27	4.67	2.23	7.90
Pr.	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
Environment 2											
Min	107	64.28	18.20	1.00	16.80	11	1.39	88	61	20.10	5.75
Max	126	130.06	35.84	1.58	56.60	44	3.72	267	153	27.12	11.25
CV	1.77	6.56	8.59	5.55	7.06	7.59	12.43	13.10	13.10	3.36	10.52
Pr.	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
Environment 3											
Min	100	89.46	22.60	1.08	13	8	2.70	121	103	21.55	2.70
Max	118	153.38	42.60	2.12	23	17	6.73	263	215	28.90	5.95
CV	5.35	3.28	7.44	12.12	10.49	8.59	6.36	6.22	5.90	1.57	7.40
Pr.	NS	0.0001	0.0001	0.01	NS	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001

NDF: number of days 50% of flowering; PLH: plant height at harvest; NTH: number of tillers per hole at maturity; NPH: number of panicles per hole; PLW: panicle leaf width; PLL: panicle leaf length; PAW: average panicle weight; NGP: number of grains per panicle; NFG: number of full grains per panicle; TGW: thousand grain weight; GYI: grain yield; not significant: $P > 0.05$

10.21% in environments 1 and from 1.99 to 12.47% in environments 2 and from 1.23 to 13.37% in environments 3. Only grain yield showed a coefficient of variation greater than 10% in environments 1 and 2. On the other hand, in environment 3, panicle leaf length and width recorded a coefficient of variation greater than 10%.

Varietal stability indices based on variance

The results recorded in Table 6 showed a variation in grain yield from 4.65 t/ha (FKR42) to 7.17 t/ha (FKR19) with Pi genotypic superiority index from 0.01 (FKR19) to 0.66 (FKR42) and environmental variance from 2.09 (FKR42) to 9.41 (FKR76). The highest grain yields and the lowest Pi genotypic superiority indices were recorded by the sativa variety FKR19 (7.17 t/ha and 0.01) and the NERICA varieties FKR62N (6.95 t/ha and 0.03), FKR58N (6.82 t/ha and 0.04), FKR56N (6.65 t/ha and 0.06) and FKR60N (6.38 t/ha and 0.09). The coefficients of variation were high and

ranged from 31.06% (FKR42) to 52% (FKR76).

Estimation of the overall mean and genetic parameters of morpho-agronomic traits in environment one

The results of the genetic parameters (genotypic variance, phenotypic variance, coefficients of genotypic variation, coefficients of phenotypic variation, the broad sense heritability, genetic gain, expected genetic gain relative to the mean) for the two years of experimentation in environment 1 are displayed in Table 7. All the traits studied showed phenotypic variances and coefficients of variation greater than the genotypic variances and coefficients of variation over the two years. For each study season, all traits recorded high heritability in the broad sense, with respective minimum and maximum values of 0.83 for grain yield and 0.99 for plant height observed in the first season of the experiment. The highest expected genetic gains were recorded for the

Table 5: Performance of agronomic parameters in each environment for the 2021–2022 campaign

Source	NDF (days)	PLH (cm)	PLW (cm)	PLL (cm)	NTH	NPH	PAW (g)	NGP	NFG	TGW (g)	GYI (t/ha)
Environment 1											
Min	108	71.10	18.20	1.04	17	11	1.23	74	52	14.80	2.10
Max	128	111.34	36.20	1.58	48	32	4.45	195	176	25.20	6.55
CV	2.55	2.87	3.26	2.59	6.66	4.49	5.34	2.81	4.00	2.56	10.21
Pr.	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
Environment 2											
Min	107	70	19.20	1.00	17	12	1.44	82	56	7.40	5.10
Max	127	127.30	34.40	1.56	58	41	3.77	269	158	26.80	11.50
CV	1.99	3.81	3.73	2.85	6.24	4.94	4.74	4.02	3.32	4.69	12.47
Pr.	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
Environment 3											
Min	98	86.46	21.20	1	14	8	2.65	122	96	21.20	2.80
Max	125	155.24	42.56	2.22	25	22	6.59	278	214	28	7.85
CV	2.20	3.27	10.20	13.37	5.34	5.79	5.37	6.46	6.32	1.23	6.02
Pr.	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001

NDF: number of days 50% of flowering; PLH: plant height at harvest; NTH: number of tillers per hole at maturity; NPH: number of panicles per hole; PLW: panicle leaf width; PLL: panicle leaf length; PAW: average panicle weight; NGP: number of grains per panicle; NFG: number of full grains per panicle; TGW: thousand grain weight; GYI: grain yield; not significant: $P > 0.05$

Table 6: Yield and stability indices of genotypes

Varieties	GYI (t/ha)	Environmental variance	CV (%)	Pi
FKR14	6.24	4.34	33.40	0.12
FKR16	5.03	4.84	43.74	0.46
FKR18	5.25	3.19	34.00	0.50
FKR19	7.17	7.12	37.23	0.01
FKR34	5.83	7.97	48.39	0.26
FKR42	4.65	2.09	31.06	0.66
FKR56N	6.65	8.89	44.86	0.06
FKR58N	6.82	8.39	42.49	0.04
FKR60N	6.38	6.93	41.28	0.09
FKR62N	6.95	8.39	41.66	0.03
FKR76	5.90	9.41	52.00	0.20
FKR78	6.13	4.33	33.95	0.18
FKR80	5.33	5.28	43.11	0.41
FKR84	5.27	4.29	39.33	0.41
IR67	5.25	5.82	45.98	0.37
IR841	6.60	8.88	45.12	0.11
SAHEL177	5.35	3.38	34.33	0.36
SAHEL328	5.48	7.15	48.77	0.29
SAHEL329	5.61	7.05	47.31	0.25
TS2	6.03	3.55	31.25	0.15

GYI: grain yield; CV: coefficient of variation; Pi: genotypic superiority index

number of grains per panicle and the number of full grains per panicle ($GA > 50$) compared with the other traits ($GA < 21$) during the two years of experimentation. High expected genetic gains relative to the average were observed over the two years of experimentation for panicle weight, number of grains per panicle and number of full grains per panicle ($GAM > 45\%$).

Estimation of the overall mean and genetic parameters of morpho-agronomic traits in environment two

The results of the estimated genetic parameters are presented in Table 8. In this environment, genotypic and phenotypic variance values were also very high for both years for the number of grains per panicle and the number of full grains per panicle. Genotypic and phenotypic coefficients of variation showed low values (< 20) for all traits except panicle weight, number of grains per panicle

and number of full grains per panicle in both crop years. High values of heritability in the broad sense ($HSL > 0.75$) were obtained for the traits studied. The lowest expected genetic gains were recorded for panicle leaf width, panicle weight, thousand grain weight and grain yield. High values of expected genetic gain relative to the mean ($> 40\%$) were also obtained with traits, mean panicle weight, mean number of grains per panicle and mean number of full grains.

Estimation of the overall mean and genetic parameters of morpho-agronomic traits in environment three

The overall mean and values of the genetic parameters estimated in environment three over the two years of experimentation are shown in Table 9. Phenotypic and genotypic coefficients of variation were relatively low for all traits ($< 21\%$). Most of the traits studied had high

Table 7: Overall mean, genotypic, phenotypic and environmental variance, coefficient of variation genotypic and phenotypic, heritability in the broad sense and response to selection for the two campaigns in environment one

Traits	NDF (days)	PLH (cm)	PLW (cm)	PLL (cm)	NTH	NPH	PAW (g)	NGP	NFG	TGW (g)	GYI (t/ha)
YEAR 2020–2021											
MG	114	87.26	23.1	1.35	39	28	2.38	126	97	22.37	4.27
σ^2_g	16.69	96.33	13.24	0.01	29.78	15.56	0.29	862.6	636	2.95	0.49
σ^2_p	17.32	96.66	13.57	0.02	31.65	16.10	0.30	872.51	642.66	3.11	0.59
σ^2_e	0.82	0.86	0.89	0.001	5.63	1.61	0.02	28.81	20.61	0.25	0.11
GCV (%)	3.57	11.25	15.75	8.76	13.99	14.09	22.63	23.39	25.93	7.68	16.39
PCV (%)	3.64	11.27	15.95	9.07	14.42	14.33	23.01	23.53	26.07	7.88	17.99
H ² _{BS}	0.96	0.99	0.97	0.93	0.94	0.96	0.96	0.98	0.99	0.94	0.83
GA	8.26	20.19	7.41	0.23	10.89	7.93	1.09	60.18	51.70	3.45	1.31
GAM (%)	7.23	23.14	32.06	17.44	27.93	28.34	45.84	47.93	53.16	15.41	30.79
YEAR 2021–2022											
MG	119	87.87	23.47	1.37	39	27	2.47	125.94	98.67	21.94	4.16
σ^2_g	21.51	81.08	14.54	0.01	29.15	16.37	0.33	936.49	703.54	3.79	0.85
σ^2_p	24.52	83.24	14.74	0.02	31.42	16.88	0.34	941.82	709.1	3.98	1.03
σ^2_e	9.21	6.38	0.58	0.001	6.80	1.53	0.02	12.51	15.58	0.32	0.18
GCV (%)	3.90	10.25	16.25	9.23	13.84	14.98	23.25	24.30	12.35	8.87	22.16
PCV (%)	4.16	10.38	16.36	10.32	14.37	15.22	23.61	24.37	26.99	9.09	24.39
H ² _{BS}	0.87	0.98	0.98	0.80	0.92	0.96	0.97	0.99	0.99	0.95	0.82
GA	8.94	18.30	7.80	0.23	10.62	8.12	1.17	62.84	54.42	3.91	1.72
GAM (%)	7.52	20.83	33.23	17.01	27.24	30.09	47.22	49.90	55.15	17.83	41.46

NDF: number of days 50% of flowering; PLH: plant height at harvest; NTH: number of tillers per hole at maturity; NPH: number of panicles per hole; PLW: panicle leaf width; PLL: panicle leaf length; PAW: average panicle weight; NGP: number of grains per panicle; NFG: number of full grains per panicle; TGW: thousand grain weight; GY: grain yield; ; GYI: grain yield; MG: overall mean; σ^2_g : genotypic variance; σ^2_p : phenotypic variance; σ^2_e : environmental variance; GCV: Coefficient of genotypic variation; PCV: Coefficient of phenotypic variation; H²_{BS}: heritability in the broad sense; GA: Expected genetic gain; GAM: Expected genetic gain relative to the mean

Table 8: Overall mean, genotypic, phenotypic and environmental variance, coefficient of variation genotypic and phenotypic, heritability in the broad sense and response to selection for the two campaigns in environment two

Traits	NDF (days)	PLH (cm)	PLW (cm)	PLL (cm)	NTH	NPH	PAW (g)	NGP	NFG	TGW (g)	GYI (t/ha)
YEAR 2020–2021											
MG	117	88.2	24.27	1.30	43	32	2.46	131	101	22.36	8.93
σ^2_g	17.75	113.07	6.74	0.02	46.12	28.95	0.28	1124.99	467.15	2.87	0.94
σ^2_p	19.37	124.64	8.55	0.03	49.26	30.92	0.31	1194.8	523.81	3.06	1.23
σ^2_e	4.31	33.43	4.35	0.005	9.42	5.90	0.09	210.25	175.36	0.56	0.88
GCV (%)	3.58	12.06	10.70	11.66	15.79	16.22	21.51	25.53	21.38	7.58	10.86
PCV (%)	3.74	12.66	12.05	11.92	12.51	17.38	22.63	26.31	22.63	7.82	12.42
H ² _{BS}	0.91	0.90	0.78	0.95	0.93	0.93	0.90	0.94	0.89	0.75	0.76
GA	8.30	20.86	4.75	0.30	10.31	10.65	1.03	67.07	42.05	2.72	1.74
GAM (%)	7.07	23.65	19.56	23.52	23.97	33.29	42.10	51.07	41.59	12.18	19.44
YEAR 2021–2022											
MG	117	88.49	24.75	1.29	44	32	2.53	129	98	22	8.88
σ^2_g	26.88	134.68	9.83	0.02	56.62	35.92	0.51	1737.19	936.19	3.23	1.49
σ^2_p	28.61	138.76	10.1	0.03	59.14	36.78	0.52	1746.27	939.72	3.58	1.90
σ^2_e	5.38	11.38	0.85	0.001	7.57	2.58	0.01	26.92	10.51	1.07	1.23
GCV (%)	4.44	13.11	12.67	12.50	17.10	18.73	28.23	32.32	31.30	8.17	13.75
PCV (%)	4.58	13.31	12.84	13.43	17.47	18.95	28.50	32.40	31.36	8.60	15.52
H ² _{BS}	0.94	0.97	0.97	0.86	0.95	0.97	0.98	0.99	0.99	0.90	0.78
GA	10.36	23.56	6.37	0.31	15.05	12.12	1.45	85.65	62.90	3.51	2.23
GAM (%)	8.87	26.63	25.73	23.98	34.20	37.87	57.54	66.41	64.34	15.98	25.06

NDF: number of days 50% of flowering; PLH: plant height at harvest; NTH: number of tillers per hole at maturity; NPH: number of panicles per hole; PLW: panicle leaf width; PLL: panicle leaf length; PAW: average panicle weight; NGP: number of grains per panicle; NFG: number of full grains per panicle; TGW: thousand grain weight; GYI: grain yield; MG: overall mean; σ^2_g : genotypic variance; σ^2_p : phenotypic variance; σ^2_e : environmental variance; GCV: Coefficient of genotypic variation; PCV: Coefficient of phenotypic variation; H²_{BS}: heritability in the broad sense; GA: Expected genetic gain; GAM: Expected genetic gain relative to the mean

broad-sense heritability values ($H < 60\%$), except for panicle leaf width and total number of tillers per cluster in the first year of experimentation and panicle leaf width in the second year. The number of grains per panicle and the number of full grains per panicle recorded the highest values of expected genetic gain ($GA > 50$). The number of days 50% of flowering showed the lowest genetic gain compared with the average in both years, 9.03 and 7.50% successively.

Combined variation in genetic parameters across environments

The results of the combined analyses of the genetic parameters are shown in Table 10. Panicle leaf width, panicle weight and yield had very low genotypic and phenotypic variances ($< 1\%$) and low genotypic and phenotypic coefficients of variation values ($< 4\%$) during the sowing– flowering cycle in all environments combined.

Table 9: Overall mean, genotypic, phenotypic and environmental variance, coefficient of variation genotypic and phenotypic, heritability in the broad sense and response to selection for the two campaigns in environment three

Traits	NDF (days)	PLH (cm)	PLW (cm)	PLL (cm)	NTH	NPH	PAW (g)	NGP	NFG	TGW (g)	GYI (t/ha)
YEAR 2020–2021											
MG	110	110.21	33.48	1.53	18	14	3.9	173	146	23.3	4.46
σ^2_g	25.45	199.35	4.26	0.01	0.67	1.83	0.47	1077.3	828.93	2.65	0.34
σ^2_p	27.44	204.24	7.61	0.03	1.87	2.32	0.51	1117.67	855.86	2.76	0.42
σ^2_e	5.98	0.12	6.20	0.03	3.60	1.43	0.06	116.55	73.90	0.16	0.11
GCV (%)	4.50	12.81	6.16	6.54	4.55	9.66	17.58	18.97	19.72	6.99	13.07
PCV (%)	4.76	12.97	8.24	11.32	7.60	10.88	18.31	19.32	20.04	7.13	14.53
H ² _{BS}	0.92	0.97	0.56	0.33	0.36	0.79	0.92	0.96	0.96	0.96	0.81
GA	9.93	28.56	3.18	0.12	1.01	2.48	1.35	66.11	57.85	3.29	1.08
GAM (%)	9.03	25.91	9.51	7.70	5.63	17.71	34.70	38.22	39.63	14.10	24.25
YEAR 2021–2022											
MG	113	109.93	33.41	1.51	20	15	3.91	173	144	24.81	4.76
σ^2_g	21.85	203.55	6.25	0.04	3.08	5.79	0.45	1130.31	869.25	2.68	0.85
σ^2_p	27.85	208.48	11.52	0.05	3.47	6.05	0.49	1175.46	900.84	2.8	0.96
σ^2_e	6.20	12.89	11.62	0.04	1.18	0.79	0.04	124.78	82.88	0.09	0.08
GCV (%)	4.14	12.98	7.48	13.25	8.77	16.04	17.16	19.43	20.47	6.60	19.37
PCV (%)	4.67	13.13	10.16	14.81	9.31	16.40	17.90	19.82	20.84	6.74	20.58
H ² _{BS}	0.78	0.97	0.54	0.8	0.89	0.96	0.91	0.96	0.96	0.95	0.88
GA	8.48	28.85	3.78	0.37	3.42	4.86	1.31	67.80	59.36	3.27	1.78
GAM (%)	7.50	26.25	11.30	24.40	17.08	32.43	33.56	39.19	41.22	13.20	37.31

NDF: number of days 50% of flowering; PLH: plant height at harvest; NTH: number of tillers per hole at maturity; NPH: number of panicles per hole; PLW: panicle leaf width; PLL: panicle leaf length; PAW: average panicle weight; NGP: number of grains per panicle; NFG: number of full grains per panicle; TGW: thousand grain weight; GYI: grain yield; MG: overall mean; σ^2_g : genotypic variance; σ^2_p : phenotypic variance; σ^2_e : environmental variance; GCV: Coefficient of genotypic variation; PCV: Coefficient of phenotypic variation; H²_{BS}: heritability in the broad sense; GA: Expected genetic gain; GAM: Expected genetic gain relative to the mean

Table 10: Overall mean, genotypic, phenotypic and environmental variance, coefficient of variation genotypic and phenotypic, heritability in the broad sense and response to selection of the three environments combined for the two years

Traits	NDF (days)	PH (cm)	PLW (cm)	PLL (cm)	NTH	NPH	PW(g)	NGP	NFG	TGW(g)	GYI (t/ha)
MG	115	95.33	27.08	1.39	34	25	2.94	143	114	23.13	5.91
σ^2_g	9.05	106.82	5.55	0.01	16.27	11.37	0.17	594.21	283.45	1.92	0.26
σ^2_p	12.00	118.17	7.28	0.02	20.37	13.48	0.25	784.12	438.88	2.35	0.51
σ^2_e	11.85	13.63	4.7	0.01	7.81	3.62	0.05	89.83	64.63	0.51	0.48
GCV (%)	2.62	10.84	8.70	8.43	11.86	13.49	14.18	17.05	14.77	5.99	8.62
PCV (%)	3.01	11.40	9.97	9.66	13.27	14.69	17.05	19.58	18.38	6.62	12.05
H ² _{BS}	0.75	0.90	0.76	0.76	0.80	0.84	0.69	0.76	0.65	0.82	0.51
GA	5.38	20.24	4.24	0.21	7.43	6.38	0.71	43.71	27.87	2.58	0.75
GAM (%)	4.68	21.23	15.65	15.14	21.85	25.52	24.28	30.57	24.45	11.15	12.70
MS	216.1	2127.1	131.1	0.32	366.62	242.67	4.52	14114.2	7899.81	42.26	9.13

NDF: number of days 50% of flowering; PLH: plant height at harvest; NTH: number of tillers per hole at maturity; NPH: number of panicles per hole; PLW: panicle leaf width; PLL: panicle leaf length; PAW: average panicle weight; NGP: number of grains per panicle; NFG: number of full grains per panicle; TGW: thousand grain weight; GYI: grain yield; MG: overall mean; σ^2_g : genotypic variance; σ^2_p : phenotypic variance; σ^2_e : environmental variance; GCV: Coefficient of genotypic variation; PCV: Coefficient of phenotypic variation; H²_{BS}: heritability in the broad sense; GA: Expected genetic gain; GAM: Expected genetic gain relative to the mean MS: mean squares

All traits recorded broad-sense heritability values below 0.90, except plant height. Panicle leaf width had the lowest expected genetic gain (0.21).

Analysis of the direct effects of agronomic traits on grain yield

The path coefficient analysis, using grain yield as the dependent variable for indirect selection, is shown in Fig. 2. The path coefficient analysis showed that half of the traits, namely panicle leaf length (0.17), panicle leaf width (5.08), number of panicles per hole (0.15), number of full grains per panicle (0.001), average panicle weight (1.06) and thousand grain weight (0.44), had a direct positive effect on grain yield. The six other traits, including the number of days 50% of flowering, plant height at harvest, number of tillers per hole at maturity, panicle length, grain length and

grain width, had a direct negative effect on grain yield (Table 11). Panicle leaf width recorded the highest positive path coefficient ($b = 5.08$, $SE = 1.59$, $P = 0.0001$), so that an increase in panicle leaf width length resulted in a 5.08-unit increase in grain yield. Grain width, on the other hand, recorded the highest negative path coefficient ($b = -1.77$, $SE = 1.44$, $P = 0.219$), therefore a one-unit increase in grain length resulted in a 1.77-unit decrease in grain yield. The fit indices were better for the overall comparative fit index (1.00), root mean square error of approximation (0.0001) and residual standard root mean square (0.0001) with significant probability ($P = 0.0001$).

Discussion

Assessing the stability of a species genetic potential is important in genotype selection and varietal improvement

Table 11: Sequential regression analysis of agronomic traits on grain yield

Parameters		Estimate	SE	Z	P-value
GYI ~	NDF	-0.12	0.03	-3.64	0.0001
GYI ~	PLL	0.17	0.05	3.58	0.0001
GYI ~	PLW	5.08	1.59	3.18	0.0001
GYI ~	PLH	-0.04	0.01	-2.48	0.015
GYI ~	NTH	-0.18	0.06	-3.28	0.001
GYI ~	NPH	0.15	0.03	5.63	0.0001
GYI ~	PAL	-0.28	0.15	-1.89	0.058
GYI ~	NFG	0.001	0.01	0.07	0.941
GYI ~	PAW	1.06	0.40	2.66	0.008
GYI ~	GRL	-0.19	0.19	-1.01	0.311
GYI ~	GRW	-1.77	1.44	-1.23	0.219
GYI ~	TGW	0.44	0.14	3.16	0.002

NDF: number of days 50% of flowering; PLH: plant height at harvest; NTH: number of tillers per hole at maturity; NPH: number of panicles per hole; PAL: panicle length; PLW: panicle leaf width; PLL: panicle leaf length; PAW: average panicle weight; NFG: number of full grains per panicle; GRL: grain length; GRW: grain width TGW: thousand grain weight; GYI: grain yield

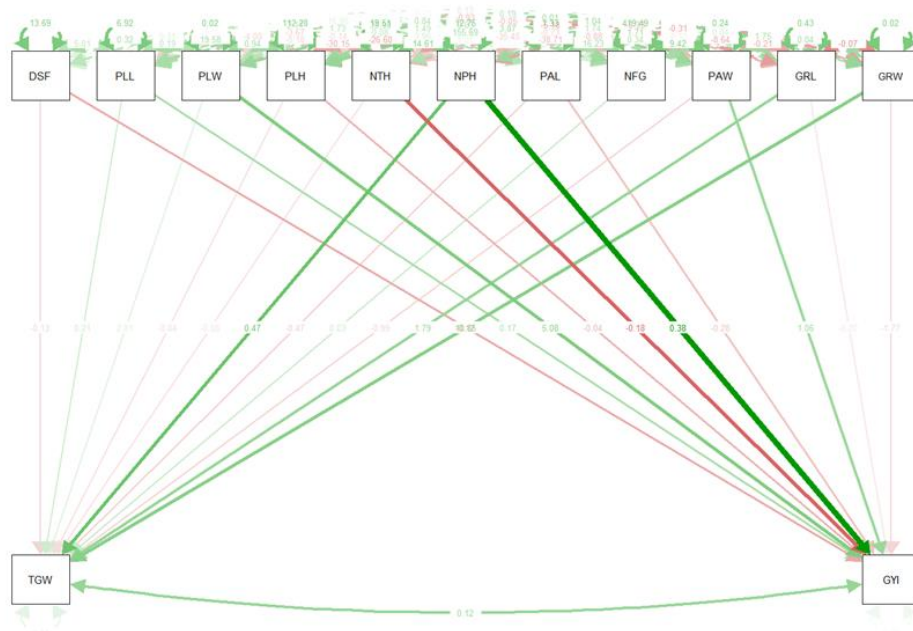


Fig. 2: Trajectory coefficient for direct effects of agronomic traits on grain yield

NDF: number of days 50% of flowering; PLH: plant height at harvest; NTH: number of tillers per hole at maturity; NPH: number of panicles per hole; PAL: panicle length; PLW: panicle leaf width; PLL: panicle leaf length; PAW: average panicle weight; NFG: number of full grains per panicle; GRL: grain length; GRW: grain width, TGW: thousand grain weight; GYI: grain yield. Red indicates direct negative impact, and green indicates direct positive impact

programs (Sebbane 2021).

The almost similar response of the varieties tested in the same environment during the two years of experimentation could be explained by the adoption of identical experimental and management conditions (irrigation, fertilization) applied within the same environment during the trials. The lack of variability observed between the two years was also confirmed by the low coefficients of variation (< 20%) for each of the traits measured (Table 4–5). According to Sawadogo *et al.* (2015), all traits with coefficients of variation below 30% indicate low variation between genotypes. Genotypic superiority is determined by the sum of the squared distances between the performance of the genotype under consideration and that of the best

genotype per environment for all environments. A stable, high-performing cultivar has a low index value. Thus, the varieties FKR19, FKR56N, FKR58N and FKR62N with a low index can be considered both productive and adaptable to different environments (Table 6). The low values of this index indicate desirable genotypes that combine performance and stability. According to Guendouz *et al.* (2021), genotypes with low Pi values are the most desirable for breeding because they are considered to be high-performing and stable genotypes. The closer values of the coefficient of phenotypic variation and the coefficient of genotypic variation for most traits in all environments and by year suggest a low impact of the environment on these traits and therefore high heritability (Table 7–9). The smaller the

difference between the genotypic variation and the phenotypic coefficient of variation, the weaker the environmental influence and the greater the genetic control in their expression (Sawadogo *et al.* 2023).

The high values of heritability in the broad sense for most traits, regardless of the year of experimentation, could indicate a more predominant role for the genotype in determining the phenotype (Table 7–9). This suggests the predominance of the effects of additive and dominant genes in the inheritance of these traits (Jimmy *et al.* 2017). The higher the heritability values of the traits, the more effective the selection (Sawadogo *et al.* 2023). However, the value of heritability in the broad sense alone, which considers additive and non-additive variance, does not provide any indication of the degree of improvement expected from selection for a given trait. The genetic gain of each trait is the most important parameter in the selection of any crop. It indicates the extent to which a given trait could be modified in its respective units by selection (Tsenov *et al.* 2022). Thus, low estimates of the average percentage genetic advance were observed in this study (Table 10). This indicates that traits governed by non-additive gene action and selection by heterosis are useful. According to several previous studies (Fellahi *et al.* 2013; Adhikari *et al.* 2018), high genotypic coefficients of variation associated with high sense heritability values and high genetic gains provide better predictive information than each parameter in isolation. The traits recorded a high value of heritability in the broad sense associated with a high genetic gain despite the importance of the interaction for effective selection. Thus, heritability should be considered in association with genetic gain to predict the effect of breeding high-yielding crop varieties (Jimmy *et al.* 2017). The expression of each trait studied was influenced by variety, the study environment (irrigation system) and their respective interactions. This could indicate the specificity of each environment and a differential response of varieties depending on the environment. This significant genotype \times environment interaction effect of the traits indicates that the irrigation systems affected the performance of the genotypes (Table 10). This led to differences between rice varieties in the three study environments.

Selection for higher grain yield in rice should not focus solely on yield because of its complexity and interaction with other yield-enhancing traits. The characteristics of yield components do not occur independently; however, they are interconnected and lead to higher grain yield in rice. Path coefficient analysis was used to determine the contribution of each agro-morphological or phenological trait to the total variance of grain yield as a dependent variable, which is a function of the other measured variables introduced as independent variables. These correlations provide information on traits likely to improve and can be used as selection criteria to increase yields. For example, panicle leaf width and harvest index showed a very high path coefficient. In fact, panicle leaf width significantly predicted grain yield;

therefore, an increase in panicle leaf width increases grain yield. In fact, the surface area of the flag leaf could be an important component in increasing grain yield because this organ is the last to remain active, along with the ear, to produce the assimilates necessary for grain filling (Table 11, Fig. 2). In this regard, key components underlying grain yield in cereal crops are positively correlated with flag leaf size (Yang *et al.* 2016). Thus, the high direct effects of the traits seem to be the main factor in their association with grain yield per plant (Sudeepthi *et al.* 2020). Therefore, these traits should be considered as an indirect selection criterion for yield improvement because, these yield components could indirectly increase yield. However, this study was based on a few pheno-agromorphological traits in a single agro-climatic zone, which is still insufficient.

Conclusion

The expression of the traits studied was influenced by variety, the study environment (irrigation system) and their respective interactions. Analysis of the genotypic superiority index (Pi) identified the FKR19, FKR56N, FKR58N and FKR62N genotypes as performing and stable. In addition, environmental factors had little influence on the expression of the agro-morphological performance of the varieties, as shown by the small differences between the phenotypic and genotypic coefficients of variation. The heritability coefficients were high for most of the parameters, suggesting the effectiveness of early selection based on the variables studied. It was found that flag leaf area, number of tillers per hole at maturity, number of panicles per hole and number of spikelets per panicle were the most important traits because they have high heritability coupled with high genetic advance. This indicates the involvement of an additive gene in controlling the gene responsible for these traits. Consequently, these traits could be improved by selection in the segregating generations. The results of this study suggest that an ideotype variety with high grain yield should have a high panicle leaf length, panicle leaf width, panicle leaf number per hole, panicle whole grain number per panicle, average panicle weight and thousand grain weight. Among these traits, panicle leaf length, panicle leaf width, number of panicles per hole, average panicle weight and thousand grain weight can be used as criteria for indirect selection of grain yield. However, this study was based on a few pheno-agro-morphological characteristics in a single agro-climatic zone, which is still insufficient. As the aim of plant improvement is to bring together or combine as many favorable genes as possible in a single variety, it is important that future studies broaden the scope of the study. Subsequent studies broaden the field of expertise in morphological, agronomic, biochemical and physiological traits. In this context, it would also be interesting to conduct multi-location trials, particularly in different agro-climatic zones, to assess the G \times E interaction and identify high-yielding and stable varieties.

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Author Contributions

This work was carried out in collaboration between both authors. The first author designed the experiment, AO, ALB, OTB and PMN analyzed the data. Both of the authors interpreted the data, read the final manuscript and agreed with all contents. IY corrected and translated into English, NS and YIS supervised the work.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability

All data are available on request to the corresponding author.

Ethics Approvals

None

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None

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