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Agromorphological and Participatory Evaluation of Aromatic Rice Lines in Burkina Faso

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Abstract

Rice is a major food crop in Burkina Faso but its productivity must increase to meet the growing demand. This study assessed agromorphological diversity, yield stability, and farmer preferences among aromatic rice lines using multi-year field evaluations and participatory approaches. Combined analysis of variance revealed highly significant effects of genotype, year, and genotype × year interaction for all quantitative traits, demonstrating substantial genetic variability and differential genotype responses across environments. Grain yield ranged from 4.94 to 9.70 t ha^{-1}, with an overall mean of 7.34 t ha^{-1}, while key agromorphological traits such as phenological cycles, plant height, panicle number, and grain characteristics exhibited wide variation among genotypes. AMMI analysis showed that the first two interaction principal component axes explained 99.2% of the genotype × environment interaction, indicating predominantly structured interaction patterns. The WAASB index enabled the identification of genotypes combining high productivity and broad adaptation. Correlation analysis revealed significant relationships among yield components, while PCA identified phenology, grain morphology, and plant architecture as the main drivers of genotypic differentiation. Qualitative trait analysis revealed morphological diversity and allowed the identification of three distinct clusters primarily differentiated by architectural traits such as flag leaf attitude, panicle orientation, and awn presence. Participatory varietal selection further indicated that farmers prioritized productivity, panicle number, early maturity, and grain characteristics, with no significant differences between men and women. Overall, the integration of agromorphological characterization, multivariate analyses, stability assessment, and farmer participation provides a comprehensive framework for identifying rice lines that are high-yielding, stable, and aligned with farmer preferences, thereby enhancing the potential for successful varietal adoption.

Keywords

Rice Genetic Diversity, Agromorphological Traits, Genotype × Environment Interaction, Yield Stability, Participatory Varietal Selection

1. Introduction

Rice (*Oryza sp*) is one of the world's most important food crops, providing the main daily source of calories for over half the world's population [1]. The crop is produced on almost every continent in over 100 countries. It adapts to a variety of environments from sea level to 3000 m altitude, between 40˚ South and 53˚ North latitudes, on plains to shallow lands except Antarctica [2]. In Africa, paddy rice production was estimated at 39 million tons of which 22 million tons were produced from West Africa [3].

In Burkina Faso, the yearly rice demand is estimated at 700,000 tons while the national production only provides around 400,000 tons [3] [4]. Therefore, substantial amounts of rice are imported to fill the gap, resulting in a significant cash outflow of 140,000 USD [5]. The reliance on imports makes the national economy vulnerable to fluctuations in global markets and weakens progress toward achieving food self-sufficiency. At least two major strategies can contribute to reducing rice imports dramatically. On the one hand, crop productivity should be improved by developing high-performance varieties. On the other hand, the country should take advantage of its huge land potential estimated at 500,000 ha of lowland that can be developed and 233,500 ha of land suitable for irrigation. Only 10% of lowland and 5% of irrigable land are currently used [6].

Besides high yields, desirable organoleptic properties are important traits that determine demand and acceptability of rice varieties by farmers, traders and consumers [7]. Aroma in rice is one of the most important properties sought out by consumers and the rice industry [8]. Participatory breeding approaches that engage farmers have proven to be a useful tool for the breeders to shape their breeding goals towards meeting end-users' preferences [9]. This approach was recently adopted in our rice breeding program while developing aromatic double haploid and recombinant lines. The aim of the present study is therefore to evaluate the aromatic rice lines using quantitative and qualitative agromorphological traits while integrating farmers' preferences into the assessment framework.

2. Materials and Methods

2.1. Plant Material

The plant materials used in this study included 65 aromatic rice lines (Table 1). Twenty-seven came from Africa Rice Saint Louis Station as part of the Korea-Africa Food and Agriculture Cooperation Initiative (KAFACI). Thirty-three recombinant lines came from our national rice germplasm at the Institut de l'Environement et de Recherches Agricoles (INERA) and the remaining five lines were obtained from the Africa Rice Senegal core collection. The Orylux6 rice variety, widely used in Burkina Faso by farmers, was included among the 65 lines and used as control.

Table 1. List of plant materials used in this study.

Number	Line	Origin[a]	Type[b]	Number	Line	Origin[a]	Type[b]
1	AFR15	KAFACI	DH	34	Kossi10	INERA	RIL
2	AFR16	KAFACI	DH	35	Kossi12	INERA	RIL
3	AFR19	KAFACI	DH	36	Kossi13	INERA	RIL
4	Basmati370	INERA	RIL	37	Kossi2	INERA	RIL
5	Burkindi	INERA	RIL	38	Kossi238	INERA	RIL
6	Fangatigui	KAFACI	DH	39	Kossi3	INERA	RIL
7	IR841	INERA	RIL	40	Kossi4	INERA	RIL
8	K20-26	KAFACI	DH	41	Kossi7	INERA	RIL
9	K20-27	KAFACI	DH	42	Kossi8	INERA	RIL
10	K20-37	KAFACI	DH	43	Kossi9	INERA	RIL
11	K20-39	KAFACI	DH	44	KossiLolo1	INERA	RIL
12	K20-40	KAFACI	DH	45	KossiLolo3	INERA	RIL
13	K20-60	KAFACI	DH	46	KWS1	KAFACI	DH
14	K20-9	KAFACI	DH	47	KWS2	KAFACI	DH
15	K20-Germ12	KAFACI	DH	48	Madiba	INERA	RIL
16	K20-Germ13	KAFACI	DH	49	Moussoni	INERA	RIL
17	K20-Germ14	KAFACI	DH	50	Nerica10	Africa Rice	RIL
18	K20-Germ15	KAFACI	DH	51	Nerica4	Africa Rice	RIL
19	K20-Germ16	KAFACI	DH	52	Orylux6	INERA	RIL
20	K20-Germ17	KAFACI	DH	53	Remar GT	INERA	RIL
21	K20-Germ18	KAFACI	DH	54	Remar11	INERA	RIL
22	K20-Germ20	KAFACI	DH	55	Remar12	INERA	RIL

Continued

23	K20-Germ25	KAFACI	DH	56	Remar13	INERA	RIL
24	K20-Germ33	KAFACI	DH	57	Remar2	INERA	RIL
25	K20-Germ35	KAFACI	DH	58	Remar28	INERA	RIL
26	K20-Germ38	KAFACI	DH	59	Remar3	INERA	RIL
27	K20-Germ39a	KAFACI	DH	60	Remar4	INERA	RIL
28	K20-Germ4	KAFACI	DH	61	Sahel177	Africa Rice	RIL
29	Kayan	INERA	RIL	62	Sahel210	Africa Rice	RIL
30	KD	INERA	RIL	63	Sahel328	Africa Rice	RIL
31	Komboka	INERA	RIL	64	Tankie	INERA	RIL
32	Kossi_plus	INERA	RIL	65	Yankadi	INERA	RIL
33	Kossi1	INERA	RIL				

[a]KAFACI: Korea Africa for Food and Agriculture Cooperation Initiative; INERA: Institut de l'Environement et de Recherches Agricoles. [b]RIL: Recombinant Inbreed Line; DH: Double Haploid.

2.2. Methods

2.2.1. Field Trials

The study was conducted at the INERA agricultural research station of Kamboinsé (12.4467˚ N, −1.5625˚ W) over two consecutive years. Each year included two cropping seasons: a rainy season (June-October) and a dry hot season (November-May). Consequently, the experiments were evaluated in four environments defined as season–year combinations: 2022 rainy season (E1), 2022 dry season (E2), 2023 rainy season (E3), and 2023 dry season (E4). These four environments were used in the genotype × environment interaction analysis.

Field trials were arranged following a Randomized Complete Block Design (RCBD) with three replications. Elementary plots (1.2 m^2) were spaced 40 cm apart lengthwise and 50 cm apart widthwise, each bearing 20 plants in 20 cm × 20 cm spacings. Soil preparation consisted of flat ploughing followed by crushing, levelling and application of bottom fertilizer composed of 2.5 t ha^{-1} of organic fertilizer and 200 kg ha^{-1} of Nitrogen Phosphate Potassium (NPK 14-23-14). Rice seedlings were transplanted 14 days after germination. Urea (46%) was used as a booster at a rate of 150 kg ha^{-1} in three equal fractions at 10, 30 and 60 days after transplanting. Irrigation was punctual in the event of pockets of drought in the wet season and permanent in the dry season. Yield (RDT) was determined from paddy rice harvested on a net plot area of 2.16 m^2, excluding border rows to minimize edge effects. Grain weight was measured and adjusted to a standard moisture content of 14% before conversion to yield expressed in t ha^{-1}.

2.2.2. Data Collection and Analysis

Field data were collected on nine qualitative traits (Table 2) and 10 quantitative traits. The qualitative traits were mainly DUS (Distinction, uniformity, Stability) descriptors [10] including basal leaf sheath pigmentation, panicle exertion, awn development, flag leaf attitude, stigma color, panicle attitude, glume length class, lemma color, and ligule shape. Quantitative variables were the following:

i) 50% panicle heading cycle (CSE) as the number of days from sowing to 50% panicles heading.

ii) 85% maturity cycle (CSM), representing the number of days from sowing to maturity of 85% of plants.

iii) plant height (HP), corresponding to the height of five random plants (cm) from each plot at maturity stage.

iv) Panicles number (NP) referring to the number of fertile panicles assessed on five random plants from each plot at crop maturity.

v) Panicles length (LP), corresponding to the length (cm) of the panicles from five random plants at crop maturity.

vi) Paddy grain length (Lg) indicating the distance (mm) between the two ends of the paddy grain on the longitudinal plane from 10 random grains for each line after harvest.

vii) Paddy grain width (lg) corresponding to the distance (mm) between the two ends of the paddy grain on the transverse plane from 10 random grains for each line after harvest.

viii) Paddy grain length/width ratio indicating ratio between the length and width of 10 random individual grains after harvest.

ix) Weight of 1000 paddy grains (PMG) measured using an electronic scale with a precision of 0.001g.

x) Paddy grain yield per hectare (RDT)indicating the grain production of the entire plot (t ha^{-1}).

Table 2. List of qualitative traits studied.

Traits	Modality	Observation phase
Basal leaf sheath pigmentation	1-absent or very weak; 3-weak; 5-medium; 7-strong; 9-very strong	Mounting
Ligule shape	1-truncate; 2-acute; 3-lobed	Maturation
Stigma color	1-white; 2-green; 3-yellow; 4-purple; 5-black	Heading
Awn development	1-absent; 9-present	Maturation
Flag leaf attitude	1-erect; 3-semi-erect; 5-horizontal; 7-moderatly reflexed; 9-strongly reflexed	Maturity
Panicle attitude	1-erect; 2-semi-erect; 3-semi-drooping; 4-droping	Maturity
Panicle exertion	1-enclosed; 2-partly exserted; 3-just exserted; 4-well exserted	Maturity
Lemma color	1-white; 2-yellowish; 3-red; 4-purple; 5-brown; 6-black	Maturity
Glume length class	1-short; 2-medium; 3-long	Maturity

2.2.3. Participatory Varietal Selection

A total of 21 female and 19 male farmers from the surrounding localities were included in the participatory varietal selection to show their preference among 65 rice lines. Participants used their own criteria for making their decisions, but they were interviewed individually.

2.2.4. Statistical Analysis

A combined analysis across the four environments was performed using the following linear model:

$$Y_{ijk} = \mu + E_i + R_j\left(E_i\right) + G_k + \left(GE\right)_{ik} + \varepsilon_{ijk} \tag{1}$$

where Y_{ijk} is the observed value of genotype k in replication j within environment i; μ is the overall mean; E_i is the fixed effect of the i^{th} environment; $R_j\left(E_i\right)$ is the effect of replication j nested within environment i; G_k is the effect of genotype k; $\left(GE\right)_{ik}$ is the genotype x environment interaction; and ε_{ijk} is the residual error.

Quantitative agronomic data were subjected to combined analysis of variance using the Additive Main Effects and Multiplicative Interaction (AMMI) model to partition the total variation into Genotype (G), Environment (E), and genotype × environment (G × E) interaction effects. The interaction component was further decomposed into Interaction Principal Component Axes (IPCAs) to assess the pattern and magnitude of genotype stability across environments. To complement AMMI, the Weighted Average of Absolute Scores from the BLUP of the GEI effects (WAASB) index was calculated to quantify genotype stability by integrating all significant interaction principal components into a single stability metric [11]. Principal Component Analysis (PCA) was performed on standardized quantitative traits using genotype mean values across environments to explore multivariate relationships among agronomic variables and to identify the main sources of phenotypic variation. The use of genotype means allowed the characterization of overall genotype performance while reducing the influence of within-environment experimental variation despite the presence of significant genotype × environment interaction. For qualitative morphological descriptors, Multiple Correspondence Analysis (MCA) was conducted to examine the structure of categorical data and to detect morphologically distinct genotype groups. Hierarchical Clustering on Principal Components (HCPC) was applied to the MCA results to classify genotypes into homogeneous clusters. All statistical analyses were conducted using R software [12], primarily with the following main packages: metan [13], FactoMineR [14], factoextra [15], and corrplot [16].

3. Results

3.1. Quantitative Agromorphological Variability

Table 3 summarizes the responses of rice lines for the quantitative traits. The combined analysis of variance revealed highly significant effects of genotype ($F_{64;3632} = 44.14$; $p < 0.001$), environment ($F_{3;3632} = 276.04$; $p < 0.001$), and genotype × environment interaction ($F_{192;3632} = 8.77$; $p < 0.001$). Coefficients of variation ranged from 3.4% to 27.2%. The mean grain yield was higher in 2022 (7.65 t ha^{-1}) compared to 2023 (7.02 t ha^{-1}), representing a reduction of approximately 8.3% in the second year. Yield variability also differed between years. The Coefficient of Variation (CV) reached 28.69% in 2022 and increased to 31.61% in 2023, indicating greater dispersion of genotype performance under the environmental conditions in 2023.

The 50% panicle heading cycle (CSE) parameter ranged from 59.33 days in rice line Kayan to 98 days (rice line KD) with an average of 87.18 days. The control line Orylux6 had a CSE of 79 days which was significantly different ($p < 0.05$) from CSE of 47 lines.

CSM ranged from 79.25 days (rice line Kayan) to 127.83 days (rice line Moussoni), with an average of 114.56 days. The Orylux6 control matured in 105 days. A total of 45 lines had a maturity cycle significantly different from that of the control. Plant height (HP) varied between 91.67 cm (in line K20-9) and 175.33 cm (in line K20-60) with an average of 116.4 cm.

Table 3. Summary of quantitative trait values.

Traits[a]	Mean	Minimum	Maximum	CV (%)
CSE	87.18	59.33	98.00	8.26
CSM	114.56	79.25	127.83	6.02
HP	116.40	91.67	175.33	17.2
LP	25.69	21.50	29.90	9.1
NP	13.01	6.90	19.35	27.2
PMG	25.41	16.59	34.08	7.99
Lg	2.33	2.00	2.83	7.2
lg	9.21	6.26	11.50	3.4
Ratio	3.99	2.74	5.13	7.6
RDT	7.34	4.94	9.70	26.46

[a]CSE-50% = time (days) from sowing to 50% panicle heading; CSM-85% = time (days) from sowing to 85% crop maturity; HP = plant height (cm); lg = grain width (mm); Lg = grain length (mm); ratio = grain length/grain width ratio; LP = panicle length (cm); NP = panicles number; PMG = weight of 1000 grains (g); RDT = grain yield (t ha^{-1}), CV = Coefficient of Variation, P = Probability.

The mean plant height for the control Orylux6 was 115.8 cm and differed significantly from plant height in 40 lines. Panicle length (LP) ranged from var 21.51cm (rice line Kossi2) to 29.91cm (rice lines K20-60 and Basmati370), the average LP being 25.59 cm. With a mean LP of 24.85 cm, the control line differed significantly from seven other lines. Per plant panicle number (NP) was lowest in

Remar11 (NP = 6.9) and highest in Fangatigui (NP = 19.35) with an average of 13.01 across the lines. The NP in control line Orylux6 was 16.0 which made it significantly different from 30 lines. The 1000-grain weight (PMG) was also highly variable, ranging between 16.56 g in line Kayan and 34.15 g in line Remar13. The overall average PMG was 25.41 g. The control had a PMG of 20.84 g and differed from 60 lines. Variable grain dimensions were found in grain length (Lg: 6.27 - 11.51 mm), grain width (lg: 2 - 2.71 mm) and grain ratio (2.7 - 5.1). The overall average values for the three parameters were 9.23 mm (Lg), 2.33 mm (lg) and 3.9 (ratio), respectively. Grains of the control line Orylux6 were 9.04 mm long, 2.03 mm wide and 4.5 ratio, respectively. In total, the control line differed from 48 lines in Lg, 59 lines in lg and 59 lines in Lg/lg ratio. Finally, grain yield (RDT) strongly discriminated among the evaluated lines, ranging from 4.94 t ha^{-1} (in line Kayan) to 9.7 t ha^{-1} (in line Fangatigui) and averaging at 7.1 t ha^{-1}. The control produced 6.7 t ha^{-1}, which made it significantly different from 19 rice lines.

3.2. AMMI and WAASB stability analysis

The combined ANOVA revealed a highly significant genotype × environment (G × E) interaction ($F_{192;3632} = 8.77$; $p < 0.001$). Therefore, the additive main effects and multiplicative interaction (AMMI) model was used to partition interaction patterns. Genotype effects were highly significant ($p < 0.001$), indicating substantial genetic variability for grain yield among the evaluated lines. Although the main environmental effect was not significant ($p = 0.143$), the magnitude of the G × E Interaction (GEI) confirmed differential genotype responses across environments.

The first two interaction principal component axes (IPCA1 and IPCA2) explained 60.3% and 38.9% of the GEI sum of squares, respectively, accounting for 99.2% of the total interaction variation. The statistical significance of these axes indicated that the interaction was largely structured rather than random, supporting the adequacy of the AMMI2 model for describing genotype performance.

To complement AMMI2, the Weighted Average of Absolute Scores (WAASB) was computed to quantify stability. The joint evaluation of mean yield and WAASB in a performance × stability quadrant enabled the identification of genotypes combining high productivity and broad adaptation (high yield, low WAASB) (**Figure 1**). This integrated approach strengthened selection decisions by simultaneously considering productivity and stability across environments.

The WAASB stability analysis identified several genotypes combining high productivity and stability across environments (**Table 4**). Kossi4 and IR841 showed the highest mean grain yield (9.7 t ha^{-1}) with WAASB values of 0.1622 and 0.3108, respectively, indicating strong performance with acceptable stability across environments. Other genotypes such as Burkindi, Sahel210, and K20-Germ4 exhibited very low WAASB values, reflecting high stability, although their mean yields were comparatively lower.

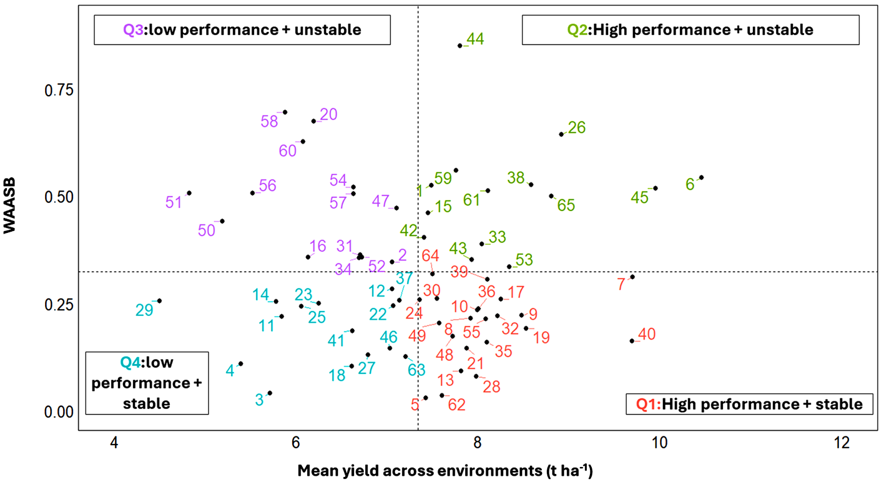

Figure 1. Performance × Stability quadrant base mean grain yield and WAASB index. Quadrants (Q1 - Q4) are indicated along with their description.

Table 4. High yielding and stable rice genotypes identified in the study.

Rice line	Number	Mean yield (t ha^{-1})	WAASB index
Burkindi	5	7.4	0.0298
Sahel210	62	7.6	0.0351
K20-Germ4	28	8.0	0.0795
K20-60	13	7.8	0.0931
K20-Germ18	21	7.9	0.1457
Kossi12	35	8.1	0.1589
Kossi4	40	9.7	0.1622
Madiba	48	7.7	0.1729
K20-Germ16	19	8.5	0.1921
Moussoni	49	7.6	0.2043
Remar12	55	8.1	0.2133
K20-26	8	7.9	0.2159
Kossi_plus	32	8.2	0.2204
K20-27	9	8.5	0.2224
K20-37	10	8.0	0.2348
Kossi13	36	8.0	0.2378
K20-Germ33	24	7.4	0.2584
K20-Germ14	17	8.3	0.2592
KD	30	7.5	0.2605

Continued

Kossi3	39	8.1	0.3058
IR841	7	9.7	0.3108
Tankie	64	7.5	0.3189

3.3. Relationships between Yield Components and Grain Productivity

Correlation analysis (Table 5) indicated a strong positive association between CSE and CSM (r = 0.96). Plant height (HP) was positively correlated with LP (r = 0.64) and negatively correlated with NP (r = −0.58). NP showed negative correlations with lg (r = −0.40) and PMG (r = −0.32) but was positively associated with the ratio variable (r = 0.39). A positive correlation was also observed between Lg and PMG (r = 0.70), while the ratio trait was positively correlated with Lg (r = 0.55) and negatively correlated with lg (r = −0.64). Grain yield (RDT) was moderately correlated with CSM (r = 0.52), CSE (r = 0.46), and NP (0.30).

Table 5. Pearson correlation matrix among agronomic traits[a].

	CSE	CSM	HP	LP	NP	Lg	lg	ratio	PMG	RDT
CSE	1.00									
CSM	0.96*	1.00								
HP	0.28*	0.22	1.00							
LP	0.14	0.07	0.64*	1.00						
NP	0.06	0.18	−0.58*	−0.28*	1.00					
Lg	0.22	0.28*	0.23	0.16	0.07	1.00				
lg	0.28*	0.24	0.30*	−0.02	−0.40*	0.27*	1.00			
Ratio	−0.08	0.01	−0.06	0.17	0.39*	0.55*	−0.64*	1.00		
PMG	0.19	0.18	0.37*	0.22	−0.32*	0.70*	0.41*	0.19	1.00	
RDT	0.46*	0.52*	−0.03	−0.04	0.30*	0.18	0.06	0.09	0.05	1.00

[a]CSE = time (days) from sowing to 50% panicle heading; CSM = time (days) from sowing to 85% crop maturity; HP = plant height (cm); lg = grain width (mm); Lg = grain length (mm); ratio = grain length/grain width ratio; LP = panicle length (cm); NP = panicles number; PMG = weight of 1000 grains (g); RDT = grain yield (t ha^{-1}); correlation coefficients with a star sign are significant at $p < 0.05$.

3.4. PCA Biplot of Agronomic Traits

Principal Component Analysis (PCA) revealed that the first two components explained 39.5% of the total phenotypic variation among the evaluated rice lines, with PC1 and PC2 accounting for 20.7% and 18.8% of the variance, respectively (Figure 2). PC1 was primarily associated with phenological traits, namely days to 50% panicle heading (CSE; 0.80) and days to 85% maturity (CSM; 0.81), together with grain-related traits such as grain length (Lg; 0.57) and thousand-grain weight (PMG; 0.45). This pattern indicates that differences in crop cycle duration and grain morphology were major sources of variation among genotypes.

The strong alignment between CSE and CSM reflects the close developmental relationship between flowering and maturity timing. PC2 was characterized by positive loadings for plant height (HP; 0.57) and small grain length (Lg; 0.70), and negative loadings for number of panicles (NP; −0.59) and the ratio trait (−0.47), suggesting a contrast between plant architectural traits and reproductive allocation. Grain yield (RDT) showed relatively low loadings on both PC1 (0.22) and PC2 (0.004), indicating that yield variation was not strongly structured along the first two principal components but rather distributed across multiple trait dimensions.

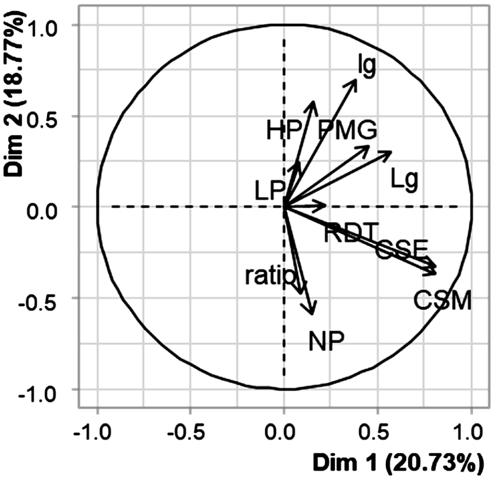

Figure 2. Principal component analysis biplot of evaluated traits. CSE = time (days) from sowing to 50% panicle heading; CSM = time (days) from sowing to 85% crop maturity; HP (cm) = plant height (cm); lg = grain width (mm); Lg = grain length (mm); ratio = grain length/grain width ratio; LP = panicle length (cm); NP = panicles number; PMG = weight of 1000 grains (g); RDT = grain yield (t ha^{-1}).

3.5. Morphological Diversity and Clustering Structure

Multiple Correspondence Analysis (MCA) performed to explore the structure of qualitative agromorphological traits indicated that the first two dimensions explained 23% and 22% of the total inertia, respectively (**Figure 3**). This accounted for 45% of the overall variation. The projection of individuals on the factorial plane revealed a clear structuring of genotypes. Hierarchical Clustering on Principal Components (HCPC) identified three distinct morphological groups.

The association between cluster membership and categorical traits was highly significant, as confirmed by chi-square tests for flag leaf attitude ($p = 3.89 \times 10^{-27}$), ligule shape ($p = 1.09 \times 10^{-16}$), lemma color ($p = 1.09 \times 10^{-16}$), panicle attitude ($p = 7.68 \times 10^{-15}$), and awn presence ($p = 9.39 \times 10^{-11}$). Cluster characterization based on v-test statistics revealed that architectural traits were the primary drivers of separation. Cluster 1 was strongly defined by erect flag leaf attitude (v-test = 6.64,

$p < 0.001$) and the presence of awns (v-test = 5.79, $p < 0.001$), while semi-erect leaves and awn absence were significantly underrepresented (negative v-tests). Cluster 2, representing most genotypes, was significantly associated with semi-erect flag leaf attitude (v-test = 7.12, $p < 0.001$), awn absence (v-test = 5.10, $p < 0.001$), and semi-drooping panicle attitude (v-test = 2.22, $p < 0.05$). In contrast, Cluster 3, composed of two highly divergent genotypes, was characterized by drooping panicle attitude (v-test = 3.49, $p < 0.001$) and strongly reflexed flag leaf attitude (v-test = 3.49, $p < 0.001$), with complete absence of semi-erect leaf types.

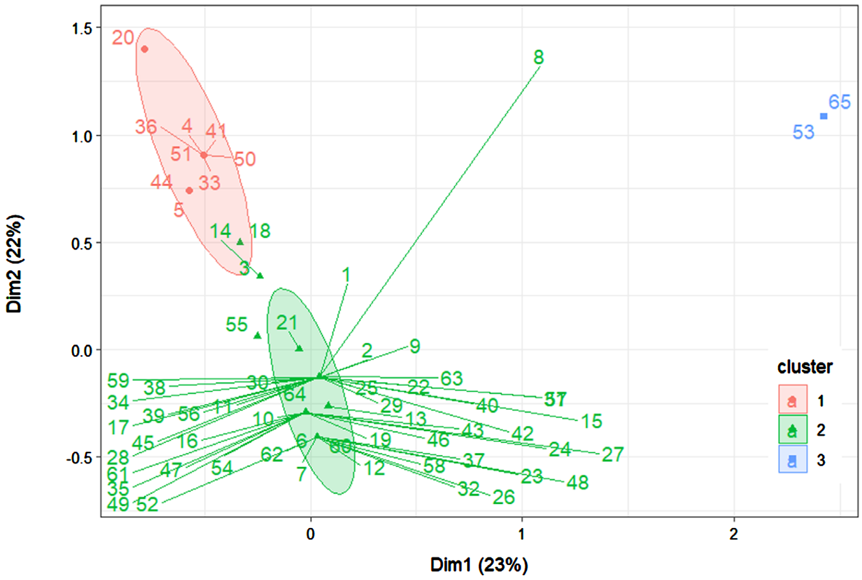

Figure 3. Factorial map of genotypes based on Multiple Correspondence Analysis (MCA) of qualitative agromorphological descriptors.

3.6. Participatory Line Selection

As summarized in **Table 6**, participatory varietal selection revealed similar preferences between men and women farmers across evaluated criteria ($p > 0.05$ for all traits). Productivity was highly prioritized by both groups (80% of men vs. 71.42% of women), although the difference was not statistically significant ($\chi^2 = 0.033$, $p = 0.86$). Early maturity was slightly more emphasized by women (71.42%) than men (60%), but this difference was also non-significant ($\chi^2 = 0.318$, $p = 0.57$). Similarly, plant height was considered important by 76.19% of women compared to 60% of men ($\chi^2 = 0.802$, $p = 0.37$), while grain length was valued by 90.48% of women and 80% of men ($\chi^2 = 0.332$, $p = 0.56$). Panicle number received the highest overall priority, being selected by all men (100%) and 90.48% of women, without significant gender differences ($\chi^2 = 0.427$, $p = 0.51$).

4. Discussion

The significant effects of genotype, year, and genotype × year (G × Y) interaction indicate substantial genetic variability among the evaluated rice lines. Such variability in yield and agronomic traits is commonly observed in rice germplasm and reflects differences in genetic background and adaptive capacity [17]. The significant effects of year and genotype × year interaction highlight the strong influence of environmental conditions on crop performance and indicate that rice lines responded differently to environmental variation (wet and dry seasons) across years [18]-[20]. The coefficients of variation (3.4% - 27.2%) indicate acceptable experimental precision for most traits [21]. However, the lower mean yield observed in 2023 compared with 2022 suggests that environmental conditions during the second year were less favorable. Rice yield is known to be highly sensitive to climatic fluctuations, particularly water availability and temperature stress during flowering [18]. Substantial variation was also observed for phenological traits, with heading ranging from 59.33 to 98 days and maturity from 79.25 to 127.83 days. Such diversity is valuable for breeding programs targeting diverse agro-ecological zones because flowering time strongly influences adaptation to rainfall regimes and cropping systems [22]. Similarly, the wide range in plant height (91.67 - 175.33 cm) suggests the presence of contrasting plant architectures, which may be exploited to select ideotypes with improved lodging resistance and yield potential [23].

Table 6. Farmers' varietal selection criteria by gender and associated chi-square test statistics.

Selection criteria	Men	Women	χ^2	p-value
Productivity	80	71.42	0.033	0.86
Earlyness	60	71.42	0.318	0.57
Plant heigth	60	76.19	0.802	0.37
Grain length	80	90.48	0.332	0.56
Panicle number	100	90.48	0.427	0.51

The AMMI analysis showed that the first two interaction principal component axes accounted for 99.2% of the total GEI variation, indicating that most of the interaction structure was captured by a low-dimensional model. Such a high proportion of explained variance suggests that genotype responses across environments were largely systematic rather than random, as commonly observed in multi-environment yield trials analyzed using AMMI models [24] [25]. Similar patterns have been reported in rice studies, where the first few IPCAs typically explain the majority of the interaction variation and provide a reliable basis for interpreting genotype × environment interactions [26] [27]. The statistical significance of IPCA1 and IPCA2 therefore confirms the adequacy of the AMMI2 model for describing genotype performance across environments and for capturing the major structure of GEI. Complementing the AMMI analysis, the WAASB stability index used to complement the AMMI analysis and to integrate the absolute contributions of all significant IPCAs, provided a robust and comprehensive measure of genotype stability across environments [28].

The joint evaluation of mean yield and WAASB through a performance × stability quadrant enabled the identification of genotypes combining high productivity with broad adaptation. Such integrated approaches are increasingly recommended in multi-environment trials because they simultaneously consider yield performance and stability, thereby improving the reliability of genotype selection for breeding and varietal development [29].

Correlation analysis revealed several relationships between agronomic traits and grain yield, highlighting the variables associated with productivity in the evaluated rice lines. The very strong correlation between CSE and CSM (r = 0.96) indicates a close developmental linkage between these phenological traits, reflecting synchronized progression of reproductive stages. Grain yield showed moderate positive correlations with CSM (r = 0.52), CSE (r = 0.46), and NP (r = 0.30), suggesting that productivity was partly associated with phenological development and the number of panicles produced per plant.

The negative correlations between NP and both lg (r = −0.40) and PMG (r = −0.32) reflect the common trade-off in cereals between panicle number and grain size or weight [30]. Conversely, the positive relationship between Lg and PMG (r = 0.70) indicates coordinated grain development during the grain-filling stage. Altogether, these relationships suggest that grain yield results from the combined effects of phenology, panicle production, and grain development [31].

Principal Component Analysis further clarified the structure of trait variation among genotypes. The first two principal components explained 39.5% of the total phenotypic variation. PC1 was mainly associated with CSE, CSM, Lg, and PMG, indicating that variation in phenological timing and grain characteristics was a major source of differentiation among genotypes. In contrast, PC2 separated vegetative growth traits from reproductive traits, suggesting potential trade-offs between plant architecture and reproductive development [32]. The relatively low contribution of grain yield to the first two components indicates that yield is influenced by multiple interacting traits rather than a single dominant factor, reflecting the complex genetic basis of yield formation in rice [19]. These results highlight the importance of considering multiple agronomic traits when identifying promising genotypes under the tested environmental conditions.

The use of qualitative agromorphological descriptors revealed noticeable phenotypic diversity between the rice lines. Qualitative descriptors are commonly used for the characterization of genetic resources to facilitate the selection of desirable traits for varietal improvement [33] [34]. The observed diversity among qualitative traits therefore provides useful information for the identification of distinct phenotypic groups and potential parental lines for breeding programs.

The participatory varietal selection results indicated a shared perception of desirable varietal traits within the farming community. Productivity and panicle number received the highest priority, highlighting the importance farmers placed on yield potential and its key morphological determinants. This is in line with the primary goal of rice breeding programs which strive to develop high-yielding varieties [22] [31]. The emphasis on early maturity, particularly among women farmers, likely reflects the need to reduce production risks and adapt cropping cycles to local climatic conditions or labor constraints [35]. Similarly, the importance given to plant height and grain length indicates that farmers consider both agronomic performance and grain quality characteristics when selecting varieties. Altogether, the PVS results are consistent with participatory breeding studies showing that farmers often prioritize traits directly linked to productivity, adaptation, and market or consumption preferences [36]. Integrating such farmer-preferred agromorphological traits into breeding programs can therefore enhance varietal adoption and ensure that improved lines meet both agronomic and socio-economic needs.

5. Conclusions

The present study on agromorphological characterization of aromatic rice lines revealed substantial genetic variability between the evaluated rice lines for both quantitative and qualitative traits, highlighting the potential of this germplasm for varietal improvement. The significant genotype × environment interaction confirmed that genotype performance varied across environments, emphasizing the importance of multi-environment testing to identify stable and widely adapted lines. The AMMI analysis effectively captured the structure of the interaction, while the WAASB stability index enabled the simultaneous evaluation of yield performance and stability, facilitating the identification of promising genotypes. Overall, Kossi4 and IR841 emerged as the most promising rice lines due to their combination of high grain yield and stable performance across the tested environments.

Correlation and PCA analyses further demonstrated that phenological traits, plant architecture, and grain characteristics contributed significantly to phenotypic differentiation among genotypes. These agromorphological traits play a key role in shaping yield potential and adaptation. The diversity observed in qualitative traits also confirmed the presence of exploitable agromorphological variability within the studied germplasm. Participatory varietal selection revealed that farmers strongly prioritized productivity, panicle number, early maturity, and grain characteristics, indicating that both agronomic performance and grain quality influence varietal preference. The alignment between farmer-preferred traits and the agromorphological determinants of yield highlights the relevance of integrating farmers' perspectives into breeding programs. Overall, the combined use of statistical stability analyses, agro-morphological characterization, and participatory evaluation provides a robust framework for identifying rice lines that are not only high-yielding and stable but also meet farmers' needs, thereby increasing the likelihood of successful varietal adoption.

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Conflicts of Interest

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

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