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Performance of New Lines from Anther Culture, Mutation Breeding and Interspecific Crosses, under Lowland and Irrigated Condition in Mali

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Abstract: Rice productivity is still low in Mali due to many factors such biotic and abiotic stresses, and the immense rice-growing potential is underutilized. There is a need to enhance rice productivity through a development of new varieties more productive and stable. Under the partnership between the Institute of Rural Economy, AfricaRice and Korea-Africa Food and Agriculture Cooperation Initiative (KAFACI) nine new lines selected among 300 fixed lines were evaluated in 8 sites under irrigated and lowland conditions. The plant material included 4 KAFACI lines derived from Anther culture (series K), 2 lines from interspecific crosses (series DKA), one line (DKA-M50) from induced mutation on wild rice (*Oryza longistaminata*), and other lines from simple crosses. The objective of the study is to identify genotypes adapted to irrigated, or lowland and/or both conditions. Analysis of variance revealed the genotypes differed significantly (p < 000.1) at all environments except Kadiolo, Longorola and Manikoura, which implies that the geno types constitute a pool of germplasm with adequate genetic variability. Heritability was high with 0.76 suggesting high component of heritable portion, therefore selection for the improvement for this trait can be achieved directly based on their phenotypic performance. The combined analysis of variance indicated significant effects of environment (p < 000.1), genotype (p < 000.1) and genotype × environment interaction (GEI) (p < 000.1) on grain yield. The significance of genotype and environment interaction suggests that genotypes behaved differently in different environment and demonstrated that GEI had remarkable effect on genotypic performance in different environments. The highest environment mean grain yield was observed in San (5,197 kg/ha), followed by Baguineda (4,960 kg/ha). The genotype SIK 442-2-2 was identified as genotype adapted to wider environments, and hereby recommended for cultivation in Mali. Wild rice derivative genotypes DKA 42, DKA-M50 and DKA 37 exhibited low yield and high stability. These genotypes are more suitable for breeding specific traits. Analysis also revealed that ARS 100-5-1-B, K150849 and K150810 exhibited low yield along with low stability. GGE biplot depicted the presence of three mega environments among the test environments used for evaluation of genotypes and revealed the nature of mega-environment. Based on this, the test environment could be grouped into three diverse mega-environments. The environments of Selingué 2, Selingué 1, Manikoura, Mopti and San grouped into the same mega-environment and the interspecific line SIK 442-2-2 was identified as the best performing and candidate genotype for this mega-environment. Kadiolo and Longorola grouped into the same mega-environment with the check variety as candidate genotype for this mega-environment. In Baguineda mega-environment, K150014 was identified as the best performing genotype.

Key words: Adaptability, rice, stability, yield.

1. Introduction

Rice is one of the main sources of food for more than 3.5 billion people in the world and increased demand is expected necessitating enhanced production in Asia, Africa and Latin America.

In Mali, rice is the third most important cereal, after millet/sorghum and maize, in terms of production and consumption. Domestic production of paddy rice, currently estimated at 2.9 million tonnes, covers only 70% of the country's demands, hence the use of imports to fill the gap. This low production is due to the low productivity of farms, particularly in rice systems without total control of water, and the low exploitation

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of the immense potential of cultivable land with rice estimated at more than 3,000,000 ha. Hence, self-sufficiency in the country may be achieved either by making more agricultural land available for rice cultivation or increasing rice yield per unit area by growing improved varieties that are stable and high yielding with minimal input requirements [1]. The development of high yielding varieties requires detailed knowledge of the genetic variability that presents in the germplasm of the crop, the association among yield components, inputs requirements, cultural practices. Most traits of interest in breeding are quantitatively inherited, dependent on the cumulative action of many genes or quantitative trait loci (QTL) and their interaction with the environment that can vary among individuals over a given range to produce a continuous distribution of phenotypes [2].

Rice is a crop that has the ability to grow under a varied range of agro-climatic conditions ranging from upland to lowland and irrigated to rainfed situations, leading to wide phenotypic variation [3]. In the same ecosystem and under the same management conditions, rice grain yield is subject to variation which is principally explained by the effects of genotype and environment. This coupled with changes in the climate observed over recent decades, makes cultivation in these delicate ecosystems rather intricate. In several regions, climate variability explained more than 60% of the yield variability in maize, rice, wheat and soybean [4]. This variability is due to genotype × environment interaction (GEI) which is habitually observed in multi-environment trials (METs). This GEI is the result of changes in a genotype's relative performance across environments, due to differential responses to various abiotic and biotic factors [5] and means that the precision and predictive power of individual field trials is very low.

Studies on various crops including rice [6-10], maize [11-13], cassava [14-17] showed that most of the economic quantitative traits such as grain yield are influenced by GEI.

Assessment of GEI offers breeders the opportunity to select genotypes which show a positive interaction in some environments and under specific environmental conditions or conversely, to select genotypes with wide adaptation characterized by above-average yield performance and low variation between environments.

The most commonly used statistical technique for analyzing GEI is two-way cross classification analysis of variance (ANOVA). Although this model can adequately explain the main effects and identify GEI as a source of variation, it fails to analyze the inherent effects of GEI. This is because the additive nature of the ordinary ANOVA model does not allow the inclusion of a non-additive interaction component and other statistical techniques are therefore required to identify interaction relationships [14]. Failure related to the analysis of variance has been also shown by other earlier studies including those of Gauch and Zobel [18] and Manrique and Hermann [19]. The use of stability analysis instead of ANOVA may also help in predicting adaptability of genotypes [20].

Under the partnership between the Institute of Rural Economy, AfricaRice and Korea-Africa Food and Agriculture Cooperation Initiative (KAFACI) several promising varieties have been developed. Nine stable lines resulting from this collaboration were evaluated on 8 sites under irrigated and lowland conditions.

Hence, the objective of this study was to explore the effect of genotype and genotype × environment interaction on grain yield and to assess yield stability of 9 rice lines from interspecific crosses, from induced mutation on wild rice (*Oryza longistaminata*), and other lines from simple crosses along with 1 check variety across diversified environments of Mali using different parametric stability models.

2. Material and Method

2.1 Plant Material and Field Conditions

A total of 9 rice lines plus 1 check variety were used as experimental material. These genotypes were

evaluated across 6 environments over two years.

The experiments were conducted in the crop seasons 2018 at the Africa Rice research at the Institute of Rural Economy (IER) experimental station in Longorola, Mali and in 8 farmers field in Baguineda Kadiolo, Longorola, Manicoura, Mopti, Selengué 1, Selengué 2 and San. Experimental layout was an alpha lattice design with two replications for each experiment. For all experiments, compound fertilizer (NPK 15-15-15) was applied at the rate of 200 kg/ha at time of transplanting, followed by 100 kg/ha urea (46% N) 15 and 30 days after transplanting.

The nursery was sown in raised beds and healthy nursery was raised at all the locations following uniform package of practices. Thirty days old seedlings were transplanted following a spacing of 20 × 20 cm with a row length of 5 m for each entry.

A set of 9 rice entries, along with 1 check were analyzed for grain yield at the 9 locations.

2.2 Statistical Analysis and Procedures

2.2.1 Analysis of Variance of AMMI

In order to investigate the GEI, the grain yield was subjected to AMMI model analysis, which combines standard ANOVA with principal component analysis [21].

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^{N} \lambda n Y_{gn} \delta_{en} + \rho_{ge}$$

where Y_{ge} = yield of the genotype (g) in the environment (e); μ = grand mean; α_g = genotype mean deviation; β_e = environment mean deviation; N = number of Interaction Principal Component Axis (IPCAs) retained in the model; λn = singular value for IPCA axis n; Y_{gn} = genotype eigenvector value for IPCA axis n; δ_{en} = environment eigenvector values for IPCA axis n and ρ_{ge} = the residuals.

Stability Parameters. Five stability measures were computed using the following formulae:

Environmental Variance (S^2_{xi}).

$$S^2_{xi} = \frac{\sum(X_{ij} - \bar{X}i.)^2}{(E-1)}$$

where, X_{ij} = grain yield of genotype i in environment j, $\bar{X}i.$ = mean yield of genotype i and E is the number of environments.

Superiority Index (P_i). Genotypic superiority index P_i for each genotype is the sum of the squares of the difference between the mean in each environment and the mean of the best genotype [22]. Genotypes with smaller P_i values tend to be more stable and to approach the best genotype of each environment. The low values of P_i are the most desirable selection because they are the hallmark of efficient and stable genotypes [23]:

$$P_i = \frac{\sum_{j=1}^{n}(X_{ij} - M_j)^2}{2E}$$

where, X_{ij} = the grain yield of genotype i in environment j, M_j = the yield of the genotype with maximum yield at environment j and E = the number of environments.

Wricke's Ecovalence (W_i). The Wricke's Ecovalence is the contribution of each genotype, to the genotype x environment sum of squares, in an unweighted analysis of the genotype x environment means (GEI) [24]. A zero or near zero value of W_i indicates that genotype responds in a consistent manner to changes in environment. Thus, low value of W_i is indicator of stability while the high value is indicator of instability.

$$W_i^2 = \sum(X_{ij} - \bar{X}i. - \bar{X}.j + \bar{X}..)$$

where, X_{ij} = mean of genotype i in environment j; $\bar{X}i$ = environment mean; and $\bar{X}.j$ = mean grain yield of genotypes across environments; $\bar{X}..$ = overall mean.

AMMI Stability Value (ASV). The additive main effect and multiplicative interaction effect stability analysis (ASV) is used to decompose the interaction effect. The two principal components have their own extremis, but calculating the AMMI stability value (ASV) is a balanced measure of stability [25]. The

genotype with lower ASV value is considered stable and genotype with higher ASV is unstable. It was calculated according to:

$$ASV_i = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}}(IPCA1score)\right]^2 + (IPCA2score)^2}$$

where, $\frac{SS_{IPCA1}}{SS_{IPCA2}}$ = weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares.

Finlay and Wilkinson Joint Regression Coefficient (b_i). It aims to assess how the expected performance of a genotype varies depending on the environmental effects. Usually this is achieved by a decline in performance of each genotype on the mean environment [26].

$$b_i = 1 + \frac{\sum(Xij - \bar{X}i - \bar{X}.j + \bar{X}..)(\bar{X}.j - \bar{X}..)}{\sum(\bar{X}.j - \bar{X}..)^2}$$

$$b_i = \frac{\sum y_{ij} I_j}{\sum ij^2}$$

where, b_i = the regression coefficient; y_{ij} = the performance of the i^{th} genotype in the j^{th} environment; i_j = the environmental index which is the mean of all genotypes at the j^{th} envionments.

3. Results

3.1 Yield Performance over Environments

Analysis of variance performed on yield data of the eight environments showed significant ($p < 0.001$) differences among genotypes except in Kadiola, Longorola and Manicoura. The pooled analysis of variance indicated significant variation among genotypes. Heritability across the combined data of the 8 experiments was high heritability (0.76) suggesting the narrow effect of environment of the expression of this trait therefore the variation observed is controlled by additive gene effects or a few major genes, and selection for this trait would be more effective for improvement (Table 1).

3.2 Analysis of Additive Main Effect and Multiplicative Interaction Effect

The AMMI ANOVA performed on 10 lines in 8 environments revealed significant difference between, genotypes ($p < 0.05$), environments ($p < 0.05$) and significant interaction between genotypes and environments ($p < 0.05$). The analysis showed that 67.18% of the sums of squares were attributable to environmental effects, 20.38% to GEI and only 12.43% to genotypic effects. A substantial part of the GEI unexplained by the first two axes forms part of the residual and accounted for 4.93% of GEI (Table 2).

3.2.1 Yield Adaptation across Environments

The AMMI analysis allowed the selection of the best genotype according to the environment (Table 3). Genotypes SIK 442-2-2 showed the best performance across 5 environments and can be considered as well adapted to these environments. In the same way genotype K150014 performed well and ranked second in 4 environments. Genotypes K150510 and K150849 showed their best performance and ranked third in 3 and 2 environments respectively. Genotypes DKA 37 ranked third and fourth in 1 and 5 environments respectively while genotypes ARS 100-5-1-B ranked fourth in a single environment (Baguineda). On the other hand the highest grain mean yield 4,960 kg/ha has been recorded in Baguineba.

3.2.2 Correlation between Environments

According to AMMI-2 biplot environment scores are connected to the origin of the plot by blue vector, and angles between environments vectors translate the correlation between environments [27, 28]. Acute angles between vectors indicate a positive correlation between environments. A right angle between lines indicates low or no correlation between environments, and an obtuse angle indicates negative correlation.

According to Fig. 1 there is an acute angle between vectors of Selingué 1, Seligué 2 and San indicating positive correlation of these three environments. In the same way Longorola and Kadiolo were strongly

Table 1 Summarize statistic of grain yield of 10 rice genotypes evaluated across 8 environments.

No.	Variety	Site								
		Baguineda	Kadiolo	Longorola	Manicoura	Mopti	San	Selingué 1	Selingué 2	Overall mean
1	K150849	5,339.6	1,062.1	3,632.0	3,484.2	6,666.7	5,080.8	3,075.0	2,540.4	3,346.7
2	K150014	6,547.4	1,062.1	3,561.5	4,632.4	4,000.0	6,348.7	2,467.9	2,771.7	3,863.1
3	K150510	5,512.1	1,158.6	4,072.3	3,376.5	4,851.9	4,557.9	2,042.8	2,366.9	3,337.2
4	K150810	5,397.1	1,190.8	3,804.4	3,627.7	4,620.4	4,441.7	2,285.7	2,598.2	3,346.2
5	DKA 37	4,246.8	1,078.2	4,008.1	3,914.8	5,058.3	5,080.8	2,164.3	2,713.9	3,342.6
6	DKA 42	2,924.0	1,255.1	3,913.0	3,268.9	4,133.3	4,956.6	1,435.7	1,962.1	2,885.4
7	DKA-M50	4,074.3	1,206.9	3,856.0	3,233.0	4,958.0	4,035.0	2,225.0	2,598.2	3,057.0
8	ARS 100-5-1-B	5,454.6	1,174.7	3,809.8	3,233.0	2,866.7	4,301.5	1,557.1	1,846.5	3,044.4
9	SIK 442-2-2	5,339.6	1,223.0	4,132.1	4,417.1	4,401.8	8,276.3	4,046.5	4,101.8	4,500.9
10	Check	4,764.5	1,255.1	4,261.5	3,412.4	5,592.6	4,616.0	3,500.1	2,366.9	3,515.4
	Heritability	0.86	0.24	0.57	0.54	0.22	0.88	0.87	0.91	0.766
	Mean	4,960.0	1,166.7	3,905.1	3,660	4,715	5,169.5	2,586.7	2,480	3,423.9
	LSD	839.3	280.0	737.7	978.4	2,633.7	1,083.6	503.5	545.1	536.8
	CV	15.0	40.3	20.3	30.0	33.0	17.6	17.2	19.0	21.3
Genotype significance		$p < 0.001$	0.62	0.30	0.16	0.1416176	$p < 0.001$	$p < 0.001$	$p < 0.001$	$p < 0.001$

Table 2 AMMI analysis of variance of 10 genotypes evaluated in 8 environments.

Source	d.f.	s.s.	v.r.	*F* pr
Genotypes	9	24,633,883 (12%)	4.27	< 0.001
Environments	7	133,123,056 (67.18%)	29.67	< 0.001
Interactions	63	40,387,687 (20.38%)	-	-
IPCA 1	15	18,828,012	4.27	< 0.001
IPCA 2	13	11,278,329	2.95	0.0054
Residuals	35	10,281,346 (4.93%)	-	-

d.f. = Degree of freedom; s.s. = sum of squares; v.r. = variance, *F* pr = probability of *F*-test.

Table 3 First four superior genotype per environment by AMMI analysis.

Environment	Mean (kg/ha)	Score	1	2	3	4
Longorola	3,919	41.16	Check	DKA 42	K150510	SIK 442-2-2
Kadiolo	1,207	25.05	Check	SIK 442-2-2	K150510	DKA 37
Mopti	4,500	10.75	SIK 442-2-2	Check	K150510	DKA 37
Selingue 2	2,480	-0.54	SIK 442-2-2	K150014	Check	DKA 37
Selingue 1	2,587	-2.53	SIK 442-2-2	K150014	Check	DKA 37
Manicoura	3,660	-19.65	SIK 442-2-2	K150014	K150849	DKA 37
Baguineda	4,960	-22.71	K150014	K150810	K150849	ARS 100-5-1-B
San	5,197	-31.52	SIK 442-2-2	K150014	DKA 37	K150849

correlated positively. Obtuse angle between Kadiolo, Longorola and Baguineda indicated that these two environments showed negatively correlated with Banguineda. Manicoura was positively correlated with Selingué and San (Fig. 1).

3.3 Stability Analysis

In order to investigate the sensitivity and the stability of genotypes, yield data were subjected to four types of stability analysis: The Cultivar-Superiority Measure Analysis, Static Stability Measures Coefficients, Wricke's ecovalence and AMMI stability values (ASV) (Table 4).

Cultivar-Superiority Measure revealed that the genotype SIK 442-2-2 was the most stable with the smallest values of P_i (337,000) followed by K150014,

while genotypes of DKA serial were the most unstable. Since the superiority index was calculated based on distance between the performance of tested cultivar and the best performance in considered environment the genotypes SIK 442-2-2 and K150014 are the most superior in term of stability and grain yield. Conversely, DKA 42 and DKA-M50 were the most unstable because of their high P_i values (3,891,795 and 2,657,767 respectively).

Contrary to Cultivar-Superiority Measure, DKA-M42, DKA 37 and DKA-M50 were respectively selected as the most stable genotypes by Static Stability Measures, AMMI stability values and Finlay-Wilkinson joint regression and the genotype K150014 was selected as the most unstable.

3.3.1 Association among Stability Measures and Yield Parameters

Spearman's rank correlation coefficients were computed for the stability measures and yield parameters including the mean yield in favorable environment (GY_{favo}) and the average grain yield over all environments (GY). Results showed negative correlation between P_i and all others stability coefficients. The strongest positive correlation was recorded between W_i and ASV followed by S_i and b_i while the strongest negative correlation is observed

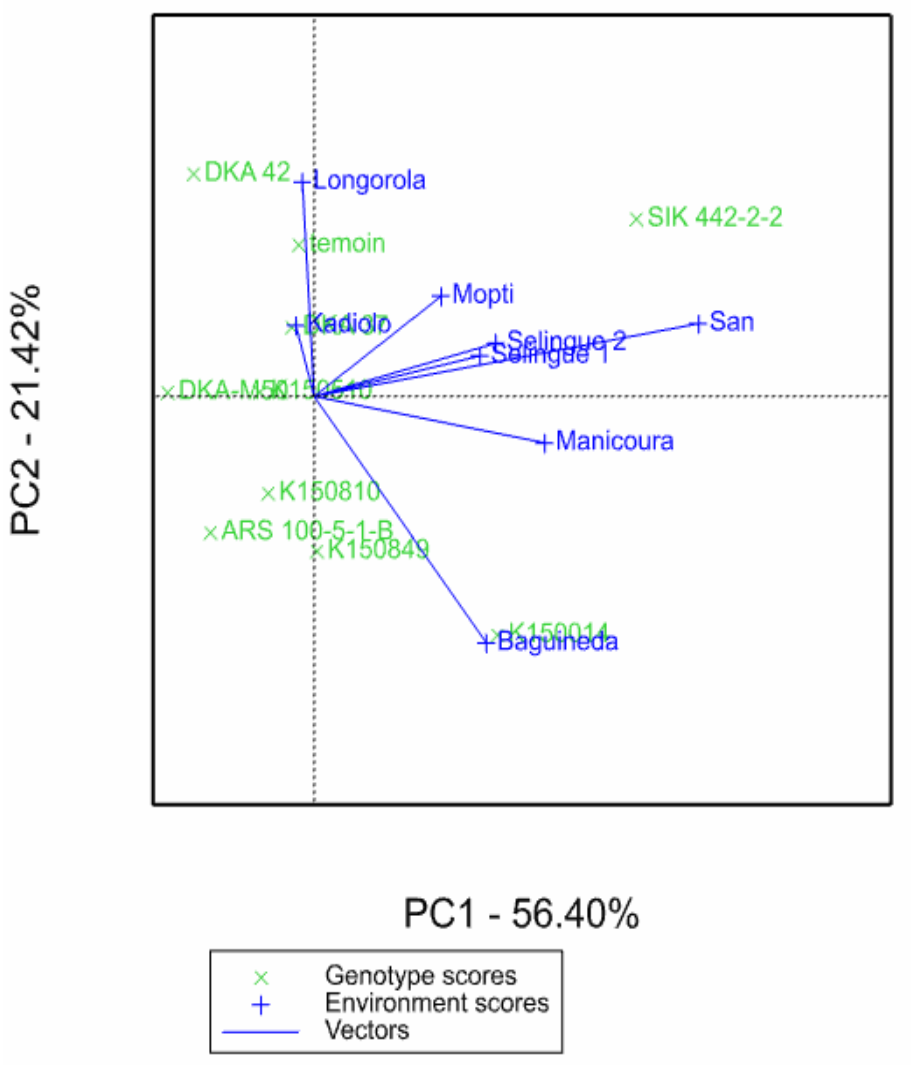

Fig. 1 AMMI biplot showing correlation between environments.

Table 4 Genotypes ranked by four stability parameters.

	Superiority genotypique			Stability statistic			Ecovalence of Wrick			AMMI sability value			Finlay and Wilkinson		
Rank	Genotype	P_i	GY	Genotype	S_i	GY	Genotype	W_i	GY	Genotype	ASV	GY	Genotype	b_i	GY
1	SIK 442-2-2	337,000	4,916	DKA 42	95,711	3,058	K150810	1,136,828	3,408	DKA 37	13.88	3,477	DKA-M50	0.5979	2,940
2	K150014	632,618	4,054	DKA-M50	496,850	2,940	DKA 37	1,275,428	3,477	K150810	16.85	3,408	DKA 42	0.8312	3,058
3	K150510	1,103,885	3,534	DKA 37	496,945	3,477	ARS 100-5-1-B	2,276,914	3,093	ARS 100-5-1-B	21.70	3,093	Check	0.8433	3,816
4	Check	1,208,322	3,816	Check	545,094	3,816	K150510	2,655,687	3,534	DKA-M50	24.74	2,940	DKA 37	0.8973	3,477
5	K150810	1,214,329	3,408	K150510	1,961,758	3,534	K150849	2,780,300	3,340	K150510	28.61	3,534	K150810	0.9112	3,408
6	K150849	1,418,426	3,340	SIK 442-2-2	2,043,546	4,916	DKA-M50	3,111,551	2,940	K150849	29.99	3,340	K150849	1.0059	3,340
7	ARS 100-5-1-B	1,597,613	3,093	K150810	2,342,218	3,408	Check	3,982,880	3,816	Check	38.33	3,816	ARS 100-5-1-B	1.0498	3,093
8	DKA 37	1,856,745	3,477	ARS 100-5-1-B	2,972,499	3,093	DKA 42	6,349,473	3,058	DKA 42	48.63	3,058	K150510	1.0589	3,534
9	DKA-M50	2,657,767	2,940	K150849	3,563,964	3,340	SIK 442-2-2	7,732,767	4,916	SIK 442-2-2	55.47	4,916	SIK 442-2-2	1.2966	4,916
10	DKA 42	3,891,795	3,058	K150014	6,587,642	4,054	K150014	9,085,858	4,054	K150014	72.55	4,054	K150014	1.4812	4,054

ASV = AMMI stability value; W_i = Wrick ecovalence; P_i = genotype superiority index; S_i = Wrick's ecovalence index; b_i = Finlay and Wilkinson joint regression coefficient; GY_{favo} = mean grain yield in favorable environment; GY = mean grain yield over all environments.

between the b_i and P_i. A strong negative correlation was also observed between P_i and S_i. Positive correlation was observed between the two yield parameters. Static stability coefficient S_i was positively correlated with b_i. W_i showed positive correlation with GY and b_i.

To better understand the relationships between the various indices stabilities used in our study, we performed a principal component analysis from the matrix correlation on the basis of values taken by the stability index. The relationships among different parameters are graphically displayed in a biplot of PCA1 and PCA (Fig. 2). The first axis (PC1) and the second axis (PC2) explained 48.2 and 29.50%, of the variance of the original variables respectively and the two components accounted for a total of 77.69% of the variance. PC1 and PC2 mainly distinguish the stability measures in agronomic stability and biological stability, respectively. The PCA1 axis distinguishes the method of superiority genotypes analysis (P_i) from the other stability methods (Fig. 3).

The weak positive correlation between GY_{fav} and S_i ($r = 0.42$; $p < 0.01$) shows that successful genotypes in the favorable environment are relatively unstable. The use of this stability parameter in breeding involves determining the weight to be given to stability relative to yield potential, particularly in semi-arid conditions in the Sahelian regions, where farmers are looking for varieties with stable performance to meet the inter-annual climate variability. Indeed in arid or semi-arid areas, such as the Sahel, the inter-annual variability of rainfall is a major constraint for the choice of varieties, and is the main cause of GEI [29]. On the other hand, the partial sacrifice of stability to the benefit of yield potential, selects genotypes which moderately contribute to the interaction. Such genotypes significantly valorize better the favorable years (or environment) and respond better than

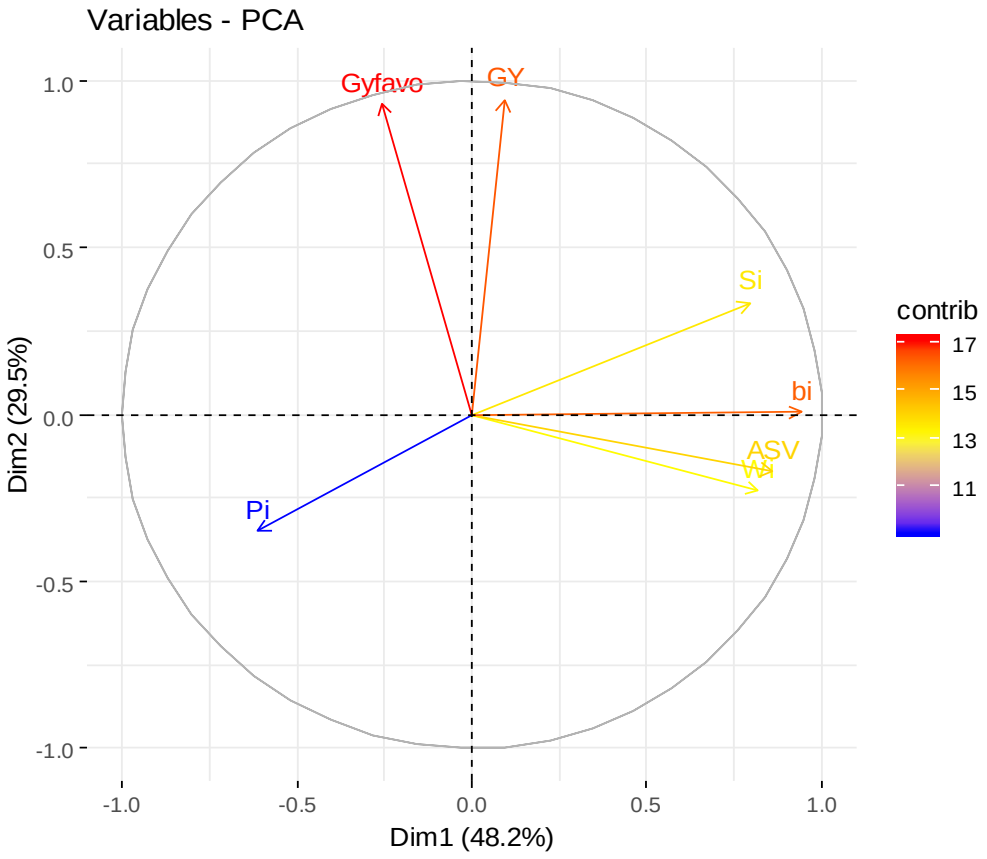

Fig. 2 Biplot of PC1 versus PC2 for 5 parametric stability methods and 2 yield parameters of 240 rice genotypes.

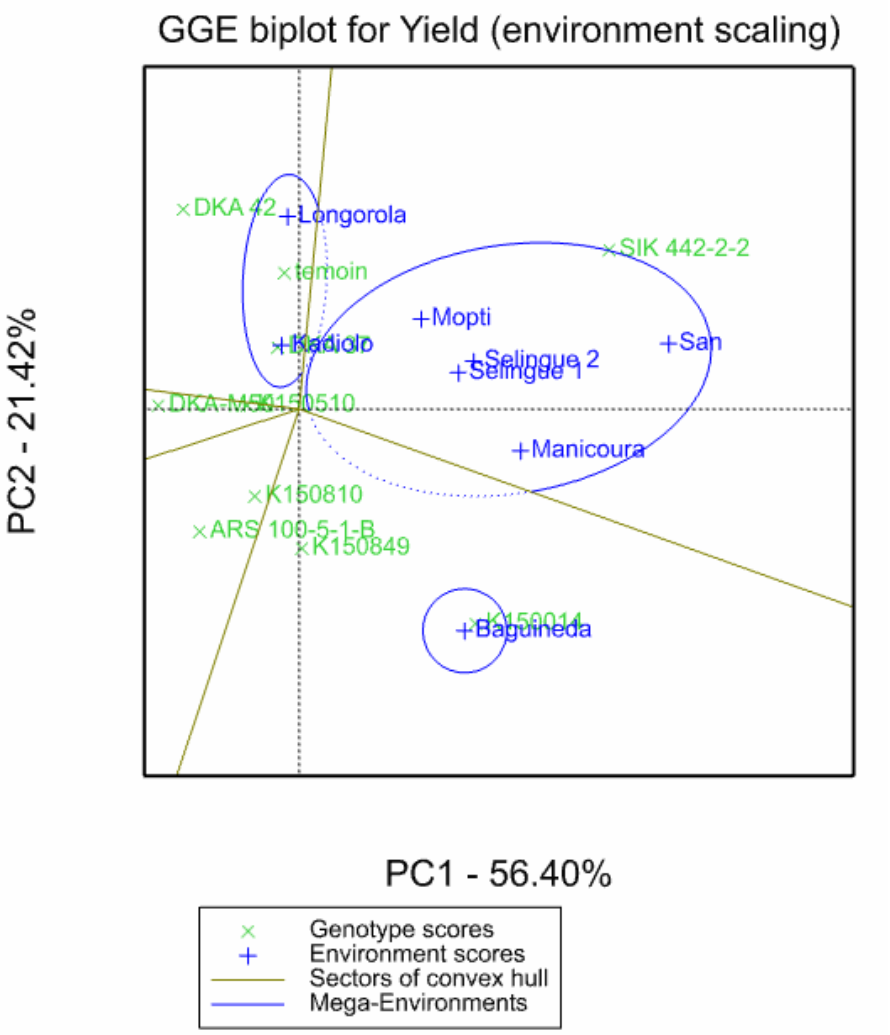

Fig. 3 GGE biplot identification of winning genotypes and their related mega-environments.

Table 5 Mega-environments and performance of wining genotypes.

Mega env.	Site	Genotypes	AMMI estimates
1	Baguineda	K150014	6,850
2	Selingue 2	SIK 442-2-2	3,921
	Selingue 1	SIK 442-2-2	4,215
	Manicoura	SIK 442-2-2	5,553
	Mopti	SIK 442-2-2	5,731
	San	SIK 442-2-2	8,577
3	Kadiolo	Check	2,042
	Longorola	Check	5,109

unstable genotypes during constraining years as emphasized by Benmahammed et al. [30]. They can therefore be recommended to be used in Sahelian regions.

In order to evaluate the possibility of subdividing the 8 sites into different environmental groups and to determine the cultivars that optimized performance in those mega-environments the genotype main effect (G) plus genotype × environment interaction (GGE) has been used to generate biplots (Fig. 3). The biplot based on environment-focused partitioning revealed the relationships among the test environments. The

biplot explained the 77.82% of the total G + GE and adequately represents the environment-centered data. The eight tested environments fall in to three mega-environments (Table 5). The environments comprising, Selingué 2, Selingue 1, Manicoura, Mopti and San were considered similar and, therefore, grouped into the same mega-environment (quadrant). In the same way Kodiolo and Longorola were considered similar and grouped into the same mega-environment. Manicoura constituted in itself 1 mega-environment. In the GGE plot environment grouping in relation to genotype performance revealed that the genotype SIK 442-2-2 was the highest yielder in test environment Selingué 2, Selingue 1, Manicoura, Mopti and San. Among the test environments San was the highest yielder.

It is important to notice that the national check was the highest yielder in Longorola and Kodiola that constitute the mega-environment 3.

The best performing and candidate genotypes were identified for each sub-mega-environment. Among the eleven test environments, three sites were the most discriminative of the genotypes, hence to evaluate a large number of genotypes in these regions three ideal test environments can be deployed thus saving time, resources and energy.

4. Discussion

Breeding for the improvement of rice production through the development of high yielding rice varieties has been a major challenge for plant breeders especially from sub-Saharan regions where self-sufficiency in rice is declining. Over the last decades, some varieties in sub-Saharan regions have been developed and have become popular among farmers because of their high yield potential and preferred grain quality. Unfortunately, grain yields of most of these farmer-preferred varieties are subject to considerable fluctuation with according to environmental conditions. Hence, to increase the adaptability of these appreciated varieties, it is crucial to incorporate cultivars with high yielding potential and reasonable stability for yield. This involves evaluation of rice varieties across diverse environments to identify the best genotypes with broad or specific adaptation due to genotype by environment interaction.

AMMI analysis of variance showed a large difference between the environments studied ($p < 0.001$) (Table 2). The difference between genotypes was significant ($p < 0.05$). The genotype × environment interaction (GEI) was also significant ($p < 0.001$). The sum of squares was significantly higher for environments, for genotypes and their interaction showing that the genotypes interacted significantly with the environments. These results are in agreement with previous findings [31, 32]. The considerable variation due to GEI suggests that rice genotypes respond differently to environmental changes for grain yield. Similar results have been reported by previous studies [33-35].

The first two principal components explained 82.10% of the total variation. Similar results were obtained in investigations on wheat [36], faba bean [37], barley [38] and rice [9, 39].

From the results of AMMI analysis, we suggest three possible alternatives for the breeder. The first is to adopt genotypes which have general adaptation as K150014. The second alternative is to take advantage of interaction by choosing genotypes specifically adapted to favorable environments, coupled with the choice of genotypes with large adaptation for low production potential environments. In this case, SIK 442-2-2 is retained for San environment and K150510 and check variety for the other environments which will form a region with more or less similar potentials. The third alternative is to assign to each environment a specific genotype. Under this scenario the genotypes DKA 42 and K150510, are suitable for Longorola environment; check variety, SIK 442-2-2, K150510 and DKA 37 are suitable for Kadiolo environment, SIK 442-2-2, K150510, DKA 37 are suitable for

Mopti, SIK 442-2-2, K150014, are suitable for the environments of Selingué 1, Selingué 2, Manicoura as well as San and finally K150014, K150810, K150849 for Baguineda.

Genotype-by-environment interactions are important sources of variation in any crop and the term stability is sometimes used to characterize a genotype, which shows a relatively constant yield, independent of changing environmental conditions. On the basis of this idea, genotypes with a minimal variance for yield across different environments are considered stable [38]. According to Becker and Léon [40], this concept of stability may be considered as a biological or static concept of stability. This type of stability, therefore, is not acceptable to most agronomists, who would prefer an "agronomic" or "dynamic" concept of stability [41]. Here we used 4 stability parameters to rank genotypes. The positive correlation observed between GY and W_i (r = 0.36) and S_i (r = 0.38) indicates that the use of W_i and S_i to evaluate the performance of rice genotypes in future breeding programs could promote the simultaneous development of stable and high yielding genotypes. Conversely the negative correlation recorded between GY and P_i (i = -0.25; $p < 0.01$) shows that a selection based on this parameter of stability will be less useful if *yi*. These results contradict those obtained in the previous studies in which there was a positive correlation between GY and P_i in wheat (*Triticum* spp.) and barley (*Hordeum vulgare* L.) [30, 42]. But they confirm other findings which reported negative correlation between GY and P_i in faba beans (*Vicia faba*) and wheat [42-44]. An almost perfect correlation was observed between ASV and W_i (r = 0.95; $p < 0.001$) showing that these two stability parameters have very similar characteristics in the selection of genotypes for stability.

The principal component analysis separated the different indices in two concepts of stability, representing the agronomic stability and biological stability. Agronomic stability is measured by P_i and b_i, while the biological stability is measured by W_i, S_i and ASV. Fig. 3 showed that b_i, ASV as well as S_i are gathered along the positive part of axis 1 contrary to P_i which contributed negatively to the axis. This result underscores the similarity of the performance based on low P_i ranking values and that defined on the basis of high ranking values of b_i and S_i. The ASV and W_i are relative to the static of stability concept and were not correlated with the yield. Although neither of these 2 parameters is significantly correlated with the GY, they may allow identification of genotypes adapted to unfavorable environments.

Breeders use Finlay-Wilkinson regression to assess the sensitivity of genotypes in different environments. The genotypes with high sensitivity indices (b_i) and acceptable performance can positively exploit the improvement of environmental conditions. Here in the average environment SIK422-2 and K150014 have the highest means, and perform better than the other tested genotypes. Although SIK422-2 performs slightly better than K150014 in the average environment, K150014 has a higher sensitivity value and will exploit improved environmental conditions better than SIK422-2. Similarly, DKA 37 performs better than ARS 100-5-1-B in the average environment, but has low sensitivity and will not benefit from the better environmental conditions and hence will not perform as well as 100-5-1-B in these conditions.

5. Conclusion

This study identified SIK422-2 as wide-adaptation genotypes and K150014 as genotypes with specific adaptation to favorable environments represented in the study by San. Overall, the most promising genotypes SIK422-2, K150014 and K150510 with high mean yield and stability could be used for commercial cultivation across rice growing region of Mali. The present study highlights the effectives of use of superior genotype index to select genotypes if both yield and stability are desired. The study merged

the 8 sites in 3 mega-environments; the use of these meg-environments would decrease the cost of conducting field trials without compromising the repeatability of the trials. For the time being, continuity of the testing locations for more years and improving the efficiency of the less discriminating sites could be a better option for strengthening the results obtained so far.

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