



International Journal of Environmental Science and Green Technology

<https://journals.ayu.edu.kz>



Multivariate Analysis of Agro-Morphological Traits in Rice (*Oryza sativa* L.) Germplasm from Morocco

Fathalah Elwahab^{*1}, Mohamed Sedki², Sang-bok Lee³, Hanae Marjaa⁴,
Siham Belkacemi⁴, Najiba Brhadda¹, Rabea Ziri¹

¹Biotechnologies and Plant Protection, Faculty of Science, Ibn Tofail University, B.P. 133, Kenitra 14000, Morocco

²Regional Center of Agricultural Research of Kenitra, B.P. 257, 14000, Kenitra, Morocco

³Korea-Africa Food & Agriculture Cooperation Initiative (KAFACI), Rural Development Administration (RDA), Republic of Korea

⁴Natural Resources and Sustainable Development Laboratory, Faculty of Sciences, Ibn Tofail University, Kenitra B.P. 242, Morocco

*Corresponding Author e-mail: fathalah.elwahab@uit.ac.ma

Keywords	Abstract
Rice	The assessment of agro-morphological diversity in rice (<i>Oryza sativa</i> L.) plays an important role in determining superior performing cultivars that adapt well to their environmental settings. The present study was carried out to investigate the genetic diversity and agronomic performance of 34 accessions of rice grown in the Moroccan environment through the application of both descriptive and multivariate statistical analysis methods. Ten agro-morphological characteristics, including plant height, number of tillers per plant, number of panicles per plant, panicle length, heading cycle, maturity cycle, thousand grain weight, grain weight, straw weight, and grain yield, were taken into account. As the result of the analysis of variance, it can be said that there is a certain level of difference among accessions according to many analyzed parameters, reflecting the existence of genetical variability of germplasm. The grain yield varied from 6.06 t/ha up to 12.44 t/ha. In order to classify diversity between such materials and establish relationships between them, the following analysis (PCA and clustering) was conducted. It must be noted that there were two main components of principal component analysis accounting for more than 50% of total variability related to productive characters and cultivation period. It should be highlighted that the best accessions among all investigated were KF190022 owing to the highest yield (12.44 t/ha), as well as KF190114 and KF190006 owing to their high agro-economic value. High correlations between panicle length, thousand-grain weight, and grain yield could be revealed on the basis of correlation analysis.
<i>Oryza sativa</i> L	
Agro-morphological	
Genetic diversity	
PCA	
Morocco	
Cite	
Elwahab, F., Sedki, M., Lee, S.- bok., Marjaa, H., Belkacemi, S., Brhadda, N., & Ziri, R. (2026). Multivariate Analysis of Agro-Morphological Traits in Rice (<i>Oryza sativa</i> L.) Germplasm from Morocco. <i>International Journal of Environmental Science and Green Technology</i> , 1(3), 14-26. doi: 10.5281/zenodo.23494476	
Article Process	
Submission Date: 16.05.2026; Revision Date: 10.06.2026; Accepted Date: 02.07.2026; Published Date: 30.09.2026.	

1. INTRODUCTION

Rice (*Oryza sativa* L.), among other cereal grains, is considered to be the most significant agricultural plant in the world and is regarded as the staple diet of more than half of the global population. The rising need for rice, which arises from the increasing population, climate change, and depletion of agricultural land, presents a severe threat to global food security and sustainable agriculture (FAO, 2023; Ray et al., 2013).

Genetic variation is vital in crop breeding because it forms the genetic pool necessary for selecting plants with favorable agronomic attributes like productivity, stress resistance, grain quality, and disease resistance (Acquaah, 2012). Rice germplasm collection and characterization are thus indispensable in breeding sustainable rice varieties under changing environments (Tanksley & McCouch, 1997; Elwahab et al., 2025).

Agro-morphological analysis still represents one of the most popular methods for studying genetic variation within the rice germplasm collection. Parameters such as height, tillering capacity, panicle structure, grain weight, and growth period are critical criteria for identifying promising genotypes and selecting superior breeding stocks (IRRI, 2013). Various scientific works have proven high agro-morphological variation within rice populations grown under different agro-ecological zones (Roy et al., 2015).

The multivariate statistical approach, especially PCA and hierarchical clustering, is an efficient means of studying genetic diversity and genetic relationships between different rice genotypes. Multivariate statistics allow the detection of those traits that account for phenotypic variation and the classification of germplasm on the basis of agronomic performance into separate groups (Mohammadi & Prasanna, 2003). Traits related to rice yield, including panicle length, number of panicles, and thousand grain weight, are often linked to genetic diversity in rice.

Although rice production is rather low compared to other cereal crops in Morocco, it represents an important crop for agricultural diversification and food security in irrigated zones (FAO, 2023). Although the demand for improved rice is constantly increasing, there are few studies on the morphological variability of rice germplasm in Morocco (Elwahab et al., 2025).

It is therefore important to identify high-performing and well-adapted accessions for the development of new improved rice varieties which will ensure productive cultivation in Moroccan conditions. Therefore, this study aimed at evaluating the agro-morphological diversity of rice (*Oryza sativa* L.) germplasm grown in Morocco through descriptive and multivariate statistical analyses, such as PCA and correlation analysis. The main purpose was to find high-performing accessions suitable for future rice breeding in Morocco.

2. MATERIAL AND METHOD

The plant material consisted of 33 carefully selected rice accessions along with the control variety Lagostino, all cultivated under the experimental conditions of Sidi Allal Tazi. The KAFACI accessions were selected from a collection of 100 accessions introduced by the Africa Rice Center located in Saint-Louis, Senegal. The evaluated accessions included KF190136, KF190006, KF20005, KF190112, KF20017, KF20018, KF190114, KF20036, KF20058, KF20045, KF20046, KF20006, KF20013, KF20034, KF20059, KF190018, KF20019, KF190061, KF20035, KF18045, KF18046, KaWS 9294292, KF18044, CB MS11, KF190063, KF190026, KF190051, KF190027, KF190052, KF190064, KF190065, KF190022, KF190066, and Lagostino (Table 1).

Table 1. List of the 33 rice accessions used in the study

N° accession	Serial	Entry n°	Pedigree
1	KF190136	2019WS /9230343	HR32057F1-4-4-1-1-5-1
2	KF190006	2019WS / 9210008	KR55-2-4

N° accession	Serial	Entry n°	Pedigree
3	KF20005	2020WS/ 20210008	HR32058F1-1-10-1-4-1-1
4	KF190112	2019WS / 9230259	HR32054F1-2-17-1-1-3-3
5	KF20017	2020WS/ 20220007	KR55-2-1-1-2-1
6	KF20018	2020WS / 20220008	KR55-2-3-4-1-1
7	KF190114	2019WS / 9230265	HR32054F1-2-17-1-1-5-1-2
8	KF20036	2020WS/ 20270275	Ohselfed-1-4-2-3
9	KF20058	2020WS/ 20120139	HR32058F1-4-18-1-2-3-3
10	KF20045	2020WS/ 20120083	HR32051F1-3-11-1-5-4-2
11	KF20046	2020WS/ 20120007	HR32054F1-2-17-1-1-5-1-2
12	KF20006	2020WS/ 20210013	HR32058F1-4-18-1-3-1-1
13	KF20013	2020WS/ 20220029	HR32056F1-4-14-1-4-2-2
14	KF20034	2020WS/ 20270262	ARS1960-5-1-1-2
15	KF20059	2020WS/ 20120106	HR32058F1-4-18-1-5-1-2
16	KF190018	2019WS / 9210033	SR35266-2-11-4-1-1
17	KF20019	2020WS/ 20220009	KR55-2-3-4-1-2
18	KF190061	2019WS / 9220061	SR35266-HB3580-110
19	KF20035	20270273	Ohselfed-1-4-2-1
20	KF18045	2018WS / 8220057	SR35357F1-1-3-4-1
21	KF18046	2018WS / 8220058	SR35357F1-1-3-4-1
22	KaWS 9294292	2019ws	-
23	KF18044	2018WS / 8220056	SR35357F1-1-3-4-1
24	CB MS11	2019ws	-
25	KF190063	2019WS / 9220065	SR35285-HB3573-48
26	KF190026	2019WS / 9210046	ARS1974-5-2
27	KF190051	2019WS / 9220038	SR34574-HB3565-285
28	KF190027	2019WS / 9210047	ARS1974-5-3
29	KF190052	2019WS / 9220039	SR34574-HB3565-290
30	KF190064	2019WS / 9220066	SR35285-HB3573-72
31	KF190065	2019WS / 9220067	SR35285-HB3573-75
32	KF190022	2019WS / 9210037	SR34045-HB3487-11-1-1
33	KF190066	2019WS / 9220069	SR34567-HB3573-113
34 (Témoin)	Lagostino	-	-

Experimental Site

The experiment was conducted at the experimental station of Sidi Allal Tazi, located in northwestern Morocco (34°31'14.758" N, 6°14'34.169" W). The study area is part of the Gharb Plain, which extends along the Atlantic coast between 34° and 34°45' N and covers approximately 7,500 km² of

hydrogeographic territory. This region is characterized by a Mediterranean climate with mild winters and warm summers, conditions that are favorable for rice cultivation.

The Gharb Plain is well known for its diversity of soils. From Oued Sebou towards inland areas, different soil types are encountered, including Dehs, Shots, and Merjas, each with specific physico-chemical characteristics. In this region, rice is mainly cultivated on grey alluvial soils, which are predominantly clayey, low in organic matter (humus), deficient in phosphorus, and often poor in nitrogen. These soils generally exhibit a slightly alkaline pH.

The climate of the region is Mediterranean, and agricultural production benefits from important water resources provided by the Sebou River, its tributaries, the Merjas, and groundwater reserves (Figure 1).

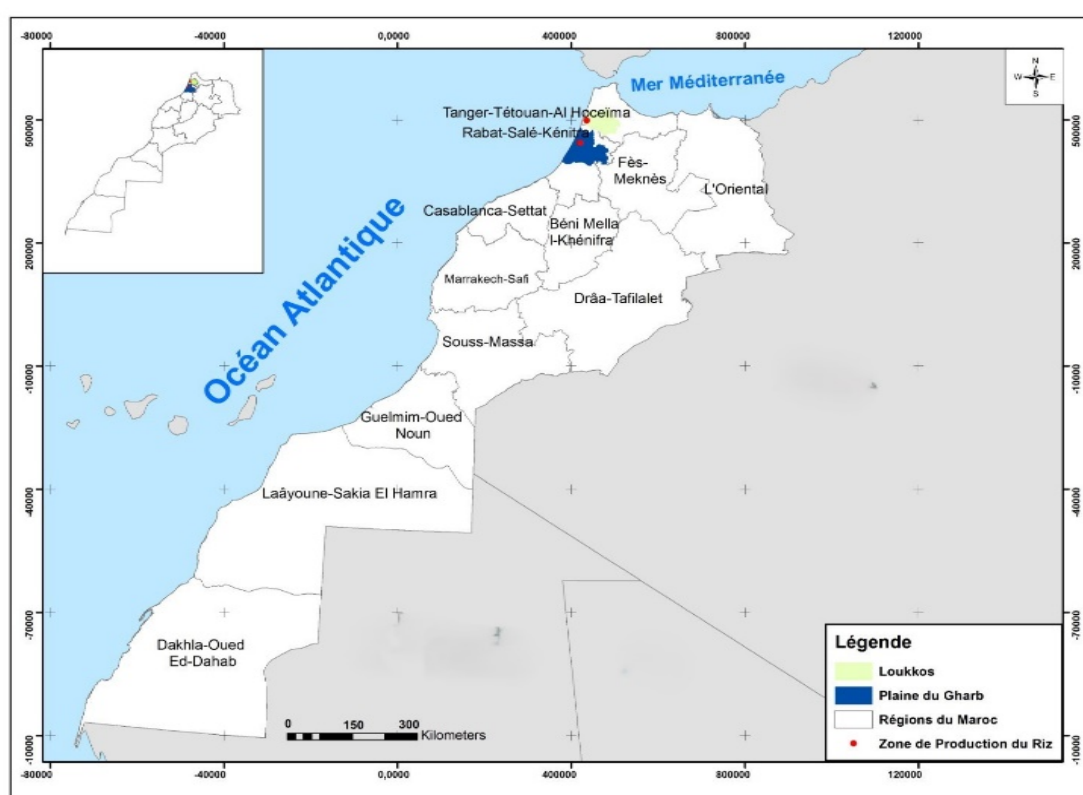


Fig. 1. Geographic map of study area

Experimental Design and Crop Management

The trial was set up based on a randomized complete block design (RCBD) with three replicates. Agronomic practices that were recommended by standards for the production of rice in Morocco were followed during the experiment, including irrigation, fertilization, weed, and pest control. All accessions were grown under similar environmental and management conditions in order to reduce variation in the experiment.

Measured Traits

Ten agro-morphological traits and productivity traits were observed during the crop cycle. These traits include plant height (H, cm), number of tillers per plant (NTP), number of panicles per plant (NPP), and panicle length (LP, cm). All these traits indicate some important components for rice

plants. Phenology traits, which are cycle to heading (CSE, days) and cycle to maturity (CSM, days), were used to determine the time of crop growth.

Parameters of biomass and yield traits were also considered, which include thousand-grain weight (PMG, g), grain weight (kg), straw weight (kg), and grain yield (RDT, t/ha). Thus, these traits show both the quality and productivity of the observed rice varieties.

Statistical Analysis

Statistical description was used to assess the variability within accessions. The variance analysis method was used to test whether there was any significant difference among genotypes regarding the investigated features. Comparisons of means were done by applying Duncan's Multiple Range Test at a 5% level of significance, and all statistical analyses were done using the RStudio software package.

Correlation matrix analysis with the use of Pearson's correlation coefficients was done to analyze the relationship between various traits. It helped reveal both positive and negative correlations between agronomic and morphologic traits.

Multivariate statistics analysis such as PCA were also applied using the RStudio software tool to identify the principal traits responsible for the differences between accessions.

3. RESULTS AND DISCUSSION

The result of the analysis of agro-morphological traits indicated a considerable phenotypic variability existing between Moroccan rice germplasm under evaluation. Most of the quantitative characters exhibited considerable differences in their values. The characters with the greatest variability included plant height, the number of tillers per plant, panicle length, number of grains per panicle, 1000-grain weight, and grain yield. This considerable variation observed between accessions confirms the presence of high genetic diversity between studied rice germplasm, representing a useful material for future rice improvement projects. Accessions coming from different agro-ecological regions presented various phenotypes suggesting the influence of both genetic and environmental factors. The results obtained from the analysis of grain yield (RDT, t/ha) showed a great variability among different accessions, indicating that there is a great effect of genetic factors on yield (Fig. 2). Grain yield was found to vary from about 5.9 t/ha up to 12.5 t/ha. These observations confirm that there is a wide genetic diversity between the studied rice germplasm. Such variability suggests that Moroccan rice germplasm is a valuable source of desirable genetic materials for yield improvement programs (Singh & Chaudhary, 1985; Mohammadi & Prasanna, 2003).

KF190022 proved to be the best accession in terms of yield (yielded the highest yield of about 12.5 t/ha) and statistically was classified into the highest class "a", signifying that it performed much better than others in the sample. The accessions KF190114, KF200018, and KF190006 were also found to have the same statistical classification and thus had a great potential for yielding. This is consistent with Singh and Chaudhary's (1985) findings on high adaptability and efficient assimilate partitioning for grain yield of productive genotypes.

The second set of accessions that included genotypes like KF190061, KF200017, KF190064, and KF191036 produced moderate yields (approximately 9.5–10 t/ha). Such genotypes were normally classified under groups "b" and "bc". As stated by Kumar et al. (2014), moderate-yielding genotypes could serve as valuable breeding materials because they were environmentally stable and capable of contributing adaptive qualities in crossbreeding programs.

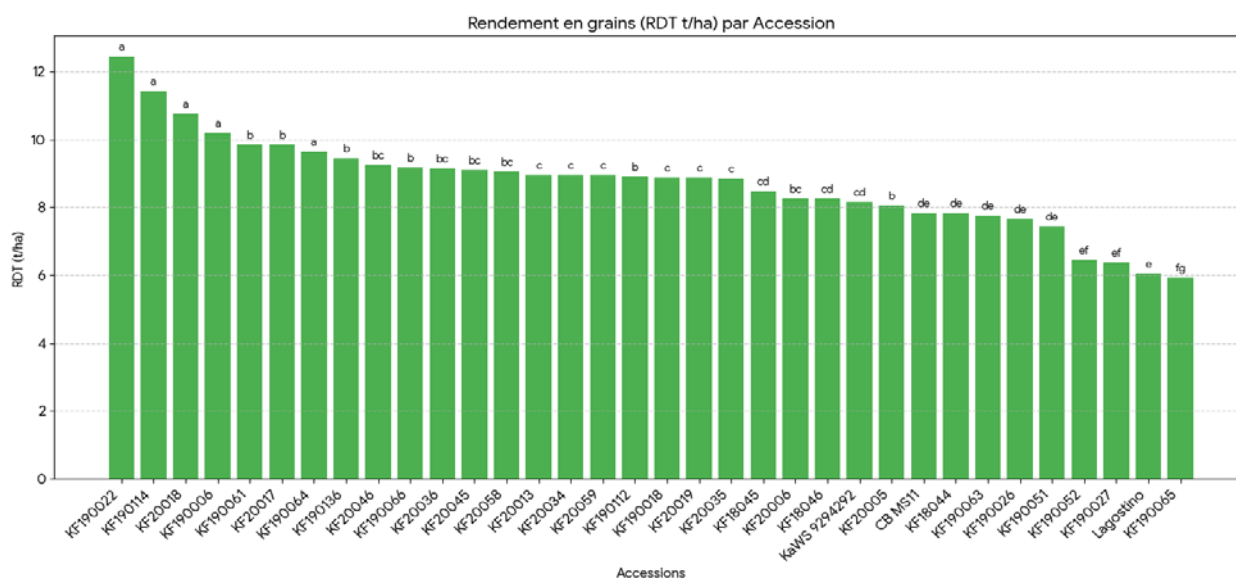


Fig. 2. Comparison of Grain Yield (t/ha) across different Accessions

Many accessions were also classified into the intermediate classes ("c", "cd", and "de"), signifying moderate levels of performance. They can still be used due to their adaptability and may be considered genetic materials for particular traits, not just for high yield alone. This level of diversity corresponds with what has been observed in a study conducted by Kirchmann & Bergström, (2001).

On the other side of the spectrum, accessions KF190065, KF190027, KF190052, and Lagostino recorded relatively low yield rates (under 7 t/ha) and formed the last statistical groups ("e", "ef", and "fg"). This suggests that their potential is not high when grown under the current conditions and may need improvement. Nevertheless, they may have some other characteristics, which are of great importance but do not relate to their productivity. IRRI (2013) supports this view by stating that traditionally cultivated genotypes with low yield rates often have desirable genes missing from elite cultivars.

In general, the findings indicate the presence of considerable genetic variation for grain yield which is a key trait for rice breeding programs. In addition, high-yielding genotypes such as KF190022 and KF190114 can be regarded as useful parents for developing new varieties of rice that fit the agro-climatic conditions in Morocco. Furthermore, the differences observed among the Duncan statistical groups ("a" to "fg") indicate that the Duncan multiple range test can be used effectively for differentiating rice genotypes according to their grain yield (Fig. 2). These results are also in line with existing literature indicating that the agro-morphological characterization of rice is a valid strategy to identify elite rice lines (Mohammadi & Prasanna, 2003).

The correlation between TGW and grain yield (GY) showed positive association between these two agronomic traits (Fig. 3). From the scatter plot presented in Figure 3, it is possible to infer that genotypes that have higher TGW values generally give higher yields of grain

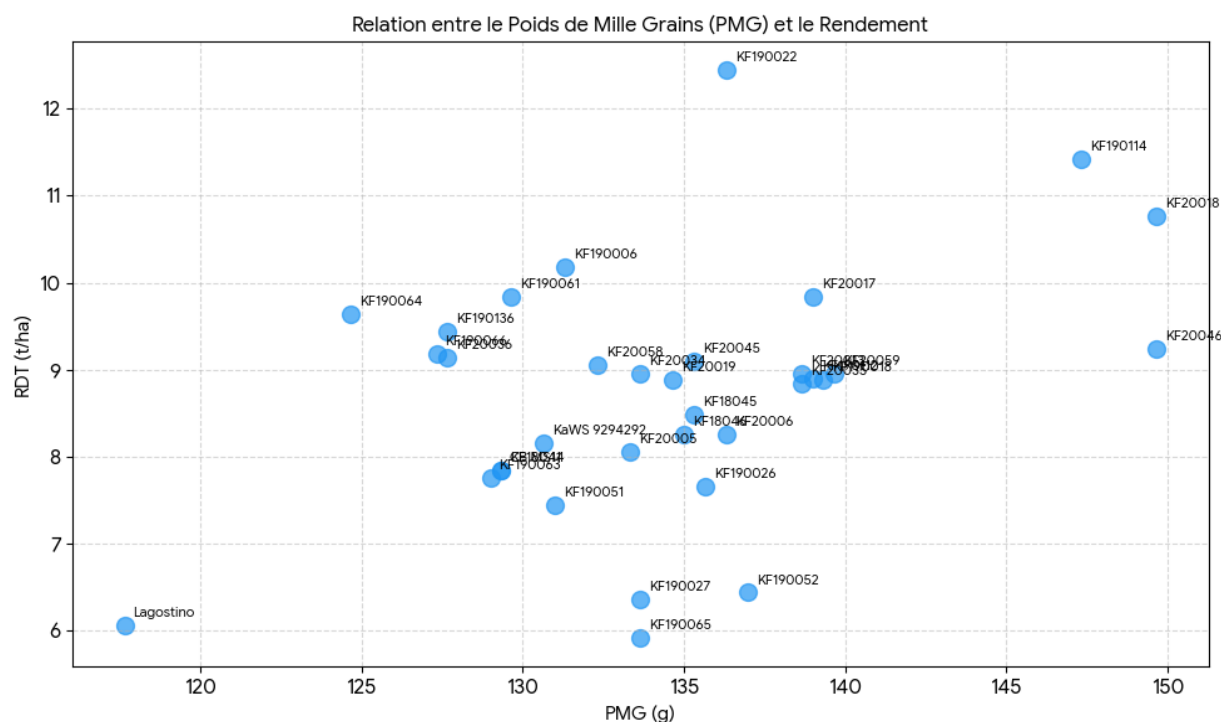


Fig. 3. *Corrélation entre le poids de mille grains et le rendement (t/ha) pour les différentes accessions.*

The TGWs of all lines ranged from 118 to 150 g, while the grain yields were within the range of 5.9 to 12.5 t/ha. The line KF190022 demonstrated the highest grain yield (≈ 12.5 t/ha), which was linked to the highest TGW value (≈ 136 g). Likewise, genotypes KF190114 and KF20018 were characterized by high agronomic performance, showing grain yields above 10 t/ha along with TGWs ranging from 148 to 150 g. On the contrary, some genotypes had relatively low yields in spite of possessing TGWs in the middle to upper range. This is evident for the genotypes KF190065, KF190027, and KF190052, which had grain yields less than 6.5 t/ha. These results imply that the grain yield cannot be attributed only to TGW but is also influenced by other agronomic factors, including panicle density and number of grains per panicle. The lowest TGW was obtained from the genotype Lagostino which coincided with a low yield (≈ 6 t/ha). Thus, there is a positive correlation between TGW and yield since a higher TGW results in a higher yield. Nonetheless, the scattered pattern of the data points shows that there exists only a weak correlation. In any case, these findings show that an increase in TGW leads to an increase in the yield of grains, although genotype performance relies on several factors (Fig. 3). These findings concur with other investigations that have revealed grain yield in rice is a polygenic character that depends significantly on its yield components, such as TGW, panicle number, and grains per panicle (Yoshida, 1981; Peng et al., 2008; Huang et al., 2013).

From the biplot analysis of the principal component analysis (PCA), it was evident that there is variability between the rice genotypes considered in terms of their agronomic characters. The first two principal components account for 31.0% and 19.2%, respectively, explaining a total percentage variance of 50.2%. This trend is comparable to what has been observed in the study of rice germplasm collections. It is indicative of high genetic diversity associated with their yield attributes (Fu et al., 2016; Sanni et al., 2012).

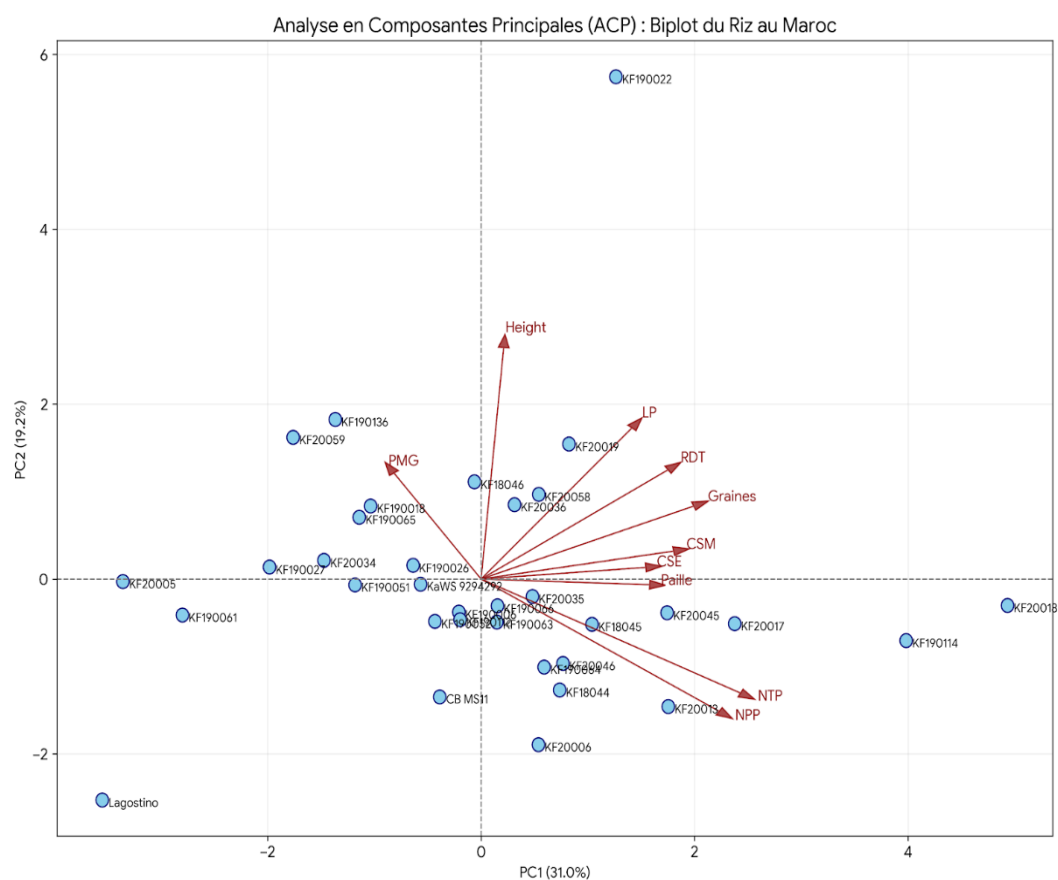


Fig. 4. PCA Biplot of Agronomic and Morphological Traits of Rice Varieties Evaluated in Morocco

From the PCA biplot, it was observed that characters such as RDT, the number of grains, LP, and CSM were positively correlated and made a significant contribution to the positive side of PC1. This suggests that genotypes falling on the right-hand side of the biplot possessed good agronomic characters and higher productivity. This is because according to previous studies conducted on the genetic relationship among yield components in rice, there existed a strong positive correlation between yield components (Omer et al., 2018; Akhundzada et al., 2020).

The genotypes KF20018 and KF190114 were distinctly positioned in the positive direction of PC1, highlighting their significant relationship with the yield characteristics and high potential for production. Similarly, the genotype KF190022 was isolated based on the highest value of PC2 in a positive direction, which is significantly linked to plant height. This implies that the morphological characters of this genotype are different from those of the other genotypes. It has been documented that phenotypic divergence among elite lines of rice contributes significantly to the success of breeding programs (Roy et al., 2019). In contrast, genotypes on the negative side of PC1, including Lagostino, KF190061, and KF20005, had a negative correlation with the primary yield-related traits. They had poor agronomic performance with limited productivity potential, typical of low-yielding rice genotypes with unfavorable traits (Sanni et al., 2012).

Additionally, the vectors used to represent the agronomic characteristics of the study can be used to analyze correlations between different traits. The traits represented by vectors showing a close direction, such as yield, grains per plant, and panicle length, had positive correlations, implying that an increase in one characteristic tends to coincide with an increase in other variables as well. On the

other hand, characteristics showing vectors oriented oppositely were negatively correlated. Such correlations are very common during multivariate studies on rice genotypes (Kumar et al., 2020; Zhang et al., 2016).

In addition, the close proximity of certain genotypes in the middle of the graph also indicates some level of phenotypic similarity among them concerning the evaluated characters. On the other hand, the location of some genotypes at a considerable distance from the center also reveals a high degree of phenotypic variability and serves as a great source of information for future breeding programs.

Generally, the present PCA analysis provided evidence of considerable genetic and agronomic diversity among the rice genotypes. It identified a number of promising genotypes that exhibited high yield potential and possessed desirable trait associations for further breeding programs under Moroccan production conditions (Roy et al., 2019). The correlation matrix analysis resulted in identifying some key associations between the studied agronomic traits of rice genotypes (Fig. 5). The heatmap provided information on both positive and negative correlations to reflect the strength of the relationship among different variables affecting grain yield performance. Such relationships among yield-associated traits have been frequently observed in past research on rice (Yoshida, 1981; Fageria et al., 2011).

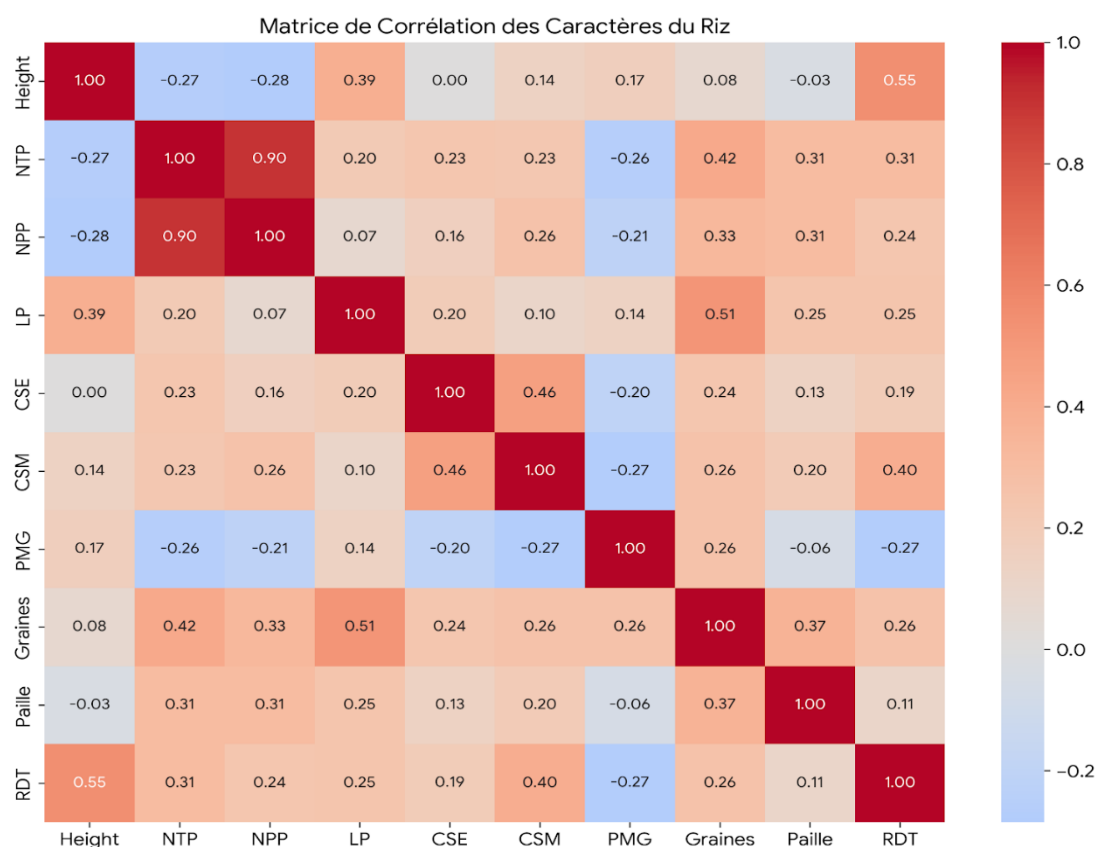


Fig. 5. Correlation Matrix of Agro-Morphological Traits in Rice Genotypes Cultivated in Morocco

Rice grain yield (RDT) was found to have a significant positive correlation with the height of the plant (Height) ($r = 0.55$). This implies that plants with higher height had better grain yields compared to plants with shorter height under the given circumstances. RDT was also significantly positively

correlated with culm dry matter (CSM) ($r = 0.40$). The results indicate the role of biomass accumulation in the development of grains. These results corroborate the literature findings that biomass production and plant vigor were significantly related to the productivity of rice grains (Peng et al., 2000).

A significant positive correlation was detected between the number of tillers per plant (NTP) and the number of productive panicles (NPP) ($r = 0.90$). The result implies that varieties with more tillers had a greater number of productive panicles, which would positively impact crop productivity. Similar correlations were reported by Calviño et al. (2004) that indicated the significance of tillering capability in panicle formation and yield potential.

Panicle Length (LP) had positive relationship with Grain Number (Graines) ($r = 0.51$). Hence, it is clear from this observation that panicle length positively affects the number of grains. Moreover, grain number has shown positive correlation with NTP ($r = 0.42$) and NPP ($r = 0.33$). Thus, both of these traits prove to be important for assessing reproductive performance. This is in line with the studies of Seyoum et al. (2012) on reproductive success, wherein panicle structure and grain number have proven to be an important parameter for improved rice cultivars.

However, Thousand Grain Weight (PMG) showed negative correlation with various yield-related parameters, which include RDT ($r = -0.27$), NTP ($r = -0.26$), and CSM ($r = -0.27$). It can be deduced that there exists a trade-off between grain size and productivity of productive structures, meaning that increasing grain number is accomplished by reducing its weight. Trade-offs between grain weight and grain number have long been established in cereals (Sadras, 2007).

The correlation coefficient between straw biomass (Paille) and yield of rice grains was low ($r = 0.11$), meaning that vegetative biomass does not serve as an adequate indicator of future grain yield. It means that it is better to use effective allocation of assimilates in reproductive organs than to increase vegetative biomass.

In general, the correlation analysis has revealed that the yield of rice grains depends on a complex interaction of many parameters in rice plants, including plant height, biomass production, structure of panicles, and grain number. This data is essential for rice breeding programs to select productive varieties with specific agronomic traits.

4. CONCLUSION

In the present investigation, great variations were found between the tested rice genotypes based on their agromorphology in Morocco. The grain yield exhibited great variation among the genotypes, suggesting promising genotypes with great agronomic potential. Positive correlation was found between some yield traits and the number of panicles and tillers.

Principal Component Analysis and correlation matrices have clearly identified the principal traits involved in the differentiation of the genotypes and in the variation within the genotypes. The findings of this study suggest that the rice genotypes studied are an important genetic material in developing rice varieties in Morocco.

AUTHOR CONTRIBUTIONS

Conceptualization, F.E. and R.Z.; methodology, F.E., M.S. and R.Z.; fieldwork, F.E., M.S. and H.M.; software, F.E.; title, F.E., M.S. and R.Z.; validation, F.E., M.S., S.-b.L., N.B. and R.Z.; laboratory work, F.E., M.S. and H.M.; formal analysis, F.E.; investigation, F.E. and M.S.; resources, M.S., S.-b.L. and R.Z.; data curation, F.E.; manuscript—original draft preparation, F.E.; manuscript—review and editing, M.S., S.-b.L., N.B. and R.Z.; visualization, F.E.; supervision, M.S. and R.Z.; project administration, R.Z.; funding acquisition, S.-b.L. and R.Z. All authors have read and agreed to the published version of the manuscript.

ACKNOWLEDGEMENT

The authors would like to express their sincere gratitude to the Biotechnologies and Plant Protection Laboratory, Faculty of Sciences, Ibn Tofail University, Kenitra, Morocco, and to the Regional Center of Agricultural Research of Kenitra (INRA), Morocco, for providing the facilities, technical assistance, and experimental support necessary for this study. The authors also gratefully acknowledge the Korea-Africa Food & Agriculture Cooperation Initiative (KAFACI), Rural Development Administration (RDA), Republic of Korea, for supplying the rice germplasm and supporting research activities related to rice improvement and agricultural development. Special thanks are extended to the Natural Resources and Sustainable Development Laboratory, Faculty of Sciences, Ibn Tofail University, Kenitra, Morocco, for their scientific collaboration and support throughout the research work.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

REFERENCES

- Acquaah, G. (2012). Principles of plant genetics and breeding (2nd ed.). Wiley-Blackwell.
- Akhundzada, K., Murthy, P. V., Reddy, V. R., & Sathyanarayana, B. N. (2020). Standardization of cytokinins (BAP and kinetin) concentrations and their combination with NAA on regeneration through seeds in lime (*Citrus aurantifolia*). *International Journal of Current Microbiology and Applied Sciences*, 9(8), 1245–1252. <https://doi.org/10.20546/ijcmas.2020.908.140>
- Elwahab, F., Sedki, M., Boukita, H., Karidioula, L. C., Brhadda, N., & Ziri, R. (2025a). Grouping rice varieties in Morocco based on key agronomic traits: A PCA and HCA approach. *Journal of Water and Land Development*, 65(IV–VI), 230–237. <https://doi.org/10.24425/jwld.2025.154267>
- Elwahab, F., Sedki, M., Sock, M., Clément, K. L., Boukita, H., Brhadda, N., & Ziri, R. (2025b). Assessment of the agronomic performance of newly introduced rice varieties in Morocco. *International Journal of Agriculture and Biology*, 33, 330–401. <https://doi.org/10.17957/IJAB/15.2291>
- FAO. (2023). *FAOSTAT statistical database*. Food and Agriculture Organization of the United Nations. <https://www.fao.org/faostat/>
- Fageria, N. K., Barbosa Filho, M. P., Moreira, A., & Guimarães, C. M. (2011). Foliar fertilization of crop plants. *Journal of Plant Nutrition*, 32(6), 1044–1064. <https://doi.org/10.1080/01904160902872826>

- Fu, P.-C., Gao, Q.-B., Zhang, F.-Q., Xing, R., Khan, G., Wang, J.-L., Liu, H.-R., & Chen, S.-L. (2016). Responses of plants to changes in the Qinghai-Tibetan Plateau and glaciations: Evidence from phylogeography of a *Sibiraea* (Rosaceae) complex. *Biochemical Systematics and Ecology*, 65, 72–82. <https://doi.org/10.1016/j.bse.2016.01.006>
- Huang, X., et al. (2013). A map of rice genome variation reveals the origin of cultivated rice. *Nature*, 490(7421), 497–501. <https://doi.org/10.1038/nature11532>
- IRRI. (2013). *Rice knowledge bank*. International Rice Research Institute. <https://www.knowledgebank.irri.org>
- Kirchmann, H., & Bergström, L. (2001). Do organic farming practices reduce nitrate leaching? *Communications in Soil Science and Plant Analysis*, 32(7–8), 997–1028. <https://doi.org/10.1081/CSS-100104101>
- Mohammadi, S. A., & Prasanna, B. M. (2003). Analysis of genetic diversity in crop plants—Salient statistical tools and considerations. *Crop Science*, 43(4), 1235–1248. <https://doi.org/10.2135/cropsci2003.1235>
- Omer, A., Mulualem, D., Classen, H., Vatanparast, H., & Whiting, S. J. (2018). A community poultry intervention to promote egg and eggshell powder consumption by young children in Halaba Special Woreda, SNNPR, Ethiopia. *Journal of Agricultural Science*, 10(5), 1–12. <https://doi.org/10.5539/jas.v10n5p1>
- Peng, S., Cassman, K. G., Virmani, S. S., Sheehy, J., & Khush, G. S. (2000). Yield potential trends of tropical rice since the release of IR8 and the challenge of increasing rice yield potential. *Crop Science*, 40(6), 1542–1549. <https://doi.org/10.2135/cropsci2000.4061542x>
- Peng, S., Khush, G. S., Virk, P., Tang, Q., & Zou, Y. (2008). Progress in ideotype breeding to increase rice yield potential. *Field Crops Research*, 108(1), 32–38. <https://doi.org/10.1016/j.fcr.2008.04.001>
- Ray, D. K., Mueller, N. D., West, P. C., & Foley, J. A. (2013). Yield trends are insufficient to double global crop production by 2050. *PLOS ONE*, 8(6), e66428. <https://doi.org/10.1371/journal.pone.0066428>
- Roy, S., et al. (2015). Agro-morphological characterization and genetic diversity in rice germplasm. *Journal of Crop Improvement*, 29(3), 1–15.
- Sadras, V. O. (2007). Evolutionary aspects of the trade-off between seed size and number in crops. *Field Crops Research*, 100(1), 15–24. <https://doi.org/10.1016/j.fcr.2006.06.008>
- Sanni, K. A., Fawole, I., Ogunbayo, S. A., & Tia, D. D. (2012). Multivariate analysis of genetic diversity in lowland rice (*Oryza sativa* L.) germplasm. *Journal of Crop Improvement*, 26(4), 464–480. <https://doi.org/10.1080/15427528.2011.653006>
- Seyoum, M., Alamerew, S., & Bantte, K. (2012). Genetic variability, heritability and genetic advance of yield and yield related traits in upland rice (*Oryza sativa* L.). *Journal of Plant Sciences*, 7(13), 1390–1397. <https://doi.org/10.3923/jps.2012.1390.1397>
- Singh, R. K., & Chaudhary, B. D. (1985). *Biometrical methods in quantitative genetic analysis*. Kalyani Publishers.

Tanksley, S. D., & McCouch, S. R. (1997). Seed banks and molecular maps: Unlocking genetic potential from the wild. *Science*, 277(5329), 1063–1066.
<https://doi.org/10.1126/science.277.5329.1063>