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Yield Stability and Adaptability of Elite Doubled Haploid (DH) Rice Genotypes in Different Locations in Central Clay Plains of the Sudan

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Abstract

Stability analysis of grain yield is an efficient tool for the selection of varieties adapted to fairly wide cultivation zone. A study aims to determine adaptability and stability for grain yield and agronomic performance of 10 elite Doubled Haploid (DH) rice genotypes generated through anther culture technique, along with local cultivar Umgar as a check under irrigated lowland conditions in three different environments in the central clay plains of the Sudan; during two cropping seasons 2019 and 2020. The trials were conducted in a randomized complete block design with three replications. Grain yield stability was studied, using the Additive Main effect and Multiplicative Interaction (AMMI) model. Bi-plots were developed following GGE bi-plot methodology over the six environments. The combined analysis of variance revealed significant to highly significant (P < 0.001) effects of genotypes, environments, and genotype by environment interaction. Moreover, the analysis of variance based on AMMI indicated significant genotypes, environments, and GE interaction with a total variation of 43.16%, 44.26% and 12.58% respectively. A biplot-AMMI analysis and yield stability index incorporating the AMMI stability value and yield in a single non-parametric index were used to identify the genotypes with the highest and stable yield. The overall mean for grain yield was 5.69 t/ha, with a range of 5.77 to 4.12 t/ha. The genotypes k150147, k150870, k150032, k150912, and k150307 out yielded the local check Umgar by 40%, 38%, 34%, 34% and 33% respectively. The most genotypes were mid-early maturities which were harvested at 107, 113, 108, 109 and 112 days after sowing, respectively. These five genotypes also showed grain yield stability along with their high mean yield performance according to the AMMI analysis and widely adaptable to the tested locations. Therefore, the five out yielding genotypes

will be considered for cultivation under irrigated system condition in central clay in the Sudan.

1. Introduction

Rice (*Oryza sativa* L.) is the primary food source for more than 3.5 billion people in the world [1]. Rice provides 20 percent of the world's dietary energy supply, while wheat and maize supplies 19 and 5 percent respectively [2]. From this perspective, rice is the most important strategic crop for food and nutrition security globally [3]. Rice Production in 2019 was 499.07 million tons. 2020 year's estimation of 496.08 million tons could represent a decrease of 2.99 million tons or 0.6% in rice production around the globe and could be due to climatic changes [4]. Rice is the most rapidly growing food commodity in sub-Saharan Africa (SSA) and is now grown and consumed in more than 40 African countries, where about 20 million farmers are engaged in its production and about 100 million people depending on it directly for their livelihood [5]. There is an urgent need of developing high yielding varieties to increase rice productivity in Africa [6].

Climate change scenarios are predicting increases in future incidences and intensities of floods, especially in the tropics and subtropics [7]. Most dry land cereals such as maize, wheat and barley are sensitive to waterlogging, which causes up to 20% yield losses in irrigated areas and even greater losses in rainfed ecosystems exceeding 40% [8]. Rice is the only crop that can be grown in many flood-prone areas and that was made possible by the most striking progress of the discovery and deployment of the (*SUB1*) locus in rice conferring tolerance to complete submergence [9]. The submergence lowland rice is traditionally grown in bounded fields that are continuously flooded from crop establishment to close to harvest. The rice types corresponding to these ecosystems are rice grown under controlled irrigated conditions, deepwater rice and rice in tidal wetlands. Rice grown in the submergence lowland ecosystem distinguishes itself from most modern rice varieties by its ability to survive in water depths of more than 50 cm for at least 1 month [10].

In the Sudan, submergence lowland rice is grown normally around river banks and their floodplains mainly in back swamps and natural levees mainly in White Nile, South Darfur, Gedarif and Blue Nile States. The nature of the flood is important for success of lowland rice, with timing and the rate of rise of water affecting survival and crop density [11]. Generally, in the White Nile State the flood rice-producing areas comes from rainfall or water over spilling from river Nile, when Jabil Awelye damp closes up. Small scale farmers with farm holdings of less than two hectares cultivate most of the rice produced in White Nile State with low yields of (0.98 - 1.2) tha^{-1}. However, rice productivity and production

at the farm level are constrained by several factors including insufficient appropriate technologies, using traditional varieties, biotic factors, poor supply of input, ineffective farmer organization, poor milling quality of local rice varieties, poor marketing arrangements, poor extension system and environment constrains including poor drainage and iron toxicity in undeveloped lowland swamps, poor maintenance of developed lowland swamp, drought, deficiencies of N and p, insufficient rain at crop establishment and poor soil management [12]. When seeds are sown directly into the soil, the seedlings and young plants can be damaged by drought conditions before floods arrive. During this stage, the plants can also suffer due to competition from weeds. Sudden flooding, where a large volume of water enters the field in a short time, can lead to a high level of seedling death. Floating rice faces additional problems due to the depth and time of the water in which it grows. Water conditions such as turbulence and temperature can adversely affect the crop [13]. Efforts to improve yield and grain quality of irrigated rice have been met with adequate success and cultivars with increased yield and growth potential were developed in lowland areas and recently, high yield and retention of floating ability have been combined in one single cultivar [10].

Rice production is affected by emerging problems of climate change and the over-utilization of resources. To obtain consistent yield across diverse environments, a variety should have adaptability and stability to fit into various growing conditions. Evaluation of grain yield under multi-environments is one of numerous approaches to verify the stability of genotypes. However, the interaction of genotypes and environment always contributes to the stability of rice varieties [13]. Currently, the AMMI model is a hybrid model involving both additive and multiplicative components of a two-way data structure which enabled a breeder to get precise predictions on genotypic potentiality and environmental influences on it. AMMI is a powerful tool for the evaluation of G × E interaction with a high degree of accuracy, while also allowing easy interpretation from single graphs [14] [15] [16]. Moreover, the bi-plot approach is also helpful in breeding programs for the selection of a suitable environment for crop evaluation, genotypic selection for a specific location and stability of crop genotypes. Grain yield is a complex trait that is influenced by a number of component characters along with the environment directly or indirectly. Hence, we could develop high yielding stable DH rice which adopted on diverse environments, to play a vital role in future food security of Sudan. The main objectives of the present study are to identify higher yielding promising DH rice genotypes having a wide to environment and environment interaction for their yield stability and adaptability across the six environments in a center clay plain of the Sudan.

2. Materials and Methods

2.1. Plant Materials

In this study, a total of 285 Double haploid lines, were produced through anther culture of the (F_2 – F_3) generations derived from interspecific crosses among

Korean Tongil-type (Semi-dwarfism, high-yielding potential with medium amylose and short grain) and Japonica (Earliness, low-medium amylose, soft and sticky endosperm) with African varieties and land-races (high biomass, disease resistance and low yield) were established at (Tissue culture laboratory *Africa-Rice St. Louis*). Of these 10 promising Double Haploid lines were selected from on station and on-farm advanced yield trials based on their high yielding potential, submergence tolerance and early maturity along with the local cultivar Umgar as a check were used. The pedigree, source, origin and ecology of the studied genotypes were presented in Table 1.

2.2. Environments

A field experiments were conducted at three agricultural research corporation stations under different environmental conditions to maximize the influence of the interaction of phenotypic values with environments. The three locations, namely Kosti, Medani and Maatug in 2019 to 2020 rainy seasons, making a total of six environments, are shown in Table 2.

2.3. Cultural Practices

The genotypes were randomly assigned to plots of 3 × 6 m size and consisted of 10 rows spaced 30 cm a part. The seeds were drilled on July 1^{sd} to 5th, at all the five environments. Sowing was done by hand drilling on a seed rate of 60 kg/ha and then thinned after seedling establishment to about 3 - 5 cm intra row spaced plants. Fertilizers were applied at the rate of 86 kg N ha^{-1} and 43 kg P_2O_5 ha^{-1} in the form of urea and triple super phosphate (TSP), respectively. P_2O_5 was applied as a basal dose during final land preparation. Urea was top dressed in two

Table 1. Rice doubled haploid (DH) genotypes, code, designation, pedigree and ecology.

SN	Code	Name	Pedigree	Crossing	Ecology
1	G1	k150912	SR34038-HB3420-44	MS11/HB4052	Irrigated/Areobic
2	G2	k150870	SR34038-HB3420-2	MS11/HB4052	Irrigated/Areobic
3	G3	k150307	SR34042-HB3475-7	HB4057/Japonica 1	Irrigated/Areobic
4	G4	k150874	SR34038-HB3420-6	MS11/HB4052	Irrigated/Areobic
5	G5	k150659	SR33703-HB3482-31	Ilpum/IR84421-4-47-B-1-3	Irrigated/Areobic
6	G6	k150451	SR34035-HB3477-62	HB4057/Ungwang	Irrigated/Areobic
7	G7	k150032	SR34034-HB3471-10	HB4052/Ungwang	Irrigated/Areobic
8	G8	k150223	SR34039-HB3366-1	HB4055/MS11	Irrigated/Areobic
9	G9	k150426	SR34035-HB3477-37	HB4057/Ungwang	Irrigated/Areobic
10	G10	k150147	SR34034-HB3471-125	HB4052/Ungwang	Irrigated/Areobic
11	G11	UMGAR	Situppatenggang	Indonesian lines	Irrigated/Areobic

Table 2. Locations, seasons, altitude, latitude and longitude of testing locations.

Code	Location	Seasons	Altitude (m)	Latitude	Longitude	RH %	Temperature	
							Max	Min
E1	Kosti	2019	410	13˚06"	32˚38"	64	35.6	24.4
E2	Kosti	2020	410	13˚06"	32˚38"	75	38.4	21.6
E3	Medani	2019	413	14˚23"	33˚32"	77	34.4	22.7
E4	Medani	2020	413	14˚23"	33˚32"	74	36.7	22.2
E5	Maatug	2019	403	14˚14"	33˚46"	75	39.1	26.2
E6	Maatug	2020	403	14˚14"	33˚46"	74	36.6	23.2

equal split doses one at 21 days after sowing and the other before panicle initiation. Irrigation at every 3 - 7 days intervals was kept under the saturated submerged condition at first four weeks and drainage was conducted whenever heavy rains resulted in pounding at this stage then whole plots were flooded gradually until reaching the peak (10 to 20 cm) at reproductive and ripening stages. In all environments, a uniform package of practices and necessary precautions were taken to maintain the crop in its best condition.

2.4. Pests and Diseases

Hand weeding was performed three times per season across the six environments following the local recommendations. Insect damage and disease incidence were not recorded during the cropping season at all environments.

2.5. Data Collection

Data on quantitative traits at appropriate growth stages of rice plants were collected according to the standard evaluation system (SES) for rice, [17]. Data on days to flowering (DF) (days from sowing time when the 50% of the plants reached flowering), days to maturity (DM) (days from sowing time when 50% of the panicles reached full maturity), number of panicle/m², 1000 grain weight (g) and grain yield (t/ha) were collected on a plot basis. At harvest, ten randomly selected plants in the middle of the row of each plot were used to collect data on plant height (cm), panicle length (cm), number of tillers/plant, number of filled grains/panicle, number of unfilled grains/panicle.

2.6. Statistical Analysis

The trials were conducted using a randomized complete block design (RCBD) with three replications.

Analysis of variance (ANOVA) for individual experiments was carried out to assess the genotypic effects and their interaction for all studied characters using the general linear model (GLM) procedure. A combined analysis on mean grain yield and its components was conducted after testing the homogeneity of va-

riances. The GE interaction of 11 rice genotypes over the six environments were assessed by the AMMI model as proposed by [18], using the statistical analysis program GenStat 12th edition [19].

The AMMI model is:

$$Y_g = \mu + \propto_g + \beta_e + \sum_{n=1}^{N} \lambda n \gamma_g \delta_n + p_g$$

where Y_g = yield of the genotype (g) in the environment(e); μ = grand mean; $\propto_g$ = genotype mean deviation; β_e = environment n = mean deviation; N = No. of IPCAs (Interaction Principal Component Axis) retained in the model; λ_n = singular value for IPCA axis n; γ_g = genotype eigenvector values for IPCA axis n; δ_n = environment eigenvector values for IPCA axis n and p_g = the residuals.

2.6.1. AMMI Stability Value (ASV)

Was calculated using sum of squares and scores of both Interaction Principal Component Axis 1 and 2 (IPCA1 and IPCA2). The genotype recording the lowest ASV was the most stable one across the tested environments and the genotype recording the highest ASV was the most unstable. In the same manner, the genotype having IPCA1 - 2 scores near zero reveals more stability, while large values indicate more responsive and less stable genotypes.

$$ASV_i = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}}\right]^2 + \left[IPCA2\ Score\right]^2}$$

where SS_{IPC1} is the interaction principal component one sum of the square, SS_{IPC2} is the interaction principal component two sum of the square, IPCA2 Score is interaction principal component 2.

2.6.2. GGE Bi-Plot Methodology

Which is a combination of AMMI bi-plot and GGE concepts [14], was used for visual interpretation of patterns of GEI. Polygon view of GGE biplot based on symmetrical scaling for determining "which-won-where" pattern of genotypes with test locations and average-environment coordination (AEC) view of bi-plot based on environment-focused scaling for interpreting mean performance of the genotypes vs. their adaptability patterns were used to understand the pattern of genotype by environment interaction.

3. Results and Discussion

3.1. Analysis of Variance for Agronomic Traits

The combined analysis of variance for yield and other agronomic characteristics is presented in Table 3. The main effect of genotypes mean squares was significant for number of panicle per m², number of filled grain per panicle and number of unfilled grain per panicle (0.05) and highly significant for other agronomic traits (0.01), indicating that genotypes differed in their genetic potential for

Table 3. Mean squares of combined analysis of variance for measured traits across the environments for the 11 genotypes.

Sources of variations	Genotypes	Environments	G x E	Error
Traits	df = 10	df = 5	df = 50	df = 130
Days to 50% flowering	233.32***	705.52**	60.12**	4.47
Days to 50% maturity	157.16***	1532.1***	71.12***	6.77
Plant height (cm)	667.9***	199.65***	79***	26.32
Panicle length (cm)	59.31***	35.71**	4.62ns	7.2
No. of tillers/plant	16.35***	17.36***	0.568*	0.78
No. of panicles/m^2	14971.87*	58015.26**	3382.4*	6485.5
No. of filled grain/panicle	695.38**	2621.9**	118.18*	106
No. of unfilled grain/panicle	117.04**	837.9**	34.22*	23.49
Thousand grain weight (g)	34.15***	29.67***	5.02***	2.18
Grain yield t/ha	6.5***	13.33**	0.379*	0.43

*, ** significant at 0.05 and at 0.01 probability level, respectively.

these traits. Main effects of season × genotype mean squares were highly significant for all studied traits, indicating varietal differential seasonal response and thus agree with the results found by [13]. Mean square for genotype × location was highly significant (p < 0.01) for grain yield and its most components indicating that some genotypes performed differently in different locations.

3.2. Grain Yield and Its Stability Performance

Mean grain yields ranged between 5.77 tha^{-1} for k150147 to 4.12 tha^{-1} for UMGAR (Table 4). k150147, k150870, k150032, k150912, and k150307 had significantly higher grain yield than the local check Umgar over the six environments. They produced a grain yield increase of 40%, 38%, 34%, 34% and 33% over Umgar, respectively (Table 5).

Grain yield stability and wide adaptation of rice varieties are becoming increasingly important in mitigating the adverse effects of climate change, which is becoming more prominent over the last years. The analysis of variance as per AMMI model revealed that there was significant contribution for variation by main effects (genotypes and environments) and interaction effects for yield (Table 6). Significant mean sum of squares due to genotypes indicate that there existed genotypic differences and significance of environment explains that environmental effects differ across different locations and test locations were diverse. In addition, G × E interaction effects signify that genotypes behave differently across different environments. Grain yield showed that 43.2% of the total sum of squares was attributable to genotypes, 44.2% to environments and 12.6% to G × E effects (Table 6). A large sum of squares for genotypes (43.2) near to environments (44.2) indicated that the genotypes were diverse, with large

Table 4. Means of grain yield (t/ha) for seven lowland rice genotypes evaluated over five environments during 2017 to 2019.

Locations	Kosti		Medani		Maatug		Mean
Genotypes	E1 (2019)	E2 (2020)	E3 (2019)	E4 (2020)	E5 (2019)	E6 (2020)	
k150912	6.42	6.33	5.51	5.13	4.93	5.27	5.51[A]
k150870	6.41	6.26	5.69	5.16	5.36	5.77	5.69[A]
k150307	6.05	6.36	5.48	5.04	5.40	5.17	5.48[A]
k150874	5.34	5.33	4.84	4.94	4.03	4.03	4.84[BC]
k150659	5.13	5.33	4.38	3.84	4.47	3.20	4.38[D]
k150451	5.58	5.44	4.99	4.38	4.37	5.47	4.99[B]
k150032	6.55	6.67	5.53	5.15	5.00	4.93	5.53[A]
k150223	5.33	5.44	4.43	3.82	4.50	3.53	4.43[D]
k150426	5.35	5.78	4.48	3.73	3.93	4.30	4.48[D]
k150147	6.91	6.58	5.77	5.16	5.17	5.83	5.77[A]
UMGAR	4.82	5.00	4.12	3.53	3.43	4.07	4.12[D]
Mean	5.81	5.86	5.02	4.53	4.59	4.68	5.019
CV%	8.97	8.88	14.4	12.53	15.77	18.16	13.16
SE±	0.14	0.122	0.13	0.14	0.148	0.199	0.073
Pro.	**	**	*	**	*	**	**

*, ** Significant 0.05 and at 0.01 level of probability, respectively.

Table 5. Mean grain yield and stability parameters for eleven DH rice genotypes over six environments.

Genotypes	Mean	Graph ID	Rank	% increased over check	IPCA1	IPCA2	ASV	Rank	GSI
k150912	5.51A	G1	4	**33.7**	−0.10965	−0.02612	**0.05**	1	**5**
k150870	5.69A	G2	2	**38.1**	−0.30649	−0.06854	**0.12**	2	**4**
k150307	5.48A	G3	5	**33.0**	0.01265	0.17423	**0.31**	3	**8**
k150874	4.84BC	G4	7	**17.5**	0.5651	−0.87018	**1.54**	11	**18**
k150659	4.38D	G5	10	6.3	0.74607	0.18588	0.33	5	15
k150451	4.99B	G6	6	21.1	−0.56105	−0.42327	0.75	9	15
k150032	5.53A	G7	3	34.2	0.09933	0.26795	0.47	7	10
k150223	4.43D	G8	9	7.5	0.41901	0.43673	0.77	10	19
k150426	4.48D	G9	8	8.7	−0.22722	0.35156	0.62	8	16
k150147	5.77A	G10	1	40.0	−0.44633	0.17898	0.32	4	5
UMGAR CK	4.12D	G11	11	0.0	−0.19141	−0.20721	0.37	6	17
Mean	5.69								

Table 6. AMMI analysis of variance for grain yield t/ha of eleven double haploid (DH) rice genotypes over five environments.

Source of variation	Degree of freedom	Sum of Squares	Mean Squares	F ratio	SS explained	
					% total	% G x E
Treatments	65	150.66	2.318***	5.43		
Genotypes	10	65.03	6.503***	15.23	43.16	
Environments	5	66.68	13.335***	27.06	44.26	
Block	12	5.91	0.493*	1.15		
GBI	50	18.95	0.379*	0.89	12.58	
IPCA 1	14	9.4	0.671**	1.57		49.61
IPCA 2	12	6.46	0.539*	1.26		34.02
Residuals	24	3.09	0.129	0.3		
Error	120	51.25	0.427	*		
Total	197	**207.82**	1.055	*		

*, **, *** indicate highly significant at 0.05, 0.01 and 0.001 respectively. GEI = Genotypes by Environments Interaction. IPCA = Interaction Principal Component Axis.

differences among environmental means causing most of the variation in grain yield, also genotypic has a strong influence on grain yield. Present results are in harmony with results of [20], who observed that mean sum of square due to genotypic main effect was high for grain yield when rice genotypes were evaluated in different growing seasons. These results suggest that variations in environment means are mainly due to location differences than seasonal variations. In the other hand our study on lines with [21], he evaluated fifteen upland rice varieties in two locations and they found that environmental mean variations were higher than genotypic mean variations for yield and hence the tested locations were diverse. The magnitude of the genotypes sum of squares was also higher than that for G × E interaction, indicating that there were substantial differences in genotypic response across environments, which is in agreement with previous reports of [22].

The multiplicative variance of the treatment sum of squares due to G × E interaction was further partitioned into two principal components IPCA1 and IPCA2. The two principal components were highly significant for grain yield. The percent contribution of each of the IPCAs to the sum of squares of the G × E interaction for grain yield is tabulated in Table 6. [23] proposed that two IPCAs for AMMI model were sufficient for a predictive model. Therefore, the interaction of the eleven rice genotypes evaluated over the six environments were best predicted by the first two principal component axes, which explained 90.33% of the total interaction effects of which the contribution of PC1 was 49.61% and that of PC2 was 34.02%. The rest of the variations were taken as residual effect. Therefore, IPCA2 vs IPCA1 biplots were generated to illustrate the genotype and environment effects simultaneously (Figure 1).
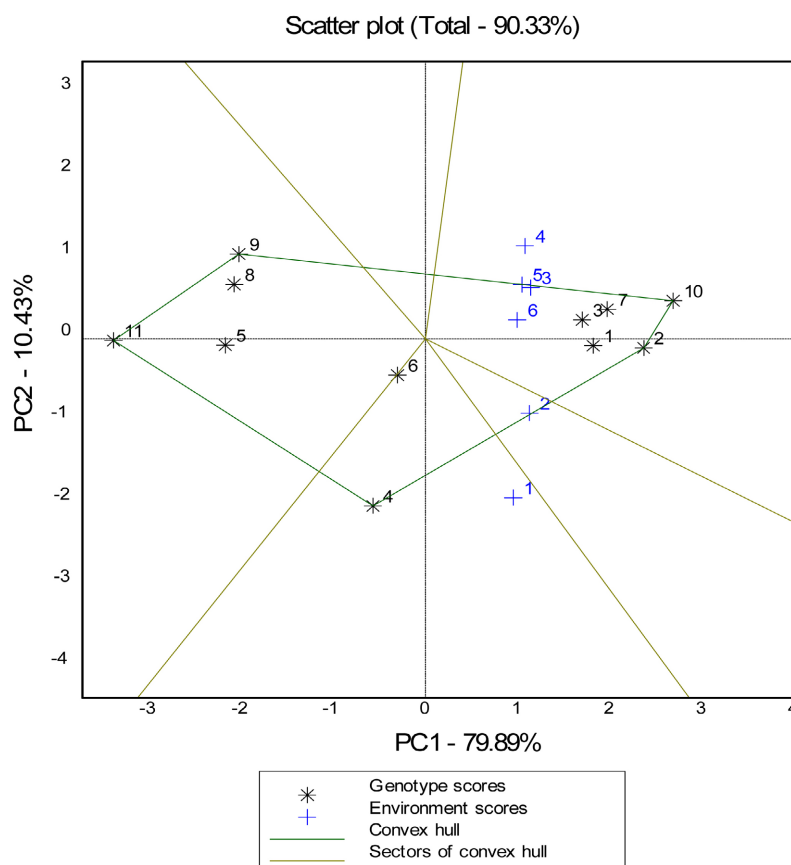
Figure 1. The which-won-where view of the GGE biplot for the ten DH lines respect to the environments for grain yield.

The PC 1 biplot indicated that the environments E3, E1, E2 and E5 were high yielding locations with high additive genotypic main effects, while the yields in the other environments were below the environmental mean. The scatter plot of the genotypes in this biplot indicated that genotype G7, G1, G2, G6 and G4 were the highest yielding genotypes. The AMMI biplot indicated that the genotypes G6, G4, G3, G7 and G5 were located close to the origin and proved highly stable, although their mean yields were on the high side and should therefore be recommended. Similar results regarding the stability of genotypes due to first two IPCAs values were recorded by [22] Vaezi *et al.*, (2017) and [24] Baraki *et al.*, (2020). The genotypes G11, G10 and G9 located far away from the origin, were unstable and expressed higher positive or negative GxE interactions. The AMMI-based stability parameter, the AMMI stability value (ASV), was calculated based on the first two PCAs to produce a balanced measurement between them and can be useful in situations where the two first IPCs explain a considerable part of the GxE interactions (Table 5).

According to ASV, genotypes k150912, k150870, k150307 and k150147 were identified as high yielding and stable for having lower ASV values, whereas genotypes k150874, k150223 and k15451G5 were identified as being more stable and low-yielding genotypes based on the genotype stability index, which takes

both the overall mean yield and ASV into consideration (Table 5). Similar results were reported by [22], who studied AMMI stability parameters to identify stably performing barley lines. According to the AMMI-based stability results, the four genotypes k150912, k150870, k150307 and k150147 are considered as prospective DH genotypes having higher grain yield, stability and wide adaptability and deserve to be released for irrigated system condition (aerobic rice) commercial production in the central clay plains of the Sudan.

3.3. Morphological Traits

Flowering and maturity: Genotypes differed significantly in flowering and maturity times, 50% flowering and maturity ranged between 76 and 91 days and 104 and 113 days after sowing, respectively, (Table 7). Generally, genotypes were harvested between 98 to 120 days after planting or 21 days after 50% flowering. Plant height: Ranged from 69.7 to 95.5 cm for KF150659 and Umgar, respectively. According to IRRI, aerobic rice plant height is classified as semi-dwarf if it is less than 110 cm. In the present study, most of the tested genotypes are classified under semi-dwarf class (Table 7). This indicated that the tested genotypes had inherent variability in stature to develop lodging resistant rice and will have higher response to nitrogen fertilization similar result was reported by [25].

Table 7. Means of all measured traits for the ten DH rice genotypes combined over six environments.

Genotypes	DF	DM	PLH	PL	NT	NP	NUF	FGP	TGW
k150912	90.2	109.0	73.0	24.0	6	366	12.6	93	24.3
k150870	94.5	113.1	76.0	23.9	5	373	15.9	92	24.0
k150307	90.8	112.3	71.5	23.3	5	336	15.3	95	23.3
k150874	91.2	109.6	75.0	20.4	4	300	21.9	83	22.8
k150659	88.6	105.2	69.7	19.4	3	291	18.4	84	21.8
k150451	87.7	104.5	73.0	19.8	4	332	17.1	84	21.5
k150032	89.5	108.1	77.2	23.2	5	358	16.7	101	22.7
k150223	89.6	107.3	70.6	20.2	4	345	18.8	88	22.4
k150426	89.7	107.2	70.0	20.3	3	356	15.3	80	22.4
k150147	87.3	106.6	74.2	23.2	5	363	13.8	92	25.0
UMGAR	79.8	104.0	91.5	22.3	4	302	17.6	88	25.9
Mean	89.0	107.9	74.7	21.8	4.4	338.4	16.7	89.1	23.3
CV%	2.37	2.41	6.86	12.30	25.0	23.7	29	11.5	6.3
SE±	0.5	0.6	0.6	0.2	0.1	6.7	1.0	0.5	0.2

(DF) = days to 50% flowering, (DF) = days to maturity, (PH) = plant height, (PL) = panicle Length, (NT) = number of tillers per plant, (NP) = number of panicles per meter square, (FG) = number of filled grains/panicle, (UG) = number of unfilled grain/panicle, (TGW) = 1000 grain weight.

Panicle length: Significantly different among genotypes at each location (Table 7). The grand mean was 21.8 cm, genotype KF150659 having the shortest (19.4 cm) and KF150912 has having the longest panicle length (24.0 cm). The number of productive tillers per plant: Significantly varied with the genotype at each locations and all combined location (Table 7). It ranged from 3 for KF150659 and KF150426 and 6 for KF150912. These numbers are relatively low compared to other findings. For instance, [26] reported number of productive tillers in the range of 4 - 7 tillers per plant. The low number of productive tillers could be due to soil type and fertility and also could be due to water stress especially waterlogging. Number of panicles/m^2: The highest number of panicles/m^2 of 373, 366 and 363 were exhibited by genotypes KF150870, KF150912 and KF150147, respectively, while, the lowest of 291 and 300 were exhibited by the genotypes KF150659 and KF150874, respectively (Table 7). For high grain yield in rice, the plant should have large number of panicles per m^2 with good grain filling and panicle size. Number of filled grains/panicle: The highest number of filled grains per panicle was recorded for KF150032 (101), KF150307 (95), KF150912 (93), KF150870 (92) and KF150147 (92). While the lowest for KF150426 (80) (Table 7). This trait offers a prime scope for the development and selection of high yielding upland rice genotypes. Number of unfilled grains per panicle: In order to increase yield, it is important to reduce spikelet sterility or increase spikelet fertility. Genotypes differed significantly in number of unfilled grains which ranged between 13 and 22 (Table 7). This could be due to drought and high temperature during flowering time. The 1000-grain weight: There is significantly different among genotypes (Table 7). Umgar recorded the heaviest 1000 grain weight (25.9 g), while KF150451 recorded the lightest (21.5 g) over the six environments. According to the standard measurement of the international Rice Research Institute (IRRI), the highest yielding varieties range between 25 to 28 g for 1000 grain weight, which indicates variability among the tested genotypes in their efficiency of partitioning, assimilates into grain yield.

4. Conclusion

In conclusion, the present study indicated that rice grain yield was significantly different under different environmental conditions. The genotypes k150147, k150870, k150032, k150912, and k150307 out-yielded the local check Umgar by 40%, 38%, 34%, 34% and 33% respectively. Analysis of variance for the AMMI model of grain yield revealed that genotypes, environments, G × E interaction and AMMI components 1 and 2 were significant Based on the static stability value. Therefore, the five out-yielding genotypes will be considered for cultivation under irrigated system conditions in central clay in Sudan.

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Conflicts of Interest

The authors declare that they have no conflict of interest.

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