

Research Article

Performance of Doubled Haploid Elite Rice (*Oryza sativa* L.) Germplasm for Grain Yield and Associated Traits in Harare, Zimbabwe

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A field experiment was conducted in 2018/2019 growing season at the Scientific Industrial Research and Development Center under irrigated conditions using the simple alpha lattice (7 * 7) design, with three replications. The objective of the study was to determine the performance of 44 elite rice lines that were selected and shared from elite doubled haploid germplasm and five cultivars were used as checks. All evaluated genotypes exhibited significant variation in the traits measured except for number of grains/panicle, total tillers/plant, and effective tillers/plant. Elite line 70462 was found to be the highest yielding, with yield advantage of 66% over the high yielding local check (Nerica 7). High values for broad sense heritability were recorded for days to 50% heading, panicle length, culm length, number of filled grains/panicle, 1000-grain weight, grain length, grain shape, and grain yield and indicated lesser influence of environment in expression of these traits, hence amenable to simple selection. Correlation analysis revealed that grain yield manifested significantly positive correlation with filled grains/panicle contributing the highest correlation ($r = 0.784$), followed by culm length ($r = 0.605$), spikelet fertility/panicle ($r = 0.677$), grain length ($r = 0.551$), 1000-grain weight ($r = 0.518$), panicle length ($r = 0.449$), and number of grains/panicle ($r = 0.328$). Based on grain yield, number of filled grains/panicle and spikelet fertility/panicle, panicle length, and earliness, lines 70462, 60143, 70383, Arica 3, Sahel 177, 6040, 70537, 60409, and 70476 had the best performance. Selection of these traits would be more effective for yield improvement in rice and these promising lines could be used in the varietal development and can be tested in multilocational trials and on-farm trials in Zimbabwe with the possibility of release and commercialization.

1. Introduction

Rice is an important cereal crop that can easily meet both food and nutritional requirements of more than 50% of the world's population [1]. It is grown mostly in Asian countries [2] but has become the fastest-growing food source in Sub-Saharan Africa [3]. Statistics show a consumption growth of

around 6% per annum in Southern Africa, while production increased by an average of 4% per annum; this can be associated with changing climate and lifestyles, increased population, and rapid urbanization [4]. Also, its easiness of preparation and versatility and the fact that it requires less energy to cook have helped raise its popularity among the population and especially the youth [5]. In Zimbabwe, rice is

the third most important cereal crop after maize and wheat. It is grown under three ecologies, namely, rainfed lowlands, rainfed uplands, and irrigated lowlands, with shares of 60%, 35%, and 5%, respectively. Until now, farmers have been growing local rice cultivars particularly Blue Bell and Mhara in cultivable vleis in the major production areas that include Mutoko and Seke, Zvimba, Murehwa, Rusape, and Chivhu [6]. However, these cultivars have shortcomings such as low yield and being susceptible to rice blast and prone to lodging. The total rice production in Zimbabwe reached 192 tonnes with a national average of 0.19 t/ha in 2020 growing season, while the national requirements stand at 300,000 tonnes [7]. Rice production needs to be increased to keep pace with the growing demand and improve food security as specified by Zimbabwe Agenda for Sustainable Socio-Economic Transformation [8].

The need for expansion of rice cultivation relies not only on cultural practices but also on their inbuilt genetic variability and breeding improvements [9]. Several advanced methods have been used by breeders to develop new varieties in a much quicker way than anticipated and at the same time to achieve a doubling speed in yield increase [10]. Similarly, several doubled haploid germplasms were produced through anther culture in South Korea, where plantlets were obtained from the second generation (F2) or third generation (F3) by applying tissue culture techniques [11, 12]. Anther culture breeding system helps to reduce the varietal development cycle by 3 to 5 years, allowing breeders to improve local varieties [13, 14]. Mohiuddin et al. [15] and Akbar et al. [11] stated that inbreeding of rice required repeated self-pollination for about seven to nine generations to get sufficiently homozygous inbred lines. In this study, germplasms that were selected and shared from elite doubled haploid germplasm of a collaborative project of KAFACI (RDA) and Africa Rice Center in Senegal were systemically tested and evaluated to generate best genetic material, exploited for selection and production of high yielding cultivars.

Breeding and adoption of rice varieties with high yield potential is one of the common objectives of the plant breeders [16, 17]. But rice grain yield is correlated with different yield contributing traits as well as environmental factors; therefore, breeding strategies of rice crop mainly depend on the nature and extent of variation of different yield attributes and their interrelationship [18–20]. It is important to have good knowledge of those traits that are significantly correlated with yield because the traits can be used in the direct selection criteria [21]. According to Alsabah et al. [22] and Anshori et al. [23], this type of selection will be more effective if heritability of those characters, which determines whether the characters can be exploited as a selection criterion or not, is known. The objective of this research study was to evaluate doubled haploid elite rice lines for grain yield and associated traits with the view of identifying traits and genotypes that can be utilized in the genetic improvement of rice or be introduced as cultivars in Zimbabwe.

2. Materials and Methods

2.1. Study Site. The field trial was conducted at the Scientific Industrial Research and Development Centre in Harare, Zimbabwe, during the 2018/19 growing season. The area is located in the northern part of Harare and lies on longitude of 30°7'E and latitude of 17.8°55'S, at an altitude of 1488.35 m above sea level (MASL). The area falls under region IIa which normally receives annual rainfall with a range of 750–1000 mm [24]. Average summer temperatures during the day and night are 26.1°C and 15.7°C, respectively. Average winter temperatures during the day and night are 22.2°C and 6.3°C, respectively. The predominant soils in this area are Fersiallitic soils. Nyamapfene [25] described the soils as 40% clay, 80% sand separate, and 90% silt and being of good agricultural value.

The soil was sampled in the topsoil layer (0–30 cm) over the experimental blocks. It was sampled in both diagonals at the four corners of the block, at the middle, between the corners, and between the middle of diagonals and corners to give 10 subsamples. The samples were analyzed separately and since they had almost the same values, these were composited and averaged [26]. The soil analysis was carried out at Food and Biomedical Research Institute (FBTI) of the Scientific Industrial Research and Development Centre and had the properties shown in Table 1. Soil pH was determined by weighing a 15 g of soil sample in a 200 ml glass jar to which 75 ml 0.1 M CaCl₂ was added. The mixture was mechanically shaken for 30 minutes and pH was determined using a digital pH meter (model: Orion 701). The optimum phosphorus available to rice occurs at a pH lower than 6.5. Phosphorus is usually available when the soil Ph is between 6.0 and 6.5. In acid soils (pH < 6.0), phosphorus is associated with aluminium and iron compounds which are slowly available to most plants [27]. When pH is above 6.5, phosphorus is associated with magnesium and calcium [28].

Total nitrogen was measured by Kjeldahl method using concentrated KCl to digest the sample [29]. Soil phosphorus was extracted using anion exchange resin [30]. In this method, anion exchange resin and soil were suspended in water at the ratio of 4 : 5 : 100 and shaken for 16 hours after which phosphorus sorbed by resin was eluted and estimated. The extraction of potassium, calcium, and magnesium was performed using NH₄Cl [31]. Each sample of the cations was deposited in a glass vessel to which 25 mL of the extraction was added and Mg, K, and Ca were estimated.

2.2. Experimental Design and Treatments. Forty doubled haploid elite rice lines were obtained from Rural Development Administration (RDA), Suwon, South Korea, under the Korea Africa Food and Agriculture Cooperative Initiative (KAFACI) and four other lines were obtained from Africa Rice Center, Senegal, which had acceptable yields, plant architecture, high grain quality, and resistance to pest and diseases and were early maturing (Table 2). Five local checks (Nerica 1, 3, and 7, Macheke land race, and Mhara 1) were used in this experiment (Table 2). These plant materials were planted during the rainy season of December 2018. The experiment was laid out in a simple alpha lattice design (7 × 7) replicated three times.

TABLE 1: Soil properties at scientific industrial research and development centre, Harare location.

Parameter	Values	High	Medium	Low	Very low
pH (CaCl ₂)	5.8				
% nitrogen	0.16	>0.25	0.12–0.25	0.05–0.12	<0.05
Resin extractable phosphorous (ppm)	17.42	>18	10–7	5–9	<5
NH ₄ Cl extractable potassium (ppm)	39	>131	91–130	61–90	<61
NH ₄ Cl extractable calcium (ppm)	1132				
NH ₄ Cl extractable magnesium (ppm)	362.4				

TABLE 2: List of plant materials used in the study.

Designation	Genotype	Source
70011	SR33705F2-76-1-1-HV-1	Korea
70033	SR34605-HB3446-3-1	Korea
70048	SR34609-HB3483-78-1	Korea
70140	SR34592-HB-1-HV-1	Korea
70148	SR34598-HB-7-HV-1	Korea
70149	SR34598-HB-8-HV-1	Korea
70186	SR34054-1-12-4-3-2-2	Korea
70274	SR34796-1-4-6-3-2-1	Korea
70314	SR34796-1-15-7-5-4-1	Korea
70322	SR34034F3-71-2-1-1-3	Korea
70340	SR34042F3-22-1-1-5-3	Korea
70363	SR34053(#5-52)-1-4-2-10-1-2	Korea
70381	SR35274-5-1-1-2	Korea
70383	SR35274-5-1-2-1	Korea
70462	SR35250-2-15-2-2	Korea
Sahel 177	Sahel 177	Africa Rice Center
70473	SR35250-2-19-3-1	Korea
70474	SR35250-2-19-3-2	Korea
70476	SR35266-2-4-1-1	Korea
70481	SR35266-2-5-2-1	Korea
70482	SR35266-2-5-3-1	Korea
70484	SR35266-2-6-1-1	Korea
70495	SR35266-2-11-1-1	Korea
70497	SR35266-2-12-1-1	Korea
70500	SR35266-2-12-4-1	Korea
70502	SR35266-2-16-1-1	Korea
70510	SR35266-2-18-3-1	Korea
Sahel 210	Sahel 210	Africa Rice Center
70528	SR34590-HB3433-1-3-1	Korea
Arica 3	Arica 3	Africa Rice Center
70537	SR34590-HB3433-6-1-1	Korea
70540	SR34590-HB3433-7-1-1	Korea
70541	SR34590-HB3433-7-2-1	Korea
70542	SR34590-HB3433-7-3-1	Korea
70552	SR35230-1-12-1-1	Korea
70553	SR35230-1-12-1-2	Korea
Sahel 134	Sahel 134	Africa Rice Center
Check 1	Nerica 7	Zimbabwe
Check 2	Nerica 3	Zimbabwe
Check 3	Mhara 1	Zimbabwe
60573	SR35255-HB3409-11	Korea
60040	Milyang23	Korea
60409	SR35239-HB3403-78	Korea
60143	SR34599-HB3474-20	Korea
60199	SR34604-HB3479-10	Korea
60323	SR35229-HB3400-47	Korea
Check 4	Macheke	Zimbabwe
Check 5	Nerica 1	Zimbabwe
60345	SR35239-HB3403-14	Africa Rice Center

2.3. Trial Establishment and Agronomic Management.

Genotypes were first established in a nursery and transplanted, one seedling per hill at 30 days after sowing. The seedlings were transplanted in beds with a net plot of 1 m² maintaining a 20 cm * 20 cm plant spacing of individual plant and all recommended cultural practices for rice were observed. A thin film of water of 1-2 cm was maintained at the time of transplanting. Afterward, the water level was increased up to 5 cm. From flowering to maturity, water was allowed to stagnate in the field up to two weeks before harvest; later on, water was removed subsequently. A pre-drilling base application of 300 kg per ha of NPK (7:14:7) fertilizer was made followed by a total of 100 kg of urea (46% N) in two applications of 35 kg at 21 days after transplanting and 65 kg at panicle initiation.

2.4. Data Collection and Analysis.

Data was collected on days to 50% heading (days from planting to the period when 50% of the rice plants were headed), panicle length (cm), culm length (cm), number of total tillers/panicle, number of effective tillers/plant, number of grains/panicle, number of filled grains/panicle, spikelet fertility/panicle (%), 1000-grain weight (g), grain yield (t/ha), grain length (cm), and grain shape. The data were recorded according to the International Rice Research Institute [32] procedures.

Analysis of variance was computed using general statistics (GenStat 14th addition) computer statistical package [33]. The correlation coefficient was calculated to determine the extent of relationship between grain yield and other important variables, using ARiS [34].

Grain shape is defined as the ratio of the brown rice length and brown rice width [35]. The scale shown in Table 3 was used to describe grain shape as suggested by IRRI [36].

Broad sense heritability (H^2) or repeatability was estimated using variance components as follows:

$$H^2 = \frac{\sigma_G^2}{\left[\sigma_G^2 + (\sigma_E^2/r)\right]}, \quad (1)$$

where σ_G^2 represents genotypic variance, σ_E^2 represents error variance, and r represents the number of replications [37].

3. Results and Discussion

3.1. Agronomic Performance of Rice.

The results of the current study revealed significant amount of variability among the tested genotypes. Genetic variability in the initial breeding materials is important in producing the desired

TABLE 3: Grain size and grain shape classification.

Grain size classification					
Grain length			Grain shape		
Scale	Size (mm)	Class	Scale	GL:GW ratio	Class
1	>7.50	Extra long	1	>3.0	Slender
3	6.60–7.50	Long	3	2.1–3.0	Long
5	5.51–6.60	Medium	5	1.1–2.0	Medium
7	<5.50	Short	9	<1.1	Short

Source: IRRI [36]. GL:GW ratio = grain length/grain width ratio.

recombinants for crop improvement. Analysis of variance revealed significant and exploitable variability due to genotypes ($p < 0.05$) for days to 50% heading, panicle length, culm length, number of filled grains/panicle, spikelet fertility/panicle, 1000-grain weight, grain yield, grain length, and grain shape but not for number of tillers/plant, number of productive tillers/plant, and number of grains/panicle (Table 4). The variation for these traits could be due to genotype composition and differed to adapted current environmental conditions. Similar results were reported by Anis et al. [16] and Khalifa [38].

Mean agronomic performance of rice for the tested genotypes is shown in Table 5. Regarding days to 50% heading, which is a good indicator of maturity, the early heading genotype was 70462 (72 days), closely followed by 70497 (74 days) and 70033 (74 days). The elite rice lines 70540 and 70340 revealed the longest days to 50% heading (117 and 108 days, respectively). Li et al. [39] reported that average heading period of 97 days was ideal for high yielding cultivars. The mean heading period of this study was 82 days, suggesting the chance of selecting early maturity genotypes which can escape terminal moisture and drought stress. Genotypes that revealed early heading date would have prolonged grain filling duration to give high yields [6]. However, in this study, lines with prolonged grain filling duration did not always give higher yields. Sheehy et al. [40] suggested that yield is influenced by not only duration in grain filling but also the efficiency in partitioning of photoassimilates to their respective sinks. Lodging is one of the major factors limiting the yield potential of rice. The results for culm length varied from 55.3 cm to 125.7 cm. Elite line 60323 produced the shortest culm length (55.3 cm), while genotype 70462 produced the longest culm length (125.7cm). It was noted that a number of genotypes in this study have short sturdy culm length. A study by Mazarire et al. [6] has shown that such genotypes could be useful in crop improvement because they do not suffer much from both root and stalk lodging and will have higher response to nitrogen application. Panicle length is one of the important parameters assessed by rice breeders in yield related studies, because longer panicles with more filled grains led to higher yields. Furthermore, studies conducted previously [41, 42] have shown that panicle length alone does not determine high grain yield as traits such as percentage of filled grains per panicle, grain size, grain shape, and longer panicles ultimately contribute to higher grain yield. The mean values for panicle length ranged from 19.1 cm to 35.7 cm. Simultaneously, rice genotypes 70462, Sahel 177, Nerica 7 (check), and 70383 recorded the highest panicle lengths of 35.7, 32, 32,

and 31 cm, respectively. On the other hand, genotypes 70528 and 70033 gave the lowest values of 19.1 and 19.8 cm for panicle length, respectively. Based on the IRRI irrigated rice panicle classification [36], the findings of the study revealed that there is enough variability for panicle length among lines for improving panicle architecture and grain yield due to high correlation of this trait to number of grains/panicle. Concerning the number of filled grains/panicle, rice genotype 70462 (204) produced the highest number, closely followed by 60409 (183) and Arica 3 (120.6). Elite line 60143 produced the highest (90.3%) spikelet fertility/panicle, followed by 70462 (90%) and Arica 3 (81.2). Generally, doubled haploid lines had high number of filled grains/panicle than local checks. These results were earlier reported by Hidayatullah et al. [12]. The mass of grains of individual plants directly determines the yield of a population [43]. Most of the lines were in the range of 20 g to 30 g for 1000-grain weight. Maximum 1000-grain weight was calculated for genotypes Sahel 177 (31 g) and Arica 3 (31 g). Adequate number of fertile grains/panicle and heavy grains are important characters, which should be exploited in the selection of high yielding genotypes [10, 44]. The genotypes significantly varied for grain yield (14.61-0 t/ha), with high yielding genotype 70462 producing 66% higher grain yield compared to high yielding local check (Nerica 7). On the basis of performance, elite line 70462 (14.61 t/ha) produced the highest grain yield, closely followed by 60143 (13.33 t/ha) and 70383 (10.80 t/ha) compared to local check Nerica 7 with 4.94 t/ha. On the other hand, genotypes Arica 3, Sahel 177, 60040, 70537, 60409, 70476, Sahel 134, and 70482 gave mean performances above the high yielding local check, with corresponding yields of 9.18, 8.38, 7.76, 7.58, 7.36, 7.11, 5.79, and 5.42 t/ha, respectively. This suggests the existence of enough variability among genotypes was highly significant. This gives a better scope for selection of promising genotypes in rice breeding program for further testing, because selection based on yield is reliable [23].

Grain size and shape are among the top rice quality properties that breeders consider when developing new varieties because preferences for these traits differ from one group to another [45]. Grain length ranged from 10.6 mm to 6.2 mm (Table 5). Arica 3 produced the highest grain length of 10.6 mm, followed by 60409 (10 cm) and 70462 (9.9 cm). According to Standard Evaluation System for rice on brown rice [36], genotypes were classified into three groups, namely, extra long (41 genotypes), long (7 genotypes), and medium (2 genotypes) grained types. Grain shape varied from 3.9 mm (Nerica 3) to 2.1 mm (70474). The classification for grain shape has led to two categories, namely, slender (31 genotypes) and long (18 genotypes) grained types out of four possible types [36]. Joachim [46] and Fitriah et al. [47] reported that long grained rice and slender grained rice are highly preferred by rice-consuming people and this is also in line with consumers in Zimbabwe; therefore the traits could be exploited to improve the grain properties of rice.

3.2. Correlation Analysis. Yield is a complex character being influenced by several quantitative traits. Some characters are highly correlated with grain yield. The association among

TABLE 4: Mean squares analysis for agronomic traits of forty-nine rice genotypes under irrigated conditions.

SOV	DF	DH (days)	PL (cm)	CL (cm)	TT	PDT	NFG	NG	TGW (g)	SF (%)	GY (Kg/ha)	(mm)	GS
Replication	2	32.33	13.359	1191.21**	4.19	7.52	894	25784**	90.84	617.3	25.83	0.7043	0.1208
Rep*block	18	159.01**	21.321**	540.86**	14.21	12.26	3750	2206	91.81**	1365.7	15.19	0.7086	0.2047
Genotypes	48	250.09**	31.328**	853.08**	17.33	14.55	5139**	3375	80.97**	1506.4**	14.55**	2.1551**	0.5079**
Residual	76	33.94	2.678	83.38	9.48	7.37	1408	1883	34.96	526.6	13.11	0.5673	0.22
Total	144	121.6	14.707	412.52	12.62	10.38	3004	2753	58.25	978.2	14.06	1.1161	0.3189

DH: days to 50% heading, PL: panicle length, CL: culm length, NFG: number of filled grains/panicle, NG: number of grains/panicle, TT: total number of tillers/plant, PDT: total number of effective tillers/plant, GL: grain length, GS: grain shape, SF: spikelet fertility, TGW: 1000-grain weight, and GY: grain yield. ***Probability level at 5%.

TABLE 5: Mean grain yield, yield components, and growth parameters of forty-nine rice genotypes under irrigated conditions.

Genotype	DH	PL	CL	TT	PDT	NFG	NG	GL	GS	TGW	SF	GY
70011	74.3	26	68.7	17.14	16.18	35.4	184.6	7.8	2.4	24	17.7	1.31
70033	74	20	66.7	8.8	8.1	32	93.9	6.2	2.3	23	32.6	1.32
70048	104	21	94.3	15.66	11.44	10	146.8	8	3.2	20	5	0.66
70140	74.1	25	59.7	11.74	10.4	26.9	143.1	7.2	2.3	21	21.8	4.38
70148	83	24	69.7	13.34	10.7	43.9	167.8	7.6	2.7	21	27.5	4.59
70149	103	23	60.7	13.06	12.12	37.9	171.9	6.9	2.3	19	20.6	2.06
70186	74.3	22	70.3	14.06	12.98	29.6	142.1	8	2.6	22	54.5	2.61
70274	82.9	21	87.5	14	12.36	75.9	153	7.4	2.2	24	54.5	2.01
70314	75.6	24	92.5	11.4	10.38	34.9	146.5	7.8	2.2	21	29.1	3.76
70322	79.1	24	88.3	9.34	8.92	62.8	128.9	8.1	2.6	22	51.4	3.03
70340	108	26	85.3	14.4	9.76	15	170.7	8.4	3.6	26	10	1.02
70363	83.1	25	72	12.46	8.94	36.9	126.3	9.3	3.3	28	32.8	2.02
70381	80.6	23	71	16.46	14.08	111	142.7	8.8	3.4	21	78.5	2.68
70383	75.4	31	120.7	13.26	13.12	117	157.2	7.7	2.5	29	74.1	10.80
70462	72	36	125.7	14.2	14	204	228.1	9.9	2.7	29	90	14.61
Sahel 177	89	32	90.3	10	9.74	123.7	199.8	9.7	2.8	31	70.2	8.38
70473	82.2	24	71	14.2	12.62	63.9	137.2	8.3	3.2	25	54.6	2.41
70474	83.3	31	108	8.6	7.28	80.4	167.4	7.2	2.1	26	54.3	2.54
70476	78.9	33	104	7.2	6.64	109.6	186.4	7.2	2.5	30	68.8	7.11
70481	91.5	23	64.3	13.6	11.44	65.5	119.8	7.7	2.3	22	50	2.08
70482	78.8	23	69	12.2	10.88	63.6	90.9	8.6	2.9	18	59.4	5.42
70484	77.5	23	64.7	10.3	9.24	20.1	119.6	7.8	2.5	22	20.7	2.89
70495	82.4	23	73.7	12.2	11.1	39.1	193	7.8	2.6	23	19.8	2.96
70497	74	22	71	9.3	8.84	52.7	168.3	7.5	2.7	23	30.5	1.98
70500	78.6	24	72	10.2	9.26	54	207.4	8	2.5	24	30.9	3.23
70502	74.6	23	72	12.14	11.48	31.2	146.3	8	2.5	22	20	1.57
70510	80.5	23	67.7	11.3	10.28	65.2	139.8	7.6	2.6	18	44	2.92
Sahel 210	85.3	25	61.7	9.7	9.34	47.1	187.9	8.6	2.9	23	25	3.35
70528	96.1	19	59.3	16.2	12.08	30.8	140.4	8.2	2.9	28	25	3.24
Arica 3	74.4	22	96	12.2	12	129	152.8	10.6	3.6	31	81.2	9.18
70537	76.2	22	75.7	11.3	10.12	107	180.5	9	3.1	23	58.9	7.58
70540	117	23	80	5	4.8	0	65.5	8.2	3.4	0	0	0
70541	83.6	23	68.7	12.9	12.44	30.4	130.1	8.1	3	20	25.9	2.96
70542	76.8	22	67.3	17.3	15.24	48.4	142.1	7.6	2.2	23	35.7	3.84
70552	84.4	23	79.3	12.8	12.72	60.3	199.8	8.1	2.4	21	46.7	3.17
70553	91.1	22	69.7	10.8	9.64	23.1	140.4	7.8	2.6	20	15.8	1.50
Sahel 134	87.2	30	85	10.78	10	62.9	165.2	8	2.3	25	33.9	5.79
Nerica 7	83.2	32	114	11.9	9.12	92.9	207.5	8.6	2.5	29	46.9	4.94
Nerica 3	87.1	23	70	16.1	13.26	94.2	166.1	9.3	3.9	22	53.8	1.62
Mhara 1	76.1	23	82	9.3	6.82	66.8	122.1	8	2.8	29	65.9	4.23
60573	77.7	23	61.3	12.54	11.46	70.9	213.1	7.6	2.7	20	35.8	3.56
60040	86.7	23	111.7	11.34	10.12	98.8	129.1	9.6	3.1	27	72.4	7.76
60409	76.1	25	110.7	8.74	8	183	218.5	10	3.4	28	86.6	7.36
60143	74.3	20	95.7	15.1	12.96	121	133.3	9.4	2.9	27	90.3	13.3
60199	95.9	24	80.3	12.6	12.42	24.2	162.1	7.7	2.3	24	14.2	2.90

TABLE 5: Continued.

Genotype	DH	PL	CL	TT	PDT	NFG	NG	GL	GS	TGW	SF	GY
60323	75.7	25	55.3	12.8	9.94	24.8	131.8	8	2.8	22	37	1.80
Macheke	74.1	23	90.3	8.2	6.2	69.1	125.9	7.6	2.3	27	54.6	2.30
Nerica 1	77.6	22	97.5	11.5	10.72	59.7	112	7.4	2.2	21	41.8	4.04
60354	76	22	88.3	8.14	6.23	25.4	125.2	7.7	2.4	21	18.3	3.48
Mean	82.6	24	81.67	12.29	10.66	61.1	153.69	8.16	2.72	22.46	41	4.05
LSD	10.69	3.00	16.75	NS	NS	72.31	NS	1.38	0.92	10.33	43.92	4.09
CV (%)	7.05	6.73	11.18	25.06	25.48	58.11	28.42	9.17	16.92	24.34	54.57	32.42

DH: days to 50% heading (days), PL: panicle length (cm), CL: culm length (cm), TT: total number of tillers/plant, PDT: total number of effective tillers/plant, NFG: number of filled grains/panicle, NG: number of grains/panicle, GL: grain length (mm), GS: grain shape, SF: spikelet fertility (%), TGW: 1000-grain weight (g), GY: grain yield (t/ha), and NS: not significant.

TABLE 6: Correlation coefficient of grain yield and other component traits.

Trait	GY	DH	PL	CL	TT	PDT	NFG	GL	GS	SF
Dh	-0.374**									
PL	0.449**	-0.075								
CL	0.605***	0.072	0.604**							
TT	-0.242	0.372**	-0.303	-0.286						
PT	-0.021	-0.153	-0.265	-0.206	0.651***					
NFG	0.754***	-0.413	0.426**	0.561***	-0.197	0.008				
NG	0.328*	-0.131	0.499***	0.262	-0.185	0.099	0.469***			
GL	0.551***	-0.025	0.182	0.329*	0.02	-0.032	0.566***			
GS	0.067	0.291	-0.121	-0.041	0.227	-0.116	0.201	0.698***		
SF	0.677***	-0.523**	0.21	0.435**	-0.132	0.081	0.884***	0.495***	0.179	
TGW	0.518***	-0.421**	0.389**	0.424**	-0.318	0.088	0.497***	0.335*	-0.023	0.484**

DH: days to 50% heading, PL: panicle length, CL: culm length, TT: total tillers/plant, PDT: productive tillers/plant, NFG: number of filled grains/panicle, NG: number of grains/panicle, GL: grain length, GS: grain shape, SF: spikelet fertility, TGW: 1000-grain weight, and GY: grain yield. Significance: * $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$.

these traits and their association with grain yield in rice is an important criterion in the selection of desirable genotypes [48]. However, if more of the characters are involved in correlation study, it becomes difficult to predict the traits which really contribute towards grain yield. Results on the correlation between 12 quantitative traits are presented in Table 6. Correlation revealed that grain yield was significantly positively correlated to filled grains/panicle (0.784), culm length (0.605), spikelet fertility/panicle (0.677), grain length (0.551), 1000-grain weight (0.518), panicle length (0.449), and number of grains/panicle (0.328) (Table 6). Similar research findings were reported by Kimani [5] who worked on correlation analysis of some important yield contributing traits in rice. This was further supported by Butta et al. [49]. Conversely grain yield was significantly negatively correlated to days to 50% heading (-0.37). Agahiet et al. [50] suggested that priority should be given to these yield contributing traits in selection for grain yield while 1000-grain weight and grain length are considered as copartners in the grain yield gain. The significantly positive association of these characters with grain yield suggests that these traits have an influence in improving grain yield; therefore direct selection towards these traits would be more effective in ensuring high grain yield. These results agree with the findings of Ogunbayo et al. [51] and Akbar et al. [11] who reported a significantly positive correlation of grain yield and number of filled grains per panicle. Kato et al. [52] also reported similar results. The negative correlation of grain yield with days to 50% heading indicates

that grain yield can be improved by selecting early maturing lines.

3.3. Broad Sense Heritability. The broad sense heritability is the relative proportion of genotypic and phenotypic variances for the characters and is used as a predictive measure in selection criteria. Heritability of a particular trait assists plant breeders in determining the total variation ascribable to genotypic effects, which are useful portion of variation [19]. In this study, the magnitude of broad sense heritability ranged from 43% to 93% (Table 7). The characters that show high heritability estimates (above 60%) were culm length (92), panicle length (93), days to 50% heading (88), number of filled grains/panicle (67), 1000-grain weight (82), grain yield (78), grain length (78), and the grain shape (64). Similar results were reported by Liangaiah et al. [53] for days to 50% heading, Arpita et al. [54] for culm length, Vanisree et al. [55] for panicle length, Tuhina-Khatun et al. [56] for the number of filled grains/panicle, Kiani et al. [57] for grain length, Abdul Fiyazet et al. [58] for 1000-grain weight, and Ammar et al. [59] for grain yield. Meanwhile, moderate heritability estimates (50–60%) were recorded for the total number of tillers/plant (52) and spikelet fertility/panicle (57). Similar results were reported by Tuhina-Khatun et al. [56] for the number of total tillers/plant, Ammar et al. [59] for spikelet fertility/panicle, and Hussain et al. [60] for L/B (grain shape). High-to-moderate heritability estimates indicate that these traits are less likely to be influenced by the environmental conditions

TABLE 7: Estimates of range, mean, standard error, and broad sense heritability.

Traits	Range	Mean	Standard error	$h^2B\%$
DH	72–117.1	82.59	0.49	88
PL	19.1–35.7	24.24	0.14	93
CL	55.3–125.7	81.67	0.77	92
TT	5–17.3	12.29	1.29	52
PDT	4.8–16.18	10.66	1.14	43
NFG	0–204.3	61.14	3.5	67
NG	65.5–228.1	153.7	3.96	43
GL	6.2–10.6	8.15	0.06	78
GS	2.1–3.9	2.71	0.04	64
TGW	0–31	22.46	0.03	82
SP	0–90.3	41	2.13	57
GY	0–14.615	4.052	220.6	78

GY: grain yield (t/ha), DH: days to 50% heading (days), PL: panicle length (cm), CL: culm length (cm), TT: number of total tillers/plant, PDT: productive tillers/plant, NFG: number of filled grains/panicle, NG: number of grains/panicle, GL: grain length (cm), GS: grain shape, SF: spikelet fertility (%), TGW: 1000-grain weight (g), and $h^2B\%$: broad sense heritability (%).

[61]. Therefore, selection based on the phenotypic expression of these characters can be effective by using simple selection methods. Low heritability estimates were recorded for the number of productive tillers/plant (43) and number of grains/panicle (43). This is in conformity with the finding of Rafii et al. [62] for the number of productive tillers/plant and that of Osekita et al. [63] for the number of grains/panicle, indicating ineffectiveness for direct selection.

4. Conclusion

From the current study, the presence of adequate genetic variability was identified among the tested genotypes. Based on the number of filled grains/panicle, earliness, spikelet fertility/panicle, panicle length, and grain yield, it is concluded that lines 70462, 60143, 70383, Arica 3, Sahel 177, 60040, 70537, 60409, and 70476 had the best performance. These promising genotypes would be more valuable materials to rice breeders in the development of high yielding climate resilient rice cultivars. Therefore, it is advisable to select and grow these high yielding genotypes in multinational yield trials and to do farmers' preferences and grain nutrient profiling before making sound recommendations for release. The results of the studied genotypes showed that number of grains/panicle, number of filled grains/panicle, panicle length, culm length, spikelet fertility/panicle, and 1000-grain weight had a significant and positive correlation with grain yield. The results of the studied genotypes also revealed that days to 50% heading, panicle length, culm length, number of filled grains/panicle, 1000-grain weight, grain length, grain shape, and grain yield had higher broad sense heritability. Selection of these traits would be more effective for yield improvement in rice.

Data Availability

Data used to support the research findings are included in this article. Any additional data can be made available upon request.

Disclosure

This research was part of the B.Sc. research of the first author, and the other authors were research supervisors and management team who also assisted with the paper preparation.

Conflicts of Interest

The authors declare that there are no conflicts of interest.

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