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Genetic and heritability estimates of landrace upland rice accessions grown in rainforest agro-ecological zone of Nigeria

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Key Message: Genetic variability among the prominent landrace upland rice accessions grown in the rainforest zone of Nigeria was unveiled. Accession by location interaction influence on rice grain yield was proven. A breeding strategy for upland rice was established in the agro-ecological zone.

Abstract: The basic understanding and knowledge of genetic variability within a plant population are highly fundamental for its improvement by the plant breeders. Research work was conducted to estimate the extent of genetic variability, heritability, and genetic advance as percent of mean of landrace upland rice accessions that are predominantly grown in the rainforest agro-ecological zone of Nigeria. Ten landrace upland rice accessions constituted the treatment and were laid in randomized complete block design with three replications in three locations between March to November 2019. Analysis of variance revealed significant differences ($P < 0.01$) among the accessions and the environments except for the number of tillers per plant while accession by environment interaction differs

significantly for all the traits though at different levels except the numbers of tillers per plant. Accession 1 recorded the highest grain yield (1.72) followed by accession 2 (1.38), accession 8 (1.36), accession 3 (1.29), and accession 4 (1.04) accordingly while accession 7 (0.75) had the least grain yield across the locations. Heritability (broad-sense) estimates ranged from (61.4393%) grain yield to (99.6028%) plant height. Moderate to high phenotypic and genotypic coefficients of variation and genetic advances as a percent of mean were recorded for all the traits. Moderate to high estimates of genotypic and phenotypic coefficients of variation, and genetic advances as a percent of mean coupled with high heritability (broad-sense) for these traits is an indication that the traits are governed by additive genetic action. Hence, improvement of these traits can be made through selection. © 2021 Department of Agricultural Sciences, AIOU

Keywords: Additive genetic action, Genetic advance, Genetic variability, Heritability, Upland rice, Non-additive genetic action

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Introduction

Rice is regarded as the most important staple cereal crop cultivated across the globe (Li et al., 2019; Cheng, et al., 2020; Long et al., 2020; Shahriar et al., 2020). Nwanze et al. (2006) estimated that almost twenty million farmers are involved in rice production across the world. Rice is at the top of the list of the consumed staple food commodity in different forms globally (Kumar et al., 2020). More than 50% of the world population solely relies on the crop for their daily calories and about a billion households across the globe depend on its cultivation, processing, distribution, and marketing for a living (Asante et al., 2019). The rice by-products are used in feeding livestock. The rate of rice production in Nigeria was lower than its consumption (Graham-Acquaah et al., 2018; Agbowuro et

al., 2020) which makes its importation becomes unavoidably necessary to meet up with the shortage in supply, thereby resulting in a price increase of the product and making it unaffordable to the poor citizens. It was reported by Chen et al. (2020) that the demand for high quality rice grains is increasing in China, this may reduce the quantity of rice grains going to some countries like Nigeria that depend on Asian Nations for rice importation.

Globally, it was estimated that upland rice encompasses about 11% of total rice grain production grown on about 14 million hectares of land across the globe (Sohrabi et al., 2012). Though the percentage that the upland rice contributed to the total rice production may seem to have a minor role in the entire world rice production, it is a major rice type cultivated in the tropics (Sohrabi et al., 2012). Comparing the grain yield in upland rice to wetland rice, upland rice yield is extremely low.

The average grain yield of wetland rice is about 3.30 tons per hectare, however, if good agronomic practices are adopted under good conditions, 10 tons per hectare can be achieved. Grain yield in upland rice ranges from 0.46 to 1.50 tons per hectare. To achieve self-reliance in rice production and meet up with Nigeria ever-increasing population demand for rice grain in the tropical region where a greater percentage of rice grown is low in yield, an urgent call for the development of high yielding upland rice varieties becomes necessary (Ogunbayo et al., 2007; Mulugeta et al., 2012) and one of the ways to achieve this is by improving the existing landrace accessions.

Comprehensive knowledge of the components of variance and their effects, genetic advance as percent of mean, and the heritability of the desired traits(s) in any crop will assist the plant breeders to determine the appropriate breeding method to adopt in a crop improvement programme (Agbowuro et al., 2019). Successful improvement of a plant population is proportional to the level of the genetic variation that is within the crop population and the level of desired traits that are heritable from one generation to another (Aladele, 2009; Tiwari et al., 2011). Broad sense heritability is a degree of the ratio that exists between the genotypic and phenotypic variance. Selection of best genotype(s) out of numerous gene populations in plants by the plant breeders could be achieved with the help of heritability (Neji et al., 2019). Moderate to high heritability estimate of the desired trait in a crop is an indication of making progress in its improvement through selection as a breeding strategy. Likewise, a low heritability estimate in any trait shows that improvement in the trait will be made through hybridization. Relying solely on heritability estimates may not give a better insight of the predictable genetic gain in the future generation, hence, Johnson et al., (1955) and Ibrahim and Hussein (2006) stated that genetic advance should be incorporated with heritability estimate in a crop improvement programme for efficient result. The objectives of this study were to assess the extent of genetic variability existing within landrace upland rice accessions grown in the rainforest agro-ecological zone of Nigeria and also to estimate heritability and genetic parameters for their agronomic traits.

Materials and Methods

Description of the research locations

The research work was conducted in three locations via (Biological Garden of Elizade University, Ilara-Mokin; Teaching and Research Farm of Ekiti State University, Ado-Ekiti, and Oke-Ako Farm Settlement, Oke-Ako-Ekiti) all at the rainforest agro-ecological zone of Nigeria between March to November 2019. The research site's climate is tropical humid with two distinct seasons; (rainy and dry seasons). The research sites have been left to fallow for two years before the commencement of the research work. A topsoil compost sample (0-15cm) of the

research sites was collected randomly with the aid of a soil auger immediately after manually slashing the vegetation before the preparation of the land. The slashed vegetation residues were hand-packed, ploughed, and harrowed mechanically. The collected soil samples from each location were properly prepared, packed, and labelled for physio-chemical analysis at the laboratory of the Department of Environmental Toxicology and Management, Elizade University, Ilara-Mokin, Nigeria.

Experimental materials and design

Ten landrace upland rice accessions used for the research work were prominent landrace upland rice accessions obtained across the rainforest agro-ecological zone in Nigeria. Table 1 shown where the ten accessions used for the research work were collected at the rainforest agro-ecological zone in Nigeria. The accessions served as the treatment and were laid in randomized complete block design in three replications in all three locations. The influence of environmental factors that are usually associated with large plot size was reduced to the minimal by planting each of the accession in a separate single-row plot. Excellent agronomic practices were adopted to raise good crops throughout the experiment.

Table 1 List of ten Landrace upland rice accessions showing their source of collections in rainforest agro-ecological zone of Nigeria

Accessions Code	Place of Collection
Acc. 1	Igbemo – Ekiti, Ekiti State
Acc. 2	Abeokuta, Ogun State
Acc. 3	Ilesha, Osun State
Acc. 4	Ogbomoso, Oyo State
Acc. 5	Ikare-Akoko, Ondo State
Acc. 6	Ido-Ekiti, Ekiti State
Acc. 7	Okuku, Osun State
Acc. 8	Ijebu Ode, Ogun State
Acc. 9	Aba-Ife (Ondo Town) Ondo State
Acc. 10	Iseyin, Oyo State

Data collection and statistical analysis

20 rice plants from each plot were randomly selected and tagged for record purposes. Data were collected on plant height (cm) at 85 days after planting, leaf area (cm²) at 85 days after planting, number of tillers per plant at 80 days after planting, panicle weight (g), panicle length (cm), days to 50% flowering, number of filled grains per panicle, the weight of 1000 grains (g) at 12% moisture, grain yield (ton/hac.) at 12% moisture. Analysis of variance was carried out using Statistical Tools for Agricultural Research software (STAR, version 2.0.1, 2014). Table 2 shows the expected means squares for the analysis of variance. Means were separated using the Duncan Multiple Range Test at P (≤ 0.05) level of significance. Genotypic and phenotypic variance components were computed according to Burton and Devance (1953). Phenotypic and genotypic coefficient of variation was calculated based on Burton (1952) while broad-sense heritability and the genetic advance were

determined using the model suggested by Johnson et al. (1955).

Table 2 Analysis of variance (ANOVA) model showing mean squares and expected means squares for each trait

Source of variation	Df	MS	Expected MS
Env.	s-1		
Rep. within Env.(s)	s(r-1)		
Cultivars (V)	g-1	MS1	$\sigma^2e + \sigma^2gs + sr \sigma^2g$
V × S	(s-1)(g-1)	MS2	$\sigma^2e + r \sigma^2gs$
Pooled error	S(r-1)(g-1)	MS3	σ^2e

δ^2e = Environmental variance; δ^2g = Genotypic variance

Results and Discussion

Soil analysis

The soil physio-chemical properties of the research sites were shown in Table 3. The soils at the three locations were slightly different from each other. The soil pH value at each location was 5.50, 5.77, and 5.30 at Oke-Ako-Ekiti, Ilara-Mokin, and Ado-Ekiti respectively. These values

indicated that the research site is slightly acidic and will still make plant nutrients readily available for plant uptake (Golla, 2019). Organic matter, carbon content, and nitrogen were presented in percentage. Soil organic matter in the soils ranges from 1.42-1.60. Olugbemi et al. (2018) stated that the roles of soil organic matter are very crucial in plant response to soil nutrient uptake especially nitrogen and phosphorus. The result revealed that the soils across the locations were sandy loam.

Table 3 Physical and chemical characteristics of the soils in the experimental sites

Properties	Locations		
	Oke-Ako-Ekiti	Ilara-Mokin	Ado-Ekiti
Sand (%)	58	60	55
Clay (%)	20	19	25
Percentage silt	22	21	20
Textural class	Sandy loam	Sandy loam	Sandy loam
pH	5.50	5.77	5.30
Carbon (%)	1.00	0.92	1.23
Organic matter (%)	1.54	1.60	1.42
Nitrogen (%)	1.10	1.20	1.16
Phosphorus (mg kg ⁻¹)	10.12	9.20	10.54
Ca ²⁺ (C mol kg ⁻¹)	1.50	1.25	1.72
Mg ²⁺ (C mol kg ⁻¹)	0.60	0.62	0.64

Analysis of variance and mean performance

The mean squares due to genotype were significant ($P < 0.05$) in all the traits studied except the number of tillers per plant (Table 4). The degree of significance among the accessions as shown in the result of this research work revealed that a high level of genetic variability exists in landrace upland rice accessions grown in the rainforest agro-ecological zone of Nigeria. This is an indication of a very rich genetic diversity that is of great importance for the crop improvement programme (Akinyosoye et al., 2017). The extent of genetic variability in crop genotypes improvement is a key in selecting superior genotypes over the existing ones. This result is in agreement with the findings of some authors that reported genetic variability among crop genotypes (Sohrabi et al., 2012; Ogunbayo et al., 2014; Sandhya et al., 2015; Edukondalu et al., 2017; Ajayi & Gbadamosi, 2020). The environment had a significant effect ($P < 0.05$) for all the traits except the number of tillers per plant. This result indicated that environments have effects on all the landrace

accessions tested. Moreover, the effects of accession by environment interaction were found to be significant among the studied traits though at different levels except for the number of tillers per plant. The level of significance detected in accession by location interaction effects in this study indicated the extent of inconsistency in the performance of accessions evaluated across the locations (Horn et al., 2018). The inconsistency in the performance of accessions in different environments is one of the limiting factors in ascertaining the effectiveness of selection as a breeding method. Odesye et al. (2018) reported similar results when cowpea was evaluated in two environments.

The combined mean values for all the traits studied were presented in Table 5. Table 6 presents the grain yield mean performance of the ten landrace upland rice accessions in the three locations. All the ten accessions studied were significantly different across the locations except accession 1. The variability across the locations could be a result of slight differences in the climatic factors prevailing in each of the locations and the little differences in the soil properties. The highest grain yield was recorded in all the ten accessions at the

Ilara-Mokin research location compared to the other two locations except in accession 4 and accession 8. The soil test revealed that the Ilara-Mokin research station soil is slightly higher in nitrogen and organic matter; this could be the reason for higher grain yield in the research station. The combined mean performance for the ten landrace upland rice accessions traits studied across the three locations was presented in Table 7. Accession 1 gave the

highest grain yield (1.72) followed by Accession 2 (1.38), Accession 8 (1.36), Accession 3 (1.29), and Accession 4 (1.04) accordingly while accession 7 (0.75) recorded the least mean performance for grain yield across the three locations. Hence, these accessions with high grain yield can be considered as the best accessions for selection.

Table 4 Mean squares for the studied traits of ten landrace upland rice accessions for the combined locations

S/N	Variables	Reps	Acc.	Env.	Acc. X Env.	Error
Degree of Freedom		2	9	2	18	40
1.	PH (cm)	49.1253	1574.8922**	82.7253**	6.2536*	6.0896
2.	LA (cm ²)	30.4484	651.1681**	42.4534**	10.8330*	0.3492
3.	NT./P	1.9003	7.5880ns	0.2293ns	0.1154ns	0.0584
4.	PW (g)	0.3430	8.6948**	0.7263**	0.0452**	0.0055
5.	PL (cm)	29.1214	30.3233**	9.5988**	0.6451*	0.2621
6.	X50%F	21.2271	616.3751**	11.2564**	27.3805**	0.8478
7.	NFG/PAN	15.1954	2786.1041**	57.9071**	41.2741**	6.4861
8.	X1000GW (g)	17.9649	156.0802**	7.8563**	8.4047**	0.3825
9.	GY/TON	0.1054	0.8381**	0.2652**	0.0323*	0.0102

*, ** Significant at 5% and 1% levels, respectively; ns = Non-significant; PH = Plant height (cm); LA = Leaf area (cm²); NT./P = Number of tiller per plant; PW = Panicle weight (g); PL = Panicle length (cm); X50%F = Days to 50% flowering; NFG/PAN = Number of filled grain per panicle; X1000GW = Weight of 1000 seeds (g) at 12 percent moisture; GY = Grain yield (ton/ha) at 12 percent moisture.

Table 5 Combined mean values of the traits studied of ten accessions of landrace upland rice for the three locations.

	Ranges	Mean±SE
PH	75.50-124.50	92.58±1.36
LA	20.10-51.40	36.07±0.88
NT/P	3.60-9.00	6.14±0.10
PW	3.00-6.70	4.50±0.10
PL	19.40-28.90	23.92±0.22
X50F	80.20-113.40	92.70±0.88
NFG/PAN	38.50-91.40	61.92±1.81
X1000W	12.40-28.40	19.21±0.45
GY/TON	0.24-2.01	1.12±0.03

PH = Plant height (cm); LA = Leaf area (cm²); NT./P = Number of tiller per plant; PW = Panicle weight (g); PL = Panicle length (cm); X50%F = Days to 50% flowering; NFG/PAN = Number of filled grain per panicle; X1000GW = Weight of 1000 seeds (g) at 12 percent moisture; GY = Grain yield (ton/ha) at 12 percent moisture.

Table 6 Mean performance of the ten landrace upland rice accessions for grain yield across the three locations

Acc. Code	Acc. Name	Ikole-Ekiti	Ado-Ekiti	Ilara-Mokin
Acc. 1	Igbemo – Ekiti, Ekiti State	1.5767a	1.7600a	1.8367a
Acc. 2	Abeokuta, Ogun State	1.2967ab	1.3400b	1.5067b
Acc. 3	Ilesha, Osun State	1.1533bc	1.3467b	1.3567bc
Acc. 4	Ogbomoso, Oyo State	0.8733cde	1.0300c	0.9700de
Acc. 5	Ikare-Akoko, Ondo State	1.0033bcd	1.0133c	1.0767cde
Acc. 6	Ido-Ekiti, Ekiti State	0.9700cde	1.0533bc	1.1100cd
Acc. 7	Okuku, Osun State	0.7000de	0.7633c	0.7900e
Acc. 8	Ijebu Ode, Ogun State	1.1767bc	1.6933a	1.2000cd
Acc. 9	Aba-Ife (Ondo) Ondo State	0.7167de	0.9833c	1.0433de
Acc.10	Iseyin, Oyo State	0.6933e	0.7933c	0.9100de

Means with the same letter are not significantly different

Table 7 Combined mean performance for the 10 landrace upland rice accessions traits studied across the three locations

Acc. Code	Acc. Name.	PH	LA	NT/P	PW	PL	X50F	NFG/PAN	X100W	GY/TON
Acc. 1	Igbemo, Ekiti State	86.16	44.76	7.91	6.24	7.91	6.24	21.91	109.63	1.72
Acc. 2	Abeokuta, Ogun State	102.92	34.88	8.76	5.00	8.76	5.00	23.81	97.11	1.38
Acc. 3	Ilesha, Osun State	88.89	48.84	9.73	5.49	9.73	5.49	27.07	94.37	1.29
Acc. 4	Ogbomoso, Oyo State	78.20	37.31	10.04	3.39	10.04	3.39	24.17	87.43	0.96
Acc. 5	Ikare-Akoko, Ondo State	120.28	27.77	10.08	4.00	10.08	4.00	25.66	95.18	1.03
Acc. 6	Ido-Ekiti, Ekiti State	89.41	28.94	11.21	4.29	11.21	4.29	24.04	98.02	1.04
Acc. 7	Okuku, Osun State	83.20	43.28	10.22	3.38	10.22	3.38	20.99	83.28	0.75
Acc. 8	Ijebu-Ode, Ogun State	92.57	41.71	9.71	5.33	9.71	5.33	23.92	94.16	1.36
Acc. 9	Aba-Ife (Ondo) Ondo State	105.16	30.26	7.87	4.33	7.87	4.33	25.33	84.48	0.91
Acc. 10	Iseyin, Oyo State	79.06	22.94	6.86	3.54	6.86	3.54	22.28	83.39	0.80

PH = Plant height (cm); LA = Leaf area (cm²); NT/P = Number of tiller per plant; PW = Panicle weight (g); PL = Panicle length (cm); X50%F = Days to 50% flowering; NFG/PAN = Number of filled grain per panicle; X1000GW = Weight of 1000 seeds (g) at 12 percent moisture; GY = Grain yield (ton/ha) at 12 percent moisture.

Phenotypic and genotypic variations

When estimating the extent of variation that occurs in yield and other agronomy traits among various accessions, it should be noted that overall variability in any trait relies heavily on the heritable and non-heritable components (Al-Tabbal & Al-Fraihat, 2012). The degree of variability existing within a plant population could be measured by the coefficients of variation while heritability and genetic advances estimates provide useful information in deciding the appropriate breeding programme to adopt. Moreover, the development of improved varieties and adopting a suitable breeding method rely on the levels of genotypic and phenotypic variations that exist among the crop varieties to be developed (Agbowuro et al., 2019). According to Burton and De Vane (1953), genotypic and phenotypic coefficients of variation were reported to be one of the key parameters used in estimating variability in crops. Whenever the genotypic coefficient value is lower than the phenotypic coefficient value for any trait, this showed that environmental factors have effects on the trait expression (Al-Tabbal & Al-Fraihat, 2012). The phenotypic coefficient of variances values was slightly higher than the genotypic coefficient of variances values in this research work. The differences recorded between the phenotypic and genotypic coefficient of variation show that a robust genetic effect exists in the studied traits (Ajayi et al., 2017). Sivasubramaniam and Menon (1973) categorized the phenotypic and genotypic coefficient variance values as low, moderate and high from 0-10%, 10-20, 20%, and above to respectively.

Phenotypic and genotypic coefficient values for the studied traits were present in Table 8. Leaf area (cm²), panicle weight, number of filled grains per panicle, grain yield, and weight of 1000 seeds had phenotypic and genotypic coefficient variance values greater than 20% which is regarded high while other studied traits phenotypic and genotypic coefficient variance values were greater than 10% but lesser than 20% which is moderate but days to 50% flowering and panicle length that are lesser than 10% (low). This is in accordance with the

findings of Sumanth et al. (2017). Moderate to the high magnitude of phenotypic and genotypic coefficient of variance is due to additive genetic actions; therefore better improvement of these traits can be achieved through selection (Ibrahim & Hussein, 2006; Krishnamurthy et al., 2013).

Heritability and genetic advance estimates

It is noted that the genotypic coefficient of variation indicates the degree of genetic variability that exists in the genotypes for different traits, but, this does not give the full opportunity to estimate the heritable variation (Al-Tabbal & Al-Fraihat, 2012). Genotypic coefficient variance coupled with heritability estimates will give more reliable information on the quantity of genetic advance expected through phenotypic selection compared to the total reliance on the genotypic coefficient of variation (Burton, 1952; Johnson et al., 1955). Heritability and genetic advances as a percent of the mean are shown in Table 8. Heritability is a biometrical tool that cannot be underestimated which helps plant breeders in deciding a suitable breeding strategy to adopt in a crop improvement programme.

The total influence of the genotypic variance on the phenotypic variance of a trait can be estimated with the aid of broad-sense heritability. Heritability could be described as the percentage of the inherited observed variation in offspring from its parents. Its understanding becomes non-negotiable when determining particular traits that would benefit from a plant breeding programme. Heritability was categorized by Robinson et al. (1955) in percentage as 0-30%, 30-60%, >60% as low, moderate, and high accordingly. Ansari et al. (2004); Acquah (2012) stated that moderate to high heritability percentage indicated a large heritability variance with the likelihood of making improvement through selection. A low heritability percentage of any trait(s) is associated with a non-additive gene while a high heritability percentage is related to an additive gene. For this research work, heritability estimates in percentage ranged from (61.4393 %) for grain yield to (99.6028 %) in plant height. Broad sense heritability values above 60% were obtained for all the traits studied in the experiment. This showed that additive genetic genes govern the inheritance of all these traits and improvement of these

traits can be made through selection. A similar result was reported by Raffi et al. (2014); Rashid et al. (2017). Heritability estimates in a broad sense were high for all the traits studied (Table 8), this showed the likelihood of improvement in these traits to be through selection.

Johnson et al. (1955) described genetic advances as a percent of the mean (GAM) at 5% selection intensity as low, moderate, and high at 0-10 %, 10-20%, 20%, and above respectively. Singh and Narayanan (1993) reported that whenever the value(s) of genetic advance is high, an additive gene is in action likewise low genetic advance

values show that the non-additive gene is in control. The genetic advances as percent of the mean (GAM) at 5% selection intensity ranged from 15.3922 for panicle length to 57.6675 for number filled grains per panicle. The genetic advances as percent of the mean for all the studied traits values were above 20% except panicle length (15.3922%) and 50% days to flowering (17.5731%). The values for panicle length and 50% days to flowering were still moderate. This is an indication that these studied traits were controlled by additive genes and improvement can be made on these traits through selection.

Table 8 Combined estimates of genetic parameters of the studied traits of ten accessions of landrace upland rice for the three locations

	σ^2_g	σ^2_{ph}	GCV (%)	PCV (%)	GA	GAM	H ² bs (%)
PH	174.2931	174.9880	14.2601	14.2885	27.1420	29.3174	99.6028
LA	71.1483	72.3520	23.3849	23.5819	17.2308	47.7705	98.3363
NT/P	0.8302	0.8431	14.8396	14.9544	1.8625	30.3338	98.4699
PAN.WE	.09610	0.9660	21.7845	21.8411	2.0141	44.7599	99.4824
PL	3.2975	3.3692	7.5915	7.6736	3.6818	15.3922	97.8718
X50F	65.4438	68.4861	8.7267	8.9273	16.2903	17.5731	95.557
NFG/PAN	304.9811	309.5671	28.2036	28.4149	35.7077	57.6675	98.5185
X1000W	16.4083	17.3422	21.0186	21.6782	8.1166	42.2523	94.6148
GY/TON	0.0572	0.0931	21.3540	27.2431	0.3861	34.4802	61.4393

PH = Plant height (cm); LA = Leaf area (cm²); NT/P = Number of tiller per plant; PW = Panicle weight (g); PL = Panicle length (cm); X50%F = Days to 50% flowering; NFG/PAN = Number of filled grain per panicle; X1000GW = Weight of 1000 seeds (g) at 12 percent moisture; GY = Grain yield (ton/ha) at 12 percent moisture; σ^2_g = Genotypic variance; σ^2_{ph} = Phenotypic variance; GCV = Genotypic coefficient of variation; PCV = Genotypic coefficient of variation; GA = Genetic advance, GAM= GA as 5 % of mean, H²bs = Heritability in broad sense.

Conclusion

The present research work estimated the degree of genetic variability, heritability, and genetic advance as percent of mean of ten landrace upland rice accessions that are predominantly grown in the rainforest agro-ecological zone of Nigeria. The results indicated that the ten accessions under study were significantly different ($P > 0.05$) from each other across the three locations as shown by combined analysis of variance. The analysis of variance shows that the environment influenced rice accessions. Accession 1 gave the highest grain yield followed by accession 2, accession 8, accession 3, and accession 4 respectively while accession 7 recorded the least grain yield across the locations. Accession 1, accession 2, accession 8, accession 3, and accession 4 can be considered as the best accessions for selection in all the locations. Moreover, a high heritability estimate along with moderate to high genetic advance as percent of the mean in all the traits studied indicated that the traits are controlled by additive gene effects. Hence, selection as a breeding strategy should be adopted for the improvement of these studied traits.

Authors Contribution: G.O.A. conceived the research idea, laid out the experiment, collected and wrote the manuscript. A.E.S. analyzed the collected data and edited the manuscript. M.A. and

O.O.O. interpreted the data analyzed and edited the manuscript and M.S.A. did the final editing.

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References

- Acquaah, G. (2012). Principles of plant genetics and breeding. 2nd ed. Wiley-Blackwell, Oxford.
- Agbowuro, G. O., Salami A. E., Awoyemi S. O., Ogunwale G. I., Kehinde-Fadare A. F., & Olajide O. O. (2019). Genetic variations, heritability and genetic advance studies among Okra accessions grown in different ecological zones in Nigeria. *International Journal of Food Science and Agriculture*, 3(1), 130-135.
- Agbowuro, G. O., Afolabi, M. S., Olamiriki, E. F., & Awoyemi, S. O. (2020). Rice blast disease (*Magnaporthe oryzae*): A menace to rice production and humanity. *International Journal of Pathogen*, 4(3), 32-39.
- Ajayi, A. T., & Gbadamosi, A. E. (2020). Genetic variability, character association and yield potentials of twenty five

- accessions of cowpea (*Vigna unguiculata* L. Walp). *Journal of Pure and Applied Agriculture*, 5(2), 1-16.
- Ajayi, A. T., Olumekun, V. O., & Gbadamosi, A. E. (2017). Estimates of genetic variation among drought tolerant traits of cowpea at seedling stage. *International Journal of Plant Research*, 7(2), 48–57.
- Akinyosoye, S. T., Adetumbi, J. A., Amusa, O. D., Agbeleye, A., Anjorin, F., Olowolafe, M. O., & Omodele, T. (2017). Bivariate analysis of the genetic variability among some accessions of African yam bean (*Sphenostylis stenocarpa* (Hochst ex A. Rich) Harms). *Acta Agriculturae Slovenica*, 109, 493–507; doi: 10.14720/aas.2017.109.3.02
- Aladele, S. E. (2009). Morphological distinctiveness and metroglyph analysis of fifty accessions of West African Okra. *Journal of Plant Breeding and Crop Science*, 1, 273-280.
- Al-Tabbal, J. A., & Al-Fraihat, A. H. (2012). Heritability studies of yield and yield associated traits in wheat genotypes. *Journal of Agricultural Science*, 4(4), 11-22.
- Ansari, B. A., Ansari, K. A., & Khund, A. (2004). Extent of heterosis and heritability in some quantitative characters of bread wheat. *Indus Journal of Plant Sciences*, 3, 189-192.
- Asante M. D., Adjah K. L., & Annan-Affu, E. (2019). Assessment of genetic diversity for grain yield and yield component traits in some genotypes of rice (*Oryza Sativa* L.). *Journal of Crop Science and Biotechnology*, 22(2), 123-130.
- Burton G. W., & De Vane E. H. (1953). Estimating heritability in tall fescue from replicated clonal material. *Agronomy Journal*, 45, 478-481.
- Burton, G.W. (1952). Quantitative inheritance of grasses. *Proc. 6th int. Grass. Cong* 1: 277-283. *Canadian Journal of Genetics and Cytology*, 28(3), 453-458.
- Chen S., Liu S., Yin M., Zheng X., Chu G., Xu C., Wang D., & Zhang X., (2020). Seasonal changes in crop growth and grain yield of different japonica rice cultivars in southeast China. *Agronomy Journal*, 112(1), 1–13.
- Cheng F., Quan X., Zhengjin X., & Wenfu C. (2020). Effect of Rice Breeding Process on Improvement of Yield and Quality in China. *Rice Science*, 27(5), 363-367.
- Edukondalu B., Ram Reddy V., Shobha Rani T., ArunaKumari Ch., & Soundharya B. (2017). Variability, heritability, correlation and path analysis for yield, yield attributes in rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences*, 6(10), 2369-2376.
- Golla A. S. (2019). Soil acidity and its management options in Ethiopia: A review. *International Journal of Scientific Research and Management*, 7(11), 1429-1440.
- Graham-Acquaah, S., Saito, K., Traore, K., Dieng, I., Alognon, A., Bah, S., Sow, A., & Manful J. T. (2018). Variations in agronomic and grain quality traits of rice grown under irrigated lowland conditions in West Africa. *Food Science and Nutrition*, 6, 970-982.
- Horn, L., Shimelis, H., Sarsu, F., Mwadzingeni, L., & Laing, M. D. (2018). Genotype-by-environment interaction for grain yield among novel cowpea (*Vigna unguiculata* L.) selections derived by gamma irradiation. *The Crop Journal*, 6, 306–313.
- Ibrahim M. M., & Hussein R. M. (2006). Variability, heritability and genetic advance in some genotypes of roselle (*Hibiscus sabdariffa* L.). *World Journal of Agricultural Science*, 2(3), 340-345.
- Johnson H. W., Robinson H. F. & Comstock R. E. (1955). Estimation of genetic and environmental variability in soybeans. *Agronomy Journal*, 47, 314–318.
- Krishnamurthy S. L., Reddy K. M., & Rao, A. M. (2013). Genetic variation, path and correlation analysis in crosses among Indian and Taiwan parents in chilli. *Vegetable Science*, 40(2), 210–213.
- Kumar A., Raman A., Yadav S., Verulkar S. B., Mandal N. P., Singh O. N., Swain P., Ram T., Badri J., Dwivedi J. L., Das S. P., Singh S. K., Singh S. P., Kumar S., Jain A., Chandrababu R., Robin S., Shashidhar H. E., Hittalmani S., Satyanarayana P., Venkateshwarlu C., Ramayya J., Naik J., Nayak S., Dar M. H., Hossain S. M, Henry A., & Piepho H. P., (2020). Genetic gain for rice yield in rainfed environments in India. *Field Crops Research*, 260, 107977. doi: 10.1016/j.fcr.2020.107977
- Li, R., Li, M., Ashraf, U., Liu, S., & Zhang, J. (2019). Exploring the relationships between yield and yield-related traits for rice varieties released in China from 1978 to 2017. *Frontiers in Plant Science*, 10, 543; doi: 10.3389/fpls.2019.00543
- Long, Z., Ning, L., Huimin, F., Linglong, Z., Ke, G., Jing, Z., Qiaoquan, L., Ling, J., & Cunxu, W. (2020). Morphological characteristics and seed physiochemical properties of two giant embryo mutants in rice. *Rice Science*, 27(2), 81-85.
- Mulugeta S., Sentayehu A., & Kassahun B. (2012). Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). *Journal of Plant Sciences*, 7(1), 13-22.
- Neji, M., Kouas, S., Gandoura, M., Aydi, S., & Abdelly, C. (2019). Genetic variability of morpho-physiological response to phosphorus deficiency in Tunisian populations of *Brachypodium hybridum*. *Plant Physiology and Biochemistry*, 143, 24–256.
- Nwanze, K. F., Mohapatra, S., Kormawa, P., Keya, S., & Bruce-Oliver, S. (2006). Rice development in sub-Saharan Africa. *Journal of the Science of Food and Agriculture*, 86, 675- 677.
- Odeseye, A. O., Amusa, N. A., Ijagbone, I. F., Aladele, S. E., & Ogunkanmi, L. A. (2018). Genotype by environment interactions of twenty accessions of cowpea [*Vigna unguiculata* (L.) Walp.] across two locations in Nigeria. *Annals of Agrarian Science*, 16, 481–489.

- Ogunbayo, S. A., Ojo, D. K., Popoola, A. R., Ariyo, O. J., Sie, M., Sanni, K. A., Nwilene, F. E., Somado, E. A., Guei, R. G., Tia, D. D., Oyelakin, O. O., & Shittu, A. (2007). Genetic comparisons of landrace rice accessions by morphological and RAPDs techniques. *Asian Journal of Plant Science*, 6(4), 653-666.
- Ogunbayo, S. A., Sie, M., Ojo, D. K., Sanni, K. A., Akinwale, M. G., Toulou, B., Shittu, A., Idehen, E. O., Popoola, A. R., Daniel, I. O., & Gregorio, G. B. (2014). Genetic variation and heritability of yield and related traits in promising rice genotypes (*Oryza sativa* L.), *Journal of Plant Breeding and Crop Science*, 6(11), 153-159.
- Olugbemi, O., Aboyeji, C. M., Olofintoye, J. T. A., & Eifediyi, E. K. (2018). Growth and ethanol yield responses of sweet sorghum (*Sorghum bicolor* (L.) Moench) varieties to nitrogen fertilizer rates. *The Journal of Agricultural Sciences*, 13(1), 1-14.
- Raffi, M. Y., Zakiah, M. Z., Asfaliza, R., Iffah, H. M. D., Latif, M. A., & Malek, M. A. (2014). Grain quality performance and heritability estimation in selected rice genotypes. *Sains Malaysiana*, 43(1), 1-7.
- Rashid, M., Nuruzzaman, M., Hassan, L., & Begum, S. N. (2017). Genetic variability analysis for various yield attributing traits in rice genotypes. *Journal of the Bangladesh Agricultural University*, 15(1), 15-19.
- Robinson, H. F., Comstock, R. E., & Harvey, P. H. (1955). Estimates of heritability and the degree of dominance in maize. *Agronomy Journal*, 41, 353-359.
- Sandhya, A., Lok, K., Rngare, N. R., & Vidyakar, V. (2015). Study of genetic variability of Indian and exotic rice germplasm in Allahabad agro-climate. *The Bioscan*, 8(4), 1345-135.
- Shahriar, S. A., Imtiaz, A. A., Hossain, M. B., Husna, A., & Eaty, N. K. (2020). Review: Rice blast disease. *Annual Research & Review in Biology*, 35(1), 50-64.
- Singh, P., & Narayanan, S. S. (1993). *Biometrical techniques in plant breeding*. Kalyani, Publishers. New Delhi, India.
- Sivasubramaniam, S., & Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agricultural Journal*, 60, 1139-1140.
- Sohrabi, M., Rafii, M. Y., Hanafi, M. M., SitiNorAkmar, A., & Latif, M. A. (2012). Genetic diversity of upland rice germplasm in malaysia based on quantitative traits. *The scientific World Journal*, 2012, 1-9. doi: 10.1100/2012/416291
- STAR, version 2.0.1 (2014). Biometrics and breeding informatics, PBGB Division, International Rice Research Institute, Los Baños, Laguna.
- Sumanth, V., Suresh, B. G., Jalandhar Ram, B., & Srujana, G. (2017). Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, 6(4), 1437-1439.
- Tiwari, R., Suresh, B. G., Mishra, V. K., Kumar, A., & Kumar, A. (2011). Genetic variability and character association in direct seeded upland rice (*Oryza sativa* L.). *Environment and Ecology*, 29(4A), 2132-2135.



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