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Original Research Article

Genetic Variability, Heritability and Genetic Advance among Lowland Rice (*Oryza sativa* L.) Genotypes at Woreta, Ethiopia

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Abstract: Rice (*Oryza sativa* L.) is a versatile crop globally, though it has relatively short history of production and research in Ethiopia. Hence, genetic improvement is of paramount importance to increase the production and productivity of the crop, which requires understanding of genetic variability in the crop. The study was conducted during 2017/2018 main cropping season at Fogera, Ethiopia, to determine the magnitude of genetic variability for yield and yield related traits in 30 lowland rice genotypes. The experiment was laid out using randomized block design with three replications. Data were collected for 17 agronomic characters and analysis of variance revealed significant differences among the genotypes for all characters. Grain yield ranged from 2766.7 to 7062 kgha^{-1} with a mean of 4736.13kgha^{-1}.Genotypes G26 (7062kg), G14 (6900kg), G8 (6583.1kg), G27 (6486.9kg), G29 (6400.6kg) and G30 (6343.1kg) were found to be high yielding. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) ranged from 8.44 and 8.53 for days to maturity to38.30 and 39.37 for number of unfilled grains panicle^{-1}. Broad sense heritability value ranged from 77.45% for number of panicles per plant to 99.16 % for plant height. Characters viz. days to heading, days to flowering, tillers plant^{-1}, panicle plant^{-1}, culm length, panicle length, plant height, flag leaf length, flag leaf width, filled grains panicle^{-1}, unfilled grains panicle $^{-1}$, panicle weight, biomass, grain yield and harvest index had high heritability and high genetic advance as percent of mean, showing presence of additive genes and selection based on these traits would be successful. For future, six rice genotypes with grain yield above 6 tons ha^{-1} have been identified and are recommended to advance further towards release as new varieties. Moreover, the future rice research should be supplemented by molecular characterization to further confirm the obtained current results.

Keywords: Genetic advance, Heritability, *Oryza sativa* L., Variability.

INTRODUCTION

Rice is one of the most significant food crops of the world's population. It belongs to the family Poaceae and genus Oryza [1, 2]. The genus *Oryza* consist 22 wild species (2n=24, 48) and two cultivated species i.e.;*O. sativa* (2n=24=AA) and *O. glaberrima* Stued (2n=24=AA) [3]. The primary center of origin of Asian rice is found in the river valleys of Yangtze and Mekon River area in China [1]. African rice is originated in the upper valley of the Niger River and it is cultivated in the western tropical Africa [4]. Cultivated rice (*O. sativa*) is predominantly self-pollinating and has lower out crossing ability. A cross-pollination rate of O. sativa is less than one percent [5]. However, the estimated out crossing rates among wild rice populations ranges from 4.3% to 55.9% [6]. Rice is a highly diverse crop species with wide geographic dispersal from sea level up to 3000 m.a.s.l. in both temperate and tropical climate [6, 7].

Rice is the second most-produced cereal in the world after wheat and assists as a chief food basis for more than half of the world's population [8, 9]. Most of the world's rice is cultivated and consumed in Asia [10]. Although Asia is the main place of rice cultivation, rice is also produced in other continents like Latin America, Europe, USA and Africa [11]. Asia accounts the largest portion (about 144.25 million tons), whereas Africa produces approximately 11.58 million tons [12]. China, India and Indonesia are the largest rice producing countries in the world, with percentage share of 32.9 %, 24.4% and 11.0 %, respectively. Worldwide the area covered by rice exceeds 163.1 million hectares with a production of 748 million tons [13]. The world's average productivity (kg/ha) has doubled during the last 25 years, largely due to the use of improved

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technologies such as high yielding varieties [14]. High average yields of rice was found in 2014 from Japan, China, Egypt, Vietnam, Indonesia and USA with productivity of 6.69, 6.75, 9.52, 5.75, 5.13 and 8.48 tons ha^{-1}, respectively [12].

Rice was introduced in to Ethiopia during the 1970s and its production was progressively increased [15]. Presence of huge potential under both irrigation and rain fed, long shelf life and acceptance of rice amongst rural population due to the possibility of using rice to a range of traditional food recipes, relatively higher productivity as compared to other main staple crops and the by-products from rice such as straws and husks that shall be fed to livestock and/or used as alternate source, are the main attracting factors for rapid increase in rice production in the country [16].

In Ethiopia, rice covered about 48,418.09 hectares of land and 136,000.726 tons of grain was produced per annum in 2016/17 with average productivity of 2.81 tons per hectare [17]. As the demand of rice production is increasing in alarming rate, the area of production almost doubled from 18000 ha in 2006 to 48,418.09 ha in 2016/2017 [18, 17]. According to CSA [17] the number of participant farmers increased from 115,832 in 2012 to 150,041 in 2017 cropping season and the demand for improved rice technologies is also increasing rapidly from time to time.

Rice is a nutritious cereal crop, used mainly for human consumption. It is the main source of energy and protein [19]. In Ethiopia, rice offers a variety of uses. It is used in the preparation of local foods (*injera*, *dabbo*, *genffo*, *kinchie*,*shorba*) and local beverages (*tella* and *katikalla*/*Areki*) either alone or mixed with other cereal grains [20].

However, the average rice productivity in Ethiopia is estimated at 2.81 t ha^{-1} [17], which is much lower than the world's average of 4.6t ha^{-1} [12]. Despite the fact that rice has been recognized by Ethiopian government as "the new millennium crop of Ethiopia" to attain food security, lack of improved varieties, lack of recommended crop management, lack of pre and postharvest management coupled with biotic and abiotic stresses limit the production and productivity of the crop in the country [21, 16, 22]. Among these problems, lack of improved varieties for different agro ecologies of the country is the most serious [23, 22]. In many countries, rice is a long established crop and cultivars have been selected that are well adapted to local conditions and the local market. It is estimated that more than120, 000 varieties of rice exist in the world [24]. But in Ethiopia which has diverse agro-ecologies, there are no more than eleven lowland rice varieties in the whole country.

Farmers of South Gondar, especially those in Libokemikem, Fogera and Dera districts, largely produce lowland rice under rain-fed condition. Due to swampy nature of the study area, crop production was limited before rice adoption. Fogera and surrounding districts are swampy areas which are ideal for lowland rice cultivation. However, one of the major constraints in the area is the absence of high yielding improved lowland rice varieties resistant to diseases and to terminal water deficit (terminal moisture stress). Hence, as rice is a potential crop in study area, increasing its productivity per unit area and its total production will enable farmers get encouraging returns and improves its role in achieving food self-sufficiency. To increase the productivity of rice in the country, research has been conducted mainly at Fogera National Rice Research and Training Center (FNRRTC). The center introduced a bulk of genotypes from International Rice Research Institute (IRRI) and African Rice Center (WARDA), which are sources of variability for future rice improvement in Ethiopia.

The success of plant breeding research depends on the availability of genetic variation. However, full information is lacking on the genetic variability of recently introduced low land rice genotypes in the study area. Genetic improvement mainly depends on the amount of genetic variability present in the population which is a universal property of all species in nature [25]. Variability in genotypes for yield and yield component traits forms the basic factor to be considered while making selection [26]. The character yield reflects the performance of all plant components and might be considered as the final result of many other traits. i.e. every plant contains an inherent physiological production capacity that operates on energy required for normal plant performance. Not all genotypes have the same inherent physiological capacity to yield [27].

Heritability along with genetic advance as percent of mean may provide a clearer picture for selection of a particular trait. Therefore, keeping in view these urgent needs, the present study has been undertaken to examine the extent of genetic variability among twenty seven rain-fed lowland rice genotypes with three check varieties for yield and yield related traits.

MATERIALS AND METHODS

Experimental Site Description

The experiment was conducted in the North-Western part of Ethiopia at Fogera National Rice Research and Training Center (FNRRTC) (Figure1) during 2017 cropping season (June-December) under rain-fed condition. The experimental site is located $11^0$58' N , 37° 41' E and elevated 1810m.a.s.l. Ten years' average meteorological data showed that the annual rainfall and mean annual minimum, maximum and average air temperatures are 1300mm, 11.5°C, 27.9°C and 18.3°C,respectively. The soil type is predominantly black *Vertisol* with pH of 5.90 [2].

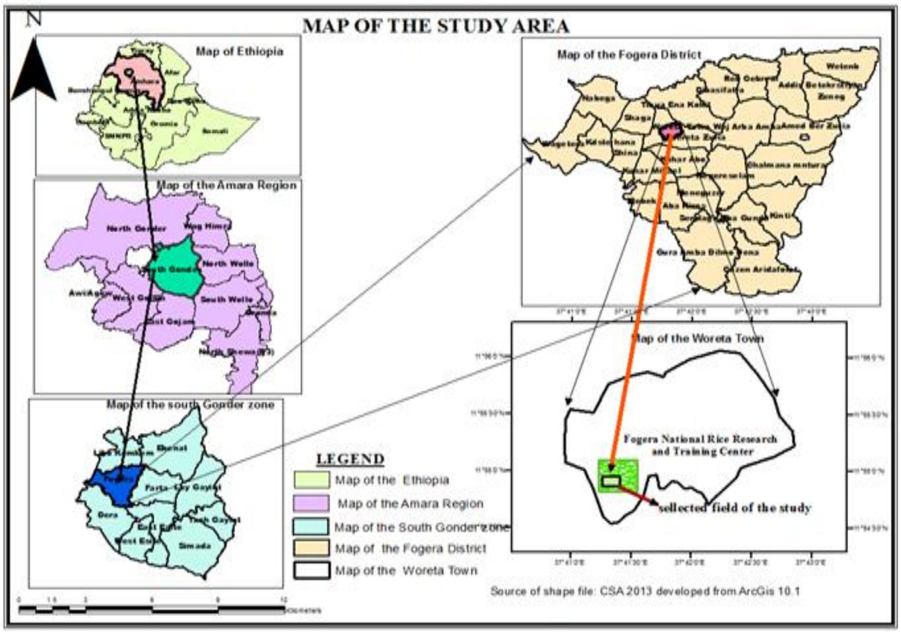

Fig-1: Diagrammatic descriptions of experimental site

Experimental Materials

Thirty rice genotypes, 27 introduce from Africa Rice and three obtained from FNRRTC, were used for this study. List of genotypes and their origin is presented in Table 1.

Experimental Design

The experiment was laid out in randomized complete block design with three replications. Each plot had six rows each 4m long, with a spacing of 25 cm between rows and 15cm between plants. The plot size was 4 x 1.5m = $6m^2$. Net plot size was 4 rows x 4m $=4m^2$. The distance between plots and replications was 0.3 m and 1 m, respectively. Three healthy and uniform sized seeds were drilled per hill on date 28 June 2017 and thinning was conducted after germination to ensure single plant per hill.

Fertilizer in the forms of N and P_2O_5 was applied at a rate of 69/23 Kg/ha, Urea and NPS, respectively. All the NPS was applied at sowing. Urea was applied as split three times, 1/3 at sowing, 1/3 at tillering and the remaining at panicle initiation stage. All other agronomic practices were applied as per recommendation.

Table-1: List of lowland rice genotypes used for this study

No.	Genotype	Code	Source	No.	Genotype	Code	Source
1	B6144F-MR-6-0-0-0	G1	Africa Rice	**16**	MERING	G16	Africa Rice
2	CHOMRONG	G2	Africa Rice	**17**	NERICA L-19	G17	Africa Rice
3	DEMIR	G3	Africa Rice	**18**	OSMANLIK-97	G18	Africa Rice
4	DIAMANTE	G4	Africa Rice	**19**	PADISASHAL	G19	Africa Rice
5	DURAGAN	G5	Africa Rice	**20**	PARTAO	G20	Africa Rice
6	(Edgt)WAB189*	G6	FNRRTC	**21**	SCRID2-1-2-4	G21	Africa Rice
7	FARO-35	G7	Africa Rice	**22**	SILEWAH	G22	Africa Rice
8	FOFIFA160	G8	Africa Rice	**23**	SIM2SUMADEL	G23	Africa Rice
9	HIBIR*	G9	FNRRTC	**24**	4181-SOAMOVA	G24	Africa Rice
10	HS379	G10	Africa Rice	**25**	WITA 4	G25	Africa Rice
11	IR64	G11	Africa Rice	**26**	X-243	G26	Africa Rice
12	KIRKPINAR	G12	Africa Rice	**27**	X-265	G27	Africa Rice
13	MACHAPACHURI	G13	Africa Rice	**28**	X-JIGNA	G28	FNRRTC
14	MAKALOIKA34	G14	Africa Rice	**29**	YUN-KENG	G29	Africa Rice
15	4182—MANJAOVE	G15	Africa Rice	**30**	ZONG-ENG	G30	Africa Rice

*=released varieties at FNRRTC.

DATA COLLECTION

Based on the standard evaluation system developed by International Rice Research Institute [28], seventeen quantitative traits were recorded on plot and plant basis with close follow up of growth stages. These data were recorded from pre-tagged ten randomly sampled plants in the four central harvestable rows of each experimental unit (plot). However, yield per plot and phenological traits were taken on plot basis. Details of all recorded parameters are described below.

Measurements on plot basis

Days to heading (DH): is number of days from seedling emergence up to the date when the tips of the panicle first emerged from the main shoots on 50 % of the plants in each plot.

Days to 50% flowering (DF): is number of days from seedling emergence up to the date of appearance of flowers at the panicle on about 50% of the plants in each plot.

Days to maturity (DM): Number of days from seedling emergence to the date when 85% of the stems, leaves, and floral bracts in a plot are changed to light yellow color.

Thousand-grain weight (TGW) (g): Measured by randomly taking 1000 grains from harvested grain and weighed in grams by using a sensitive balance; finally adjusted at 14% moisture content

Biomass yield (BY) (kg): The total above ground biomass yield produced from the four central harvestable rows of each plot was measured after harvest and converted it to kilograms per hectare.

Grain yield (GY) (kg): Grain yield was measured from the net middle plot area of $4m^2$ by using an electronic sensitive balance and converted to kilograms per hectare at 14% moisture content.

Harvest index (HI) (%): The ratio of grain yield per hectare adjusted to 14% moisture to sun-dried biological yield per hectare was calculated and expressed in percent.

Measurements on plant basis

Number of tillers per plant (TP): Number of both ear bearing and non-bearing tillers per plant were counted at the time of harvest.

Number of panicles per plant (PP): It was recorded by actual counts of the total number of tillers bearing panicles per plant at harvest.

Culm Length (CL) (cm): It was taken from ground level to the base of panicle neck node of main stem at maturity stage.

Panicle length (PL) (cm): Actual measurement in centimeters was taken from panicle base to tip of panicle of the main stem.

Plant height (PH) (cm): It was taken at maturity stage from ground level to the tip of the longest part.

Flag-leaf length (FL) (cm): It was measured from the point of attachment of the ligule to the tip of the blade on the main stem after anthesis.

Flag-leaf width (FW) (cm): Width of flag leaf was measured on the main stem after anthesis. Number of filled grains per Panicle (FGPP): The number of filled grains per panicle was recorded from the central panicles of sampled plants at harvest.

Number of unfilled grains per panicle (UGPP): Number of unfilled grains was measured by counting only unfilled grains from the central panicles of sampled plants at harvest. Panicle weight (PW) (g): Panicle weight of main stem was measured after it lost its moisture content by sun drying.

STATISTICAL ANALYSIS

Analysis of variance (ANOVA)

The data was subjected to analysis of variance as the procedure for randomized complete block design as stated by Gomez and Gomez [29] using proc GLM of SAS computer Software program (SAS, [24], Version 9.0) to assess the significance of the difference between the genotypes (the F-test). For traits where significant difference among the genotypes has been obtained, mean comparisons was carried out using least significance difference test (LSD) at $p=0.05$.

The General Linear Model (GLM) equation of RCBD ANOVA is as follows:

$yij = \mu + g_i + r_j + \mathcal{E}_{ij}$

Where, Yij = the observation of trait Y in the i^{th} genotype and the j^{th} replication, μ = the grand mean of trait Y, rj = the random effect of the j^{th} replication, gi = the fixed effect of the i^{th} genotype, εij = experimental error effect

Table-2: Analysis of variance for RCBD design

Source of variation	DF	MS	EMS
Replication	**(r-1)**	**MSr**	$\sigma^2 e + g\sigma^2 r$
Genotypes	**(g-1)**	**MSg**	$\sigma^2 e + r\sigma^2 g$
Error	**(r-1)(g-1)**	**MSe**	$\sigma^2 e$
Total	**gr-1**		

r= number of replications, g= number of genotypes DF= degree of freedom, MS= mean square, MSr= mean square of replications, MSg= mean square of genotypes, MSe= mean square of error, $\sigma^2 g$ = genotypic variance, σ^2 e = error variance,^{2}e = MSe

Estimation of phenotypic and genotypic variances

The variability present in the population was examined by the range, standard error, phenotypic and genotypic variances and coefficients of variations (GCV and PCV). The phenotypic and genotypic variances of each trait were determined from the analysis of variance, as per the methods suggested by Burton and Devane [30].

Phenotypic variance $(\sigma^2 p) = \sigma^2 g + \sigma^2 e/r$

Genotypic variance $(\sigma^2\ g) = \frac{(Msg - Mse)}{r}$

Where, $\sigma^2 p$ = phenotypic variance**,** σ^2 g = genotypic variance, $\sigma^2 e$ = error variance, Msg = mean square of genotypes**,** Mse = mean square of error**,** r = Number of replications.

Phenotypic and genotypic coefficients of variation were calculated as follows:

Phenotypic coefficient of variation, PCV $= \frac{\sqrt{\sigma^2 p}}{\bar{x}} * 100$

Genotypic coefficient of variation, GCV $= \frac{\sqrt{\sigma^2 g}}{\bar{x}} * 100$

Where: $\sigma^2 p$ = Phenotypic variation; $\sigma^2 g$= Genotypic variation and $\bar{x}$= Grand mean of the trait under consideration.

According to Sivasubramanian and Madhavamenon [31] PCV and GCV values were categorized as low (0–10%), moderate (10–20%) and high (20% and above).

Estimation of heritability and expected genetic advance

Heritability in broad sense (H^2b)

Heritability in broad sense estimates the ratio of genotypic to the phenotypic variance [32]. Heritability in percent was computed for each character based on the formula suggested by Johnson *et al.* [33] and Hanson *et al.* [34].

$H^2 = \frac{\sigma_g^2}{\sigma_p^2} * 100$ Where, H² =heritability in broad sense,$\sigma^2 p$ = phenotypic variance, $\sigma^2 g$ = genotypic variance

According to Johnson *et al.* [33], heritability estimates were classified as low (below 30%), moderate (30-60%) and high (above 60%).

Expected genetic advance

Genetic advance (GA) in the original units and in percent of the mean (GAM), assuming selection of superior 5% of the genotypes were estimated in accordance with the methods illustrated by Johnson *et al.* [33] as:

GA = (K) (σp) (H^2b), where, GA = expected genetic advance, σp = the phenotypic standard deviation, H^2b = broad sense heritability, K = Selection differential (where K = 2.06 at 5% selection intensity).

Genetic advance as percent of mean (GAM) was computed to compare the extent of predicted genetic advance of different traits under selection, using the formula:

GAM $= \frac{GA}{\bar{x}}$ *100 Where, GAM = Genetic advance as percent of mean, $\bar{x}$ = population mean

The GA as percent of mean is categorized as suggested by Johnson *et al.* [33] as follows.0 - 10% = Low, 10 – 20 = Moderate and > 20 = High

RESULTS AND DISCUSSION

Analysis of Variance

The analysis of variance showed highly significant differences among genotypes for all evaluated traits (*P<0.05* and *0.01*) (Table3).

Table-3: Mean squares for 17 traits of 30 lowland rice genotypes during 2017at Fogera

		Mea Square		
Trait	**Replication(df=2)**	**Genotype(df=29)**	**Error(df=58)**	**CV (%)**
DH	4.43	431.32**	4.38	2.19
DF	6.01	432.86**	4.67	2.16
DM	12.31	408.54**	8.27	2.10
TP	4.80	14.45**	2.59	16.81
PP	8.61	12.25**	2.76	18.24
CL	1.47	782.93**	6.61	3.69
PL	3.68	36.50**	1.84	6.59
PH	3.49	1057.74**	8.88	3.30
FL	5.08	125.03**	3.90	7.52
FW	0.01	0.06**	0.00	5.22
FGPP	4.52	967.30**	65.11	7.44
UGPP	5.55	49.07**	2.62	15.76
PW	0.13	2.97**	0.13	13.70
TGW	0.95	26.07**	3.75	6.79
BY	3071253.40	17631908.70**	1596423.70	12.08
HI	23.66	299.32**	25.36	10.92
GY	50031.40	5285966.40**	228372.20	10.09

* and **= significance levels of p-value at 5% and 1%, respectively , CV= coefficient of variability, LSD= least significance difference ,DH= days to heading, DF= days to flowering, DM= days to maturity, TP= number of tillers per plant, PP= number of panicles per plant, CL=culm length, PL= panicle length, PH= plant height, FL= flag- leaf length, FW= flag- leaf width , FGPP= filled grain per panicle, UGPP= unfilled grain per panicle , PW= panicle weight, TGW=1000 grain weight, BY=Biomass yield per ha in Kg, HI=harvest index, GY=paddy grain yield per ha in Kg

This significance difference indicates the presence of acceptable amount of variability among rice genotypes in growth parameters, in grain yield and yield components. This provides a great opportunity for breeders to improve desired traits through selection and hybridization. Similar finding was previously described by Rashid *et al.* [35] in 10 rice genotypes for all the traits they studied. Konate *et al.* [36] reported significant differences among 17 rice genotypes evaluated in different years. Khare *et al.* [37] also found similar results among the accessions for all studied traits.

Performance of the genotypes

Crop phenology traits

The number of days to 50% heading ranged from 79 days to 117.67 days with over all mean of 95.7. Among all the genotypes, G13 was earliest to time of heading (79 days) while G23 was found to be late (117.67days). Tefera *et al.* [38] and Bitew *et al.* [39] evaluated 34 and 22 rice genotypes, respectively and noted the presence of significant variations among genotypes for days to 50% heading ranging from 82.5 to 110 days and 67.3 to 87.3 days, respectively.

The number of days to flowering ranged from 83 days to 121.33 days with a mean of 99.78. Among all the genotypes tested for days to flowering, G13 was earliest onset of flowering (83 days), while G23 was found to be late (121.33 days). Osman *et al.* [40] evaluated 13 genotypes in Sudan and reported days to 50% flowering ranged from 64 to 79 days.

Genotypes displayed a highly significant difference in days to maturity that varied from 118 to 158.33 days with over all mean of 136.81. The maximum maturity period of 158.33 days was registered for G7 genotype followed by G20 (158 days) and the early maturity days was recorded for G2 (118 days) succeeded by G13 (119.33). Among 30 genotypes, 46.7% genotypes showed days to maturity lower than the average that indicates half of studied genotypes had earlier maturity period than the others. On the other hand, as compared to the standard check varieties, Ediget and Hibir, 46.7 % and 16.7% of the genotypes showed earlier maturity period, respectively. However, 26.7% of genotypes were earlier maturing than the locally available check variety (X-Jigna). This gives the opportunity of screening early maturing materials which can escape terminal moisture stress.

Growth related traits

The average values of total tillers number per plant varied from 4.97(G22) to 14.1(G13) with a mean of 9.57 tillers. Number of panicles per plant varied from 4.97 (G22) to 13.27 (G13) with a mean value of 9.11 panicles. Culm length varied from 44.37 cm for a genotype G11 to 122.07 cm for a genotype G22 with a mean of 69.79cm. The maximum panicle length was 28.17cm (G22) and the minimum value 13.27cm (G18) with a mean of 20.59 cm. Bioversity International [26] classified panicle length as very short less than 11 cm, short (~15 cm), medium (~25 cm), long (~35 cm) and very long greater than 40 cm. According to this classification, 3 genotypes grouped under the short class; 26 genotypes group under medium and another genotype (G22) fall within a class of the long panicle length. This variability of panicle length between the genotypes is crucial for improving architecture of panicle.

Minimum and maximum values of plant height, 64.93 and 150.23cm, were recorded for genotypes G11 and G22 respectively, with average value of 90.38 cm (Table 4). IRRI [28] classified lowland rice plant height as semi-dwarf less than 110 cm, intermediate 110-130 cm and tall more than 130 cm. According to this classification, 28 genotypes grouped under the semi-dwarf class; a genotype (G24) group under intermediate and another genotype (G22) grouped within the tall class. From here on, the studied genotypes had inherent variability in stature to develop lodging resistant varieties which will have higher response to nitrogen application. Shahriar [41] also reported variation in plant height in the evaluated rice genotypes.

The maximum flag-leaf length was observed for the genotype G20 (38.6 7cm), while the minimum for the genotype G18 (14.27cm) with a mean value of 26.26 cm. Tefera *et al.* [38] reported flag leaf length ranged from 16.15 to 30.95cm. On the other side, flag leaf-width was ranged from 1.64cm (G22) to0.92cm (G9) with a mean value of 1.16cm.

Table-4: Mean for phenology and growth characters of30 lowland rice genotypes

Genotypes	DH	DF	DM	TP	PP	CL	PL	PH	FL	FW
G1	100.00	104.00	140.00	8.87	8.80	68.07	21.60	89.67	31.27	1.23
G2	79.67	83.67	118.00	12.50	11.17	76.00	19.50	95.50	21.10	1.03
G3	80.67	84.33	123.00	12.70	11.70	51.17	15.60	66.77	14.87	0.98
G4	84.00	88.00	126.00	12.77	11.60	60.83	18.57	79.40	21.83	1.00
G5	81.67	85.67	126.33	9.23	8.73	56.00	13.50	69.50	15.40	1.24
G6(Edgt)	86.67	90.67	133.00	6.07	5.80	63.67	19.40	83.07	21.90	1.07
G7	112.33	116.33	158.33	9.90	9.70	45.90	22.07	67.97	26.43	1.20
G8	103.00	107.00	140.67	11.63	11.53	80.37	22.43	102.80	28.87	1.15
G9(Hibir)	91.00	95.67	124.33	8.75	8.15	61.40	19.50	80.90	19.33	0.92
G10	81.33	85.67	128.33	11.59	10.09	54.33	17.00	71.33	23.93	1.05
G11	105.00	109.00	141.00	12.80	12.50	44.37	20.57	64.93	25.40	1.09
G12	84.00	88.00	131.33	9.20	7.83	54.17	14.90	69.07	20.68	1.08
G13	79.00	83.00	119.33	14.10	13.27	77.80	18.77	96.57	21.00	1.06
G14	105.67	109.67	143.67	10.13	10.07	76.10	22.97	99.07	29.10	1.19
G15	82.33	86.33	124.00	7.97	6.70	81.93	24.77	106.70	27.25	1.01
G16	83.00	87.00	130.00	7.77	7.60	64.50	16.63	81.13	23.53	1.23
G17	102.00	107.00	143.33	6.50	6.43	73.47	24.97	98.43	35.50	1.21
G18	90.33	94.33	131.67	9.73	9.13	55.80	13.27	69.07	14.27	1.23
G19	104.67	108.67	152.67	8.17	8.13	84.53	23.57	108.10	33.83	1.28
G20	117.00	121.00	158.00	8.40	8.30	80.50	22.13	102.63	38.67	1.30
G21	90.00	94.33	124.00	6.50	6.00	71.40	21.13	92.53	23.63	1.13
G22	107.33	111.00	145.67	4.97	4.97	122.07	28.17	150.23	31.00	1.64
G23	117.67	121.33	152.33	10.27	10.17	61.23	21.10	82.33	24.63	1.20
G24	97.00	100.33	140.67	10.10	9.90	88.53	23.27	111.80	28.77	1.07
G25	109.00	114.33	157.33	9.07	8.67	50.50	21.30	71.80	29.10	1.15
G26	103.67	107.33	141.33	10.43	10.43	82.17	22.47	104.63	30.47	1.25
G27	108.67	112.67	142.33	9.77	9.77	82.07	22.80	104.87	30.30	1.23
G28(X-J)	87.67	92.00	128.00	11.10	9.93	63.17	19.07	82.23	23.40	1.00
G29	96.00	99.67	139.00	8.43	8.43	75.97	22.77	98.73	34.33	1.30
G30	100.67	105.33	140.67	7.83	7.80	85.63	23.87	109.50	38.10	1.24b
Range	79-117.67	83-121.33	118-158.33	4.97-14.10	4.97-13.27	44.37-122.07	13.27-28.17	64.93-150.23	14.27-38.67	0.92-1.64
Mean	95.7	99.78	136.81	9.57	9.11	69.79	20.59	90.38	26.26	1.16
LSD(0.05)	3.42	3.53	4.7	2.63	2.72	4.2	2.22	4.87	3.23	0.1

DH=days to heading, DF= days to Flowering, DM= days to maturity, TP= tillers per plant, PP=Panicles per plant, CL=culm length, PL= panicle length, PH= plant height, FL=flag leaf-length, FW: flag leaf-width, CV: coefficient of variability, LSD: least significance difference

Yield and yield related traits

Number of filled grains per panicle ranged from 81.9 to 141 for the genotype (G12) and (G30) with over all mean of 108.44. Number of unfilled grains per panicle ranged from 3.57 (G21) to 22.43 (G25) with a mean of 10.27. Jember *et al.* [42] reported number of unfilled grains per panicle ranged from 4.66 to 8.8 with a mean of 5.8. Panicle weight varied between genotypes with a range of 1.21-5.29g. Maximum panicle weight (5.29) was found in G30 followed by G29 (4.59g) and G17 (4.33g). It was observed that genotypes showing low number of filled grains had also shown low panicle weight and vice versa. Thousand seed weight ranged from 21.64 to 33.18g. Highest thousand seed weight value was noted in G16 followed by G6 (32.92g) and G2 (32.39g), while the lowest value was exhibited in G23 succeeded by G14 (24.34g) and G15 (24.88g). Abayneh *et al.* [43] found that1000 grain weight ranged from 26.33 to 33.67 g among evaluated rice genotypes.

The maximum and minimum above ground biomass yields were obtained from G2 (6713 kg ha-^{1}) and G20 (14861kg ha^{-1}). From here on, biomass yield of 43.33% or 13 genotypes higher than the overall mean (10457.13 kg ha^{-1}) of the tested genotypes while 63.33% and 70% of genotypes biomass yield exceed the standard check (Ediget) and local check, respectively**.** Harvest index was ranged from G23 (23.38%) to G29 (62.57%) that indicates variability among the studied genotypes in their efficiency of assimilate partitioning into grain yield. In addition, G29 (62.57%), G3 (61.8%) and G21 (56.51%) were the most efficient genotypes as compared to the included check varieties which had less than 55% of harvest index.

Paddy grain yield was ranged from 2766.7 to 7062.0 kg ha^{-1} with a mean of 4736.13kg ha^{-1}. The genotypes were significantly varied for grain yield and about forty seven (46.67%) of the genotypes grain yield exceeded the standard check G6 (Ediget) while 90% of the tested genotypes grain yield exceeded locally available check variety G28 (X-Jigna). Based on the studied the genotypes, G26, G14, G8, G27 and G29 were the top yielders with corresponding grain yield of 7062, 6900, 6583.10, 6486.90 and 6400.60kgha^{-1}, respectively. While lower yield was recorded for genotype G12 (2766.7kgha^{-1}) exceeded by genotype G23 (2830.70kgha^{-1}) and the local check (X-Jigna) (2925.80kgha^{-1}).

Tefera *et al.* [38] evaluated 34 rice genotypes with 2 checks and reported that grain yield ranged between 2886 and 6759 kgha^{-1}which showed wide range of variation among the genotypes. Similarly, Bitew *et al.* [39], Akinwale *et al.* [44] and Ekka *et al.* [45] evaluated 22, 20 and 96 rice genotypes in Ethiopia, Philippines and India respectively, addressed the presence of significant variations among genotypes for grain yield. The existence of such variation for the different characters showed presence of variable genetic materials for rice improvement.

Table-5: Mean for yield and yield related components of low land rice genotypes

Genotypes	FGPP	UGPP	PW	TGW	BY	GY	HI
G1	136.00	19.70	3.22	25.39	9722.00	5123.90	52.87
G2	91.33	8.82	1.66	32.39	6713.00	3631.30	53.95
G3	88.03	6.88	2.00	27.64	8426.00	5210.60	61.80
G4	86.94	7.96	1.67	28.87	7593.00	3905.30	51.47
G5	100.44	7.88	2.04	31.77	7963.00	4022.30	50.57
G6(Edgt)	94.67	12.33	2.95	32.92	8704.00	4759.20	54.67
G7	108.00	13.20	2.92	27.87	11769.00	4753.90	40.66
G8	132.67	6.80	2.79	26.14	12222.00	6583.10	54.75
G9(Hibir)	94.67	8.01	2.11	31.38	7741.00	3725.30	48.25
G10	85.43	11.48	1.32	29.35	7870.00	3115.40	40.23
G11	106.33	9.00	2.02	26.90	10741.00	5014.10	46.89
G12	81.90	14.49	1.21	31.67	7778.00	2766.70	35.40
G13	103.00	6.33	1.60	29.98	10593.00	5740.10	54.06
G14	134.75	10.10	3.14	24.34	13657.00	6900.00	50.92
G15	108.00	15.27	3.27	24.88	13102.00	5587.10	43.81
G16	103.33	8.43	2.15	33.18	8333.00	4409.70	52.80
G17	135.96	7.87	4.33	25.36	11574.00	5628.00	48.93
G18	102.33	7.56	2.02	31.26	8991.00	3666.90	41.06
G19	106.00	12.20	2.60	28.68	10093.00	3075.80	30.94
G20	107.67	10.70	2.48	27.62	14861.00	5066.70	34.01
G21	107.67	3.57	3.80	31.01	7500.00	4219.10	56.51
G22	111.94	9.07	3.59	29.64	10417.00	3297.30	31.93
G23	95.19	13.93	1.52	21.64	12074.00	2830.70	23.38
G24	105.67	9.60	3.03	31.48	12315.00	6104.20	50.24
G25	100.00	22.43	2.42	26.45	13750.00	3728.70	27.33
G26	134.07	10.07	2.94	25.03	14259.00	7062.00	49.64
G27	122.67	11.90	2.91	25.46	14259.00	6486.90	45.60
G28(X-J)	87.70	10.31	1.55	27.58	8148.00	2925.80	36.10
G29	139.83	4.67	4.59	30.88	10231.00	6400.60	62.57
G30	141.00	7.67	5.29	28.89	12315.00	6343.10	51.92c
Range	81.90-141	3.57-22.43	1.21-5.29	21.64-33.18	6713-14861	2766.7-7062	23.38-62.57
Mean	108.44	10.27	2.64	28.52	10457.13	4736.13	46.11
LSD(0.05)	13.19	2.65	0.59	3.17	2065.1	781.05	8.23

FGPP=filled grain per Panicle, UGPP= unfilled grain per Panicle, PW=panicle weight, TGW=1000 grain weight, BY= Biomass yield per ha in Kg, HI= harvest index, GY= paddy grain yield per ha in Kg, CV= coefficient of variability, LSD= least significance difference

Estimation of Variance Components

The results pertaining to mean, range, component of variance, genotypic and phenotypic coefficient of variability, heritability, genetic advance and genetic advance expressed as percent of mean of 30 genotypes of lowland rice has been presented at Table 6.

Estimates of PCV and GCV

The trait above ground biomass kg ha^{-1} exhibited the highest genotypic and phenotypic variance i.e. 5,345,161.67 and 5,877,302.90 respectively and followed by grain yield ha^{-1} that had genotypic variance of1,685,864.73 and phenotypic variance of 1,761,988.80. The lowest for both genotypic and phenotypic variance was recorded as 0.02 for the trait flag-leaf width (Table 6). However, these variation influenced by the measuring units of the traits while coefficient of variation is more useful in comparing the population, which is independent of the magnitude of the measuring units.

The genotypic coefficient of variation (GCV) ranged from 8.44 for days to maturity to 38.30 for number of unfilled grains per panicle. The maximum genotypic coefficient of variability was observed for number of unfilled grains panicle^{-1} (38.30 %) followed by panicle weight (36.91%). The result of genotypic coefficient of variability was in agreement with phenotypic coefficient of variability. Phenotypic coefficient of variation ranged from 8.53% for days to maturity to 39.37% for number of unfilled grains panicle^{-1}. The maximum PCV was observed for unfilled grains panicle^{-1}(39.37%) followed by panicle weight (37.74%) (Table6).

According to Sivasubramanian and Madhavamenon [31], genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were categorized as low (0-10%), moderate (10-20%) and high (greater than 20%). Based on this classification high GCV and PCV values were obtained for number of tillers per plant, culm length, plant height, flag-leaf length, number of unfilled grain per panicle, panicle weight, grain yield, biomass yield and harvest index, which suggests the chance of these traits improvement through selection. The result in this study agrees with Satheeshkumar and Saravanan [46] and Hoque [47] who found high GCV and PCV for biomass yield and plant height. Rashid *et al.* [35] found similar results for number of unfilled grains panicle^{-1}, filled grains paicle^{-1}, plant height and yield panicle^{-1}.

On the other hand, low GCV and PCV values were recorded for days to maturity (8.44%, 8.53%). The result of this study is in conformity with the reports presented by Pandey *et al.* [48]. Generally, a high coefficient of variation showed that there is a scope of selection and improvement of these traits while low coefficient of variation indicated the need for creation of variation by hybridization or mutation followed by selection [49].

The values of PCV were slightly higher than the corresponding GCV values for all traits and the magnitude of differences between the two values were low for most of the traits. This indicated that the traits were less influenced by the environment. The environmental influence on any character is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation. Babu *et al.* [50], Konate *et al.* [30] and Srivastava *et al.* [51] Indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the traits studied in rice and noted the characters were less influenced by the environment. The authors suggested that selection on the basis of phenotype alone can be effective for the improvement of the traits in which the magnitude of differences between GCV and PCV are low.

Estimates of broad sense heritability

As suggested by Johnson *et al*. [33] heritability was classified as high (above 60%), medium (30-60%) and low (below 30%). Based on this delineation, high broad sense heritability values were recorded for all the studied traits ranged from 77.45 to 99.16%. The maximum and minimum broad sense heritability value was observed for plant height (99.16%) and number of panicles per plant (77.45%), respectively. High broad sense heritability values estimates indicated the additive genes were more effective than non- additive effects that the studied traits were less influenced by environment in their expression. Thus, rice breeders get a possibility of selecting superior genotypes based on phenotypic performance of these characters.

Rashid *et al.* [35] found comparable results for all studied traits in rice ranged from number of panicles per plant (75.14%) to plant height (98.79%). Abayneh *et al.* [43] also obtained similar results for plant height, days to heading, thousand grains weight and panicle length in rice. This result indicated the major role of additive gene action in the inheritance of the traits that would help breeders to select superior genotypes based on these phenotypic performances.

Estimates of genetic advance and genetic advance as percent of mean

Broad sense heritability alone gives no indication of the magnitude of genetic improvement from the result of selection of individual genotypes. Therefore, heritability coupled with genotypic coefficient of variations and genetic advance would give a more reliable index of selection. As stated by Johnson *et al.* [33] genetic advance as percent of mean classified as low (0 to 10%), moderate (10 to 20%) and high (20% and above).

The genetic advance as percentage of the mean (GAM) values varied from 17.24 (days to maturity from the date of seedling emergence) to 76.87 (number of unfilled grains per panicle). High GAM was exhibited by unfilled grains per panicle number followed by panicle weight (74.45), grain yield (55.32), flag leaf length (49.13) and culm length (47.35) (Table 6). In this study, high heritability coupled with high GCV and high GAM exhibited by unfilled grains per panicle, panicle weight, culm length, plant height, flag leaf length, biomass yield, grain yield and harvest index.

These characters were controlled by few major genes that simply inherited in nature which indicated the presence additive gene effects, that are fixable in the next generation and selection in next population based on these traits, would be ideal. The present finding was in correspondence with the investigation of Shrivastava *et al.* [52] and Shrivastava *et al.* [53] for the number of unfilled grain panicle^{-1}. In contrary, Tefera *et al.* [38] reported low heritability with low genetic advance as percent mean for flag leaf length and harvest index. The results of high heritability with a moderate GAM for days to maturity and thousand-grain weight also agreed with the finding of Abayneh *et al.* [43] for thousand grain weight.

Table-6: Estimate of phenotypic and genotypic variances and coefficient of variations, habitability in broad sense and genetic advance for 17 traits of 30 low land rice genotypes

Traits	$\sigma^2 g$	$\sigma^2 e$	$\sigma^2 p$	GCV	PCV	H^2(%)	GA	GAM
DH	142.31	4.38	143.77	12.47	12.53	98.99	24.49	25.59
DF	142.73	4.67	144.29	11.97	12.04	98.92	24.51	24.57
DM	133.43	8.27	136.18	8.44	8.53	97.98	23.59	17.24
TP	3.95	2.59	4.82	20.76	22.92	82.07	3.72	38.81
PP	3.16	2.76	4.08	19.52	22.18	77.45	3.23	35.44
CL	258.77	6.61	260.98	23.05	23.15	99.15	33.05	47.35
PL	11.55	1.84	12.17	16.51	16.94	94.96	6.83	33.19
PH	349.62	8.88	352.58	20.69	20.78	99.16	38.41	42.50
FL	40.38	3.90	41.68	24.19	24.58	96.88	12.90	49.13
FW	0.02	0.00	0.02	11.60	11.99	93.69	0.27	23.16
FGPP	300.73	65.11	322.43	15.99	16.56	93.27	34.55	31.86
UGPP	15.48	2.62	16.36	38.30	39.37	94.66	7.90	76.87
PW	0.95	0.13	0.99	36.91	37.74	95.61	1.96	74.45
TGW	7.44	3.75	8.69	9.56	10.34	85.61	5.21	18.25
BY	5345161.67	1596423.70	5877302.90	22.11	23.18	90.95	4548.53	43.50
HI	91.32	25.36	99.77	20.73	21.66	91.53	18.86	40.90
GY	1685864.73	228372.20	1761988.80	27.41	28.03	95.68	2620.12	55.32

$\sigma^2 g$ =Genotypic variance, $\sigma^2 e$ =Environmental variance, $\sigma^2 p$=Phenotypic variance, DH= days to heading ,DF= days to flowering, DM=days to maturity, TP=number of tillers plant $^{-1}$, PP= panicles plant $^{-1}$, CL= culm length, PL= panicle length, PH= plant height, FL= flag-leaf length ,FW= flag-leaf width , FGPP= filled grain panicle^{-1} ,UGPP=unfilled grain panicle $^{-1}$, PW= panicle weight, TGW=1000 grain weight, BY= biomass yield ha^{-1} in Kg, HI= harvest index, GY=paddy grains yield per ha in Kg.

CONCLUSION

The analysis of variance showed highly significant differences among the tested genotypes for all 17 studied traits, which indicates that there is a considerable genetic variability in the tested rice genotypes. Paddy grain yield ranged from 2766.7 kg ha^{-1} for G12 to 7062.0 kg ha^{-1} for G26 with a mean of 4736.13kg ha^{-1}. Among the genotypes, G26, G14, G8, G27, G29 and G30 were the six top yielders with corresponding mean grain yield of 7062, 6900, 6583.10, 6486.90, 6400.60 and 6343.10 kg ha^{-1}. About 46.7% and 90% of the genotypes exhibited higher mean grain yield than the check varieties G6 (Ediget) and the local check G28 (X-Jigna), respectively. Phenotypic variance was slightly higher than the genotypic variances for all characters. The PCV and GCV value of the studded traits ranged from high to low. High PCV and GCV values were recorded for number of tillers per plant, plant height, culm length, flag-leaf length, number of unfilled grain per panicle, panicle weight, grain yield, biomass yield and harvest index indicating high scope for improvement through selection. However, genotypic and phenotypic coefficients of variation were low for days to maturity.

High heritability values were observed for all the studied traits ranged from 77.45 to 99.16%. The highest heritability value was observed for plant height (99.16%) followed by culm length (99.15%).High heritability coupled with high genotypic coefficients of variation (GCV) and high genetic advance as percentage of mean were exhibited by unfilled grains per panicle, panicle weight, panicles per plant, culm length, plant height, flag leaf length, biomass yield, grain yield and harvest index; reflecting the presence of additive gene action for the expression of these traits, which is fixable in the next generation, and suggesting that the genotypes under consideration are a good source of material to develop varieties with high yield.

It is recommended to repeat the study at more seasons and locations with more number of genotypes to predict genotypic performance across seasons and locations which helps to validate the obtained current results. Moreover, the future rice research should be supplemented by molecular characterization to further confirm the outcome of current study findings.

Conflict of Interests

The authors have not declared any conflict of interests.

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REFERENCE

1. Gross, B. L., & Zhao, Z. (2014). Archaeological and genetic insights into the origins of domesticated rice. *Proceedings of the National Academy of Sciences*, *111*(17), 6190-6197.
2. Singh, G., Singh, A., & Shrivastav, S. P. (2018). Genetic Variability, Heritability and Genetic Advance for Yield and its Contributing Traits in Garlic (Allium sativum L.). *Int. J. Curr. Microbiol. App. Sci*, *7*(2), 1362-1372.
3. Singh, S. K., Bhati, P. K., Sharma, A., & Sahu, V. (2015). Super hybrid rice in China and India: current status and future prospects. *Int. J. Agric. Biol*, *17*, 221-232.
4. ANSARI, M. U. R., Shaheen, T., BUKHARI, S., & Husnain, T. (2015). Genetic improvement of rice for biotic and abiotic stress tolerance. *Turkish Journal of Botany*, *39*(6), 911-919.
5. Messeguer, J., Fogher, C., Guiderdoni, E., Marfa, V., Catala, M. M., Baldi, G., & Melé, E. (2001). Field assessments of gene flow from transgenic to cultivated rice (Oryza sativa L.) using a herbicide resistance gene as tracer marker. *Theoretical and Applied Genetics*, *103*(8), 1151-1159.
6. Oka, H.I. (1988). Weedy forms of rice. Origin of cultivated rice. Elsevier, Amsterdam, 107-114.
7. Mickel A., Donini B., & Maluszynski, M. (1990). Induced mutations for crop improvement. Mutuation Breeding Review, No.7. *IAEA, Vienna*. pp1-16
8. Luz, V. K. D., Silveira, S. F. D. S., Fonseca, G. M. D., Groli, E. L., Figueiredo, R. G., Baretta, D., ... & Oliveira, A. C. D. (2016). Identification of variability for agronomically important traits in rice mutant families. *Bragantia*, *75*(1), 41-50.
9. Dejen, B. (2020). Improvement of Rice Breeding for Salinity Tolerance. *Journal of Environment and Earth Science*; 10:5, 14
10. Chakravarthi, B. K., & Naravaneni, R. (2006). SSR marker based DNA fingerprinting and diversity study in rice (Oryza sativa. L). *African Journal of Biotechnology*, *5*(9).
11. Zibaee, A. (2013). Rice: importance and future. *J. Rice Res*, *1*, e102.
12. FAO. (2015). International Year of Rice 2015, Statistical database of the food and agriculture of the United Nations.
13. FAO. (2017). Food and Agriculture organization of the United Nations. (http://faostat.fao.org.)
14. Rahman, M. M., Syed, M. A., Adil, M., Ahmad, H., & Rashid, M. M. (2012). Genetic variability, correlation and path coefficient analysis of some physiological traits of transplanted Aman rice (Oryza sativa L.). *Middle East Journal of Scientific Research*, *11*(5), 563-566.
15. Girma, B. T., Mohammed, H., & Abegaz, K. (2016). Physical characteristics and nutritional quality of salt tolerant rice genotypes. *Journal of Cereals and Oilseeds*, *7*(2), 7-13.
16. Mo ARD (Ministry of Agriculture and Rural Development). (2010). National Rice Research and Development Strategy of Ethiopia. The Federal Democratic Republic of Ethiopia, Ministry of Agriculture and Rural development, Addis Ababa, Ethiopia; 48.
17. CSA (Central Statistical Agency). (2017). Agricultural Sample Survey Series: Report on Area and Production for Major Crops (Private Holdings, Main Season). Statistical Bulletin No. 578. Addis Ababa, Ethiopia, 14-16.
18. Kirub, A., Alemu, D., Shiratori, K., & Assefa, K. (2011). Challenges and opportunities of rice in Ethiopian agricultural development.
19. FAO. (2002). Food and agriculture organization. The agricultural production domain covers: Quantity produced Producer price, Area harvested and Yield per hectare. FAO Statistics Division
20. Gebrekidan, H., & Seyoum, M. (2006). Effects of mineral N and P fertilizers on yield and yield components of flooded lowland rice on vertisols of Fogera Plain, Ethiopia. *Journal of Agriculture and Rural Development in the Tropics and Subtropics (JARTS)*, *107*(2), 161-176.
21. Tesfaye, Z., Befekadu, A., & Akililu, A. (2005). Rice production consumption and marketing: The case of Fogera, Dera and Libokemikem districts of Amhara region Paper presented on the national workshop on the status of rice research and promotion in Ethiopia.3-4 June 2005, Bahir Dar, Ethiopia.13.
22. EIAR/FRGII. (2011). Challenges and opportunities of Rice in Ethiopia Agricultural development. Addis Ababa, Ethiopia.
23. MoARD (Ministry of Agriculture and Rural Development). (2009). National Rice research and

development strategy of Ethiopia. MOARD, Addis Ababa, Ethiopia.

24. SAS (statistical Analysis Software). (2002). Statistical analysis systems SAS/STAT user's guide vesion 9 cary NC: SAS Institute Inc.USA.
25. Dutta, P., & Borua, P.K. (2013). Morphological traits as selection indices in rice: A statistical view. *Universal Journal of Agricultural Research*, *1*(3):85-96.
26. Bioversity International. (2007). Descriptors for wild and cultivated rice (*Oryza Sativa* L.). International Rice Research Institute Los Banos, Cotonou, Benin. 63pp.
27. Welsh, J. R. (1981). Fundamentals of Plant Genetics and Breeding. John Willey and Sons, Inc., New York. 290.
28. IRRI (International rice research institute). (2002). Rice Almanac, source book for the most important economic activity on earth. Third edition. Maclean J.L., Dawe D.C., Hardy B., and Hettel G.P. (Eds.) International Rice Research Institute, Manila, Philippines, 1–253.
29. Gomez, K.A., & Gomez, A.A. (1984). Stastical procedures for agricultural reseach. John Wiley L.pak. *J.Bot*. *22*(2):160-167.
30. Burton, G.W., & Devane, E.H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, *45*(10).478-481.
31. Sivasubramanian, S., & Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agric* J .60:1093-1096.
32. Raiz, R., & Chowdhry, M. A. (2003). Estimation of variation and heritability of some physio-morphic traits of wheat under drought condition. *Asian Journal of Plant Science*, *2*(10), 748-755.
33. Johnson, H.W., Robinson, H.P., & Comstoc, R.E. (1955). Estimation of genetic and environmental variability in soy beans. *Agron. J.* 47: 314- 318.
34. Hanson, G., Robinson, H. F., & Comstock, R. E. (1956). Biometrical studies on yield in segregating population of Korean Lespedeza. *Agron. J.* 48:268-274.
35. Rashid, M. M., Nuruzzaman, M., Hassan, L,. & Begum, S. N. (2017). Genetic variability analysis for various yield attributing traits in rice genotypes, Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU), Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh-2202, Bangladesh. *J. Bangladesh Agri. Univ*, *15*(1): 15–19.
36. Konate, A. K., Zongo, A., Kam, H., Sanni, A., & Audebert, A. (2016). Genetic variability and correlation analysis of rice (Oryza sativa L.) inbred lines based on agro-morphological traits.
37. Khare, R., Singh, A. K., Eram, S., & Singh, P. K. (2014). Genetic variability, association and diversity analysis in upland Rice (Oryza sativa L). *SAARC Journal of Agriculture*, *12*(2), 40-51.
38. Abebe, T., Alamerew, S., & Tulu, L. (2017). Genetic variability, heritability and genetic advance for yield and its related traits in rainfed lowland rice (Oryza sativa L.) genotypes at Fogera and Pawe, Ethiopia. *Adv. Crop Sci. Tech*, *5*(272), 10-4172.
39. Bitew, J. M., Mekbib, F., & Assefa, A. (2016). Genetic Variability among Yield and Yield Related Traits in Selected Upland Rice (Oryza sativa L. and Oryza glaberrima Steud) Genotypes in Northwestern Ethiopia. *World Scientific News*, *2*(47), 62-74.
40. Osman, K. A., Mustafa, A. M., ALI, F., Yonglain, Z., & Fazhan, Q. (2012). Genetic variability for yield and related attributes of upland rice genotypes in semi-arid zone (Sudan). *African Journal of Agricultural Research*, *7*(33), 4613-4619.
41. Shahriar, M.H. (2014). Morphological characterization and SSR-based molecular screening of advanced breeding lines of rice for short growth duration. The thesis submitted to the school of graduate studies of Bangladesh Collegeof Agricultural University
42. Bitew, J. M., Mekbib, F., & Assefa, A. (2016). Genetic Variability among Yield and Yield Related Traits in Selected Upland Rice (Oryza sativa L. and Oryza glaberrima Steud) Genotypes in Northwestern Ethiopia. *World Scientific News*, *2*(47), 62-74.
43. Kampe, A. K., Tassew, A. A., & Gezmu, A. T. (2018). Estimation of phenotypic and genotypic correlation and path coefficients in rainfed upland rice (Oryza sativa L.) genotypes at Guraferda, Southwest Ethiopia. *J Rice Res*, *6*, 195.
44. Akinwale, M. G., Gregorio, G., Nwilene, F., Akinyele, B. O., Ogunbayo, S. A., & Odiyi, A. C. (2011). Heritability and correlation coefficient analysis for yield and its components in rice (Oryza sativa L.). *African Journal of plant science*, *5*(3), 207-212.
45. Ekka, R. E., Sarawgi, A. K., & Kanwar, R. R. (2015). Genetic variability and inter-relationship analysis for various yield attributing and quality traits in traditional germplasm of rice (Oryza sativa L.). *Plant Archives*, *15*(2), 637-645.
46. Satheeshkumar, P., & Saravanan, K. (2012). Genetic variability, correlation and path analysis in rice (Oryza Sativa L.). *International Journal of Current Research*, *4*(09), 082-085.
47. Hoque, A. (2013). *Morphophysiological and molecular characterization of rice (Oryza sativa L.) advanced breeding lines for earliness* (Doctoral dissertation).
48. Pandey, V. R., Singh, P. K., Verma, O. P., & Pandey, P. (2012). Inter-relationship and path coefficient estimation in rice under salt stress environment. *International Journal of Agricultural Research*, *7*(4), 169-184.
49. Tiwari, D. K., Pandey, P., Tripathi, S., Giri, S. P., & Dwivedi, J. L. (2011). Studies on genetic

variability for yield components in rice (Oryza sativa L.). *Advances in Agriculture & Botanics*, *3*(1), 76-81.

50. Babu, V. R., Shreya, K., Dangi, K. S., Usharani, G., & Shankar, A. S. (2012). Correlation and path analysis studies in popular rice hybrids of India. *International Journal of Scientific and Research Publications*, *2*(3), 1-5.
51. Srivastava, N., Babu, G. S., Singh, O. N., Verma, R., Pathak, S. K., Behra, M., ... & Chanda, M. (2017). Genetic variation, heritability and diversity analysis of exotic upland rice (Oryza sativa L.) germplasms based on quantitative traits. *The Pharma Innovation Journal*, *6*(12), 316-320.
52. Shrivastava, A., Mishra, D. K., Koutu, G. K., & Singh, S. K. (2014). Heritability and genetic advance estimation from parental lines of hybrid rice. *International journal of scientific research*, *3*(7), 11-13.
53. Shrivastava, A., Mishra, D. K., & Koutu, G. K. (2015). Estimation of genetic parameters of variability for yield and its attributing traits in parental lines of hybrid rice. *Plant Archives*, *15*(1), 571-574.

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