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Genetic Variability and Advance among Rice (*Oryza sativa* L) Genotypes in Northwestern Ethiopia

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Abstract **– Rice is staple food for more than half of the world's population and a new flagship crop to ensure food security for Ethiopians. This research was conducted with the aim of quantifying the extent of phenotypic and genotypic variability, and estimating broad sense heritability and genetic advance among 100 rice genotypes in Northwestern Ethiopia. The experimental design was triple lattice design which laid out with 10×10 in 2021/22 main cropping season. Analysis of variance indicated high significant ($P<0.01$) differences among genotypes for all studied traits, which reveals the presence of sufficient variability for selection. The genotypic coefficient of variation/GCV, phenotypic coefficient of variation/PCV, heritability/H^2 and genetic advance as percent of mean/GAM were varied from 8.52% to 72.18%, 8.64% to 86.62%, 63.34% to 98.76% and 17.32% to 136.05%, respectively. Traits that had high heritability coupled with high/moderate GCV and high GAM per small difference between GCV and PCV are best for direct selection. Accordingly, to improve panicle length G18 and G68, thousand grain weight G21 and days to 50% heading G57 and G87 are recommended donor rice genotypes for future crossing works.**

Keywords **– Genetic Advance, Genotypes, Heritability, Rice, Trait, Variability.**

I. INTRODUCTION

Rice is the second most produced cereal in the world after wheat (Luz *et al.*, 2016) and grown worldwide (Loitongbam *et al.*, 2017). In Ethiopia, rice is considered as "Millennium crop" and expected to ensure food security of the country (Dessie *et al.*, 2018). In Amhara region, rice is introduced in the early 1980s through the technical support of North Korean experts in Fogera plain; where the most successful and potential area of the country (Tadesse, 2020). As rice is a recent crop in Ethiopia, the source of germplasm until now is through introduction. The major source of genotypes includes Africa Rice Center, International Rice Research Institute (IRRI), IRRI-ESA (Tanzania, Kenya and Burundi), China and Japan (Asmelash, 2014; Dessie *et al.*, 2019). Since 2007 to 2018 a total of 3336 genotypes were introduced and evaluated for variety release (Dessie *et al.*, 2019).

Variability is differences among individuals due to variations in their genetic composition and or environment (Allard, 1960; Falconer and Mackay, 1996). Phenotypic variability is observable variation present in a character within a population, which includes both genotypic and environmental variation. As a result, its magnitude differs under different environmental conditions. On the other hand, genotypic variability is the genotypic differences among individuals within a population and it is the main concern of plant breeders (Singh, 2001). Hence genetic variability could be transferred to the progeny and proper management of this diversity could produce permanent gain in the performance of the plant (Welsh, 1981). The magnitude of genetic variability present in the base population of any crop species is also vital for crop improvement, which must be exploited by plant breeders for yield improvement (Idahosa *et al.*, 2010). The amount of variation present in a population is measured and expressed in terms of variance (Falconer and Mackay, 1996). So, information on the nature and magnitude of genetic variation within agronomic traits of the species greatly helps in formulating a sound crop breeding program and efforts to breed better varieties (Sharma, 1998).

Moreover, genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful for distinguishing the amount of variability present in the germplasm (Idris *et al.*, 2012). The extent of the environmental influence on any trait is the magnitude of the differences between GCV and PCV. Large differences reflect high environmental influence, while small differences reveal high genetic influence (Allard, 2000; Osman *et al.,* 2012).

Heritability is defined as the measure of the correspondence between breeding values and phenotypic values (Falconer and Mackay, 1996). Heritability is classified into broad and narrow sense (Acquaah, 2012). Heritability in the broad sense is defined as the proportion of phenotypic variance that is attributable to an effect for the whole genotype, comprising the sum of additive, dominance and epistatic effects (Nyquist, 1991). While, narrow sense heritability is a ratio of the additive genetic variance to the phenotypic variance. It expresses the extent to which phenotypes are determined by the genes transmitted from the parents to the off springs. Heritability in the narrow-sense determines the degree of resemblance between relatives and measures the relative importance of additive portion of the genetic variance that can be transmitted to the next generation. Therefore, it has great importance in breeding programs to predict gain expected from selection for characters (Falconer and Mackay, 1996).

Heritability estimates can be used to predict genetic advance under selection so that breeders can anticipate improvement from different types and intensities of selection. Heritability estimates and genetic advance should always be considered simultaneously, because high heritability will not be always associated with high genetic advance (Johnson *et al.,* 1955). High heritability associated with equally high genetic advance is mainly due to additive gene effect, but if the heritability is due to dominance and epistasis, the genetic advance would be low (Nirmaladevi *et al.,* 2015).

Genetic advance under selection is a genotypic value, which depends on three things such as genetic variability, heritability or masking effect of non-genetic variability on the genetic variability and the selection intensity applied (Allard, 2000). Genetic advance under selection can be computed by product of broad sense heritability, phenotypic standard deviation and selection differential (Allard, 1960; Johnson et al., 1955). The estimate of genetic advance as percent of mean provides more reliable information regarding the effectiveness of selection in improving the traits (Ghosh and Sharma, 2012). In addition, genetic advance provides information on expected genetic gain resulting from selection of superior individuals (Satheesh kumar and Saravanan, 2012).

In general, even though a total of 3336 genotypes were introduced and evaluated for variety release in Ethiopia since 2007 to 2018; their genetic variability, heritability and genetic advance study was limited. Hence, the present research was studied 100 rice genotypes on their genetic variability, heritability and genetic advance.

II. MATERIALS AND METHODS

A. *Description of the Study Area*

The experiment was conducted at Fogera National Rice Research and Training Center (FNRRTC) on-station in 2021/22 main cropping season. FNRRTC is located 57km away from Bahir Dar, capital city of Amhara National Regional State and 607km away from the capital of Ethiopia, Addis Ababa in the north-western part of Ethiopia (Figure 1). Specifically, the experimental site was located at 11°58' N latitude, 37° 41' E longitude and at an elevation of 1810m above sea level. Based on ten years' average meteorological data, the annual rainfall is 1300mm and the annual minimum and maximum temperatures are 11.5°C and 27.9°C, respectively. The soil type is *Vertisol* (black) with pH of 5.90 (Abebe, 2016).

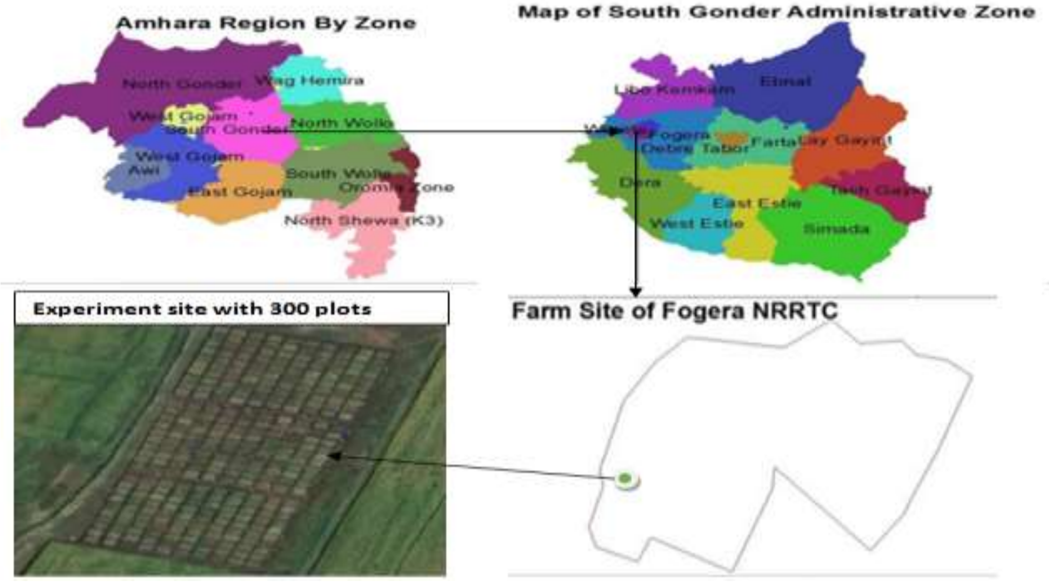

Fig. 1. Map locating the study area, Fogera National Rice Research and Training Center.

B. *Experimental Materials*

The experimental material was composed of 100 rain fed rice genotypes including 10 released varieties (Table 1). All genotypes were found from FNRRTC, which was sourced from different rice research organization mainly from IRRI and Africa Rice Center. These genotypes were maintained for future breeding work.

C. *Experimental Design*

The experiment was laid out in 10 × 10 triple lattice designs. The plot size was 7.5m^2 and the net harvestable plot size was 6m^2, excluding two boarder rows. The space between rows, plots and blocks were 0.25m, 0.5m and 1m, respectively. The plot size, space between rows, plots and blocks were done based on the national rice research protocol for breeding activities of rain fed rice (Atnaf *et al.*, 2019; Zewdu *et al.*, 2020).

D. *Agronomic Practices*

A seed rate of 60kg ha^{-1} was applied with direct seeding methods in a row. Fertilizer application and weeding were done based on the local recommendations.

E. *Data Collected*

Data were collected on plot and plant basis according to standard evaluation systems and descriptors for wild and cultivated rice (Bioversity International, 2007; IRRI, 2013) and most of important agronomic standard evaluation systems for rice is also directly adopted by FNRRTC, rice breeding as follows:

On Plant Basis

Plant Height (cm):

The height of the plant was measured by taking five plants randomly in the harvestable plot and measured starting from the base of the main stem to the tip of the main panicle at physiological maturity.

Panicle Length (cm):

The panicle length was measured from 5 randomly taken rice plants of the main tiller panicle at physiological maturity.

Number of Filled and Unfilled Spikelets /Panicle:

The number of filled and unfilled spikelets per panicle was counted from 5 randomly selected plants at maturity.

Tillering Ability, Number of Fertile and Non- Fertile Tillers Per Plant:

Three time counting was done since the sowing method was drilling. First, number of seedlings were counted before tillering at 50cm row length from two sampled harvestable rows and tagged. Second, maximum tillers were counted at maximum tillering stage from the pre tagged samples. Third, Fertile tillers were counted at maximum tillering from the pre tagged samples too. Then, tillering ability was calculated by dividing the number of tillers at maximum tillering stage by the number of seedlings and the number of non-fertile tillers were obtained by calculating the difference between tillering ability and fertile tillers.

On Plot Basis

Days to 50% Heading:

It was recorded by visual judgment in whole plot, which was number of days counted from sowing to 50% heading.

Days to 85% Maturity:

Maturity was recorded by visual judgment of the whole plot, which was number of days from sowing to 85% physiological maturity.

Above Ground Biomass Yield (kg/plot):

It was measured in each harvestable plot after two days sundry.

Grain Yield Per Plot (g):

Cleaned paddy rice yield and moisture were measured. Then, the grain yield was adjusted at 14% moisture content as follows: $Grain\ \text{yield} = \frac{(Akg(100-B))}{(100-mc)}$ Where, A = actual measured weight, B = Measured moisture content, mc= moisture content.

Harvest index (HI %):

It was calculated as follows: $HI\ \% = \frac{(\text{Economic grain yield per plot})}{(\text{Biological yield per plot })}*100$

Thousand Grain Weights (g):

It was counted by seed counter by taking whole grains randomly from clean and sun dried for each of harvestable plot and then weighed by using sensitive balance and adjusted at 14% moisture content.

Table 1. List of the one hundred rice genotypes tested at Fogera district, Ethiopia.

Genotype #	Genotype Designations	Genotype #	Genotype Designations
G1	GSR IR1-17-Y16-Y3-Y2	G51	MET-HE-17-10
G2	GSR IR1-15-D4-D1-Y1	G52	MET-HE-17-14
G3	GSR IR1-5-D1-D1	G53	MET-HE-17-16
G4	GSR IR1-12-Y4-Y1-D1	G54	MET-HE-17-23
G5	GSR IR1-8-S9-D2-Y2	G55	MET-HE-17-25
G6	GSR IR1-12-S2-Y3-Y2	G56	Aromatic-1
G7	GSR IR1-5-D20-D2-D1	G57	Edirne
G8	GSR IR1-5-S10-D3-Y2	G58	Trakya
G9	GSR IR1-12-S8-Y1-S1	G59	Halilbey
G10	GSR IR1-8-S14-S1-SU1	G60	Osmancik-97
G11	GSR IR1-12-D10-S1-D1	G61	Tunca
G12	GSR IR1-12-Y4-D1-Y2	G62	Condai
G13	GSR IR1-12-S8-Y1-Y2	G63	Hangamchal
G14	GSR IR1-5-S10-D1-D1	G64	Hawaghaelo-2
G15	GSR IR1-8-S6-S3-S1	G65	Namcheobyeo
G16	GSR IR1-5-S12-D3-Y2	G66	Samgangbyeo
G17	GSR IR1-5-S8-D2-S1	G67	Suitou Chuukanbohon Nou 11
G18	ROJOMENA271/10	G68	PCT-11\0\0\2, Bo\2\1>487-1-6-2-3-3-M
G19	IRGA370-38-1-1F-B1-1	G69	CT11231-2-2-1-3-M-5-2-M-3-M
G20	PSBRC92	G70	PCT-11\0\0\2, Bo\2\1>1-M-3-1-2-M
G21	FKRS	G71	PCT-4\0\0\1>161-3-2-1-M
G22	IR75502-5-1-1-B	G72	PCT-4\0\0\1>204-1-3-3-M-3-M
G23	WAB95-B-B-40-HB	G73	PCT-4\0\0\1>295-2-3-1-3-3-M
G24	IR76999-52-1-3-2	G74	PCT-4\0\0\1>295-2-6-1-3-3-M
G25	WAB502-8-5-1	G75	IR 84639-7-76-3-2-1-2-4-2-2-2-B-Tsukuba
G26	WABC165(IAC165)	G76	IR 84633-9-16-5-11-2-2-4-3-2-2-B-Tsukuba
G27	Yungeng 45	G77	SCRID091-10-1-3-2-5
G28	SR35239-HB3403-27	G78	SCRID091-24-3-2-2-3
G29	MwuR4	G79	SCRID090-60-1-1-2-4

Genotype #	Genotype Designations	Genotype #	Genotype Designations
G30	Pakistan	G80	SCRID090-72-3-1-3-5
G31	SIM2 SUMADEL	G81	SCRID090-177-2-4-3-4
G32	WAS 127-12-1-2-1	G82	SCRID090-18-1-2-2-1
G33	IR-63275-B-1-1-13-2	G83	SCRID091-20-3-1-3-4
G34	IR-72593-B-B-2-3-14P1	G84	SCRID122-5-2-1-1-3
G35	HHZ 12-Y4-DT1-Y2	G85	SCRID122-13-1-1-4-3
G36	ARS755-5-B-B	G86	SCRID186-72-1-1-2
G37	CT18973-1-7-1-4SR-1P	G87	SCRID198-73-5-1-3
G38	HHZ12-SAL2-Y3-Y2	G88	Kb-2
G39	ARS 775-1-B-B	G89	Zongeng
G40	ARS 105-2-2-B	G90	Yuukeng
G41	Sahel134	G91	Selam (released variety)
G42	ARS-755-4-B-B	G92	Shaga (released variety)
G43	IR95786-9-2-1-2	G93	Wanzaye (released variety)
G44	IR98976-20-1-2-1	G94	Erib (released variety)
G45	IR92521-147-3-1-2	G95	Abay (released variety)
G46	IR98816-10-2-2-2	G96	Fogera-1 (released variety)
G47	IR99648-59-1-1	G97	Ediget (released variety)
G48	IR106358-B-B-AJY6	G98	NERICA-12 (released variety)
G49	IR97044-1-2-1-2	G99	X-jigina (The most cultivated cultivar)
G50	IR99637-6-1-1	G100	NERICA- 4 (released variety)

Analysis of Variance

Before running ANOVA, normality of data was checked by quantile- quantile plotting scale and box plot. All the studied traits was normal except some deviation for maximum tillering ability. For maximum tillering ability square root data transformation was done. SAS 9.4 was used for AVOVA analysis (SAS Institute Inc., 2013). Duncan's Multiple Range Test at 5% level of significance was used for genotypes mean comparisons, when genotype differences were found to be significant.

The ANOVA model for single location of triple Lattice design was as follows: $Pijk = \mu + \tau_i + \beta_{(j)} + \rho_j + \iota_k + \varepsilon_{ijk}$; where, P_{ijk} = phenotypic value of i^{th} genotype under j^{th} replication and k^{th} incomplete block within replication j, μ = grand mean, τ_i = the effect of i^{th} genotype, $\beta_{(j)}$ = j^{th} block effect (nested with in replication), ρ_j = the effect of replication j, ι_k = effect of k^{th} level of intra block error and ε_{ijk} = effect of random error.

Relative block efficiency (R.E.) of triple lattice design with respect to randomized complete block design was calculated as: $\text{R.E.} = \left[\dfrac{Block\text{ (adj.) SS+Intrablock error SS}}{r(k-1)+(k-1)(rk-k-1)}\right]\left[\dfrac{100}{\text{Error MS}}\right]$ where, 'r' = the number of replications and 'k' =

the block size (Gomez and Gomez, 1984).

Estimation of Phenotypic and Genotypic Variances:

The phenotypic and genotypic variance of each trait were estimated from the analysis of variance. Genotypic variance ($\sigma^2 g$), environmental variance ($\sigma^2 e$), phenotypic variance ($\sigma^2 p$), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was estimated using the formula adopted from Burton and De Vane (1953) as follows: $\sigma^2 g = \frac{\text{MSg - MSe}}{r}, \sigma^2 e = \text{MSe}, \sigma^2 p = \sigma^2 g + \sigma^2 e, \text{GCV}(\%) = \frac{\sqrt{\sigma^2 g}}{\text{grand mean}} * 100$ and $\text{PCV}(\%) = \frac{\sqrt{\sigma^2 p}}{\text{grand mean}} * 100$ where, MSg = mean square due to genotypes, MSe = error mean square (environ--mental variance) and r = Number of replications.

GCV and PCV values were categorized as low (0–10%), moderate (10–20%) and high (20% and above) (Johnson *et al.*, 1955).

Estimation of Broad Sense Heritability:

It was estimated by Johnson *et al.* (1955) formula: $H^2\% = \frac{\sigma^2 g}{\sigma^2 p} * 100$ where, H^2 % = heritability of broad sense in percentage, $\sigma^2 g$ = genotypic variance and $\sigma^2 p$ = phenotypic variance. According to Robinson *et al.* (1956), heritability can be categorized as low (0-40%), moderate (40-60%) and high (60% and above).

Estimation of expected genetic advance:

It was estimated by Johnson et al. (1955) formula: $\text{GA} = K * \sigma p * H^2$ where: GA= expected genetic advance under selection, K = the standardized selection differential constant at 5% selection intensity (K = 2.06), σp = phenotypic standard deviation and H^2 = heritability in broad sense. Moreover, the genetic advance as percent of mean was calculated by Robinson *et al.* (1949) formula as follows: $\text{GAM}(\%) = \frac{\text{GA}}{\text{Grand mean}} * 100$ Where: GAM (%) = genetic advance as percent of mean and GA = expected genetic advance.

Genetic advance in percent of mean can be categorized as low (0-10%), moderate (10-20%) and high (20% and above) as published by Johnson et al. (1955).

III. RESULT AND DISCUSSION

A. *Analysis of Variance*

Analysis of variance indicated that there were highly significant differences ($P < 0.01$) among 100 genotypes on maximum tillering ability, fertile tillers per plant, non-fertile tillers per plant, plant height, panicle length, filled spikelets per panicle, unfilled spikelets per panicle, days to 85% maturity, days to 50% heading, ground biomass yield, grain yield, harvest index and thousand grain weight (Table 2), which indicating the presence of sufficient variability for selection. Similarly, Ayenew *et al.* (2019) and Bekis *et al.* (2021) reported the existence of variability among their studied rain fed rice genotypes on plant height, panicle length, days to 50% heading, days to 85% maturity, filled spikelets per panicle, ground biomass yield and grain yield.

B. *Mean Performance and Range*

Grand mean values and ranges of the studied quantitative traits are presented in Table 2 and also mean performance of 100 rain fed rice genotypes on quantitative traits are presented in Table 3.

The mean values of maximum tillering ability per plant was 2.36, which ranged from 1.36 (G89) to 4.18 (G54). And the range values of fertile tillers per plant was from 1.12 to 3.38 for G58 and G54 genotypes, respectively with a mean value of 2.26. In case of fertile tillers per plant of the current result, G54, G48 and G5 genotypes showed significant result than the better check G98/NERICA-12 (1.93). These three genotypes may attracted by the view of breeders to have better fertile tiller variety for future breeding work. Similar results were reported by Bekis *et al.* (2021) and Lakew *et al.* (2021) with wide range of fertile tillers per plant among their studied rice genotypes. On the other way, the average values of non-fertile tillers per plant ranged from 0.13 to 1.56 for G52 and G40, respectively with a mean value of 0.72. Even though there was significant difference among 100 tested rice genotypes in non-fertile tillers per plant, no tested genotype that had significantly lower value of non-fertile tillers per plant as compared to the best check NERICA-12 (0.22).

Plant height ranged from 46.87 to 124.03cm with overall mean of 74.80cm. The maximum plant height was obtained from genotype G68 (124.03cm) followed by G17 (102.93cm), which were significantly different from the tallest check, Shaga (95.00cm). On the other hand, the minimum plant height were recorded at G65 (46.87cm) followed by G76 (48.93cm) and G34 (50.67cm). Hence, these wide variability in plant height gives a chance for selection and/or hybridization based on breeder’s objective. Corresponding results were reported by Dessie *et al.* (2020) and Lakew *et al.* (2021) with a wide of variation on plant height ranging from 60.4 to 87.4cm and 72.0 to 106.6cm, respectively. According to IRRI (2002), rice plant height is classified as semi-dwarf (<110cm), intermediate (110-130 cm) and tall (>130cm). Based on this classification, only G68 was classified as intermediate and the rest 99% tested rain fed rice genotypes including 10 released varieties were classified under the semi-dwarf.

Panicle length also showed significant difference among genotypes with a range of 15.07 to 22.8cm with a mean of 18.36cm. Maximum panicle length was recorded at G18 (22.8 cm) followed by genotype G68 (22.47cm), which were significantly different from the best released variety, NERICA-12 /G98 that had longest panicle length among released varieties. On the other hand, the minimum panicle length was noted at G59 (15.07cm) followed by genotype G58 (15.27cm) and G9 (16.00cm). In line with the present results, a wide range of panicle length variation (21 to 24cm) and (16.8 to 26.7cm) was reported by Bitew (2016) and Birhanu (2020) for rain fed rice genotypes, respectively. According to Bioversity International (2007), panicle length is classified as very short (<11cm), short (~15cm), medium (~25cm), long (~35cm) and very long (>40cm). Based on this classification, 87% of the tested genotypes were classified as short (>11 and $\leq$ 20) and the rest 13% genotypes were classified as medium (>20 and < 30).

The number of filled spikelets per panicle is one of the most important components of grain yield and the present study showed significant difference among the tested genotypes. The mean value was 85.51. Maximum number of filled spikelets per panicle was recorded at G4 (128.33), but it was not statistically significant from the best check Selam/G91 (125.93), which is recent released variety. And the minimum number of filled spikelets per panicle was recorded at G52 (63.13) and followed by G56 (63.2). On the hand, the maximum number of unfilled spikelets per panicle was recorded at G41 (18.47) and the minimum was G84 (3.13) with a mean value of 9.09. Although there was significant different among the studied genotypes, G84 was recorded the minimum number of unfilled spikeletss per panicle was not significant as compared to the best check, Wanzaye/G93. In line to the present study, significant variation was reported for filled and unfilled grains per panicle by Abebe (2016). Therefore these wide ranges of variability may be used for future breeding work.

Days to 50% heading showed significant difference in the tested genotypes with a range value of 39 days and grand mean of 107.04 days. The earlier days to 50% heading was recorded at G57 (89.67 days) and the longest time was recorded at G50 (128.67 days). The grand mean of days to 85% maturity was 141.13 days with a range of 47 days. The late genotype, G50 took 161 days for 85% maturity while the earlier genotype, G57 took 123.33 days. The earlier genotype for both days to 50% heading and days to 85% maturity was recorded at G57 (89.67 and 123.33 days) followed by G85 (91.67 and 124.33 days) with respective order. For days to 50% heading the two listed genotypes were significantly different from the earliest check, Wanzaye/G93 (97.67 days). These two genotypes are opportunities for developing early maturing variety through crossing that can escape terminal moisture stress. Similarly, Dessie *et al.* (2020) reported wide variations for both days to 50% heading (84.7 to 104.6 days) and days to 85% maturity (116.6 to 138.8 days) for rain fed rice.

Biomass yield showed wide range of variations from 5.45 to 11.78 tons ha^{-1} with a grand mean value of 8.68 tons ha^{-1}. The highest biomass was recorded from G86 followed by G52 and G18. And the minimum biomass was recorded at G73 followed G74. Correspondingly, Bekis *et al.* (2021) and Ayenew *et al.* (2019) found wide range of variation for their studied genotypes. This wide range of variability gives an opportunity for breeders for variety improvement.

The primary interest of breeders especially in developing countries is grain yield to ensure food security. In the present study, highly significant variability was found among the tested genotypes with range of 1.74 to 5.15 tons ha^{-1} and grand mean of 3.22 tons ha^{-1}. G43 was scored the highest grain yield followed by G4, G1, G41 and the recent released variety Selam/G91. Even though Selam is preceded by 4 genotypes, the yield difference was not statistically significant. Similarly, Dessie *et al.* (2020) and Lakew *et al.* (2021) reported wide variations on grain yield from 3.11 tons ha^{-1} to 4.84 tons ha^{-1} and 3.20 tons ha^{-1} to 5.20 tons ha^{-1}, respectively.

Harvest index also showed highly significant difference among the studied genotypes with the range of 21.78 to 54.11% and grand mean of 37.66%. The highest harvest index was recorded at G43 followed by G1 and the recent released variety, Selam/G91. While the two proceeded genotypes from Selam didn't show significant difference. The lowest harvest index was recorded by G52 followed by G58. Likewise, Abebe (2016) and Bekis *et al.* (2021) reported different range of harvest index, 17% to 36% and 23.38% to 62.57%, respectively.

Finally, thousand grain weight showed significant difference among the genotypes in a range of 19.49 to 39.18g and grand mean of 26.86g. The maximum thousand grain weight was recorded at G21 followed by G51 and G53. G21 showed significant difference from the best check, Wanzaye/G93. The minimum thousand grain weight was scored at G13 followed by G50. Similarly, Lakew *et al.* (2021) reported a wide range of thousand grain weight from 20.1 to 34.7g.

In general, the existence of a wide range of variability in most of the traits showed the presence of considerable variability among the tested rice genotypes, so this gives an opportunity for rice breeders to improve these traits through selection and crossing.

In the present study, coefficient of variation (CV) varies from 1.21% to 47.11% (Table 2). Since the value of

CV directly related to mean square of error (MSE), $\mathrm{CV} = \sqrt{(\mathrm{MSE} / \mathrm{Grand\ mean} * 100)}$ and this wide range of difference is due to the nature of character measured. Similarly, Gomez and Gomez (1984) reported that the value of coefficient of variation varies greatly with the type of experiment, the crop grown, and the character measured. On the other hand, the coefficient of determination was ranged from 0.66 to 0.98 (Table 2), which indicated that 66% to 98% the variation was due to the difference of the studied genotypes in each respective trait.

Table 2. Variability of 100 tested rice genotypes on 13 quantitative traits in Fogera district in 2021/22.

Traits	**Mean**	**Maximum Value**	**Minimum Value**	**Range**	**Mean Square**				**Coefficient of Determination (r^2)**	**Coefficient of Variation (%)**	**Relative Efficiency to RCBD by %**
					Replication (2)	**Block within Replication (adj.) (27)**	**Genotype (adj.) (99)**	**Intra Block Error (171)**			
MTA	2.36	4.18	1.36	2.82	0.03**	0.02**	0.02**	0.004	0.77	5.16	137.29
FTP	1.78	3.38	1.12	2.26	1.05**	0.55**	0.49**	0.13	0.74	20.49	143.48
NFT	0.72	1.56	0.13	1.43	0.43*	0.22**	0.31**	0.119	0.66	47.11	112.74
PH (cm)	74.8	124.03	46.87	77.16	47.43*	167.36**	493.06**	14.53	0.96	5.1	243.44
PL (cm)	18.36	22.8	15.07	7.73	1.56^{NS}	4.02**	5.02**	0.861	0.81	5.05	150.04
FSP	85.51	128.33	63.13	65.2	1021.25**	581.29**	488.83**	83.36	0.82	10.68	181.46
UFS	9.09	18.47	3.13	15.34	75.52**	21.29**	44.02**	6.803	0.81	28.71	129.03
DH	107.04	128.67	89.67	39	48.36**	25.32**	134.73**	1.69	0.98	1.21	290.62
DM	141.13	161	123.33	37.67	58.72**	31.54**	145.82**	4.185	0.96	1.45	189.14
BYD (ton/ha)	8.68	11.78	5.45	6.33	32.11**	6.15**	4.06**	1.97	0.66	16.18	128.96
AGY (ton/ha)	3.22	5.15	1.74	3.41	8.36**	1.05**	1.33**	0.232	0.82	14.93	148.15
HI (%)	37.66	54.11	21.78	32.33	98.67**	84.90**	165.69**	19.19	0.85	11.63	146.71
ATW (g)	26.86	39.18	19.49	19.69	34.12**	12.06**	45.39**	1.552	0.95	4.64	192.31

*, ** significant at 0.05 and 0.01 probability levels, respectively; NS = Non-significant; numbers in the bracket indicate degrees of freedom; MTA = maximum tillering ability; FTP = Number of fertile tillers per plant; NFT = Number of non-fertile tillers per plant; PH = Plant height; PL = panicle length; FSP = Number of filled spikelets per panicle; UFS = Number of unfilled spikelets per panicle; DM = Days to 85% maturity; DH = Days to 50% heading; BYD = Above ground biomass yield; AGY = Adjusted grain yield at 14% moisture content; HI = Harvest index; ATW = Adjusted thousand grain weight at 14% moisture content; and RCBD = Randomized complete block design.

Source: Own experiment data.

Table 3. The mean performance values of 13 yield and yield related traits of 100 rain fed rice genotypes in 2021/22.

Gen#	**MTA**	**FTP**	**NFT**	**PH**	**PL**	**FSP**	**UFS**	**DH**	**DM**	**BYD**	**AGY**	**HI**	**ATW**
1	1.69^{s-z}	1.25^{uvw}	0.49^{i-u}	79.60^{l-s}	17.47^{n-y}	98.00^{d-m}	$7.07^{p-f'}$	107.00^{t-w}	142.33^{o-v}	8.67^{b-p}	4.64^{abc}	53.88^{a}	28.30^{i-o}
2	2.60^{c-s}	2.01^{d-t}	0.70^{e-u}	$73.53^{q-a'}$	17.53^{n-y}	$81.00^{l-e'}$	$3.27^{e'-f'}$	$102.00^{c'-h'}$	$139.00^{u-a'}$	9.05^{a-o}	3.54^{d-u}	39.38^{e-s}	30.17^{d-k}
3	1.87^{p-z}	1.31^{q-w}	0.59^{g-u}	$72.60^{r-b'}$	17.87^{k-y}	100.73^{c-j}	$7.00^{q-f'}$	108.33^{o-s}	145.00^{k-r}	7.55^{g-r}	3.62^{d-s}	47.95^{a-e}	24.71^{s-z}
4	2.89^{h-y}	1.67^{j-w}	0.71^{e-u}	90.07^{e-j}	19.73^{b-k}	128.33^{a}	$6.93^{q-f'}$	107.00^{t-w}	141.00^{r-y}	10.45^{a-g}	4.79^{ab}	45.72^{a-i}	27.08^{l-s}

Gen#	MTA	FTP	NFT	PH	PL	FSP	UFS	DH	DM	BYD	AGY	HI	ATW
5	3.32^{a-i}	2.79^{abc}	0.53^{h-u}	$72.87^{r-a'}$	$16.33^{w-a'}$	$78.53^{n-e'}$	$6.13^{t-f'}$	107.67^{t-u}	143.67^{m-t}	7.45^{g-r}	3.65^{d-r}	48.65^{a-d}	26.07^{o-x}
6	1.57^{xyz}	1.25^{uvw}	0.32^{p-u}	$73.67^{q-a'}$	17.87^{k-y}	102.93^{b-g}	$6.07^{u-f'}$	108.67^{o-r}	145.33^{j-q}	8.56^{b-q}	3.86^{b-m}	44.84^{b-i}	25.57^{q-x}
7	2.07^{l-z}	1.49^{l-w}	0.61^{f-u}	$73.67^{q-a'}$	17.20^{q-y}	94.07^{e-r}	$5.87^{u-f'}$	97.33^{o-r}	$134.00^{d'-h'}$	10.17^{a-i}	$2.86^{n-f'}$	$27.98^{y-d'}$	$23.72^{x-e'}$
8	2.44^{g-x}	2.06^{c-q}	0.46^{j-u}	$70.27^{v'-d'}$	$16.13^{x-a'}$	$74.87^{s-e'}$	$3.87^{d'-f'}$	106.33^{t-x}	$138.33^{v-c'}$	9.00^{a-o}	3.43^{e-w}	39.14^{e-s}	30.06^{d-k}
9	1.87^{p-z}	1.44^{l-w}	0.47^{i-u}	$70.13^{v-d'}$	$16.00^{y-a'}$	92.53^{e-u}	$7.47^{o-f'}$	$101.33^{d'-i'}$	$136.00^{a'-g'}$	9.89^{a-j}	$2.54^{v-h'}$	$25.74^{b'-d'}$	$21.26^{f'-j'}$
10	2.60^{d-t}	1.78^{g-w}	0.82^{c-u}	$68.47^{w-f'}$	19.07^{c-q}	95.13^{e-p}	11.53^{e-t}	114.00^{f-k}	148.67^{f-k}	8.78^{b-o}	4.19^{b-h}	47.84^{a-e}	$24.63^{s-a'}$
11	3.84^{abc}	2.42^{b-i}	1.53^{ab}	$53.87^{l'-n'}$	18.00^{i-x}	91.00^{e-v}	12.27^{c-q}	117.00^{de}	153.33^{bcd}	8.55^{b-q}	3.71^{c-q}	43.43^{b-n}	$21.83^{c'-j'}$
12	2.06^{k-z}	1.88^{d-w}	0.29^{o-u}	$72.60^{r-b'}$	17.93^{j-x}	$65.20^{c'-e'}$	$6.00^{u-f'}$	$102.67^{a'-f'}$	$135.00^{a'-h'}$	8.22^{c-r}	$2.40^{x-h'}$	$29.29^{w-d'}$	30.61^{d-j}
13	2.94^{a-o}	2.00^{d-u}	1.02^{a-p}	$64.73^{c'-h'}$	19.87^{b-i}	$86.40^{f-b'}$	18.33^{a}	114.67^{e-j}	149.33^{e-j}	8.55^{b-q}	3.35^{e-x}	39.05^{e-s}	$19.49^{j'}$
14	2.77^{b-q}	1.95^{d-u}	0.91^{a-t}	$66.00^{a'-h'}$	17.47^{n-y}	$76.40^{p-e'}$	12.60^{c-o}	116.00^{efg}	150.00^{d-i}	8.22^{c-r}	$3.28^{h-a'}$	40.12^{d-s}	25.73^{p-x}
15	3.04^{a-m}	2.09^{c-p}	0.94^{a-s}	$71.13^{u-c'}$	20.00^{b-h}	101.80^{b-h}	18.07^{ab}	113.33^{h-l}	148.33^{f-k}	8.44^{c-q}	3.55^{d-u}	42.04^{c-p}	$20.69^{f'-j'}$
16	1.75^{s-z}	1.38^{n-w}	0.36^{n-u}	75.53^{p-x}	16.93^{s-z}	$79.27^{m-e'}$	$4.73^{y-f'}$	$101.00^{d'-j'}$	$133.33^{f'-h'}$	9.72^{a-k}	$2.57^{u-h'}$	$26.44^{z-d'}$	30.70^{d-i}
17	2.07^{l-z}	1.51^{l-w}	0.58^{g-u}	102.93^{b}	20.60^{bc}	$82.00^{j-e'}$	11.93^{d-s}	107.67^{t-u}	144.67^{k-s}	9.67^{a-k}	4.31^{a-f}	44.55^{b-j}	28.61^{h-n}
18	3.22^{a-k}	2.20^{c-l}	1.05^{a-o}	98.67^{bcd}	22.80^{a}	103.13^{b-g}	12.40^{c-p}	114.00^{f-k}	151.00^{d-g}	10.89^{abc}	4.34^{a-e}	40.16^{d-s}	$24.26^{u-c'}$
19	2.14^{j-z}	1.74^{g-w}	0.44^{k-u}	74.73^{p-y}	18.20^{g-w}	$68.73^{a'-e'}$	$6.73^{r-f'}$	$100.33^{f'-l'}$	$135.67^{a'-g'}$	9.72^{a-k}	$2.66^{r-h'}$	$27.40^{y-d'}$	31.83^{dc}
20	1.87^{p-z}	1.83^{e-w}	0.35^{n-u}	74.80^{p-y}	18.53^{e-v}	93.67^{e-s}	11.27^{f-u}	$99.33^{i'-n'}$	$133.00^{f'-h'}$	8.61^{b-p}	$3.20^{h-b'}$	37.20^{h-x}	26.92^{l-t}
21	2.07^{k-z}	1.61^{k-w}	0.49^{h-u}	$68.13^{x-f'}$	17.67^{m-y}	$70.53^{x-e'}$	$5.13^{x-f'}$	106.67^{t-x}	140.33^{t-z}	9.06^{a-o}	$3.01^{k-e'}$	$33.93^{p-b'}$	39.18^{a}
22	2.22^{i-y}	2.11^{c-n}	0.65^{e-u}	$94.73^{c'-f'}$	18.67^{d-u}	$74.33^{u-e'}$	$5.93^{u-f'}$	106.67^{t-x}	$139.00^{u-a'}$	8.78^{b-o}	3.74^{c-p}	42.80^{c-p}	29.40^{d-l}
23	2.07^{l-z}	1.42^{n-w}	0.69^{e-u}	$91.07^{e-i'}$	19.73^{b-k}	$79.40^{m-e'}$	$8.60^{k-e'}$	109.00^{n-q}	144.00^{l-t}	7.55^{g-r}	3.49^{d-v}	46.11^{a-i}	29.34^{d-l}
24	2.77^{b-q}	1.83^{e-w}	1.06^{a-n}	$61.53^{g'-k'}$	20.40^{b-e}	$76.33^{p-e'}$	17.40^{abc}	121.67^{b}	150.67^{d-h}	7.78^{f-r}	3.41^{e-w}	43.62^{b-m}	$24.28^{u-c'}$
25	2.60^{d-t}	1.76^{g-w}	0.86^{a-t}	92.33^{d-h}	19.60^{b-l}	$80.53^{m-e'}$	$7.13^{p-f'}$	107.67^{t-u}	141.00^{r-y}	8.89^{a-o}	3.82^{c-n}	43.32^{b-n}	29.88^{d-k}
26	2.44^{g-x}	1.75^{g-w}	0.74^{d-u}	94.00^{def}	20.27^{b-f}	$74.27^{u-e'}$	$8.27^{m-f'}$	108.00^{t-s}	141.33^{q-x}	7.89^{e-r}	3.64^{d-s}	46.09^{a-i}	30.53^{d-j}
27	2.89^{h-y}	1.77^{g-w}	0.61^{f-u}	$72.33^{s-c'}$	18.20^{g-w}	97.47^{d-n}	$6.67^{s-f'}$	109.00^{n-q}	146.33^{i-n}	8.89^{a-o}	3.99^{b-k}	44.93^{b-i}	24.69^{s-z}
28	2.76^{b-r}	1.96^{d-u}	0.86^{b-t}	$71.67^{t-c'}$	17.53^{n-y}	$70.40^{x-e'}$	$9.33^{i-c'}$	109.33^{npo}	148.33^{f-k}	5.78^{pqr}	$2.03^{e'-h'}$	$35.02^{l-a'}$	28.15^{j-p}

Table 3. The mean performance values of 13 yield and yield related traits of 100 rain fed rice genotypes in 2021/22 (continued).

Gen#	MTA	FTP	NFT	PH	PL	FSP	UFS	DH	DM	BYD	AGY	HI	ATW
29	2.01^{m-z}	1.48^{l-w}	0.55^{g-u}	74.33^{p-z}	17.87^{k-y}	96.93^{d-o}	11.53^{e-t}	$99.67^{h'-n'}$	$133.00^{f'-h'}$	9.05^{a-o}	$2.86^{n-f'}$	$31.60^{s-c'}$	26.43^{m-v}
30	1.87^{p-z}	1.51^{l-w}	0.38^{l-u}	79.13^{l-t}	17.07^{r-z}	$86.80^{e-a'}$	$3.87^{d'-f'}$	105.67^{t-y}	$139.00^{u-a'}$	10.78^{a-e}	$2.83^{n-f'}$	$26.27^{a'-d'}$	33.15^{bc}
31	3.22^{a-j}	2.42^{b-j}	0.83^{c-u}	$66.27^{a'-h'}$	17.47^{n-y}	$69.67^{y-e'}$	12.20^{c-q}	$111.33^{lm n}$	143.00^{n-u}	9.61^{a-l}	$3.08^{i-b'}$	$31.84^{s-b'}$	$19.99^{h'-j'}$
32	2.60^{c-s}	1.88^{d-w}	0.76^{d-u}	$59.13^{h'-l'}$	19.07^{c-q}	$70.67^{x-e'}$	13.93^{a-k}	$112.00^{kl m}$	146.67^{h-n}	7.45^{h-r}	$2.78^{p-g'}$	37.10^{i-x}	27.35^{l-r}
33	3.73^{a-e}	2.48^{b-h}	1.31^{a-f}	$59.27^{h'-l''}$	20.27^{b-f}	$81.53^{k-e'}$	$9.33^{i-c'}$	120.33^{bc}	153.00^{b-e}	9.56^{a-l}	4.08^{b-i}	42.39^{c-p}	25.45^{q-x}
34	3.95^{ab}	2.62^{bcd}	1.42^{a-d}	$50.67^{m'-o'}$	17.33^{p-y}	$78.53^{n-e'}$	16.13^{a-f}	115.00^{e-i}	148.67^{f-k}	7.78^{f-r}	$2.69^{r-h'}$	$34.64^{m-b'}$	$24.32^{u-b'}$
35	2.52^{e-v}	2.36^{b-k}	0.73^{d-u}	$64.93^{b'-h'}$	18.20^{g-w}	$81.53^{k-e'}$	13.60^{a-m}	112.67^{i-m}	145.00^{k-r}	9.11^{a-o}	3.75^{c-p}	41.24^{c-q}	$23.97^{u-d'}$

Gen#	MTA	FTP	NFT	PH	PL	FSP	UFS	DH	DM	BYD	AGY	HI	ATW
36	2.60 $^{c-s}$	1.54 $^{l-w}$	1.18 $^{a-h}$	56.07 $^{i'-m'}$	17.87 $^{k-y}$	74.27 $^{u-e'}$	16.07 $^{a-f}$	112.67 $^{i-m}$	147.33 $^{g-m}$	7.56 $^{g-r}$	3.09 $^{i-b'}$	41.14 $^{c-r}$	20.16 $^{g'-j'}$
37	2.77 $^{b-q}$	1.94 $^{d-u}$	0.89 $^{a-t}$	63.27 $^{d'-i'}$	19.40 $^{c-n}$	78.13 $^{o-e'}$	12.13 $^{d-r}$	112.00 $^{kl m}$	144.67 $^{k-s}$	7.33 $^{i-r}$	3.33 $^{f-x}$	45.99 $^{a-i}$	25.57 $^{q-x}$
38	3.84 ^{abc}	2.49 $^{b-g}$	1.47 ^{abc}	54.20 $^{l'-n'}$	19.00 $^{c-r}$	79.47 $^{m-e'}$	14.53 $^{a-i}$	113.00 $^{i-m}$	147.00 $^{g-n}$	8.44 $^{c-q}$	3.63 $^{d-s}$	43.01 $^{c-o}$	21.93 $^{b'-j'}$
39	3.04 $^{a-m}$	2.10 $^{c-o}$	1.02 $^{a-p}$	55.33 $^{j'-n'}$	17.47 $^{n-y}$	75.47 $^{r-e'}$	11.93 $^{d-s}$	112.00 $^{kl m}$	146.33 $^{i-n}$	7.94 $^{d-r}$	3.42 $^{e-w}$	44.25 $^{b-k}$	21.54 $^{d'-j'}$
40	3.73 $^{a-f}$	2.20 $^{c-l}$	1.56 ^{a}	56.47 $^{i'-m'}$	17.53 $^{n-y}$	81.13 $^{k-e'}$	13.73 $^{a-l}$	111.33 $^{lm n}$	145.67 $^{j-p}$	7.72 $^{f-r}$	3.36 $^{e-x}$	43.62 $^{b-m}$	20.74 $^{f'-j'}$
41	3.32 $^{a-i}$	2.08 $^{c-p}$	1.26 $^{a-g}$	57.33 $^{i'-m'}$	18.20 $^{g-w}$	85.53 $^{f-b'}$	18.47 ^{a}	111.33 $^{l m n}$	146.33 $^{i-n}$	9.33 $^{a-n}$	4.63 ^{abc}	49.81 ^{abc}	22.20 $^{a'-h'}$
42	3.13 $^{a-l}$	2.03 $^{d-s}$	1.09 $^{a-l}$	54.27 $^{k'-n'}$	17.73 $^{l-y}$	78.87 $^{n-e'}$	9.00 $^{j- d'}$	112.00 ^{klm}	146.67 $^{h-n}$	8.55 $^{b-q}$	3.80 $^{c-n}$	43.84 $^{b-l}$	21.82 $^{c'-j'}$
43	3.32 $^{a-i}$	2.18 $^{c-m}$	1.18 $^{a-h}$	60.53 $^{g'-l'}$	17.93 $^{j-x}$	72.93 $^{v-e'}$	9.47 $^{h-b'}$	110.67 $^{m n o}$	145.67 $^{j-p}$	9.56 $^{a-l}$	5.15 ^{a}	54.11 ^{a}	24.03 $^{u-c'}$
44	2.86 $^{b-r}$	1.71 $^{i-w}$	1.11 $^{a-k}$	62.20 $^{g'-j'}$	19.80 $^{b-j}$	84.47 $^{g-b'}$	14.67 $^{a-i}$	113.00 $^{i-m}$	148.00 $^{f-l}$	8.16 $^{c-r}$	3.88 $^{b-l}$	47.29 $^{a-f}$	23.79 $^{w-e'}$
45	2.14 $^{i-z}$	1.37 $^{n-w}$	0.84 $^{b-u}$	79.07 $^{l-t}$	19.27 $^{c-p}$	99.73 $^{c-l}$	17.07 $^{a-d}$	112.00 ^{klm}	147.33 $^{g-m}$	7.45 $^{h-r}$	2.78 $^{p-g'}$	37.27 $^{h-x}$	21.05 $^{f'-j'}$
46	3.22 $^{a-k}$	2.05 $^{d-r}$	1.17 $^{a-j}$	66.87 $^{z-g'}$	20.47 ^{bcd}	82.93 $^{i-d'}$	16.67 $^{a-e}$	113.67 $^{g-l}$	147.67 $^{f-m}$	9.45 $^{a-m}$	3.82 $^{c-n}$	40.34 $^{d-s}$	22.01 $^{b'-i'}$
47	3.22 $^{a-k}$	2.41 $^{b-j}$	0.90 $^{a-t}$	66.47 $^{a'-h'}$	18.80 $^{c-t}$	93.67 $^{e-s}$	14.27 $^{a-j}$	120.67 ^{b}	155.00 ^{bc}	9.33 $^{a-n}$	3.42 $^{e-w}$	37.22 $^{h-x}$	22.22 $^{a'-h'}$
48	3.95 ^{ab}	2.91 ^{ab}	1.09 $^{a-}$	61.67 $^{g'-j'}$	19.33 $^{c-o}$	88.47 $^{e-y}$	10.60 $^{h-w}$	121.67 ^{b}	151.67 $^{c-f}$	9.78 $^{a-k}$	4.01 $^{b-k}$	41.31 $^{c-q}$	22.50 $^{z-g'}$
49	2.86 $^{a-p}$	1.67 $^{i-w}$	1.17 $^{a-j}$	62.33 $^{g'-j'}$	18.33 $^{g-v}$	77.13 $^{p-e'}$	7.00 $^{q- f'}$	118.33 ^{cd}	151.67 $^{c-f}$	9.78 $^{a-j}$	3.77 $^{c-p}$	38.62 $^{u-f}$	21.86 $^{c'-j'}$
50	3.84 $^{a-d}$	2.53 $^{b-f}$	1.34 $^{a-e}$	59.13 $^{h'-l'}$	20.47 ^{bcd}	96.47 $^{d-o}$	8.40 $^{l- f'}$	128.67 ^{a}	161.00 ^{a}	9.55 $^{a-l}$	3.06 $^{j-c'}$	31.65 $^{s-c'}$	19.71 $^{i' j'}$
51	1.88 $^{o-z}$	1.45 $^{l-w}$	0.45 $^{k-u}$	79.67 $^{l-s}$	19.00 $^{c-r}$	71.60 $^{w-e'}$	5.00 $^{x- f'}$	101.00 $^{d'-j'}$	136.00 $^{a'-g'}$	8.33 $^{c-r}$	2.48 $^{w-h'}$	29.69 $^{u-d'}$	35.11 ^{b}
52	1.52 ^{yz}	1.41 $^{n-w}$	0.13 ^{u}	81.60 $^{k-p}$	18.53 $^{e-v}$	63.13 $^{e'}$	3.93 $^{c'- f'}$	102.67 $^{a'-f'}$	137.67 $^{x-e'}$	11.39 ^{ab}	2.47 $^{w-h'}$	21.78 $^{d'}$	34.52 ^{b}
53	1.69 $^{s-z}$	1.95 $^{d-u}$	0.66 $^{e-u}$	81.67 $^{k-p}$	18.80 $^{c-t}$	70.33 $^{x-e'}$	3.87 $^{d'- f'}$	102.67 $^{a'-f'}$	138.00 $^{w-d'}$	9.72 $^{a-k}$	2.51 $^{v-h'}$	26.43 $^{z-d'}$	35.06 ^{b}
54	4.18 ^{a}	3.38 ^{a}	0.85 $^{b-t}$	86.00 $^{g-l}$	19.27 $^{c-p}$	90.67 $^{e-v}$	8.93 $^{j- d'}$	108.00 $^{t-s}$	142.00 $^{p-w}$	9.28 $^{a-n}$	4.28 $^{a-g}$	46.71 $^{a-g}$	22.69 $^{y-f'}$
55	2.52 $^{e-v}$	1.90 $^{d-v}$	0.65 $^{e-u}$	101.3 ^{bc}	20.47 ^{bcd}	116.13 ^{abc}	14.80 $^{a-h}$	112.00 ^{klm}	145.67 $^{j-p}$	8.67 $^{b-p}$	4.04 $^{b-j}$	47.36 $^{a-f}$	22.57 $^{y-f'}$
56	2.44 $^{g-x}$	1.79 $^{f-w}$	0.68 $^{e-u}$	71.13 $^{u-c'}$	17.40 $^{o-y}$	63.20 $^{e'}$	9.60 $^{h- a'}$	99.00 ^{klm}	136.00 $^{a'-g'}$	8.33 $^{c-r}$	2.48 $^{w-h'}$	30.48 $^{t-d'}$	31.48 $^{c-g}$

Table 3. The mean performance values of 13 yield and yield related traits of 100 rain fed rice genotypes in 2021/22 (continued).

Gen#	MTA	FTP	NFT	PH	PL	FSP	UFS	DH	DM	BYD	AGY	HI	ATW
57	2.60 $^{e-u}$	1.74 $^{h-w}$	0.86 $^{b-t}$	71.13 $^{u-c'}$	17.33 $^{p-y}$	75.87 $^{q-e'}$	6.67 $^{s- f'}$	89.67 $^{p'}$	123.33 $^{j'}$	7.50 $^{h-r}$	3.32 $^{f-y}$	44.20 $^{b-k}$	28.17 $^{j-p}$
58	1.69 $^{s-z}$	1.12 ^{w}	0.61 $^{f-u}$	71.60 $^{t-c'}$	15.27 $^{z-a'}$	70.60 $^{x-e'}$	10.20 $^{h-x}$	100.33 $^{f'-l'}$	133.33 $^{f'-h'}$	7.50 $^{h-r}$	1.74 $^{h'}$	22.83 $^{c'-d'}$	34.60 ^{b}
59	2.89 $^{h-y}$	1.52 $^{l-w}$	0.75 $^{d-u}$	75.40 $^{p-y}$	15.07 $^{a'}$	84.87 $^{g-b'}$	9.87 $^{h- z}$	107.00 $^{t-w}$	142.00 $^{p-w}$	6.53 $^{m-r}$	2.58 $^{u-h'}$	38.52 $^{u-f}$	31.71 ^{cde}
60	1.75 $^{r-z}$	1.38 $^{n-w}$	0.39 $^{l-u}$	80.07 $^{k-s}$	18.33 $^{g-v}$	92.27 $^{e-u}$	7.27 $^{o - f'}$	106.67 $^{t-x}$	138.67 $^{v-b'}$	8.33 $^{c-r}$	2.31 $^{z-h'}$	27.52 $^{y-d'}$	31.74 ^{dc}
61	1.94 $^{n-z}$	1.69 $^{i-w}$	0.26 $^{r-u}$	79.07 $^{l-t}$	18.40 $^{f-v}$	92.47 $^{e-u}$	9.93 $^{h- z}$	105.33 $^{u-z}$	138.33 $^{v-c'}$	8.33 $^{c-r}$	2.65 $^{s-h'}$	31.94 $^{s-b'}$	29.03 $^{g-l}$
62	1.87 $^{p-z}$	1.42 $^{m-w}$	0.46 $^{j-u}$	89.53 $^{e-j}$	17.87 $^{k-y}$	103.80 $^{b-f}$	4.07 $^{b'- f'}$	104.33 $^{x-c}$	136.67 $^{a'-g'}$	10.45 $^{a-g}$	2.82 $^{n-f'}$	26.84 $^{y-d'}$	25.29 $^{r-x}$
63	1.81 $^{q-z}$	1.49 $^{l-w}$	0.34 $^{o-u}$	78.20 $^{m-u}$	16.93 $^{s-z}$	69.40 $^{z-e'}$	4.13 $^{b'- f'}$	102.00 $^{c'-h'}$	134.67 $^{b'-h'}$	7.78 $^{f-r}$	2.32 $^{y-h'}$	30.02 $^{u-d'}$	30.43 $^{d-k}$
64	2.52 $^{f-w}$	1.63 $^{k-w}$	0.91 $^{a-t}$	84.20 $^{i'-n}$	18.60 $^{d-v}$	84.40 $^{g-b'}$	7.67 $^{n- f'}$	101.00 $^{d'-j'}$	133.33 $^{f'-h'}$	9.44 $^{a-m}$	3.04 $^{k-d'}$	32.43 $^{q-b'}$	30.35 $^{d-k}$
65	2.60 $^{e-u}$	1.61 $^{k-w}$	0.98 $^{a-q}$	46.87 $^{o'}$	16.40 $^{w-a'}$	83.80 $^{h-c'}$	7.40 $^{o - f'}$	116.33 ^{def}	153.00 $^{b-e}$	7.22 $^{j-r}$	2.53 $^{v-h'}$	35.17 $^{l-a'}$	21.41 $^{e'-j'}$
66	1.57 ^{xyz}	1.27 $^{s-w}$	0.30 $^{o-u}$	77.13 $^{n-v}$	17.33 $^{p-y}$	76.33 $^{p-e'}$	5.80 $^{v- f'}$	102.67 $^{a'-f'}$	135.67 $^{a'-g'}$	10.55 $^{a-f}$	2.96 $^{l-f'}$	27.90 $^{y-d'}$	31.42 $^{c-g}$

Gen#	MTA	FTP	NFT	PH	PL	FSP	UFS	DH	DM	BYD	AGY	HI	ATW
67	2.22^{i-z}	1.75^{g-w}	0.47^{i-u}	80.20^{k-r}	17.73^{l-y}	94.67^{e-q}	$7.80^{n-f'}$	$103.00^{z-e'}$	$136.00^{a'-g'}$	9.72^{a-k}	$3.06^{j-c'}$	$32.17^{s-b'}$	28.67^{h-m}
68	2.23^{i-y}	1.65^{k-w}	0.61^{f-u}	124.03^{a}	22.47^{a}	105.33^{b-e}	$4.67^{z-f'}$	$104.67^{w-b'}$	$135.67^{a'-g'}$	10.89^{abc}	3.77^{c-p}	$34.57^{n-b'}$	$24.46^{t-a'}$
69	2.14^{i-z}	1.56^{l-w}	0.61^{f-u}	$69.27^{w-e'}$	18.67^{d-u}	$77.07^{p-e'}$	14.40^{a-i}	$99.33^{i'-n'}$	$134.67^{b'-h'}$	6.72^{l-r}	$1.82^{g'-h'}$	$28.69^{x-d'}$	26.97^{l-t}
70	2.06^{k-z}	1.49^{l-w}	0.63^{f-u}	$67.60^{y-g'}$	17.47^{n-y}	$72.07^{v-e'}$	10.13^{h-y}	106.00^{t-x}	$138.00^{w-d'}$	6.45^{n-r}	$2.26^{b'-h'}$	35.67^{j-y}	25.00^{r-y}
71	2.44^{g-x}	1.71^{i-w}	0.73^{d-u}	$71.80^{t-c'}$	17.53^{n-y}	$73.93^{u-e'}$	12.93^{b-n}	$100.67^{e'-k'}$	$137.00^{y-f'}$	6.34^{o-r}	$2.39^{x-h'}$	37.11^{i-x}	24.82^{r-z}
72	1.63^{w-z}	1.29^{r-w}	0.35^{n-u}	$69.13^{w-e'}$	17.60^{m-y}	$64.67^{d'-e'}$	12.53^{c-o}	$100.00^{g'-m'}$	$134.33^{c'-h'}$	7.61^{g-r}	$2.07^{c'-h'}$	$27.37^{y-d'}$	26.96^{l-t}
73	2.22^{i-z}	1.48^{l-w}	0.74^{d-u}	$66.73^{z-g'}$	17.00^{s-z}	$64.13^{d'-e'}$	$9.47^{h-b'}$	108.67^{o-r}	140.67^{s-z}	5.45^{r}	$2.06^{d'-h'}$	38.65^{u-f}	26.50^{m-u}
74	1.69^{s-z}	1.26^{t-w}	0.43^{k-u}	$71.47^{t-c'}$	17.67^{m-y}	87.87^{e-z}	$6.93^{q-f'}$	107.67^{t-u}	141.00^{r-y}	5.67^{qr}	$2.78^{p-g'}$	48.96^{a-d}	25.79^{p-x}
75	3.63^{a-g}	2.01^{d-t}	1.46^{abc}	$65.07^{b'-h'}$	21.27^{ab}	88.13^{e-z}	16.00^{a-g}	112.33^{j-m}	148.00^{f-l}	8.56^{b-q}	3.91^{b-l}	46.95^{a-f}	27.01^{l-s}
76	2.77^{b-q}	2.11^{c-n}	0.71^{e-u}	$48.93^{n'o'}$	18.20^{g-w}	$67.53^{b'-e'}$	12.60^{c-o}	113.00^{i-m}	148.00^{f-l}	7.45^{h-r}	3.30^{g-z}	43.95^{b-l}	$23.93^{v-d'}$
77	1.87^{p-z}	1.62^{k-w}	0.30^{o-u}	76.27^{o-v}	18.13^{h-w}	99.93^{c-k}	$6.33^{t-f'}$	$98.33^{k'-n'}$	$132.33^{g'-i'}$	8.33^{c-r}	$3.19^{h-b'}$	39.26^{e-s}	27.08^{l-s}
78	1.64^{u-z}	1.34^{o-w}	0.33^{p-u}	75.53^{p-x}	18.07^{i-w}	$82.27^{i-d'}$	$7.87^{n-f'}$	$98.00^{l''-n'}$	$132.33^{g'-i'}$	8.05^{c-r}	$2.88^{m-f'}$	35.73^{j-y}	30.33^{d-k}
79	1.81^{p-z}	1.27^{s-w}	0.59^{g-u}	$69.07^{w-f'}$	$16.67^{v-a'}$	$80.33^{m-e'}$	$5.20^{w-f'}$	$94.67^{o'}$	$129.00^{i'}$	8.33^{c-r}	$2.60^{t-h'}$	$31.37^{s-c'}$	29.86^{d-k}
80	1.94^{n-z}	1.32^{q-w}	0.64^{e-u}	80.00^{k-s}	17.80^{l-y}	93.33^{e-t}	$6.67^{s-f'}$	105.33^{u-z}	$139.00^{u-a'}$	9.06^{a-o}	$2.33^{y-h'}$	$25.64^{b'-d'}$	31.57^{c-f}
81	2.06^{k-z}	1.71^{i-w}	0.43^{k-u}	80.60^{k-q}	18.20^{g-w}	97.47^{d-n}	$8.33^{m-f'}$	$102.67^{a'-f'}$	$134.00^{d'-h'}$	9.89^{a-j}	$2.73^{q-g'}$	$27.69^{y-d'}$	29.23^{e-l}
82	2.29^{h-y}	1.41^{n-w}	0.89^{a-t}	83.13^{j-o}	19.00^{c-r}	92.00^{e-u}	$4.73^{r-f'}$	$102.33^{b'-g'}$	$133.67^{e'-h'}$	9.33^{a-n}	$2.79^{o-g'}$	$29.85^{u-d'}$	31.09^{c-h}
83	1.88^{o-z}	1.33^{p-w}	0.60^{g-u}	89.07^{e-j}	18.47^{f-v}	101.00^{b-i}	$5.13^{x-f'}$	$102.33^{b'-g'}$	$135.00^{a'-h'}$	9.44^{a-m}	$2.94^{l-f'}$	$31.53^{s-c'}$	25.49^{q-x}

Table 3. The mean performance values of 13 yield and yield related traits of 100 rain fed rice genotypes in 2021/22 (continued).

Gen#	MTA	FTP	NFT	PH	PL	FSP	UFS	DH	DM	BYD	AGY	HI	ATW
84	2.95^{a-n}	2.09^{c-o}	0.88^{a-t}	92.80^{d-g}	17.40^{o-y}	$70.47^{x-e'}$	$3.13^{f'}$	107.33^{t-v}	$139.00^{u-a'}$	8.61^{b-p}	$2.96^{l-f'}$	$34.21^{o-b'}$	28.54^{i-o}
85	3.63^{a-g}	2.08^{c-p}	1.20^{a-h}	74.73^{p-y}	17.80^{l-y}	89.73^{e-w}	$5.73^{v-f'}$	$91.67^{p'}$	$124.33^{j'}$	8.11^{c-r}	3.54^{d-u}	46.18^{a-h}	27.92^{k-q}
86	1.75^{s-z}	1.38^{n-w}	0.36^{n-u}	92.73^{d-g}	19.13^{c-q}	103.93^{b-f}	$7.13^{p-f'}$	104.33^{x-c}	$136.67^{a'-g'}$	11.78^{a}	3.42^{e-w}	$29.24^{w-d'}$	30.35^{d-k}
87	3.42^{a-h}	2.54^{b-e}	0.95^{a-r}	98.53^{bcd}	17.87^{k-y}	$74.47^{t-e'}$	$5.13^{x-f'}$	106.00^{t-x}	$138.67^{v-b'}$	10.00^{a-j}	$3.23^{h-b'}$	$32.23^{r-b'}$	28.78^{h-m}
88	2.01^{m-z}	1.41^{n-w}	0.60^{f-u}	85.07^{h-m}	18.87^{c-s}	113.33^{a-d}	$5.93^{u-f'}$	106.33^{t-x}	142.00^{p-w}	8.56^{b-q}	3.74^{c-p}	44.83^{b-i}	26.12^{n-x}
89	1.36^{z}	1.17^{vw}	0.23^{stu}	90.20^{e-j}	20.60^{bc}	113.67^{a-d}	$8.13^{n-f'}$	115.67^{e-h}	155.67^{b}	7.78^{f-r}	3.79^{c-o}	48.85^{a-d}	26.31^{m-w}
90	2.07^{l-z}	1.69^{i-w}	0.37^{n-u}	85.73^{g-m}	20.40^{b-e}	118.47^{ab}	10.73^{g-v}	112.67^{i-m}	150.00^{d-i}	8.67^{b-p}	4.17^{b-h}	47.85^{a-e}	29.17^{f-l}
91	2.36^{h-y}	1.70^{i-w}	0.69^{e-u}	$90.93^{e-i'}$	19.47^{b-m}	125.93^{a}	$6.87^{q-f'}$	106.33^{t-x}	141.67^{p-x}	8.55^{b-q}	4.43^{a-d}	51.97^{ab}	26.43^{m-v}
92	2.36^{h-y}	1.65^{k-w}	0.73^{d-u}	95.00^{cde}	17.07^{r-z}	100.00^{c-k}	$3.47^{e'-f'}$	$99.00^{i'-n'}$	$133.67^{e'-h'}$	10.56^{a-f}	3.76^{c-p}	35.63^{j-y}	$24.60^{s-a'}$
93	2.36^{h-y}	1.88^{d-w}	0.49^{i-u}	83.13^{j-o}	18.00^{i-x}	$72.87^{v-e'}$	$3.27^{e'-f'}$	$97.67^{m'n'}$	$131.33^{h'I'}$	8.61^{b-p}	3.59^{d-t}	42.77^{c-p}	34.30^{b}
94	2.07^{l-z}	1.51^{l-w}	0.54^{h-u}	$70.07^{v-d'}$	16.93^{s-z}	$80.73^{m-e'}$	$6.93^{q-f'}$	$98.33^{k'-n'}$	$132.33^{g'-i'}$	9.06^{a-o}	$2.61^{t-h'}$	$29.54^{v-d'}$	25.31^{r-x}
95	2.01^{m-z}	1.46^{l-w}	0.53^{h-u}	$69.27^{w-e'}$	16.87^{t-z}	$70.87^{w-e'}$	$5.67^{v-f'}$	106.67^{t-x}	141.33^{q-x}	6.56^{m-r}	$2.29^{a'-h'}$	35.43^{k-z}	27.26^{l-r}
96	2.01^{m-z}	1.31^{q-w}	0.72^{e-u}	$73.40^{q-a'}$	18.80^{c-t}	88.80^{e-x}	10.93^{f-v}	$98.67^{j'-n'}$	$131.00^{h'I'}$	9.45^{a-m}	3.63^{d-s}	38.45^{f-v}	28.15^{j-p}
97	1.68^{t-z}	1.29^{r-w}	0.37^{n-u}	$71.53^{t-c'}$	$16.73^{u-a'}$	$78.67^{n-e'}$	$4.40^{a'-f'}$	$102.33^{b'-g'}$	$135.00^{b'-h'}$	6.84^{k-r}	$2.00^{f'-h'}$	$29.16^{w-d'}$	29.20^{f-l}

Gen#	MTA	FTP	NFT	PH	PL	FSP	UFS	DH	DM	BYD	AGY	HI	ATW
98	2.14^{j-z}	1.93^{d-u}	0.22^{tu}	87.33^{f-k}	20.07^{b-g}	88.40^{e-z}	10.00^{h-z}	$103.33^{y-d'}$	$138.00^{w-d'}$	10.28^{a-h}	$2.97^{l'-f'}$	$28.93^{w-d'}$	31.33^{c-g}
99	2.36^{h-y}	1.84^{e-w}	0.63^{e-u}	88.93^{e-j}	18.73^{c-t}	$86.40^{f-b'}$	$9.73^{h-a'}$	$105.00^{v-a'}$	$138.33^{v-c'}$	10.83^{a-d}	$2.87^{m-f'}$	$27.05^{y-d'}$	26.16^{n-x}
100	1.63^{s-z}	1.31^{q-w}	0.38^{m-u}	$73.67^{q-a'}$	18.07^{i-w}	92.47^{e-u}	$7.93^{n-f'}$	$99.67^{h'-n'}$	$133.00^{f'-h'}$	8.61^{b-p}	$3.21^{h-b'}$	37.75^{g-w}	26.44^{m-v}
GM	2.36	1.78	0.72	74.80	18.36	85.51	9.09	107.04	141.13	8.68	3.22	37.66	26.86
SE(d)	0.04	0.21	0.20	2.20	0.54	5.27	1.51	0.75	1.18	0.81	0.28	2.53	0.72
CV%	5.16	20.49	47.11	5.10	5.05	10.68	28.71	1.3	1.45	16.18	14.93	11.63	4.64

Any two means in the same letter are not significantly different at 5% level of significance according to Duncan's Multiple Range Test. MTA = Fourth root data transformation value of maximum tillering ability; FTP = Number of fertile tillers per plant; NFT = Number of Non-fertile tillers per plant; PH = Plant height (cm); PL = Panicle length; FSP = Number of filled spikelets per panicle; UFS = Number of unfilled spikelets per panicle; DM = Days to 85% maturity; DH = Days to 50% heading; BYD = Above ground biomass yield (ton/ha); AGY = Adjusted grain yield (kg/ha) at 14% moisture content; HI = Harvest Index %; ATW = Adjusted thousand grain weight (g) at 14% moisture content; GM = Grand mean; SE(d) = standard error of treatment mean difference; whereas Gen# =genotype number and its designations are depicted in Table 1. Source: Own experiment data.

The relative efficiency of triple lattice design to randomized complete block design was varied for each trait ranging from 112.74% (number of non-fertile tillers per plant) to 290.62% (days to 50% heading) (Table 2). This implies that triple lattice design was relatively efficient over randomized complete block design with range of 12.74 to 190.62% with the respective traits if it was done by randomized complete block design. Therefore, the choice of triple lattice design over randomized complete block design was the right decision and the analysis of variance were done by triple lattice design.

C. *Estimation of Genotypic and Phenotypic Variations*

The estimation σ^2g, σ^2p, σ^2e, GCV and PCV of all the studied traits are presented in Table 4. The GCV and PCV of the studied quantitative traits were varied from 8.52% to 72.18% and 8.64% to 86.62%, respectively.

Similarly, wide range of GCV (8.44% to 38.30%) and PCV (8.53% to 39.37%) was reported by Bekis *et al.* (2021) for different traits of their studied rice genotypes.

In the present study, high GCV and PCV estimations were recorded from non-fertile tillers per plant, fertile tillers per plant, unfilled spikelets per panicle, above ground biomass yield, plant height, harvest index, thousand grain weight, filled spikelets per panicle and grain yield. Moderate GCV and PCV estimations were scored on maximum tillering ability, panicle length and days to 50% heading. And low GCV and PCV estimations were scored on days to 85% maturity.

According to Allard (2000) and Osman *et al.* (2012) the extent of the environmental influence on any trait is indicated by the magnitude of the differences between the GCV and PCV. Large differences reflect high environmental influence, while small differences reveal high genetic influence. In the present study, relatively large differences of GCV and PCV were observed from number of non-fertile tillers per plant, fertile tillers per plant, unfilled spikelets per panicle and biomass yield, which indicated that high influence of the environment and selection may not be effective for these traits. Similarly, large difference of GCV and PCV was reported for fertile tillers per plant, unfilled spikelets per panicle and biomass yield for different rain fed genotypes by Abebe (2016). Instead, small difference of GCV and PCV of the present study were scored on maximum tillering ability, plant height, panicle length, days to 85% maturity, days to 50% heading, harvest index, thousand grains weight, filled spikelets per panicle, and grain yield. These small difference of GCV and PCV indicated that high genetic influence of those traits and selection may be effective. Similarly, Bekis *et al.* (2021) and Birhanu (2020) reported small difference of GCV and PCV from plant height, panicle length, days to 85% maturity, days to 50% heading, harvest index, 1000 grains weight, filled spikelets per panicle, and grain yield of their studied rice genotypes.

D. *Estimated of Broad Sense Heritability and Genetic Advance*

Estimated H^2 %, GA and GAM of the studied traits are also presented in Table 4. Heritability estimates of the 13 studied quantitative traits ranged from 63.34% for biomass yield to 98.76% for days to 50% heading. All the studied 13 quantitative traits scored high heritability. In agreement with the current findings, Bekis *et al.* (2021) reported high heritability for fertile tillers per plant, plant height, panicle length, filled spikeletss per panicle, unfilled spikelets per panicle, days to 85% maturity, days to 50% heading, biomass yield, grain yield, thousand grain weight and harvest index for different rain fed rice genotypes. Similarly, Birhanu (2020) scored high heritability for plant height, filled spikelets per panicle, panicle length, thousand grain weight and days to 85% maturity for rain fed rice genotypes. Differently, low heritability was reported by Abebe (2016) for days to 50% heading, days to 85% maturity, filled grain per panicle and thousand grains weight. According to Atlin (2003), highly heritable traits are easily measured and can be used for rapid screening of large volumes of early generation materials for specific traits and to select indirectly for associated traits with low heritability. However, it is better to decide the traits that might be used for rapid screening in line with genetic advance as percent of mean because high heritability may not be always associated with high genetic advance (Johnson *et al.*, 1955).

The GAM values of the present findings varied from 17.32% to 136.05%. Maximum GAM was recorded unfilled spikelets per panicle followed by non-fertile tillers per plant (124.07%), fertile tillers per plant (68.36%) and grain yield (65.87%). High heritability coupled with high GAM unfilled-spikelets per panicle, filled spikelets per panicle, non-fertile tillers per plant, fertile tillers per plant, grain yield, plant height, harvest index, biomass yield and thousand grain weight. And also high heritability tied with high GAM for maximum tillering ability, panicle length and days to 50% heading. High heritability associated with high genetic advance is mainly due to additive gene effect, but when high heritability associated with low genetic advance, the heritability is due to dominance and epistasis (Nirmaladevi *et al.*, 2015). Accordingly, the present study had high heritability associated with high genetic advance of mean for 12 studied quantitative traits and high heritability associated with moderate GAM for days to 85% maturity. Therefore, all the13 studied quantitative traits were representative traits for selection.

In line with the present study, Bekis *et al.* (2021a) reported high heritability together with high GAM for unfilled spikelets per panicle, plant height, biomass yield, grain yield and harvest index for different rain fed rice genotypes. Similarly, Abebe (2016) scored high heritability joined with high GAM exhibited for plant height and biomass yield for different rice genotypes. In addition, Birhanu (2020) found similar high heritability attached with high GAM for days to 50% heading. In contrast to the present result, Abebe (2016) reported low heritability tied with low GAM for filled Spikelets per panicle, unfilled Spikelets per panicle, fertile tiller per plant, thousand grain weight and harvest index for different rice genotypes. However, the result of this study had not low heritability traits coupled with low GAM.

Table 4. Estimation of variance components for 100 tested rice genotypes studied in Fogera district in 2021/22.

Traits	σ^2g	σ^2p	σ^2e	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
MTA	0.019	0.023	0.019	11.00	12.12	82.35	0.26	20.59
FTP	0.447	0.577	0.447	37.65	42.78	77.46	1.21	68.36
NFT	0.270	0.389	0.270	72.18	86.62	69.43	0.89	124.07
PH (cm)	488.217	502.746	488.217	29.54	29.98	97.11	44.92	60.05
PL (cm)	4.733	5.594	4.733	11.85	12.88	84.62	4.13	22.48
FSP	461.043	544.403	461.043	25.11	27.29	84.69	40.76	47.67
UFS	41.752	48.556	41.752	71.12	76.69	85.99	12.36	136.05
DM	144.425	148.610	144.425	8.52	8.64	97.18	24.44	17.32
DH	134.167	135.857	134.167	10.82	10.89	98.76	23.75	22.18
BYD (ton/ha)	3.403	5.373	3.403	21.27	26.72	63.34	3.03	34.91
AGY(ton/ha)	1.253	1.485	1.253	34.76	37.84	84.37	2.12	65.87
HI (%)	159.295	178.481	159.295	33.51	35.47	89.25	24.60	65.31
ATW (g)	44.873	46.425	44.873	24.94	25.37	96.66	13.59	50.58

σ^2p = Phenotypic variation; σ^2g = Genotypic variation; σ^2e = Environmental variance; GCV (%) = Genotypic coefficient of variation; PCV (%) = Phenotypic coefficient of variation; H^2(%) =Broad sense heritability; GA (5%) = genetic advance at 5% selection intensity; GAM (%) = Genetic advance as percent of mean; MTA = Fourth root data transformation value of maximum tillering ability; FTP = Number of fertile tillers per plant; NFT = Number of non-fertile tillers per plant; PH = Plant height; PL = panicle length; FSP = Number of filled spikelets per panicle; UFS = Number of unfilled spikelets per panicle; DM = Days to 85% maturity; DH = Days to 50% heading; BYD = Above ground biomass yield; AGY = Adjusted grain yield at 14% moisture content; HI = Harvest index; and ATW = Adjusted thousand grain weight at 14% moisture content. Source: Own experiment data.

IV. CONCLUSIONS AND RECOMMENDATIONS

Analysis of variance indicated that there were highly significant differences ($P<0.01$) among 100 genotypes for all studied quantitative traits, which indicating the presence of sufficient variability. Therefore, this sufficient variability gives an opportunity to improve those traits through selection.

Traits that had high heritability coupled with high GCV and high GAM per small difference between GCV and PCV were filled spikelets per panicle, grain yield, plant height, harvest index and thousand grain weight. And also traits that had high heritability tied with moderate GCV and high GAM per small difference between GCV and PCV were maximum tillering ability, panicle length and days to 50% heading. Therefore, we conclude that filled spikelets per panicle, grain yield, plant height, harvest index, thousand grain weight, maximum tillering ability, panicle length and days to 50% heading had high heritability coupled with high/ moderate GCV and high GAM per small difference between GCV and PCV are best for direct selection of the studied rice genotypes. Accordingly, to improve panicle length G18 and G68, thousand grain weight G21 and days to 50% heading G57 and G87 are recommended donor rice genotypes for future crossing works.

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AUTHOR CONTRIBUTIONS

Assaye Berie Mekonnen; initiated the research idea, collected, organized, analyzed and interpreted the data and wrote the manuscript. Tiegist Dejene Abebe; supervised the research, structured the paper and edited the manuscript.

CONFLICT OF INTERESTS

The authors declare that there is no competing of interests.

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