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An Investigation of Phenotypic and Genotypic Variations in 100 Upland Rice Genotypes at Pawe, Northwestern Ethiopia

Gedifew Gebrie[1]*, Desta Abebe[1], Mulugeta Atnaf[2], Desalegn Wondifraw[1] and Abebaw Dessie[2]

[1]Ethiopian Institute of Agricultural Research, Pawe Agricultural Research Center, Pawe, Ethiopia
[2]Ethiopian Institute of Agricultural Research, Fogera National Rice Research and Training Center, Fogera, Ethiopia

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Corresponding authors:
✉ Gedifew G.
gebriegedifew1976@gmail.com

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ABSTRACT

Lack of improved rice varieties has been identified as one of the challenges of rice research and development in Ethiopia, hindering the national production and productivity of the crop. Hence, the national rice research program of the country has tried to introduce and evaluate the diverse upland rice genotypes under the rainfed cropping season. In this experiment, 100 upland rice genotypes were introduced and evaluated with three locally well-adapted upland rice varieties as the standard checks using the augmented randomized complete block design/RCBD experimental design with a plot size of 1.5m^2 and 3 rows per plot. The seeds were drilled in rows with a seed rate of 60 kilograms per hectare (kgh^{-1}). The Nanoparticles/NPS (124 kgh^{-1}) and urea (100 kgh^{-1}) fertilizers were applied. The days to 50% heading, days to 85% maturity, plant height, panicle length, number of filled grains per panicle, number of unfilled grains per panicle, grain yield, and 1000 seed weight in gram were collected and subjected to a statistical analysis using SAS statistical software with 9.4 version from which a significant variation for all the traits was observed showing the presence of genetic variability among the rice genotypes. The genotypes were highly and significantly varied on their grain yield (coefficient of variation/CV= 7.86***), 1000 seed weight (CV= 9.97**), and days to 85% maturity (CV= 2.38**). A lower genotypic coefficient of variance and a higher phenotypic coefficient of variance among the genotypes were obtained, indicating that the variation was more due to environmental effects.

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Introduction

Rice (*Oryza sativa* L., 2n= 2x= 24) is the second most widely cultivated cereal crop and the staple food for more than half of the world's population, providing two-thirds of caloric intake for more than three billion people in Asia and one-third of nearly 1.5 billion people in Africa and Latin America (Khan *et al.*, 2015). It is also increasingly important in Ethiopia. Though Ethiopia has a huge potential for rice production, there is a rapid increase in consumer demand and low levels of domestic production (Dawit and John, 2020). Therefore, systematic selection of appropriate rice technologies from other rice-producing countries of the world and adapting them to Ethiopian agro-ecology is one means of solving such a problem which could be attributed to various constraints in rice production, processing, and marketing subsectors. Thus, appropriate interventions are necessary to tackle the expected constraints and bring forward the rice commodity as one of the most important crops in the Ethiopian

agricultural economy. In line with this, the national rice research program is developing and releasing a significant number of improved rice technologies such as improved varieties. However, the current national rice productivity of 3.15 tons per hectare (CSA, 2021) is low when compared to the world's current rice productivity of 4.64 tons per hectare (USDA/FAS, 2021) and the crop's genetic potential. To improve the productivity of rice, the national rice breeding program introduced different rice germplasms from external sources targeting for higher yield, tolerant against abiotic and major biotic stresses (diseases and pests) stresses, and for other quality traits (white seed color, long grain size, and acceptable amylose content). Biotic stresses such as sheath rot and blasts (panicle blast and leaf blast) are significantly impacting rice productivity in the northwestern parts of Ethiopia (Taye *et al.*, 2019), including the area where this experiment was conducted. Hence, rice variety development, considering those attributes related to consumer preference and different production constraints, is critical in the research area.

Measuring the available genetic diversity is of utmost importance for effective evaluation and utilization of germplasm (Syafii *et al.*, 2015) to explore the variability present in rice germplasms for the identification of desirable agronomic attributes (Bhattarai and Subudhi, 2019). Therefore, this research was designed to assess and determine the extent and pattern of genetic diversity vested on the pool of introduced rice germplasms.

Materials and Methods

Description of the experimental site

The experiment was conducted at the experimental site of Pawe agricultural research center during the cropping season of 2019-2020 under the upland rain-fed condition. This center is found in Pawe district, Metekel zone, Benishangul-Gumuze regional state in northwestern Ethiopia (Fig.1), located at about 575 km northwest of Addis Ababa at a latitude of 11°19'N and longitude of 36°24'E and an altitude of 1120 masl. This area is characterized by hot to warm moist conditions with average minimum and maximum temperatures of 16 ^{o}C and 32 ^{o}C, respectively. It has an average annual rainfall of 1587 mm with five to seven months duration (Wasihun, 2007; Gedifew and Tsige, 2019).

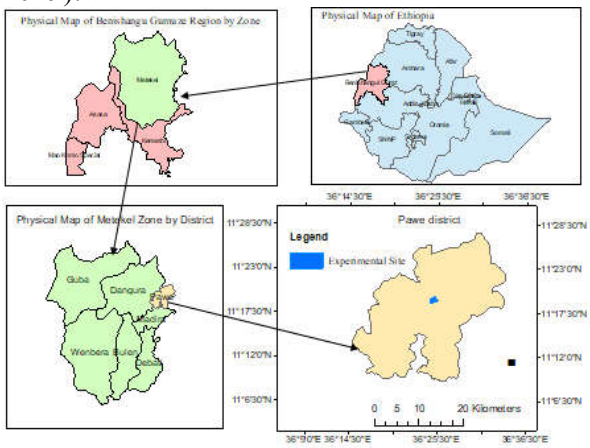

Fig. 1. The ArcGIS map projection of the experimental site.

Plant materials

The experiment comprised of 100 upland rice genotypes with 3 standard checks (Supplement 1). The genotypes were introduced by IRRI and Africa Rice Research Center.

Experimental design and procedures

Augmented randomized complete block experimental design (RCBD) was employed with a 0.5 m spacing between the plots and 1 m spacing between the blocks, respectively. A 0.26 m spacing was used between the rows and a seed rate of 60 kgh^{-1} was selected. A plot size of 2.5 m^2 (2.5m x 1m) with four rows was used. Inorganic fertilizer (NPS = 124 kgh^{-1}; Urea = 100 kgh^{-1}) was applied. The whole NPS was applied at planting, whereas Urea was applied in three stages (1/3 at planting, 1/3 at tillering after first weeding, and 1/3 at panicle initiation stages of the crop).

Data collection and statistical analysis

Data were collected on a plot and plant basis following the appropriate agronomic stages of the crop for each respectively measured trait. Three of the sown genotypes were failed to germinate and hence no measurement was

made on plots that received these genotypes. Agronomic traits such as days to 50% heading (DH), days to 85% maturity (DM), plant height (PH), panicle length (PL), number of filled grains per panicle (NFG), number of unfilled grains per panicle (NUFG), grain yield (GY) and 1000 seed weight (TSW) were collected and subjected to ANOVA using SAS 9.4 statistical software (SAS Institute, 2019). This was done following the procedures designed by Federer (1961) for augmented agricultural research design (Table 1) where the test of significance was performed using Fisher's (F) test. R^2, as the coefficient of determination, was computed to explain the variability of the modeled variable due to the explanatory variables.

Table1. The ANOVA table for augmented design.

Source	DF	SS	MS	F-Value
Blocks (Eliminating treatments)	*b-1*	*ASSB*	*MSSB*	*MSSB/MSE*
Treatments (Eliminating blocks)	*v-1*	*ASST*		
Among Tests	*w-1*	*SST*	*MSST*	*MSST/MSE*
Among Controls	*u-1*	*SSC*	*MSSC*	*MSSC/MSE*
Test Vs Controls	*1*	*SSTC*	*MSSTC*	*MSSTC/MSE*
Error	*n-v-b+1*	*SSE*	*MSE*	
Corrected Total	*n-1*	*TSS*		

b= total number of blocks; v= total number of treatments (total number of controls plus total number tested genotypes); w= total number of tested genotypes; u= total number of controls; n= total number of experimental units.

The variance components and genetic variability, including broad sense heritability (H) were estimated to determine the genetic and environmental effects on the variability of the measured quantitative traits. The phenotypic and genotypic variances were estimated from the expected mean squares using the random model considering the expected mean squares. Genotypic variances (δ2g) among the treatments on their corresponding traits were estimated according to Falconer (1981) as:

$$\delta_g^2 = \frac{MSg - MSe}{r}$$

where δ_g^2 indicates genotypic variance, MSg is the mean square of genotypes, MSe is the error mean square, and r is the number of replications (number of blocks in this case).

$$\text{Environmental variance } (\delta_e^2) = \frac{MSe}{r}, \text{ and}$$

$$\text{Phenotypic variance } (\delta_p^2) = (\delta_g^2) + (\delta_e^2) = \frac{MSg}{r}$$

Where δ_e^2 represents the environmental variance and δ_p^2 represents the phenotypic variance. Additionally, phenotypic and genotypic coefficient of variation was also used to estimate the variability based on Burton and DeVane's (1953) formula as:

$$CV = \frac{\sqrt{\delta_p^2}}{Y} x100; \quad GCV = \frac{\sqrt{\delta_g^2}}{Y} x100$$

where Y is the mean value of trait Y; Heritability in the broad sense (H) for all the quantitative traits was expressed as a percentage of the ratio of the genotypic variance (δ^2_g) to the phenotypic variance (δ^2_p) and was estimated on the genotype mean base as described by Allard (1960) as:

$$\text{Heritability (H)} = \frac{\delta_g^2}{\delta_p^2} x100$$

Where H indicates Heritability in the broad sense, δ_g^2 represents genotypic variance and δ_p^2 represents phenotypic variance.

Results and Discussion

Analysis of variance

The analysis of variance among the tested upland rice genotypes was computed based on the mean square values of the corresponding eight quantitative traits. In addition, different genetic parameters were also calculated to study the genetic variability of the genotypes. The ANOVA table showed a significant

variation (P≤ 0.05) for all the traits of the newly tested upland rice genotypes (Table 2) predicting that there was a genetic variability among the genotypes. The genotypes were highly and significantly varied on their days to 85 % maturity (DM), number of filled grains per panicle (NFG), number of unfilled grains per panicle (NUFG), grain yield per hectare (GY), and 1000 seed weight (TSW). Similarly, Girma *et al.* (2018) reported significant differences among 64 rice genotypes on their days to heading, days to maturity, plant height, and grain yield. Shrestha (2021) also studied the variability of forty rice genotypes and reported a significant variation of the tested genotypes on their plant height, panicle length, and grain yield.

While emphasizing grain yield (GY) as the most preferable quantitative trait, the model explained about 99% of the total variability among the treatments to their grain yield with a lower CV value of 7.86. The variability among the treatment (the newly tested genotypes and the check) and the newly tested upland rice genotypes was very highly significant (p-value = 0.001). However, the variability among the blocks was less significant (p-value = 0.044). On the contrary, the variability on the new upland rice genotypes versus the controls was less significant (p-value = 0.048).

Estimation of variance components and genetic variability

The Variability parameters for eight quantitative traits were measured to determine the patterns of genetic variation among the tested upland rice genotypes (Table 3). The genetic variability within the genotypes was estimated from the values ranging from 5.38% for panicle length (PL) to 52.77% for several unfilled grains per panicle (NUFG) and from 6.12% for days to 85% maturity (DM) to 58.98% for some unfilled grains per panicle (NUFG) for phenotypic and genotypic coefficients of variation (GCV and PCV), respectively.

Generally, the GCV was lower in magnitude compared to PCV for all the traits. If the PCV was higher than the GCV for the traits, the traits will be highly influenced by the environment (Hamidou *et al*., 2018). Therefore, in this experiment, the lower ratios of the GCV to PCV for the collected data indicate that the significant variability on each trait was more due to environmental influence. A higher GCV and PCV were recorded for the number of unfilled grains per central panicle, 1000 seed weight, grain yield, number of filled grains per central panicle, plant height, and days to 50% heading. This is while a lower GCV and PCV were recorded for days to 85% maturity and panicle length. Paswan *et al.* (2014) also obtained a lower genotypic coefficient of variation while studying the existence of genetic variation among 104 cultivated rice genotypes. Jember Mulugeta (2016) also reported a lower ratio of GCV to PCV for all the collected traits while evaluating 11 upland rice varieties in the same testing area.

Heritability estimates

Although the genotypic coefficient of variation revealed the degree of genetic variability in the genotypes for various traits, it does not provide the full possibility of assessing the heritable variation useful for permanent genetic improvement (Al-Tabal and AL-Fraihat, 2011). Moreover, a high broad-sense heritability (H) indicates less environmental influence in the observed variation showing is the existence of a sufficient genetic variation in the population, and implying its response to selection pressure (Ene *et al.*, 2016).

Higher heritability estimates for TSW (92.72 %), GY (87.35 %), DM (81.81%), NUFG (80.04 %), and NFG (78.14%) were obtained, indicating that the observed variation among the tested genotypes was mostly genetic and less influenced by the environment while compared to the other measured traits.

Similarly, a high heritability was reported for NFG and TSW by Islam *et al.* (2016). El-Lattef *et al.* (2011) also reported a high heritability for GY (86%). However, in contrast to this study, the author reports a higher heritability for DH (86%) and PH (91%), and a lower heritability for TSW (69%).

Table 2. Analysis of variance and performance mean value for eight quantitative traits of the tested 97 upland rice genotypes.

Source of Variation	DF	Mean Squares							
		DH	DM	PH	PL	NFG	NUFG	TSW	GY
Block (Eliminating treatment)	4	49.23*	56.10**	50.94*	9.56***	236.26ns	2.93*	10.03*	393538.14**
Treatment (Eliminating block)	96	96.28*	52.55***	87.93*	1.36*	360.56*	11.09**	15.39*	854596.26***
Among new genotypes	53	100.36*	38.09**	68.28*	0.64*	394.64*	14.90***	18.34**	905095.51***
Among controls	3	129.33*	10.25*	32.25*	0.00ns	942.67*	12.25**	2.40ns	1602644.64***
New genotypes versus controls	1	117.53*	3.65ns	285.55**	0.06ns	1665.71**	22.77**	137.54***	524761.30**
R^2		0.96	0.99	0.98	0.99	0.92	0.98	0.97	0.99
CV		7.57	2.38	7.29	3.81	20.46	28.54	9.97	7.86
Root MSE		7.12	3.11	6.25	0.80	21.53	1.71	2.62	311.28
Mean		94	130	85.75	20.97	105	6.00	26.26	3959.29

DH= days to 50% heading, DM= days to 85% maturity, PH= plant height (cm), PL= panicle length (cm), NFG= number of filled grains per panicle, NUFG= number of unfilled grains per panicle, TSW= 1000 seed weight (g), GY= grain yield (kgh^{-1}), MS= mean square of tests, CV= coefficient of variation, MSE= mean square of error, R^2= R-squared (percent of the total variability of the data related to the corresponding quantitative trait), *= significance level ((at 5%) (* = significant, ** = highly significant, and *** = very highly significant).

Table 3. Analysis of variance, performance means, components of variance, genetic variability, and heritability estimate for eight quantitative traits collected from 97 upland rice genotypes.

Traits	Component of variance		Genetic Variability		H
	σ^2g	σ^2p	GCV	PCV	
DH	82.39	143.21	9.65	12.73	57.53
DM	52.07	63.65	5.53	6.12	81.81
PH	79.64	126.54	10.41	13.12	62.94
PL	1.27	2.04	5.38	6.81	62.46
NFG	317.18	405.9	17.06	19.31	78.14
NUFG	10.02	12.52	52.77	58.98	80.04
GY	50174.9	57441.7	22.63	24.21	87.35
TSW	104.77	112.99	38.98	40.48	92.72

DH= days to 50% heading, DM= days to 85% maturity PH= plant height (cm), PL= panicle length (cm), NFG= number of filled grains per panicle, NUFG= number of unfilled grains per panicle, TSW=1000 seed weight (g), GY= grain yield (kg) per hectare, σ^2g= genotypic variance, σ^2p= phenotypic variance, GCV= genotypic coefficient of variance, PCV= phenotypic coefficient of variance, H= broad sense heritability.

Conclusion

The results of the ANOVA test shows that there is significant genetic variability among all traits of the tested upland rice genotypes and the variability is mainly due to the environment according to the lower ratio of GCV compared to PCV in all the measured quantitative traits. The observed higher heritability estimates for TSW (92.72 %), GY (87.35 %), DM (81.81%), NUFG (80.04 %), and NFG (78.14%) indicate that the observed genetic variation among the upland rice genotypes is less influenced by the environment and more caused by genetic variability. This can be seen in the obtained results (DH= 57.53, PL= 62.46, and PH= 62.94). Since a highly significant wide range of variation among the tested upland rice genotypes was observed on their days to 85% maturity (DM) and grain yield (GY), these highly preferable rice characteristics must be considered while selecting the materials for the next breeding program.

Conflict of interests

The authors declared no conflict of interest.

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بررسی تغییرات فنوتیپی و ژنوتیپی در ۱۰۰ ژنوتیپ برنج مرتفع در پاوه، شمال غربی اتیوپی

گدیفو گبری[۱*]، دستا آبه[۱]، مولوگتا اتناف[۲]، دسالگن واندیفرو[۱] و آباو دسی[۲]

[۱] موسسه تحقیقات کشاورزی اتیوپی، مرکز تحقیقات کشاورزی پاو، پاو، اتیوپی

[۲]موسسه تحقیقات کشاورزی اتیوپی، مرکز تحقیقات و آموزش ملی برنج فوگرا، فوگرا، اتیوپی

چکیده

فقدان گونه های اصلاح شده برنج به عنوان یکی از چالش های تحقیق و توسعه برنج در اتیوپی شناسایی شده است که مانع تولید ملی و بهره وری محصول می‌شود. از این رو، برنامه ملی تحقیقات برنج کشور تلاش کرده است تا ژنوتیپ های متنوع برنج مرتفع را در فصل زراعی دیم معرفی و ارزیابی کند. در این آزمایش، ۱۰۰ ژنوتیپ برنج از زمین‌های مرتفع با سه رقم برنج کوهستانی با سازگاری محلی به عنوان چک استاندارد با استفاده از طرح آزمایشی طرح بلوک‌های کامل تصادفی افزوده / طرح آزمایشی RCBD با اندازه هر قطعه ۱/۵ متر مربع و ۳ ردیف در هر قطعه معرفی و مورد ارزیابی قرار گرفتند. بذرها به صورت ردیفی با تراکم بذر ۶۰ کیلوگرم در هر هکتار (kg-1) کاشته شدند. از کودهای نانوذرات/ NPS ($124\ kgh^{-1}$) و اوره ($100\ kgh^{-1}$) استفاده شد. روزهای تا ۵۰ درصد سنبله، روزهای تا ۸۵ درصد رسیدگی، ارتفاع بوته، طول خوشه، تعداد دانه پر در خوشه، تعداد دانه پر نشده در خوشه، عملکرد دانه و وزن هزار دانه بر حسب گرم جمع آوری و مورد تجزیه و تحلیل آماری قرار گرفتند. با استفاده از نرم افزار آماری SAS با نسخه ۹/۴ تنوع معنی داری برای تمامی صفات مشاهده شد که نشان دهنده وجود تنوع ژنتیکی در بین ژنوتیپ های برنج بود. ژنوتیپ ها از نظر عملکرد دانه (CV= 7.86***)، وزن هزار دانه (CV= 9.97**) و روز تا ۸۵ درصد رسیدگی (CV= 2.38**) تنوع بالا و قابل توجهی داشتند. ضریب واریانس ژنوتیپی کمتر و ضریب واریانس فنوتیپی بالاتر در بین ژنوتیپ ها به دست آمد که نشان می دهد این تنوع بیشتر به دلیل اثرات محیطی است.

واژگان کلیدی: تنوع ژنوتیپی؛ تنوع فنوتیپی؛ وراثت پذیری؛ اجزای واریانس

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