

Variability and Correlation Study on Lowland Green Super Rice in Western Ethiopia

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Abstract

The success of plant breeding activities entirely depends on the existence of genetic variability with respect to desired traits and selection skills of plant breeders. A field experiment was conducted to evaluate the extent of variability, heritability genetic advance, and character association among yield and yield-related traits in lowland GSR. The experiment was conducted using 20 low-land green supper rice genotypes in the Northwestern part of Ethiopia at Pawe agricultural research center for three consecutive years from 2016-2018 main cropping seasons. A randomized complete block design with three replications was used. The results of the analysis of variance for yield and yield-related characters revealed that highly significant mean square due to genotypes observed for all traits studied, Higher phenotypic coefficient of variation, compared to genotypic co-efficient of variation was recorded for all the traits studied indicating the variation is not only genetic but also influence of growing environment. The highest PCV was recorded for the trait plant height (32.6) followed by panicle length (23.3). Broad sense heritability analysis showed that days to heading (56.3), plant height (49.8), Days to maturity (42.4%), and panicle length (42.3%) were high. High heritability with the high genetic advance in percent of mean was recorded by plant height (49.8 & 33.54) followed by Panicle length (42.3 & 36.55) which confirms their additive gene action and direct selection of these traits depending on phenotypic expression would be effective for yield improvement. The positive and highly significant phenotypic correlation was observed between days to heading and days to maturity (r = 9385***) plant height was positively correlated with thousand-grain weight (0.50436*) and Panicle length (0.48312*). Grain yield showed negative correlation between Days to maturity (-0.044662*), but weak positive correlation was observed for days to heading (r = 0.33472), plant height (r = 0.18729) and panicle length (r = 0.08771). Therefore, the traits recorded high heritability and higher genetic advance; and the traits showed positive correlation and could be considered as suitable traits for selection and improvement to achieve high-yielding green super rice varieties in rain-fed environments.

Keywords

GSR, Grain yield, Heritability, Variability, Yield related traits

Introduction

In Ethiopia, rice production has started three decades ago and the country has proved to have reasonable potential to grow different rice types in rain-fed lowland, upland, and irrigated ecosystems. The estimated potential of Ethiopia for upland rice production is 30 million hectares [1]. It is among the important cereal crops grown in different parts of Ethiopia as a food crop next to teff, maize, wheat and sorghum. A wide production of rice in the country is believed to make a great contribution to food security. Considering the importance and potential of the crop, it has been recognized by the Government as "the new millennium crop of Ethiopia" to attain food security [2]. However, the productivity of rice in Ethiopia is 3.04 t ha-1 which was much lower than the world's average 4.67 t ha⁻¹ [3] due to severe disease and insect pest occurrence, inspired yield increment and over application of fertilizer, water stress and terminal drought occurrence and

soil fertility depilation due to continuous cropping are the major challenges that obstruct rice production in the country. As a food security crop in the country, rice production must meet increasing requirements, in both quantity and quality, and should be in harmony with the environment thus ensuring a proper level of sustainability. This requires a gradual reduction in application of pesticides, fertilizers,

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and water while still achieving continuous yield increase and quality improvement [4]. Recently, green super rice (GSR), defined as rice varieties that can produce high and stable yields under fewer inputs (water, nutrients, and pesticides) and adverse conditions [5].

Global rice production requirements in the future need to come from increased productivity per se of improved rice varieties and require major shifts in breeding goals and objectives [6]. To achieve sustainable rice production in environmental and economic terms, GSR varieties have numerous properties, high efficiency of fertilizer use, resistance to drought and other abiotic stresses, good grain quality, and high yield potential. Development of high yielding varieties requires the existence of genetic variability and genetic variability of agronomic traits is the key component of breeding programs for broadening the gene pool [7,8]. Therefore, success on plant breeding activities entirely depends on the existence of genetic variability with respect to desired traits and selection skill of plant breeder [9]. Different genetic variability parameters, namely, Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), heritability and genetic advance for yield attributing traits is a major concern for any plant breeder for crop improvement programs [10]. Similarly, information on correlation coefficients between grain yield and its component characters is essential since grain yield in rice is a complex character and is highly influenced by several component characters [11]. While selecting the suitable plant type, correlation studies would provide reliable information in nature, extent, and the direction of the selection, especially when the breeder needs to combine high yield potentials with desirable agronomic traits and grain quality characters. It is important that breeders understand the amount of variation, correlation and inheritance of important agronomic traits. Therefore, the current study was conducted to evaluate the extent of variability, heritability genetic advance and character association among yield and yield related traits on lowland GSR.

Materials and Methods

Experimental sites

The experiment was conducted at Pawe Agricultural Research center, which is located in Metekel zone of the Benishangul Gumuze Regional State in the lowlands of the Northwestern part of the country. Its geographical location is between 11°15′and 11°23″ North latitude and 36°30′ East longitudes at an altitude of 1120 m.a.s. The mean annual temperature ranges 32 °C and 16 °C. Pawe is characterized as a lowland area with very high rainfall (unique agro ecology) and has unimodal rainfall pattern with extended rainy season from May to October, having mean annual rain fall of 1659 mm per year. Its average humidity is 54.7%, with Wind speed 53.6 km/day with sunshine rate of 7.73 hours.

Experimental materials, design and procedures

The experiment was conducted using 20 low land green supper rice genotypes in the Northwestern part of Ethiopia at Pawe agricultural research center for three consecutive years from 2016-2018 main cropping seasons. Randomized complete block design with three replications was used. Each experimental plot had a total area of 6 m² ($1.2 \text{ m} \times 5 \text{ m}$) and six rows at 0.20 m interval. There was a 0.5 m distance between two consecutive plots within a replication. Seeds were sown in rows with manual drilling at a rate of 60 kg % ha. Fertilizer was applied at a rate of 100 kg DAP and 100 kg Urea per ha. Recommended amount of DAP was applied during planting while urea was applied in three splits at planting, tillering and at panicle initiation stages.

Data collection and analysis

Data was collected on number of fertile tillers per plant, plant height, panicle length, number of filled grains per panicle and number of unfilled grains per panicle were collected on plant base from five randomly selected plants, and days to heading and days to maturity on plot base; harvest index, thousand-grain weight, biological yield and grain yield were collected on plot base from four harvestable rows. Analysis of variance (ANOVA) was carried out on the data to assess the genotypic effects and their interaction using general linear model (GLM) procedure for randomized complete blocks design (RCBD) using SAS (2004) version 9.0. Mean comparisons among treatment means were conducted by the least significant difference (LSD) test at 5% levels of significance.

Result and Discussion

Analysis of variance

The results on analysis of variance for yield and yield related characters are presented in Table 1. Highly significant mean square due to genotypes observed for traits like days to heading, days to 85% maturity, plant height and panicle length at $(p \le 0.01)$ level and significant difference $(p \le 0.05)$ among genotypes were observed for grain yield and thousand grain weight, indicating the existence of sufficient variability among genotypes for yield and yield related traits studied in the present findings, therefore; there is higher opportunities for effective selection of green super rice for the study area. Significant genetic variation among rice genotypes for yield and yield attributing traits were reported by Bandhi, et al. [12]. Berhanu, et al. [13] reported that Significant genetic variation among genotypes for various characters suggested that the genotypes were genetically diverse and could be a good opportunity for breeders to select genotypes for trait of interest. The combined analysis of variance across years showed highly significant difference ($p \le 0.01$) for days to heading, days to maturity, plant height, and panicle length; and significant difference ($p \le 0.05$) was observed for grain yield and thousand seed weight among the tested varieties. The effect of year was also highly significant on all measured traits ($p \le 0.01$) except plant height, panicle length and thousand seed weight. The interaction of variety and year revealed a significant difference ($p \le 0.05$) for plant height, grain yield and thousand seed weight, whereas days to heading, days to maturity panicle length number of filled grains per panicle, didn't show significant difference.

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Source of variation	df	Mean Squares									
		DH	DM	PH	PL	NET	NGPP	Ufgpp	GY	TSW	
Ge	19	66.78***	44.53***	78.94***	6.00***	5.14NS	151.23NS	3.15	1014264.8*	8.52*	
Rep	2	48.75 [*]	12.71NS	52.38Ns	1.74NS	1.38Ns	85.47Ns	10.73	1072094.2NS	10.12Ns	
YR	2	4780.01***	469.11***	2691.49**	28.06**	260.70***	9332.19***	157.61***	107094064.0***	506.40*	
Ge [*] YR	38	17.68NS	14.16Ns	36.93*	2.56NS	4.94Ns	126.70NS	5.74	915368.7*	5.53*	
Error	118	13.72	13.89	19.84	1.87	4.29	126.66	3.86	570649.0	3.71	
cv		3.85	2.88	6.34	7.11	26.73	10.83	36.39	18.70	9.22	

Table 1: Mean squares from analysis of variance of 9 characters of 20 genotypes of low land green super rice.

Where; "**, ***Indicate significance at 0.05 and 0.01 probability levels' = Non-Significant Where: GY = Grain Yield, DH = Number of days to Heading, DM = Number of days to Mature, PL = Panicle Length, PH = Plant Height, BMY = Biomass Yield, HI = Harvest Index, LOD = Lodging Index, NET = Number of Effective Tiller, NGPP = Number of Grains per Panicle, Ufgpp = Unfilled Grains per Panicle, TSW thousand seed weight

Estimation of variability parameters

The estimates of genetic parameters of quantitative trait in Green super rice genotypes is presented in Table 1. The result revealed a wide range of variation among 20 low land green super rice for 6 quantitative traits studied. The phenotypic variance of all traits was higher than genotypic variance. Similarly, higher phenotypic co-efficient of variation, compared to genotypic co-efficient of variation were recorded for all the traits studied in the present investigation except numbers of effective tillers per plant, indicating the variation is not only genetic but also influence of growing environment. The GCV and PCV values were categorized as low (< 10%), moderate (10 to 20%) and high (> 20) as indicated by Deshmukh, et al. [14]. The difference between PCV and GCV values were as low as (1.3) for days to maturity and as higher panicle length (17.2). The lower difference may be the lower sensitivity of the trait days to maturity (3.8 & 2.5). And days to heading (5.8 & 4.4) to the environment which indicates that these traits are less affected by the environment for expression of the trait. Sravan, et al. [15] also reported the lowest difference between PCV and GCV value for days to heading and days to maturity; Therefore, selection based on phenotypic performance for days to heading and days to maturity will be effective to bring significant genetic improvement. The highest PCV was recorded for the trait plant height (32.6) followed by panicle length (23.3). This result was in agreement with the study of Anis, et al. [16] for plant height and panicle length. Moderate PVC was recorded for the trait grain yield and thousand seed weight. In contrast the lowest PVC were recorded for the trait days to maturity (3.8) and days to heading (5.8). All traits recorded the lowest GCV. This may be due to the narrow genetic base of the trait. The lower GCV and PVC were recorded for days to heading and days to maturity. The greater difference between GCV and PCV was detected in panicle length, plant height, grain yield and thousand grain weight. The result indicates that the influence of environmental factors affects the expression of these traits than genetic factors and can be improved by growing within a proper environment. Generally, high coefficient of variability shows scope of selection in favors of traits of interest and low coefficient of variability indicates the need for creation of variability and selection Adhikari, et al. [9].

Estimates of heritability and genetic advance as percent of mean

Knowledge of heritability assists plant breeders in making selection more effective and simpler and together with heritability, genetic advance offers more attainable gain at specific selection intensity lqbal, et al. [17]. In the present study, genotypic variances were higher in magnitude than corresponding environmental variances for all the studied traits except grain yield, resulting in high heritability for most of the traits.

Among the studied traits, estimates of broad sense heritability ranged from 20.6 for grain yield to 56.3% for days to heading. Heritability is grouped as low (< 0.2), moderate (0.2-0.4) and high (> 0.4). Broad sense heritability analysis showed that days to heading (56.3), plant height (49.8), Days to maturity (42.4%) and panicle length (42.3%) was high. These findings were in agreement with Adhikari, et al. [9] for days to heading, plant height and days to maturity. Gyawali, et al. [18] reported the same findings for days to flowering and maturity. Thousand seed weight and grain yield showed moderate heritability estimate. Similar results were reported by Gyawali, et al. [18] for grain yield this may be due to the influence of environment on the yield as it is polygenic character. High heritability indicates higher response to selection for specific traits. Very low heritability indicates a greater role of environment on the expression of the trait.

Genetic advance as percent of mean ranged from 3.32 for days to maturity to 36.55 for panicle length. The highest genetic advance as percent of mean was observed for panicle length 36.55 followed by plant height 33.54. Likewise, estimates of genetic advance as percent of the mean for days to maturity, days to 50% heading, thousand grain weight and grain yield showed low genetic advance as percent of mean which indicate these traits are mostly governed by non-additive gene effect and therefore these traits can be improved through heterosis breeding, family selection and progeny test. High heritability with high genetic advance in percent of mean was recorded by plant height (49.8 & 33.54) followed by Panicle length (42.3 & 36.55). Traits with high heritability and genetic advance confirm their additive gene action, whereas low values are the indicators of non-additive gene action. In this study high heritability coupled with high

Characters	σ²g	σ² _p	σ² _e	GCV	PCV		h ² _b	EGA,	GAM
				(%)	(%)	ECV		(k = 5%)	(K = 5%)
DH	17.69	31.412	13.727	4.4	5.8	3.9	56.3	6.510	6.764
DM	10.21	24.111	13.897	2.5	3.8	2.9	42.4	4.291	3.324
РН	19.70	39.548	19.848	23	32.6	23.1	49.8	6.463	33.549
PL	1.37	3.252	1.878	6.1	23.3	17.7	42.3	2.835	36.553
GY	147871.93	718520.933	570649.0	9.5	16.1	18.7	20.6	359.886	8.911
TSW	1.60	5.317	3.713	6.1	11	9.2	30.2	1.435	6.868

Table 2: Estimation of variance components, coefficient of variability heritability and genetic advance of 6 characters.

 σ_g^2 = Genotypic variance; σ_e^2 = Environmental variance; σ^2 ph: Phenotypic variance; GCV: Genotypic coefficient of Variation; PCV = Phenotypic Coefficient of Variation; h²b = Broad sense Heritability; EGA: Expected Genetic Advance; GAM: Genetic Advance as percent of Mean; and K: Selection intensity; GY: Grain Yield; DH: Number of days to Head; DM: Number of days to Mature; PL: Panicle Length; PH: Plant Height; TSW: Thousand Seed Weight

Table 3: Phenotypic correlation coefficient for six quantitative traits of 20 low land green super Rice.

	DH	DM	РН	PL	GY	TGW
DH	1.00000					
DM	0.93857***	1.00000				
РН	-0.30419	-0.33102	1.00000			
PL	0.42420	-0.49403*	0.48312*	1.00000		
GY	0.33472	-0.44662*	0.18729	0.08771	1.00000	
TGW	-0.45979*	-0.52622*	0.50436*	0.75764***	0.15216	1.00000

genetic advance as percent of mean was observed for traits plant height and panicle length which indicates the traits were governed by additive gene effect and direct selection of these trait depending on phenotypic expression will be effective as a result of accumulation of additive genes which leads to further improvement of low land green super rice.

Correlation coefficient analysis

Correlation coefficient is a measure of the degree association and relationship between two variables. It is important in plant breeding as it can be used for indirect selection. The study of correlation between different characters may help the plant breeder to know how the improvement of one character will bring simultaneous changes in other characters. Positive highly significant phenotypic correlation was observed between days to heading and days to maturity (r = 9385***) indicating selection based on early heading types can be used to select early maturing genotypes, highly significant phenotypic correlation between heading date and maturity date was also reported by Nidhi Tiwari, et al. [19] and Adhikari, et al. [9], but days to heading was negatively associated with thousand grain weight (-0.45979^*) and plant height (r = -0.30419. Days to maturity was also negatively correlated with thousand grain weight (-0.52622*) panicle length (-0.49403*), grain yield (-0.044662^{*}) and plant height (-0.33102^{*}).

The weight of a thousand grain (0.50436^{*}) and Panicle length (0.48312^{*}) were positively correlated with plant height. lqbal, et al. (2018) [17] and Ratna, et al. [20] also reported significant positive correlation between plant height and panicle length. Rice grain yield showed a negative correlation between Days to maturity (-0.044662^{*}), but weak positive correlation was observed for days to heading (r = 0.33472), plant height (r = 0.18729) and panicle length (r = 0.08771). Similar results were found in experiments conducted by Kishore, et al. [10] for panicle length.

Conclusion and Recommendation

Development of high yielding varieties requires the existence of genetic variability and genetic variability of agronomic traits. The success of plant breeding activities entirely depends on the existence of genetic variability with respect to desired traits and selection skill of plant breeder. The results on analysis of variance for yield and yield related characters reveled that highly significant mean square due to genotypes observed for all traits studied, indicating the existence of sufficient variability among genotypes; therefore, there is higher opportunities for effective selection of green super rice for the study area. Higher phenotypic coefficient of variation, compared to genotypic co-efficient of variation were recorded for all the traits studied indicating the variation is not only genetic but also influence of growing environment. The highest PCV was recorded for the trait plant height followed by panicle length. The greater difference between GCV and PCV was detected in panicle length, plant height, grain yield and thousand grain weight. The result indicated that the influence of environmental factors affects the expression of these traits than genetic factors and can be improved by growing within a proper environment. Broad sense heritability analysis showed that days to heading, plant height, days to maturity and panicle length was high. Thousand seed weight and grain yield showed moderate

heritability estimate due to the influence of environment on the yield as it is polygenic character. High heritability with high genetic advance in percent of mean was recorded by plant height followed by Panicle length which confirms their additive gene action and direct selection of these trait depending on phenotypic expression would be effective for yield improvement. Positive and highly significant phenotypic correlation was observed between days to heading and days to maturity Thousand grain weight and Panicle length were positively correlated with plant height. Grain yield showed negative correlation between days to maturity, but weak positive correlation was observed for days to heading, plant height and panicle length Therefore, the traits recorded high heritability and higher genetic advance; and the traits showed positive correlation could be considered as suitable trait for selection and improvement to achieve high yielding green super rice varieties under rain fed environment.

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Conflict of Interest

The Author has declared that no conflict of interest exists.

Ethics Approval

Not applicable.

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