

Genetic Variability and Associations among Yield and Yield Related Traits in Upland Rice (*Oryza sativa* L.), Genotypes Evaluated at Gojeb and Guraferda, Southwestern Ethiopia

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Abstract

A field experiment was conducted using 36 rice genotypes in 2017 at two locations of Southwestern Ethiopia to estimate the extent and pattern of genetic variation and association among yield and yield related traits. The experiment was laid down in 6 × 6 simple lattice design. The combined analysis of variance over the two locations revealed that the genotypes showed significant differences for all the traits studied, except for days to heading, panicle weight, thousand seed weight, lodging incidences, leaf blast and brown spot. Although, genotype × location interactions was significant for days to maturity, plant height, fertile tillers per plant, unfilled spikelets per panicle, panicle shattering, biomass and grain yield. Moderate to high broad sense heritability was observed for days to maturity, panicle length, total tillers per plant, fertile tillers per plant, filled spikelets per panicle, unfilled spikelets per panicle, biomass yield, harvest index, panicles per square meter and plant height. Among the studied traits total tillers per plant, fertile tillers per plant, panicles per square meter, biomass yield and harvest index had moderate values of genetic advances as percent of mean. Grain yield showed positive and significant correlations with days to maturity, panicle length, fertile tillers per plant, panicles per square meter, and biomass yield and harvest index at both genotypic and phenotypic levels. Phenotypically, panicles per square meter and genotypically, harvest index exerted the maximum positive direct effect on grain yield. The study revealed that panicles per square meter and harvest index can be considered for selection in future rice breeding program and in order to give confirmative results, further studies in more locations and years, supported with molecular breeding approach should be conducted.

Keywords: Upland rice; Variability; Heritability; Genetic advance; Trait association

Introduction

Rice belongs to the genus *Oryza* within the grass family Gramineae (*Poaceae*). There are about 25 species of *Oryza*. Of these only two species are cultivated, namely *Oryza sativa* and *Oryza glaberrima*. *Oryza sativa* is originated in southern and southwestern tropical Asia [1].

The other species of cultivated rice, *Oryza glaberrima*, is indigenous to Inner delta of Niger river and some areas around Guinean coast of Africa. Rice (*Oryza sativa* L.) is the most important food crop and energy source for about half of the world's population. More than 3.5 billion people in the world depend on rice for more than 20% of their daily calories.

It is grown in more than 117 countries and covering a total area of about 163 million hectares with a global production of about 740 million metric tons. Asia is the leader in rice production accounting for about 90% of the world's production. Over 75% of the world supply is consumed by people in Asian countries.

The world largest volume of rice production is concentrated in China, India, Indonesia, Vietnam, Thailand, Bangladesh, Burma, Philippines, Brazil and Japan. The share of the above top ten rice

producing countries account for about 32.9, 24.4, 11.0, 7.0, 6.0, 5.4, 5.3, 2.9 and 1.8 % of the world production, respectively [1].

In Ethiopia, rice is important cereal crop cultivated in different parts of the country next to teff, maize, wheat and sorghum. The potential area for rice production in Ethiopia is estimated to be about 30 million hectares. The average rice productivity in Ethiopia is about 2.8 t ha⁻¹, which is much lower than that of the world's average (4.4 t ha⁻¹).

This low productivity of rice in Ethiopia is attributed to shortage of improved varieties, lack of recommended crop management practices, lack of pre and post-harvest management technologies and lack of awareness on its utilization [3].

To initiate appropriate breeding procedure in any crop improvement programme and developing genotypes with high productivity, information on the extent and pattern of genetic variation and associations among yield and yield related traits becomes a pre-requisite [2]. Previous research work on genetic variability within rice genotype has been widely reported by different researchers.

For instance, reported the presence of wide genetic variation among upland rice genotypes in their genetic variability study at Pawe, Northwestern Ethiopia. Despite the information is a pre-requisite, studies on genetic variation and association among the rice genotypes

in the study area is very limited and the information is not sufficiently available.

Hence, the present study was under taken to determine the extent of genetic variability and association among yield and yield related traits in 36 upland rice genotypes.

Experimental site	Altitude (m)	Longitude (°E)	Latitude(°N)	Temperature (°C)			
				Max	Min	Mean annual rainfall (mm)	Soil type
Gojeb	1235	036° 0' 0"	07° 15 '0"	24	16.7	1710	clay loam
Guraferda	1138	035° 17' 16"	06° 50' 368"	39	25	1266	sandy clay loam

Table 1: Agro-ecology of the study area.

Experimental materials

In this experiment, 33 upland rice genotypes, obtained from two different sets of variety trials conducted by rice breeding section of Fogera National Rice Research and Training Center (FNRRTC) and three released varieties (NERICA-12, NERICA-4 and Adet), a total of 36 upland rice genotypes were used.

Experimental design and trial management

The field experiment was laid down in 6 × 6 simple lattice designs. The gross plot size of the experiment was 7m² (4 m long and 1.75 m wide) each and there were seven rows at 0.25 m interval. The net (harvestable) plot size of the experiment was 5m² (4 m length and 1.25 m wide) each. There were a 0.35, 0.6 and 1 m distance between plots, incomplete blocks and replications, respectively [3]. Fertilizer was applied at a rate of 100kg ha⁻¹ DAP and 100kg ha⁻¹ urea as per national recommendation. The seeds were drilled in rows with seed rate of 60kg ha⁻¹.

Data collection

Based on the standard evaluation system for rice developed by International Rice Research Institute (2013)18 and Biodiversity International (2007)3 the following yield and yield related traits were collected from the central five rows of each plot. plant height, panicle length, number of tillers per plant, number of fertile tillers per plant, number of filled spikelets per Panicle, number of unfilled spikelets per panicle, panicle weight were measured from 5 randomly selected sample plants. Days to 50% heading and days to 85% maturity were recorded on plot basis. Disease severity, lodging and panicle shattering scored visually on 0-9 scale. Number of panicles was counted by random draw of 0.25m² quadrant. At harvest maturity, total above ground biomass was harvested from an area of 0.25m² (0.5 m × 0.5 m) and oven dried at 70°C for 72 hours and weighed in gram and determined as biomass yield. Harvest index is estimated to the ratio of grain yield in to biomass yield per plot. Thousand seed weight and grain yield were measured and adjusted at 14% seed moisture basis.

Statistical analysis

According to Gomez and Gomez (1984)13, scored data's were transformed using arc sin and square root transformation methods. To compute a combined statistical analysis across locations, test of homogeneity of error variances were performed by using F-max test

Materials and Methods

Description of the experimental areas

The experiment was conducted during the 2017 main rainy season in two locations namely, Gojeb and Guraferda, Southwestern Ethiopia.

method of Hartley (1950)14, which is based on the ratio of the largest mean square of error to the smallest mean square of error. Then all the characters were subjected to pooled analysis of variance over locations using the SAS (v 9.3) Mean separation among treatment means were done by using LSD at 5% probability level.

Results and Discussion

Analysis Of Variance (ANOVA): the combined analyses of variance for different characters are presented in Table 4 and revealed that significant differences among the rice genotypes for all the characters studied, except for days to 50% heading, panicle weight, thousand seed weight, lodging incidence, leaf blast and brown spot, indicates the presence of variation among the tested rice genotypes. The mean squares due to genotype × location interactions were differed significantly for panicle shattering, grain yield, days to 85% maturity, plant height, fertile tillers per plant, unfilled spikelets per panicle and biomass yield. This significant difference of genotype × location interactions indicates differential response of genotypes to the two locations for these characters [4].

Range and mean of different characters

The mean values for grain yield ranged from 1979.5 to 3562.7 kg ha⁻¹. The highest grain yield (3562.7 kg ha⁻¹) was obtained from the genotype ART15-13-2-2-2-1-1-B-1-2, while the lowest (1979.5 kg ha⁻¹) was obtained from the genotype ART16-5-10-2-3-B-1-B-1-2. Wide variation in grain yield might be due to genetic variation among the tested materials as well as influence of genotype x location interaction. Days to 85% maturity ranged from 113 to 126 days. The earliest days to maturity were recorded in the genotype NERICA-4 (113 days) and maximum were recorded in the genotype ART16-21-4-7-2-2-2-B-2-2 (126 days). Variation among genotypes for days to maturity offers opportunity for the development of upland rice varieties for different agro ecologies of Ethiopia receiving diverse distribution of rainfall. Hence, early maturing rain fed rice varieties could be developed for short season rainy areas such as for most of eastern Ethiopia and late maturing varieties could be evolved for Southwestern Ethiopia with long rainy season.

Plant height ranged from 75.15 to 93.85 cm. Maximum plant height was recorded in genotype ART16-16-1-14-3-1-1-B-1-2 (93.85 cm). The minimum plant height was recorded in genotype ART16-9-1-9-2-1-1-B-1-1 (75.75 cm). According to IRRI (2013) upland rice height is classified as semi-dwarf (<90 cm), intermediate

(90-125 cm) and tall (>125 cm). Based on this, in the present study 91.67% of the tested genotypes grouped under the semi-dwarf class whereas the remaining 8.33% genotypes fall within the intermediate statured class. Generally, genotypes that recorded 78.75 to 86.15 cm plant height measurement gave the highest grain yield. Results from this study indicated the importance of selection of semi dwarf plants in order to increase grain yield.

Estimates of variance components and coefficient of variations

The Phenotypic Coefficient of Variation (PCV) values ranged from 2.03% for days to 85% maturity to 32.95% for panicle shattering. Based on this delineation, panicle shattering had high PCV value and total tillers per plant, fertile tillers per plant, unfilled spikelets per panicle, panicles per meter square, biomass yield, harvest index and grain yield (kg ha^{-1}) had medium Phenotypic Coefficient of Variation (PCV). It indicates considerable amount of phenotypic variation is presented among the tested genotypes for these characters. While days to 85% maturity, plant height, panicle length and filled spikelets per panicle had low PCV values, indicates there is low phenotypic variation among the tested genotypes for these characters. Low PCV values for days to 85% maturity, plant height and panicle length. The Genotypic Coefficient of Variation (GCV) values ranged from 1.26 for days to maturity to 11.07% for panicle shattering. These low values indicate there was no sufficient genetic variation among the tested genotypes for these characters. Therefore, selection based on these characters may not be effective for further improvement of the crop and it is better to create genetic variability either by hybridization or introduction of more rice germplasms [5].

Estimates of broad sense heritability

Based on this delineation, high heritability estimates were recorded for plant height (75.25%) and number of panicles per meter square (60.49%). This indicates the predominance of genetic factors in the inheritance of these characters. Days to 85% maturity, panicle length, number of total tillers per plant, number of fertile tillers per plant, number of filled spikelets per panicle, number of unfilled spikelets per panicle, biomass yield and harvest index had medium heritability. Low heritability estimate was recorded from panicle shattering and grain yield, indicates the predominance of non-genetic factors in the inheritance of these characters. Low heritability estimate for grain yield could be attributed to the fact that yield is a complex character and controlled by many genes which indicates greater role of environment on the expression of this character therefore, direct selection of this character may be ineffective due to the masking effect of environment. Therefore, selection might be effective after creating variability either by hybridization or introduction of more germplasms.

Estimates of genetic advance as percent of mean

Genetic advance as percent of mean had ranged from 1.61% for days to 85% maturity to 14.65% for number of panicles per meter square. Moderate values of genetic advance as percent of mean (10% to 20%) were recorded for characters viz. total tillers per plant, fertile tillers per plant, panicles per meter square, biomass yield and harvest index. High heritability associated with moderate genetic advance as percent of mean value was observed for number of panicles per meter square and suggesting greater role of additive gene action for inheritance of this character and selection will be effective, while low

heritability coupled with low genetic advance as percentage of mean estimates were recorded for panicle shattering and grain yield which explain the dominance of non-additive gene action and genotype environment interaction played significant role in the expression of these characters.

Correlation coefficient analysis

Phenotypic and genotypic correlation estimates between various characters are presented. Grain yield had positive and significant associations with days to 85% maturity, panicle length, number of fertile tillers per plant, number of panicles per meter square, biomass yield and harvest index at both phenotypic and genotypic levels. In addition grain yield had significant and positive correlation with number of filled spikelets per panicle at phenotypic level only. This signified that for these characters which were positively and significantly associated, the improvement for one character will simultaneously improve the other. Therefore grain yield of rice can be improved by selecting genotypes having higher performances for these positively and significantly associated characters. Panicle length and filled spikelets per panicle showed positive and significant association with grain yield at both genotypic and phenotypic levels. On the other hand grain yield showed negative and significant associations with number of unfilled spikelets per panicle and panicle shattering at both phenotypic and genotypic levels. This indicated improvement in these characters and yield seems to be practically difficult as they are controlled by different genes.

Genotypic path coefficient analysis

The genotypic path coefficient analysis revealed that harvest index had the highest positive direct effect on grain yield, followed by days to 85% maturity and biomass yield. The genotypic correlation of these characters with grain yield were positive and significant, signified that there is true association between these characters and grain yield. Thus, these characters could be major selection criteria for breeding activity. On the other hand, number of unfilled spikelets per panicle and panicle shattering had negative direct effect on grain yield with negative genotypic correlation. In such situations, direct selection of genotypes with highest number of unfilled spikelets per panicle and high shattering characteristics might be ineffective for grain yield improvement in upland rice genotypes. Panicle length, number of unfilled spikelets per panicle, number of panicles per meter square, biomass yield and panicle shattering exhibited positive genotypic indirect effect on grain yield passing through harvest index. The genotypic path coefficient analysis also revealed that panicle length, number of unfilled spikelets per panicle, number of panicles per meter square and panicle shattering had positive indirect effect on grain yield through days to 85% maturity. Similarly, panicle length, number of unfilled spikelets per panicle, number of panicles per meter square and panicle shattering had positive indirect effect on grain yield through biomass yield. The genotypic path coefficient analysis exhibited the residual value of 0.443 indicated that the characters in the path analysis expressed the variability on grain yield by 55.7%, the remaining 44.3% was the contribution of other factors, such as the characters not studied and also the environment.

Conclusion and Recommendation

From the present study it can be concluded that, for increasing rice grain yield in Southwestern Ethiopia, a genotype should possess more number of panicles per square meter and high grain to biomass ratio.

The result suggests that these two characters are important yield contributing characters and selection on these characters would be most effective. Generally, the present study indicated that there was no sufficient genetic variation present for the characters studied in rice genotypes. Therefore, it is recommended that broadening the genetic bases of rice germplasms by hybridization and mutation breeding may be required for a successful breeding program in Southwestern Ethiopia. In addition, in order to give confirmative results, further studies in more years, supported with molecular breeding approach should be conducted on rice genetic variability and character association.

Conflict of Interest

There is no conflict of interest among the authors or anybody else.

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References

1. Ajmera S, Kumar SS, Ravindrababu V (2017) Evaluation of genetic variability, heritability and genetic advance for yield and yield components in rice genotypes. *Int J Curr Microbiol Appl Sci* 6: 1657-1664.
2. Burton GW, Devane EH (1953) Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agrono J* 45: 478-481.
3. Dewey DR, Lu K (1959) Correlation and path-coefficient analysis of components of crested wheat grass seed production. *Agrono J* 51: 515-518.
4. Johnson HW, Robinson HF, Comstock RE (1955) Estimates of genetic and environmental variability in soybeans. *Agrono J* 47: 314-318.
5. Khare R, Singh AK, Eram S, Singh, PK (2014) Genetic variability, association and diversity analysis in upland rice (*Oryza sativa* L). *SAARC J Agri* 12: 40-51.