RESEARCH ARTICLE

Analysis of Genetic Variability for Leaf and Yield Traits in Diverse Rice Germplasm

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Received : 12th March, 2022

Revised : 18th March, 2022

Revised: 25th March , 2022

Accepted :13th April, 2022

ABSTRACT

Ninety-nine genotypes from an association mapping panel comprising landraces, exotic genotypes, and improved varieties were evaluated for leaf and yield traits in rice. The data of plant height, number of leaves, single leaf area, single-leaf weight, leaf mass area, leaf area index (LAI), leaf angle, yield, and biomass were subjected to analysis of variance that showed significant differences among the genotypes. The genetic variability among the genotypes and the co-efficient of variation was high for all the traits analyzed except leaf mass area with 17.47%. A high coefficient of variation was recorded in the number of leaves and grain yield per plant with 42.68 and 38.55%, respectively. Frequency distribution for these traits showed that the genotypes in the category of 4 to 12 LAI fall in the category of 30 to 90 g of grain yield. Most of the traits showed symmetrical skewness and mesokurtic distribution. Besides, the correlation coefficient of LAI had a significantly positive correlation with leaf mass per area, leaf numbers, and biomass, indicating the importance of the leaf area index in determining yield and biomass. Furthermore, single leaf area had a significant positive association with leaf angle, single-leaf weight, and plant height and a negative correlation with leaf numbers and leaf mass area. The results revealed the highest genetic variability and association between two or more variables among this rice germplasm. These genotypes could act as a reservoir of variation that could possibly be utilized for improving specific traits in crop improvement programs.

Keywords: *Rice; Coefficient of variation; Frequency distribution; Correlation; Leaf traits; Yield*

INTRODUCTION

Rice is the primary source of calories for most households in Asia, Africa, and Latin America. It provides about 20- 60% of daily calories for more than 3.5 billion people worldwide. In India, rice is consumed by more than 60% of the population in their regular diet. Although, India stands first in rice cultivation area but ranks second next to china in world rice production. During 2020-2021, the total rice cultivated area is 43.78 m ha with an average production of 118.4 mt with a productivity of 2.98 t ha^{-1} (www.agricoop.nic.in). However, global food production needs to be doubled by the year 2050 to meet the demand of the growing world population. It is projected that the world population is expected to reach 9 billion by 2050, and a significant increase in population may happen in most parts of Africa and Asia. Therefore, it is imperative to improve the rice yield by ~2 fold during the coming decades. Therefore, rice production must be doubled using the same unit area or even less area to meet the food demand. In the last few decades, the rice research was focused on hybrid vigor, plant architecture, and harvest index, which have resulted in the development of short-statured, high-yielding varieties with higher productivity. After the green revolution era, the yield of high-yielding varieties/genotypes reached a plateau. On the other hand, in the face of rising atmospheric temperature, extreme rainfall events and limited land availability are challenging issues in improving rice productivity.

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At present, cultivars with maximum resource use efficiency, tolerant to abiotic and biotic stresses, are inadequate, often leading to drastic yield loss. It is essential to expand and exploit the genetic pool of rice in crop improvement programs. Understanding the magnitude of genetic variability allows the plant scientist to either develop elite cultivars or utilize them as the parental line in hybridization programs with desirable characters. In addition, estimation of correlation between yield traits or yield associated traits and grouping of genotypes into various classes using frequency distribution is essential in genotype selection in breeding programs to improve rice yield potential. Less emphasis has been given to characterizing diverse germplasm and association studies for various morpho-physiological traits to exploit the genetic diversity. Hence, the present study was carried out to utilize 99 rice genotypes from association mapping panel to assess the genetic variability for leaf and yield traits.

MATRIALS AND METHODS

Plant material

Diverse rice germplasm consisted of 99genotypes that were selected from an association mapping panel which consists of landraces, exotic genotypes, and improved varieties collected from different states of India, Argentina, Bangladesh, Brazil, Bulgaria, Uruguay, China, Indonesia, Philippines, Colombia, Taiwan, Venezuela, and the USA was used in this study. Seeds of these genotypes were obtained from the Department of Plant Biotechnology, Tamil Nadu Agricultural University, Coimbatore. The experiment was conducted in a Randomized block design (RBD) with three replications at the wetlands of Tamil Nadu Agricultural University, Coimbatore, during *Rabi,*2020 season. Fourteen-day-old seedlings were transplanted at a single seedling per hill with a spacing of 25×25 cm, and fertilizers were applied at the rate of 150:50:50 kg of NPK per hectare. The recommended cultivation practices were followed throughout the cropping period. The observations on morphological traits were recorded in the physiologically active leaf during the active tillering stage from randomly selected plants of each replication, and data on yield characters were collected during physiological maturity.

Measurement of growth and yield parameters

Plant height was measured from the ground level of the plant to the tip of the tallest leaf and expressed in cm. The number of leaves was counted in randomly selected plants of each replication. Leaf angle was measured by measuring the angle of physiologically active leaf from the main culm. Protractor is used to measure the leaf angles that are expressed in degree (°)and single-leaf area (SLA) was determined in the first, second and third leaf from the top of the primary tiller and it was calculated by linear method with the K factor of 0.78 (Ribeiro *et al.,* 2019). The average value was computed using the following equation

SLA= Leaf Length × Leaf Width × 0.78 (cm^2)

The leaves used for SLA are oven-dried at 70°C for three days, and dry weight was measured for individual leaves. The average value was taken as a single leaf weight (SLWt). Leaf area index (LAI) is measured by the ratio of leaf surface area to the ground cover occupied by the plant (Watson 1947).

$$\text{Leaf area index} = \frac{\text{Total leaf area of a plant}}{\text{Ground area occupied by the plant}}$$

Leaf mass area (LMA) was calculated by the ratio of leaf dry weight to the leaf area. It is also referred to as specific leaf weight and is presented in mg cm^{-2}. The top three leaves were collected from the primary tiller. Each leaf was measured for leaf area and oven-dried at 70°C for three days. The dry weight of each leaf was measured and the average value of leaf area and leaf weight was taken for the calculation. The dry weight of LMA is computed by the following formula

$$\text{Leaf mass area} = \frac{\text{Leaf dry weight}}{\text{leaf area}} (\text{mg/cm})$$

Plant samples were harvested at the physiological maturity stage and oven-dried at 70°C for 3 days. Above ground biomass and grain yield per plant were weighed using a weighing balance, expressed in grams.

Statistical analysis

The data collected on various leaf traits and yield parameters were analyzed in a randomized block design (RBD) and the data of all the parameters were subjected to simple statistical analysis like maximum, minimum, mean, standard deviation, and analysis of variance (ANOVA) whereas the coefficient of variation was calculated as per Burton (1952). Frequency distribution was performed to group the genotypes into different categories and Pearson's correlation coefficient was also carried out to find the association among all the characters using 'SPSS Statistics version 16.0 (SPSS Inc., Chicago, Ill., USA).

RESULTS AND DISCUSSION

The statistical analysis (mean, maximum, minimum, standard deviation, coefficient of variation)was carried out in the following traits, namely plant height, number of leaves, leaf angle, leaf area index, leaf mass area (LMA), single leaf area (SLA), single-leaf weight (SLWt), yield(Y) and biomass (Table 1). A significant variation at a 5% level was found among 99 genotypes for the nine traits such as plant height, number of leaves, single leaf area, LAI, LMA, single-leaf weight, leaf angle, yield, and biomass. Analysis of variance exhibited a highly significant difference among all the traits studied.

The frequency distribution obtained for 99 genotypes on each character is presented in figure 1. The highest coefficient of variation was recorded in the number of leaves (42.68%) with symmetric and mesokurtic distribution among the different quantitative traits observed. The highest leaf number was recorded in the genotypes G100 (225), while the lowest was recorded in G42 (12) and G26 (24). The overall mean of the number of leaves for ninety-nine genotypes was 102.85, with a range of 12 to 225 leaves (Table 1). Hence, these genotypes could be considered as a source for different ranges of leaf numbers that could be utilized for biomass and yield improvement. Since the number of leaves is regarded as an important morphological character that determines the total photosynthetic area of a plant and the total biomass of plants. The coefficient of variation for plant height was found to be high at 21.67% and ranges from 43.70-138.50 cm with a mean value of 80.80±1.02 (Table1). Skewness and kurtosis were 0.812 and 0.689 which showed symmetric and mesokurtic distribution. Minimum plant height was observed in G128 (43.70 cm) followed by G55 (45.83 cm)and maximum plant height was recorded in the genotypeG49 (138.50 cm). Plant height is a genetically controlled character that is even influenced by environmental factors (Jennings *et al.,* 1979). It has a high positive association with grain yield by remobilizing the stem reserves to the panicle (Pandey *et al,* 2009; Gosh, 2013). It is considered as an important trait since it is associated with biomass of rice. Tall plants have a higher percentage of chance for lodging; however, they have the advantage over weed competition. The success of the green revolution was owing to the development of short-statured varieties with lodging resistance. Therefore, the significant reduction in yield loss due to lodging could be narrowed by selecting semi-dwarf statured plant type.

The leaf angle of 99 genotypes ranged between 9and30° and exhibited a noticeable variation of 28.64%. It had a mean value of 14.45±0.24and most of the genotypes were in the group of 12° (Figure 1). Also, leaf angles had a significant positive skewness and leptokurtic distribution of 1.371 and 1.827, respectively. Leaf angle is a heritable trait that determines the erectness of the leaf and influences the percentage of light penetration into the canopy that decides the photosynthetic rate per unit leaf area(Sinclair and Sheehy, 1999). A higher leaf angle was observed in G100 and G71 genotypes with 9° and 9.33°, respectively, hence more erectness was observed in these genotypes and the genotype G44 showed more droopiness in leaves which recorded leaf angle of 30°. Leaf area index (LAI) is also a critical trait in determining the yield and biomass production of many crops. Predominantly it plays a major role in the light interception of the canopy (Fageria *et al.,* 2006). LAI increases with an increase in leaf number and tillers. LAI exhibited the largest variation of 37.97 percent, which shows significant symmetric and mesokurtic distribution. The mean value of LAI was 5.71±0.13 with a minimum LAI of 1.10 and a maximum of 13.00. The genotypes G115 and G114 recorded LAI of 12.61 and 12.91, respectively, whereas lesser LAI was observed in G26 and G44 with 1.35 and 1.59, respectively. The optimum range of 4 to 7 LAI is suggested to be sufficient to attain maximum yield since higher LAI leads to shading of lower leaves.

Leaf mass area (LMA) is an important leaf trait that indicates the leaf thickness, which decides the photosynthetic rate per unit leaf area. It ranged from 2.70 – 7.50 mg cm^{-2} with a less variation of 17.47. Similar findings were recorded earlier by Sowmya *et al.* (2020). The LMA had significant symmetrical skewness and mesokurtic distribution, considered normal distribution. The genotype G93 (7.50 mg cm^{-2}) recorded the highest LMA and the lowest LMA was observed in the genotype G32 (2.70 mg cm^{-2}) and the variations among ninety-nine genotypes were due to the differences in dry matter per unit leaf area of various tissues like mesophyll tissue, vascular tissues and epidermal tissues (Xiong *et al,* 2016). Single leaf area (SLA)among ninety-nine genotypes ranged between 15.16 to 97.34 cm^2 with a higher variation of 33.21percent.Skewness and kurtosis for SLA is 1.212 and 1.769, respectively which showed positive distribution. SLA is an important trait in canopy architecture and a determinant of LAI. It is even closely related to carbon exchange and biomass accumulation. Among the rice genotypes, single leaf weight showed wide variation ranging from100- 480.50 mg with the mean value of 222.36±3.55. It showed significant positive skewness and leptokurtic distribution. Among the 99 rice genotypes, the highest SLA and SLWt were recorded in G49 (97.34 cm^2 & 455.50 mg) and G42 (86.49cm^2 & 480.50 mg) , respectively whereas genotypes G125 (23.06 cm^2& 100 mg) and G5 (15. 16 cm^2 and 124.33 mg) recorded the lowest value for these traits. It was observed that the genotypes which fall on a higher range of single leaf area also fall on the higher single-leaf weight. This indicated that a larger leaf area has a maximum volume of leaf tissues that make the leaf weight higher.

A substantial variation of 38.55%was observed in grain yield per plant (Table 1). The mean grain yield was 40.24 and the genotype G93 recorded the highest grain yield of 82.16 g per plant, followed by the genotype G6 with 77.81 g per plant. In contrast, the genotypes G147 (3.03g)and G130 (5.81g) were recorded with low yield. Frequency distribution for grain yield among the 99 genotypes showed symmetrical skewness and mesokurtic distribution. Furthermore, the grain yield of rice genotypes ranged between 3.03 and 98.06g per plant, which showed a large genetic variability among these genotypes. Similar findings were reported by Priyanka *et al.(*2019) and RukminiDevi *et al.*(2017). Biomass is an important factor to be considered in plant breeding programs since higher yield is achieved by higher biomass (Amano *et al.* 1993). The genotypes G112(96.42 g) and G32 (87.29 g) recorded higher biomass whereas G125 (18.64g) and G26 (22.74g) produced lower biomass compared to other genotypes. Skewness and kurtosis coefficients were close to zero, indicating significant symmetrical skewness and mesokurtic distribution. The highest variation of about 36.61% was recorded on biomass which rangedfrom18.64g to 96.42g per plant among the rice genotypes. These results agreed with the earlier findings ofAbebe *et al.* (2017), which depicted that the diverse genotypes would be the source of novel traits for crop improvement programs.

Table 1. Minimum, maximum, mean and standard deviation for leaf traits, yield and biomass of variation of ninety nine rice genotypes

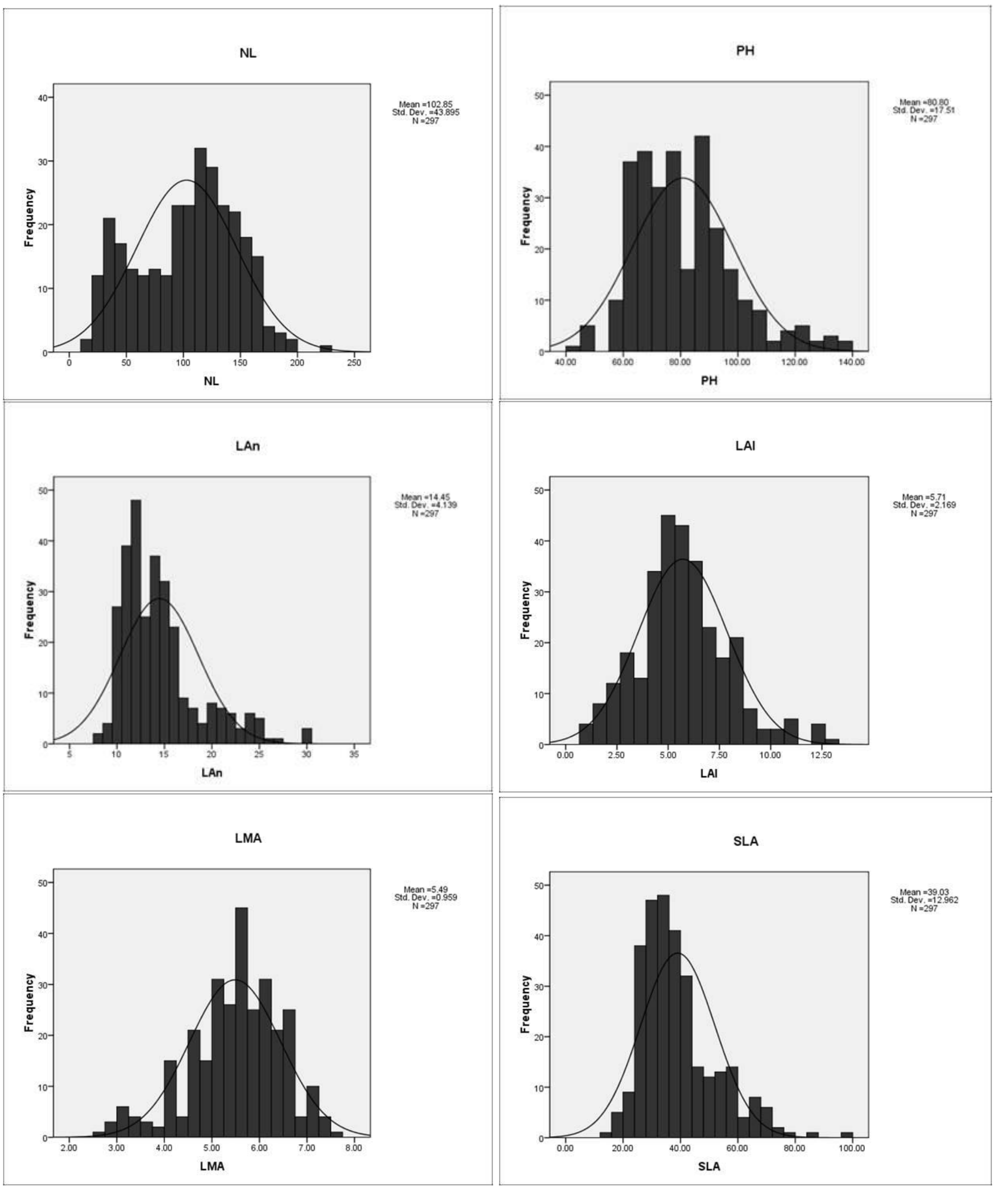
Variable	Minimum	Maximum	Mean	SD	C.V.%
PH	43.70	138.50	80.80±1.02	17.510	21.67
NL	12.00	225	102.85±2.55	43.90	42.68
LAn	9.00	30.00	14.45±0.24	4.14	28.64
LAI	1.10	13.00	5.71±0.13	2.16	37.97
LMA	2.70	7.50	5.49±0.06	0.96	17.47
SLA	15.16	97.34	39.03±0.75	12.96	33.21
SLWt	100.00	480.50	222.36±3.55	61.14	27.50
Y	3.03	98.06	40.24±0.90	15.51	38.55
Bio	18.64	96.42	48.50±1.03	17.76	36.61

PH: Plant height; NL: Number of leaves; LAn: Leaf angle; LAI: Leaf Area Index; LMA: Leaf Mass Area;
SLA: Single Leaf area; SLWt: Single leaf weight; y: Yield; Bio: Biomass.

Table 2. Correlation coefficient among leaf traits, yield and biomass of ninety nine rice genotypes

	PH	NL	LAn	LAI	LMA	SLA	SLWt	Y	Bio
PH	1								
NL	-.486**	1							
LAn	.197**	-.455**	1						
LAI	-.198**	.839**	-.345**	1					
LMA	-.381**	.450**	-.488**	.332**	1				
SLA	.621**	-.626**	.390**	-.230**	-.423**	1			
SLWt	.425**	-.402**	.071	-.016	.078	.725**	1		
Y	-.047	.158**	-.059	.183**	.179**	-.014	.080	1	
Bio	.027	.204**	-.072	.407**	.110	.121*	.252**	.413**	1

** significant at the 0.01 level * significant at the 0.05 level



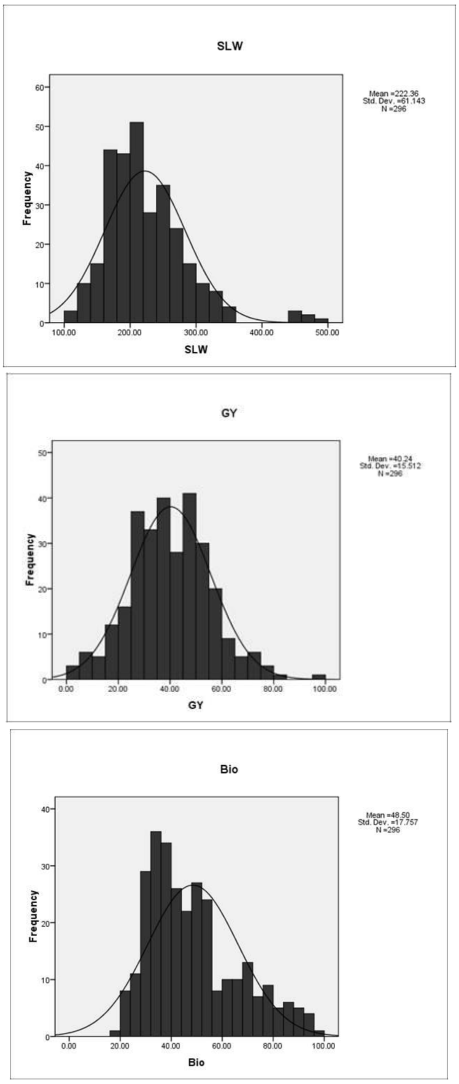


Figure 1. Frequency distribution for leaf traits, yield and biomass of rice genotypes

Conclusion

The results of the genetic variability analysis among the diverse rice germplasm showed significantly maximum variability for various leaf traits, yield and biomass. It was also observed that these genotypes exhibited significant positive and negative correlations for two or more traits (Table. 2). It is concluded from this study that the genotypes with higher diversity and association with each trait suggested that the traits with higher variability could be exploited in crop improvement programs or utilized in the direct selection of genotypes with desirable traits.

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