Analyzing Genetic Variability and Heritability in Rice Breeding: A Focus on Yield Improvement

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Abstract: *This study assesses the genetic variability and heritability of 19 agronomic traits in 431 elite rice breeding lines. Conducted in two seasons at the International Rice Research Institute, it aimed to identify traits predictive of improved rice yield. Significant genetic variability was observed, with traits like filled grains per plant showing a strong positive correlation with yield. High heritability was found for most traits, indicating their potential for use in targeted breeding programs. The study concludes that selecting for specific traits like panicles and filled grains per plant is crucial for enhancing rice yield.*

Keywords: Rice, trait evaluation, yield improvement

1. Introduction

Rice is a crucial food crop and a primary source of nutrition for more than one third of world's population [1]. In order to meet the food requirement of growing population, development of high yielding varieties is essential. The success of any breeding program depends on the selection of parents for hybridization. The parents involved in the development of varieties should be divergent. The germplasm provides immense scope for wide variability. Genetic divergence is an efficient tool for an effective choice of parents for hybridization programme. Such study also selects the genetically divergent parents to obtain desirable combinations in the segregating generations. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding program [2]. Keeping this in view, the present study was focused to assess the genetic diversity of 431 elite irrigated rice breeding lines using GenStat.

Generally researchers work with the small number of genotypes and account for phenotypic and genetic correlation coefficient. Detailed information regarding agronomic, physiological and /or yield component traits would be extremely useful for breeding to select parents for population development. However, due to limited resources typically available in public rice breeding programs, extensive trait characterization is usually not conducted. Only the critical traits such as plant height, days to fifty per cent flowering and yield are routinely measured in field trials. Once researchers have determined the total amount of genetic variation responsible for a trait, they can use this information in calculations of the trait's heritability.

The purpose of this study is to assess the genetic variability and heritability of key agronomic traits in elite rice breeding lines, and to evaluate their correlation with yield improvement, aiding in the development of high - yielding rice varieties.

The significance of this research lies in its contribution to rice breeding programs. By identifying key genetic traits correlated with higher yield, this study provides valuable insights for developing rice varieties that can meet global food demands more efficiently.

2. Materials and Methods

The research was conducted at the Plant Breeding, Genetics and Biotechnology (PBGB) Division of International Rice Research Institute (IRRI), Los Baños, Laguna, Philippines; IRRI is located at 14º 13'N latitude, 121 º 15' E longitudes, and at an altitude of about 21 m above mean sea level. Phenotyping experiments were conducted in IRRI's experimental field during 2012 dry and wet seasons.

A collection of 431 diverse *O. sativa* elite lines forms the basis for the diversity panel in this study. These elite lines were developed at IRRI from crosses between *indica* x *indica*, *indica* x temperate *japonica*, *indica* x tropical *japonica* and *indica* x aromatic basmati germplasm. The parents represent a range of geographic and genetic diversity.

All elite lines were purified for two generations by growing head rows prior to DNA extraction. Trials were grown during the dry and wet seasons of 2012 using an incomplete block design with three replications.

Important traits were identified and selected based on the literature. Phenotypic data were collected from the field grown plants in IRRI experimental station over two seasons (two replications, 8 plants per row, and 10 rows per entry). Of 431 individuals of each line grown in the field, 5 plants were randomly chosen for phenotyping from each replication. A total of 19 traits were evaluated. Plot size was 6m^2 and spacing was 20 x 20 cm.

3. Results

Phenotypic Variation
Large phenotypic variation was observed for all traits. Outliers in the data were identified based on the residuals derived from the data of all environments and were removed from further analysis. Variance components were calculated by REML. The results confirmed that genotypic variance was significant for all traits (P < 0.001). G x E interactions

were also significant (P < 0.001) but represented only a small fraction of the total variance.

The morpho - agronomic, quality and yield related trait data on 431 breeding lines grown in 2012 dry and wet season summarized in Table 2. Substantial genetic variation existed in all the 19 traits measured in the diverse germplasm set. Flowering time data was the most striking example of phenotypic variation, ranging from 73 to 110 days after sowing across two seasons. Plant height ranged from 106 to 120 cm across two seasons. Genetic variation also existed in yield and yield - related traits.

Heritability
The broad - sense heritability for agronomic traits was estimated for 2012 dry season. Plant height, flowering date, flag leaf length, peduncle length, grain length, grain width, length breadth ratio, 1000 grain weight, number of spikelets per panicle and yield per plant were highly heritable, all with an estimated $H^2 > 0.90$. Heritability for culm length panicle length and grain yield per plot was a little lower and $H^2 > 0.85$. The traits will the lower heritability were panicle exsertion, number of panicle per plant and filled grain per plant.

The broad - sense heritability for agronomic traits was estimated for wet season. Plant height, flowering date, culm length, grain length, grain width, grain length breadth ratio, were highly heritable, all with an estimated $H^2 > 0.90$. Heritability for flag leaf width, panicle length, peduncle length and 1000 grain weight was a little low and $H^2 > 0.85$. The traits with the lowest heritability were number of panicle per plant and yield per plant.

Correlation Studies
The understanding of the correlations between traits is of great importance in the studies breeding, especially if selection of one of them is impaired by low heritability or difficulties of measurement and identification [3], or when selection of one character causes modifications in other correlated traits. Generally, in a breeding program several traits are targeted simultaneously, so that the understanding of the genetic associations helps to refine the choice of the most appropriate procedures [4]. The existing relationships between traits are generally determined by the genotypic, phenotypic and environmental correlations. The phenotypic correlation measures the degree of association of two variables and is determined by genetic and environmental factors. The latter is mainly responsible for the correlation of traits of low heritability, such as grain yield, for instance [5]. The genotypic correlation on the other hand, which represents the genetic portion of the phenotypic correlation, is the only one of inheritable nature and therefore used to orient breeding programs [6].

4. Discussion

Primary objectives of this experiment were to evaluate 431 genotypes to detect the phenotypic variability of the traits and by selecting the associated traits that have better yield attributes for incorporation into the hybridization program. Normally breeding programs do not have resources for extensive phenotypic characterization. This was one of the largest phenotypic evaluations performed in elite breeding lines that ever done before that have published. Therefore the exploitation of the associated yield related traits will facilitate the development of new rice varieties.

Genetic Variation and Heritability

Genetic variability studies are important in selection of parents for hybridization [7] because crop improvement depends upon amount of genetic variability in base population [8]. Once genetic variability has been determined, crop improvement is possible through the use of appropriate selection methods. However total yield may be increased by selecting for yield components because they may be simply inherited compare to yield which is a complex trait.

Genetic improvement of a complex trait such as yield may be practiced through components approach of breeding that assumes strong associations of yield with a number of traits that make up the yield, grain weight, number of filled grains per plant and plant height are yield - determining traits that are frequently selected for the improvement of yield in breeding programs for cereals and legumes [9]. Traits are usually correlated and knowledge of the relationships among various quantitative and qualitative traits with heritability can support to the choice of appropriate factors to be used for selection.

Knowledge of relationship of the phenotypic traits among each other and their influence on yield as well as correlation of various traits will be of importance in selection of desirable lines to be incorporated in a breeding programme and in selecting suitable lines for subsequent release as new varieties.

Genetic variability was estimated by calculating broad sense heritability. The experimental result showed that most of the characters had high heritability except for number of panicle per plant. For most traits, high heritability was obtained ranging between 93 – 99.8% although low heritability was obtained for number of panicles per plant and total number of filled grain per plant. A similar result was found by [10] in rice, indicating additive gene effects. High genetic variation in the germplasm studied is a strong indication of significant genetic variation and low environmental variance indicating additive gene effects and these traits can be selected for and passed on to the progenies [11].

Calculation of heritability is used to help the breeder to select traits that are highly heritable as compared to a trait which is less heritable. High heritability value obtained in this study are days to flowering, flag leaf length and width, peduncle length, grain character, 1000 grain weight and plant height which indicated reasonable variation for these traits. This suggests that selection can be easily practiced by using these traits to improve grain yield in rice. The results support from the findings of [12] [13] [14]) who reported such type of heritability in wheat. Grain yield per plant has been found to correlate positively with the morphological characters in cereals, although days to flowering in rice was found to be significant negatively correlated. [15] evaluated yield among other components and observed the strongest

correlation between yield and yield per plant, with significant correlation also found between yield and number of panicles per plant, plant height, panicle length and 1000 - grain weight. This experimental study also detected similar results of yield with yield per plant, number of panicles per plant and 1000 grain weight.

Correlation

High yielding varieties development started since 1966. Yield per hectare is the most important consideration in rice breeding programme [16] but yield is a complex trait and may involve several related components.

Correlation analysis has been used by breeders to determine positive relationship between yield and other traits that enhance yield in rice genotypes. [16] obtained a positive correlation of number of filled grains per panicles, number of panicles per plant, 1000 - grain weight on grain yield. Correlation studies enable the breeder to understand the major traits on which selection can be based for population improvement.

The dependence of grain yield on other traits has been reported for many crops [17]. Rice yield is a product of number of panicles per unit area, number of spikelets per panicle, percentage of filled grains, and weight of 1000 seeds [18]. It is important to know the traits that influence grain yield, to determine heritability, correlation of those traits so that response to selection can be predicted.

Grain yield is a quantitative trait and a complex character for all crops. Various morphological and physiological plant traits contribute to yield. Yield components are interrelated with each other showing a complex chain of relationship and also highly influenced by the environmental conditions [19]. The breeding strategy in rice mainly depends on the degree of associated characters as well as the magnitude and nature of variation [20] [19]. For selection in rice, information on trait correlations has been helpful as a basis for selection in a breeding programme.

Most yield - related components in rice are usually significant and positive when correlated with rice yield. This gives rise to the need to identify few traits that have the highest influence on yield that could be used in rice yield improvement. The dependence of grain yield on other traits have been reported for many crops [21]. In this study grain yield was also positively correlated with all the characters except plant height, flag leaf area, grain length and length - breadth ratio.

Negative correlation between yield and days to flowering was found in this study and a similar result was obtained by [15]. The breeder must pay attention to negative correlations that present between grain yield and specific traits. Thus, in order to increase yield, it is important to minimize unfilled grain. The highest correlation with grain yield was recorded for the number of grains per plant ($r = 0.4916$) indicating the correlation of this trait with yield. This is an important findings because many research experiments use yield traits. Panicle length and flag leaf area were correlated positively and significantly, these results are in agreement with the findings of [22]. In addition, significant positive correlation

obtained between yield and panicle number ($r = 0.2556$). The findings indicated that plants with more panicles tend to have high number of filled grains thereby increasing rice yield. The positive correlation that was obtained between panicle number and filled grain per plant ($r = 0.5894$) indicating that increasing the number of panicle would also effectively increase the number of grains per plant and possibly increase grain yield. A significant correlation of traits showed that these traits could be improved simultaneously. The results also showed that differences in correlations between grain yield and yield traits present amongst the rice genotypes studied. This result is similar with the findings of [23] in maize grain, while the negative correlation between yield and plant height, flag leaf area, grain length, length breadth ratio suggest that the breeder should make careful selections negotiation if simultaneous selection for these traits is carried out in order to increase yield.

This study showed a high positive correlation of agro - morphological characters on rice yield. And this supported with the findings of [16] who obtained a positive correlation of agro morphological characters on rice yield, and the negative correlation between grain weight and number of filled grains per plant as obtained by [16] was consistent with the findings of our study.

A significant positive correlation was detected between yield and number of panicles, spikelets per panicles, filled grain per plant, yield per plant and 1000 - grain weight and while negative relationship with grain length and length breadth ratio. The findings suggest that grain yield can be improved in these rice genotypes by using these traits as selection criteria in segregating generations. The results are consistent with the findings of [19] and [20] that showed positive correlations with these traits. Plant height was found negatively correlated with number of panicle per plant, non - significant association with panicle exsertion and length breadth ratio. Negative correlation of flag leaf area with grain yield may indicate that more vegetative part in rice reduces the paddy yield due to high accumulation of photosynthates in vegetative parts as compared to reproductive parts (i. e. seed formation and grain filling) and lodging susceptibility [24] [20].

[25] reported the importance of number of filled grains per panicle in calculating of rice yield. In addition, [26] observed significant positive correlation between number of filled grains and grain yield of hybrid rice and suggested to use this trait in selecting the high yielding hybrid rice. This result coincided with the previous studies which also reported that number of filled grains per panicle had significant positive correlation on rice grain yield [25] [27]. Number of spikelets per panicle exhibited highly significant positive correlation with grain yield ($r = 0.2667$). Previous papers also mentioned that number of tillers had positive direct effect on grain yield [27] [28].

[29] described that the rice grain yield component consisted of number of spikelets, percentage of filled spikelets, and 1000 - grain weight; and among those, number of spikelets was the most important component limiting rice yield, while 1000 - grain weight rarely affected grain yield. [29]

suggested that high yield grain in rice varieties with reduced plant height associated with increase in lodging resistance of rice plant. Knowledge on contribution of each agronomic trait to grain yield could be useful to assist rice breeders as the indirect selection of grain yield during the early generation before conducting replicated yield trials [27]. Further studies are needed to elucidate relationship of grain yield and the other morpho - physiological traits.

Regression

There were several traits that were highly significantly associated with plot yield. In the dry season, flowering date was associated with yield ($R^2 = 4.1\%$) indicating that longer duration lines were lower yielding (r = - 0.20). This was not expected because high yield may be attributable to longer grain filling. Interestingly however, there was no association during the wet season.

During the wet season, flag leaf length and width were highly significantly associated with plot yield ($R^2 = 5.2\%$ and 10.5% respectively; r = - 0.23 and r = - 0.33 respectively). This strongly implies that the flag leaf physical characters are important during the wet season. However a negative correlation with leaf width was not expected because wider flag leaves may enable increased light interception when solar radiation is considerably lower compared to dry season. It is possible that wider flag leaves and higher flag leaf area may cause increased disease during the wet season.

In both seasons, number of panicles per plant was highly significantly associated with yield ($R^2 = 6.3\%$). Grain length, grain width and length breadth ratio have highly significant association with yield in wet season. Yield per plant was also highly significant association with yield in both seasons. In dry season, yield per plant was 24% and it is higher than wet season ($R^2 = 10.6\%$). The total number of filled grains per plant was also highly significantly associated with yield and in dry season ($R^2 = 17.2\%$) and it is higher than the wet season ($R^2 = 5.9\%$). In the wet season more diseases and lodging occurs so that less relation with yield in wet season and may be because plots were less uniform in wet season. Furthermore, a high and significant association of regression on flag leaf length and width in wet seasons, days to flowering in dry seasons, number of panicle per plant, grain length, grain breadth and length breadth ratio, yield per plant, number of filled grains per plant in both seasons (P < 0.001) was obtained when these traits were regressed against yield. Therefore, these traits could be used by breeders.

Use of Trait Data for Breeding

There are certain traits that are important only during dry season or wet seasons and some other traits are important across both seasons. So breeders should work with season specific materials (data not shown). Breeders have to select parents with contrasting traits and multiple trait combination and need to make specific crosses. Breeders could select the early generation segregating materials (F2 - F3) so that could make specific combination. Breeders should start selection for these traits in germplasm and should continue up to the process of developing fixed lines. This data could be used for retrospective analysis of historical varieties.

The study showed genetic variation amongst the genotypes and this is important in selection of parents for hybridization, since crop improvement depends upon magnitude of genetic variability in base population. Therefore, an understanding of the genetic variation associated with the expression of yield related traits will facilitate the exploitation of the component approach in the improvement of rice. Thus, the various analyses carried out indicated wide variability among the 431 entries for the 19 traits (i. e. based on broad sense heritability) among different traits. The wide range of variability observed for the characters evaluated may be attributed to diverse genetic backgrounds of the lines studied. These could be used for selection of the genotypes to make targeted crosses. In conclusion, days to flowering, number of panicles per plant, number of spikelets per panicle, yield per plant and filled grain per plant are most important traits for use in selection program among traits. Thus, these plant traits deserve greater attention in further breeding programs for developing new high yielding varieties.

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