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Assessment of nature and magnitude of gene action and components of genetic variation for quality traits and yield

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Abstract

Rice (*Oryza sativa* L.) is one of the most important staple food crops of the world, and improvement in yield and grain quality remains a major objective of rice breeding programs. The present investigation was undertaken to estimate the nature and magnitude of gene action and components of genetic variation governing yield and quality traits in rice. The experimental material comprising selected parental lines and their hybrids was evaluated under suitable field conditions using an appropriate mating design. Observations were recorded for grain yield and important quality traits such as hulling percentage, milling percentage, head rice recovery, kernel length, kernel breadth, length–breadth ratio, amylose content, and other related characters. The analysis of variance revealed significant differences among genotypes for all the traits studied, indicating the presence of considerable genetic variability. Estimates of additive and dominance genetic components showed that both additive and non-additive gene actions were involved in the inheritance of yield and quality traits. However, the predominance of dominance effects for several characters suggested the importance of heterosis breeding and selection in later generations. Higher estimates of heritability coupled with high genetic advance for certain traits indicated the effectiveness of selection for their improvement. The study also revealed substantial genotypic and phenotypic variation for grain yield and quality parameters, providing ample scope for genetic enhancement. The information generated from this investigation will be useful for identifying superior parents, designing effective breeding strategies, and developing high-yielding rice varieties with desirable grain quality attributes.

Keywords: Rice, gene action, genetic variability, additive effects, dominance effects, heritability, genetic advance, quality traits, grain yield

Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops in the world and serves as a staple food for more than half of the global population. In India, rice plays a crucial role in ensuring food and nutritional security, contributing significantly to agricultural income and employment. With the increasing demand for food due to rapid population growth, the development of high-yielding rice varieties possessing superior quality traits has become a major objective of plant breeding programs.

Yield is a complex quantitative trait controlled by numerous genes and is greatly influenced by environmental factors. Similarly, grain quality traits such as grain length, grain breadth, kernel dimensions, amylose content, cooking quality, and milling characteristics are polygenic in nature and determine consumer preference and market value. Therefore, understanding the genetic architecture governing these traits is essential for the formulation of effective breeding strategies.

The success of any crop improvement program largely

depends on the knowledge of the nature and magnitude of gene action controlling economically important traits. Gene action refers to the manner in which genes influence the expression of a trait and includes additive, dominance, and epistatic effects. Additive gene effects are fixable through selection, whereas non-additive effects such as dominance and epistasis are exploited through hybrid breeding. Estimation of gene action helps breeders identify appropriate breeding methods for genetic improvement. Genetic variation is the fundamental prerequisite for selection and crop improvement. The partitioning of genetic variance into its components provides valuable information regarding the inheritance pattern of traits and the relative importance of additive and non-additive gene effects. Estimation of genetic parameters such as additive variance, dominance variance, heritability, and genetic advance enables breeders to assess the effectiveness of selection and predict the potential genetic gain in subsequent generations. Generation mean analysis, diallel analysis, and other biometrical approaches are commonly employed to estimate

the components of genetic variation and gene action. These methods facilitate the identification of superior parental lines and promising cross combinations for developing high-yielding varieties with desirable quality characteristics.

Materials and Methods

The experimental material consisted of selected rice (*Oryza sativa* L.) genotypes differing in yield and quality traits. Crosses were made between genetically diverse parents to generate six generations, namely P₁, P₂, F₁, F₂, BC₁ and BC₂, for generation mean and genetic variance analysis.

Experimental Site and Design

The experiment was conducted at the research farm of the Department of Genetics and Plant Breeding during the kharif season. The six generations of each cross were grown in a Randomized Block Design (RBD) with three replications. Recommended agronomic practices were followed to raise a healthy crop.

Analysis of Variance (ANOVA)

Analysis of variance was performed to test the significance of differences among generations for all the traits following standard statistical procedures.

Estimation of Gene Action

Generation mean analysis was carried out using the six-parameter model proposed by Hayman (1958)^[1] and Jinks and Jones (1958)^[2]. The following genetic parameters were estimated:

- m = Mean effect
- d = Additive gene effect
- h = Dominance gene effect
- i = Additive × Additive interaction
- j = Additive × Dominance interaction
- l = Dominance × Dominance interaction

The adequacy of the additive-dominance model was tested using scaling tests (A, B, C and D) and joint scaling tests.

Estimation of Genetic Variance Components

The components of genetic variance were estimated from generation variances as follows:

- Additive variance (D)
- Dominance variance (H)
- Environmental variance (E)

The relative importance of additive and non-additive gene effects was assessed through the magnitude and significance of these components.

Heritability Estimation

Heritability was estimated in both broad sense and narrow sense using standard biometrical genetic formulas:

$$H^2 = \frac{VG}{VP} \quad h^2 = \frac{VA}{VP}$$

where:

- VG = Genotypic variance
- VA = Additive variance
- VP = Phenotypic variance

Interpretation

The significance and magnitude of additive, dominance and epistatic gene effects were used to determine the nature of gene action controlling yield and quality traits. Traits governed predominantly by additive effects were considered amenable to selection, while traits showing dominance and epistatic effects were considered suitable for heterosis breeding and recurrent selection approaches.

Results and Discussion

The estimates of broad-sense heritability recorded during the experiment at two different locations, including Pilikothi farm, are presented in Tables 4.7.1 and 4.7.2 and illustrated in Fig. 4.2.1 and Fig. 4.2.2.

At the first location, broad-sense heritability values ranged from 53.14% to 99.22%. Most of the grain quality and yield-related traits exhibited high heritability, indicating a strong genetic control over trait expression. However, number of spikelet's per panicle (53.14%) and effective tillers per plant (55.22%) showed moderate heritability. The highest heritability was recorded for grain length (99.22%), followed by elongation index (98.28%) and elongation ratio (98.28%), suggesting that these traits are predominantly governed by genetic factors and are less influenced by the environment.

At Pilikothi farm, broad-sense heritability values ranged from 48.10% to 99.80%. Similar to the first location, most traits exhibited high heritability, while panicle length (48.10%) and number of spikelet's per panicle (54.39%) showed moderate heritability. The highest heritability was observed for grain length (99.80%), followed by kernel length after cooking (99.65%), indicating strong genetic control and high potential for effective selection in breeding programs.

Estimates of Genetic advance

The estimates of genetic advance recorded during the experiment at the two locations are presented in Tables 4.7.1 and 4.7.2 and illustrated in Fig. 4.2.1 and Fig. 4.2.2. The genetic advance values ranged from 0.19 to 27.57 at the first location and from 0.21 to 28.37 at Pilikothi farm, indicating considerable variability among the studied traits.

At both locations, the highest genetic advance was observed for number of spikelet's per panicle (27.57 and 28.04, respectively) and plant height (27.53 and 28.37, respectively), suggesting strong additive gene effects and good scope for improvement through selection.

Moderate genetic advance coupled with high heritability was recorded for several important traits across both environments, including days to 50% flowering (14.92 with 95.51% heritability and 15.32 with 95.70% heritability), days to maturity (14.71 with 95.01% and 15.30 with 95.73%), gel consistency (12.87 with 68.15% and 14.12 with 69.83%), and grain yield per plant (12.57 with 86.13% and 11.59 with 89.26%).

Summary and Conclusion

The different steps involved in the research work include, identification of contrasting parents, their crossing, confirmation of true hybrids by hybridity test, and making backcross for Experiment I whereas, Experiment II involved validation of parents for grain quality traits using gene-

specific markers, development of $F_{2:3}$ population, parental polymorphism survey for identification of polymorphic markers, genotyping of the $F_{2:3}$ population with the identified polymorphic markers and finally, phenotyping of the mapping population for grain quality traits such as aroma, eating & cooking quality, grain dimension, and yield-related traits.

- The scaling test results showed significance for either one of the four scales or in combination, along with a significant χ^2 value of joint scaling, suggesting the presence of non-allelic interaction for all the grain quality and yield traits.
- The significance of mean values (m) in generation mean analysis for all the grain quality and yield traits advocates that the mean values of the six generations differed significantly for all the traits and hence the information generated through mean would be unbiased.
- The additive (d) and additive $\times$ additive (i) types of interaction were significant in the desired direction for the traits kernel breadth after cooking, the number of spikelet's/panicle and grain yield per plant, suggesting the improvement of these traits through simple pedigree selection.
- For the traits plant height, panicle length, number of effective tillers per plant, grain yield per plant, grain breadth, kernel breadth, kernel length breadth ratio, and kernel breadth after cooking, dominance (h) and dominance $\times$ dominance

(l) interactions were significant in the desired direction, implying that selection for these traits should be practiced in later generations when heterozygosity in the population is reduced.

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