



## **A Review on Genetic Analysis of Rice (*Oryza sativa* L.) Crop for Yield and its Contributing Characters**

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### **Authors' contributions**

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

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### **ABSTRACT**

Rice provides major source of calories in the global population. In any crop breeding programme, presence of genetic variability is essential for broadening the gene pool. For selecting a genotype having high desirable traits, high magnitude of variability should be present in the population. The heritability estimates along with amount of genetic variability give us an idea about genetic gain due to selection. Different direct traits (number of panicle/plant, filled grains/plant and test weight) and indirect traits (tiller number/plant, plant height) determine the yield component of rice. Present review draw a clear picture of how variability influences the selection process and also how yield is associated with different direct and indirect traits. Genotypes shows high variability and desirable characters can be used in further breeding programme. A glimpse of molecular advances in rice breeding also has been incorporated in the present review.

**Keywords:** *Staple food; genetic variability; desirable traits; selection; heritability; molecular breeding.*

## 1. INTRODUCTION

Rice (*Oryza sativa* L.) crop provides food for majority of the world's population, providing almost 21% of energy [1,2]. Rice is one of the most important food grain and economically viable crop which rank second (2<sup>nd</sup>) next to wheat with 497 million metric tons produced. For the expression of a particular character, different gene actions are involved. In rice crop, diallele analysis provides necessary information on gene action by using different yield and its contributing traits. In some specific scenarios, conventional breeding is also helpful to understand the type of gene action involved in the expression of a trait. In rice crop besides breeding strategies, addition of natural components- peptides, nano particles [3], amino acids herbal extracts and essential oils [4] with biological activities may increase gene expression. Grain yield is highly influenced by various biotic (bacteria, viruses, fungi) and abiotic (water-logging, salinity) stresses. Under complex environmental condition in any crop breeding programmes, direct selection for yield is error prone and creates confusion. Therefore, accurate selection process depends on the genetic variability present in the population and also the association among different morpho-agronomic traits with yield. Estimation of correlation coefficient provides an idea about relationship of the different traits with grain yield. Association analysis helps plant breeders to find superior genotypes by focusing on desirable traits. So the present paper gives an overview of the concept of genetic diversity and also describes how the yield component is determined by different direct and indirect effects.

## 2. GENETIC VARIABILITY IN RICE

Any breeding programme mainly depends on the amount of genetic variability present in the population. The phenotypic observable variation of an individual is the result of genetic variability and variability due to environment. For any crop improvement programme, estimation of genetic variability is the key requirement. So to find out the genetic and non-genetic components of a population, partitioning of total phenotypic variability is essential for any successful breeding programme. A study was conducted to evaluate thirty five (35) rice genotypes for genetic variability, genetic advance and heritability for yield and its related traits. For traits like-days to panicle initiation, plant height, days to 50 % flowering, number of panicle/plant, panicle length

(cm), number of spikelets/panicle a wide range of variation was observed [5]. Significant difference was observed among several genotypes in a study with rice crop by taking into consideration of thirteen (13) characters to estimate the nature and magnitude of variability, genetic advance and heritability. Similar significant genetic variability was also observed for all the characters in a study with rice crop. Moderate genotypic and phenotypic coefficient of variance was observed in traits like number of grains/panicle, productive tillers/plant and seed yield/plant [6]. In a recent study diversity analysis was done with forty (40) wild rice germplasm lines for twelve (12) quantitative characters using D<sup>2</sup> analysis. Seven (7) clusters were made based on the performance of genotypes in which cluster I possess maximum (32) number of genotypes followed by cluster-IV and other clusters [7].

To study the character association and genetic variability, observations were recorded for 49 rice cultivars. Path analysis was carried out with character association to find out the effect of yield with its related traits. Significant differences among genotypes were found after considering all the traits. For traits like number of grains/panicle, grain yield and test weight, PCV and GCV was found moderate to high [8]. Estimation of correlation was also done along with genetic variability and heritability for 100 rice germplasms by using alpha lattice design having three replications. ANOVA study revealed that significant differences were observed for all the traits studied [9].

## 3. CRITERION FOR SELECTION BY CORRELATION AND PATH COEFFICIENT ANALYSIS IN RICE

It is important to know the feasibility of a joint selection for several traits instead of selecting the secondary traits for genetic gain of main (primary) traits [10]. For increasing the rice production, the aim of breeding programs is to use more genetic diverse population and also apply appropriate selection methods to increase yield by its component characters. Correlation analysis helps in identifying the relationship between yield and its component traits [11], whereas path analysis is used to divide the influence of characters into direct and indirect effects. In path analysis (statistical tool) a path chart is used for estimation of relationships between prediction variables and response variables [12]. Yield is a complex character which is associated with its component traits

(number of panicle/ plant, number of grains/ spike, test weight etc.) [13,14]. Performance of rice crop depends on the relationship between yield and its related major traits. In such condition selection is ineffective if we only focus on yield trait. Therefore, Path analysis and correlation coefficient helps in segmenting the yield contributing traits into direct effect and indirect effect components [15]. Path analysis is also use as a selection criterion for improvement of rice crop [16]. A positive correlation study was observed in rice crop for grain yield and its related traits. Study found out that trait 1000 grain weight can be improved by increasing the panicle length as well as panicle number per plant [17]. Another study reveals a positive correlation of grain yield with related traits; trait 1000 grain weight can be improved by increasing the panicle length and panicle number per plant. Similar correlation was observed with the results of Kumar *et al.* [18], Khush [19], Bhutta *et al.* [20], Chhangte and Devi, [21]. Information about trait relationship helps plant breeders to find suitable genotypes in various environmental conditions [22].

#### 4. MODERN APPROACHES IN RICE BREEDING

Molecular breeding of rice for high yield, improved grain quality, and high environmental adaptability is essential for feeding the world's rapidly growing population [8]. The crop yield per unit area must be increased by 50 % to meet the security of food supply by 2030 [23]. High yield is the primary objective pursued by rice breeders. Super rice breeding using molecular design in the model of ideal plant architecture is important for future rice development programme [24]. In some recent studies with Aromatic Rice shows variation in aroma when they are grown in regions other than their normal traditional growing regions [25]. In *Biryancheera* variety aroma production is due to presence of BADH2 gene which is also present in the popular scented Basmati rice [26]. For increasing the major breeding objective that is grain yield, different associated traits like- grain number per panicle, grain shape, number of tillers, leaf angle and leaf size need to improve. Gene *OsHHLH079* is associated with the control of leaf angle and grain shape in rice through brassinosteroid biosynthesis and signaling pathways [27]. A study was conducted on grain shape and grain weight to identify the effect of 7 genes *GS2*, *GS3*, *GS5*, *GW5*, *GS7*, *SLG7*, and *GW8*. Genetic effect was estimated for each allelic

combination for the improvement of traits like grain length, grain thickness, grain width, and thousand grain weights [28]. In rice plants, a semi-dwarfism gene, *OsCYP96B4* was identified which influence the content of amino acids,  $\gamma$ -aminobutyrate (GABA), saccharides and other secondary metabolites. Molecular study on heterosis for different characters like plant height, days to heading and grain yield were also conducted [29-32]. Parental material was two (2) subspecies of rice (*O. sativa* spp. Indica and *O. sativa* spp. Japonica) and eight QTLs were detected in the study [33]. CRISPR/Cas9 technique was used to identify *OsEVL4* gene which is a regulator of character plant biomass and tiller number. A targeted mutation of rice *FLW* genes was used in the technique [34]. Over expression and knockdown transformants of the *OsNAR2.1* gene was estimated in rice crop. With the change of expression level of *OsNAR2.1* gene changes the global methylation at whole genome level which ultimately changes plant height and grain yield [35]. Another study found out that a large set of genes are expressed differentially at the shoot apical meristem and regulate traits like number of tillers per plant and panicle numbers in rice plant [36]. All these above novel approaches are used to increase the yield potential of rice crop by understanding the molecular mechanisms.

#### 5. CONCLUSION

Enhancement of yield is the prime objective in any rice improvement programme. Genetic variability with high narrow sense heritability must be present in a population for effective selection of economically important traits. For selection of traits which are preferred by farmers like large seeds, high yield potential and also for traits preferred by plant breeders like resistance against different biotic and abiotic stress, proper dissection of nature and magnitude of genetic variability is essential. A study on relationship between yield and its different component traits help plant breeders to go for direct and indirect selection. Different molecular techniques are used to find out the genes responsible for expression of traits. So more emphasize should be given to characterize diverse germplasm by using different molecular approaches so that they can be used in future breeding programme efficiently.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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