Variability parameters,correlation studies and path analysisof yield and yield-related traits in rice (*Oryza sativa* L.): A Comprehensive Review

ABSTRACT

Rice, a staple food crop of global importance exhibits substantial diversity in terms of yield and other agronomic traits, influenced by genetic, environmental, and management factors. Variability parameters, including genotypic and phenotypic coefficients of variation, heritability,correlation, and pathanalysis provide crucial insights into the extent of trait variation and their potential for improvement through breeding programs.Furthermore, correlation studies unveil the interdependencies between different traits, shedding light on potential connections influencing yield. This analysis uncovers important trait associations, guiding breeders and researchers in the pursuit of crop improvement strategies. By identifying both positive and negative correlations, this research offers a deeper understanding of trait interplay and informs targeted trait selection efforts.Path analysis, a pivotal aspect of this review, describes the underlying causal relationships between traits and their direct and indirect effects on yield. This analysis facilitates the ranking of trait contributions and guides decisions for trait prioritization in breeding programs. By illuminating the pathways through which traits influence yield, path analysis enhances the precision of trait selection for improved rice cultivars.The synergy of variability parameters, correlation studies, and path analysis presents a holistic framework for unraveling the complexities of rice yield determination. Understanding these parameters enhances our ability to select and develop high-yielding and resilient rice varieties, contributing to food security and sustainable agriculture. This abstract delves into the significance of variability parameters in unraveling the complexities of rice yield and trait dynamics, guiding effective crop improvement strategies for the future. This review provides a valuable synthesis of existing knowledge, offering insights that can aid researchers, breeders, and agronomists in their pursuit of enhancing rice yield and overall agricultural sustainability.

INTRODUCTION

Rice is one of the most important staple food crops in the world, serving as a primary food source for more than half of the global population, particularly in Asia where it is a dietary staple. It plays a critical role in ensuring food security and providing essential nutrients to billions of people.The study of yield and yield-related traits in rice is of paramount importance for several reasons.Yield in the context of rice production refers to the total amount of harvested rice grain obtained from a specific area of land, usually expressed in kilograms or tons per hectare (or any other suitable unit of measurement). It is a crucial metric in agriculture as it directly measures the productivity and efficiency of rice cultivation.Yield is a multifaceted trait, influenced by a variety of morphological and physiological attributes that collectively contribute to the production of grain (Luo *et al.*, 2001).Developing crops with high yields necessitates knowledge about the types and extent of differences present in the accessible genetic resources, the connection between yield and other related traits, and the level of impact that environmental factors have on the manifestation of these characteristics (Edukondalu *et al.,* 2017).Various genetic parameters, including measures like phenotypic coefficient of variation, genotypic coefficient of variation, heritability, and genetic advance over the mean, collectively provide a comprehensive understanding of the existing diversity within the population. This comprehensive insight assists in the identification of genotypes possessing sought-after traits (Vikas *et al.,* 2015).

Variability arises from differences in the genetic composition of individuals within a plant population or due to environmental changes. Effective selection occurs when there is a significant level of genetic variation among the breeding materials' individuals (Sumanth *et al.,* 2017).ANOVAhelps researchers identify and understand the characters that influence yield variation and ultimately aiding in the improvement of rice production strategies.In various improvement programs, the presence of genetic diversity plays a vital role in selecting superior genotypes. However, the influence of environmental factors can obscure the true genetic variation. Phenotypic variance represents the variation in the expression of traits, which arises from both genetic and environmental factors. Hence, it is essential to partition the phenotypic variance into genotypic and environmental factors when selecting genotypes (Hasan *et al*., 2019). In general, the phenotypic variance tends to be higher than the genotypic variance, indicating the coexistence of both factors.Heritability quantifies the extent to which a trait is inherited by future generations, while genetic advance illustrates the variance between the average genotypic values of the chosen group and the initial population. When heritability estimates are coupled with genetic advance, they provide a more precise prediction of the genetic progress achievable through selection compared to relying solely on heritability measurements (Demeke *et al*., 2023). While substantial genetic diversity has been previously documented for yield and quality traits, there remains a significant amount of untapped genetic variation within the germplasm. This untapped diversity holds potential for discovering appropriate parent plants and creating improved offspring that excel in both yield and quality aspects. The multitude of genes, known as polygenes, that primarily govern various genetic traits, are notably influenced by environmental factors (Manivelan*et al*., 2022).Understanding the nature and extent of genetic variation concerning quantitative traits such as yield and its components is indispensable for enhancing crop improvement efforts (Deepthi *et al*., 2021).

Due to its intricate and polygenic nature, yield selection benefits not only from measures of variability but also from association analyses, aiding in the identification of traits accountable for yield enhancement. Character association, determined through the correlation coefficient, stands as a significant biometric instrument for constructing a selection criterion, as it unveils the intensity of connections within a cluster of traits. The nature and degree of correlation between yield and other attributes aid in gauging the proportional impact of individual traits on yield enhancement, thus empowering breeders to pinpoint favorable traits crucial for augmenting yield.Understanding the correlation between a characteristic, such as yield, and other factors influencing yield components, would be advantageous for identifying suitable rice genotypes to serve as parent plants in breeding initiatives (Sreedhar *et al.,* 2019).Indirectly choosing to yield through yield components becomes feasible when the component traits exhibit high heritability and a positive correlation with yield (Asante *et al*., 2019).Nevertheless, relying solely on correlation estimates does not always lead to an accurate understanding of the actual relationship between two variables, as it can sometimes be influenced by the presence of a third variable (Bello *et al.,* 2010). Path analysis holds significance as a statistical method employed in conjunction with correlation studies, aiming to establish causal relationships between variables. It distinguishes direct influences from indirect ones, providing essential insights for effective trait selection geared towards yield improvement (Talekeret *al*., 2022).Information obtained from the variation in traits at the phenotypic and genotypic levels, heritability, and correlation studies offers valuable insights for the improvement of favorable characteristics through breeding(Bekele *et al.,* 2013).

As per Robinson *et al.* (1949), heritability estimates were categorized into three groups: high (greater than 60%), moderate (30-60%), and low (0-30%). The calculation of genetic advancement as a percentage of the mean was performed and categorized as high (greater than 20%), moderate (10-20%), and low (less than 10%), following the approach outlined by Johnson *et al.* (1955). Correlation analysis utilized the formulas proposed by Falconer (1964). The division of the correlation coefficient into direct and indirect effects was executed using the method introduced by Wright (1921) and further detailed by Dewey and Lu (1959).

Yield and its component traits

These component traits play a crucial role in determining the productivity of the crop.Understanding and optimizing these traits are essential for improving rice yield and ensuring food security. Some of the key component traits that impact rice yield include days to 50% flowering, plant height, panicle length, number of productive tillers per plant, grains per panicle, test weight etc.Optimizing rice yield involves breeding and selecting varieties that excel in these component traits, as well as implementing effective agronomic practices such as proper fertilization, irrigation, and pest management. Scientific research and breeding programs continually aim to improve these traits to enhance rice yield, increase food production, and contribute to global food security.

ANOVA (Analysis of Variance)

ANOVA helps researchers determine whether there are significant differences among various genotypes or treatments, and it quantifies the amount of variation that can be attributed to different factors.The process involves comparing the variability between groups (often referred to as "treatments" or "factors") to the variability within the groups. If the variability between groups is significantly larger than the variability within groups, it suggests that the traits being analysed have a notable impact on rice yield.The results of ANOVA provide a way to determine which characters contribute most significantly to the variation in rice yield. This information is valuable for making informed decisions about rice cultivation practices, breeding programs, and selecting the most promising rice varieties to improve overall yield and quality.

Genetic Variability

Having a wider range of genetic diversity in the starting breeding materials increases the likelihood of obtaining the desired traits in a crop plant. As a result, the main purpose of germplasm conservation is to gather and safeguard the genetic variability present in the native collection of crop species, ensuring that it remains accessible to both current and future generations. (Maurya *et al*., 2022). Genetic variability serves as the foundation upon which selection operates to enhance the genetic makeup of plants. Key indicators for direct selection, such as broad-sense heritability and genetic advance as a percentage of the mean, offer insights into the transmissibility of traits and the effectiveness of selection in improving these characteristics (Gupta *et al.*, 2022). Genetic variability research offers essential insights into the genetic characteristics of a population, forming the basis for developing breeding strategies to enhance the crop further. These studies are also valuable in understanding the nature and extent of variability arising from various factors, the crop's responsiveness to its environment, the heritability of traits, and the potential for genetic advancement (Chavan *et al*., 2022).

Heritability and Genetic advance as percent of mean

Heritability and genetic advance are additional crucial factors for selection. Heritability estimations aid plant breeders in identifying which traits would be beneficial for selection and the degree of transmissibility of traits of interest (Sabesan *et al.*, 2009). Breeders aim to choose superior genotypes based on their observable characteristics (Paikhomba*et al.*, 2014). The traits that are considered for further breeding are determined based on the estimates of heritability. Genetic advance as a percentage of mean refers to a measure used to quantify the extent of improvement in a trait or characteristic within a population. It represents the difference between the mean (average) value of the trait in the current population and the mean value of the trait in the selected improved individuals. This difference is then expressed as a percentage of the original mean value. It helps assess the effectiveness of a breeding program by indicating the relative magnitude of improvement achieved in comparison to the initial trait mean. Heritability quantifies the extent to which a trait is inherited by future generations, while genetic advance illustrates the variance between the average genotypic values of the chosen group and the initial population. When heritability estimates are coupled with genetic advance, they provide a more precise prediction of the genetic progress achievable through selection compared to relying solely on heritability measurements. When high heritability is observed along with a substantial genetic advance, it suggests the influence of additive gene action whereas high heritability with low genetic advance indicates non additive gene action of the concerned traits.When there's a combination of high genetic advance and high heritability estimations, it presents breeders with the optimal circumstances to swiftly identify and promote desirable characteristics within a population (Larik *et al.*, 2000). Consequently, making selections based on these parameters would result in more reliable outcomes (Johnson *et al*., 1955).

Coefficient of variation

GCV (Genotypic Coefficient of Variation) and PCV (Phenotypic Coefficient of Variation) are important statistical measures used to assess the variability of a trait, such as rice yield, within a population. GCV measures the proportion of genetic variation present in a trait within a population. It focuses on the inherent genetic differences among individuals. In the context of rice yield, GCV indicates the extent of variation in yield attributed to genetic factors. A higher GCV suggests that there is significant genetic diversity among the rice plants in terms of their yield potential (Oladosu *et al.*, 2014). PCV considers both genetic and environmental factors that contribute to the variation in a trait. In the case of rice yield, PCV reflects the overall variability in yield across different rice plants, considering genetic differences as well as the influence of environmental conditions such as soil quality, climate, and cultivation practices. Thus, GCV focuses on the genetic diversity underlying a trait, while PCV considers the combined effects of genetics and environment. Moreover, studies revealed that the inclusion of genotypes exhibiting substantial Genetic Coefficient of Variation (GCV) in traits related to yield is crucial for developing high-yielding varieties using hybridization and selective breeding techniques (Tiwari *et al.*, 2019). It is hypothesized that a significant level of GCV leads to diverse offspring in subsequent generations of segregation (Bose *et al*., 2007).

Correlation studies

Correlation analysis offers insights into the nature and strength of relationships among different traits, enabling the identification of key component traits. These component traits serve as the basis for selecting traits that can be genetically improved to enhance grain yield ((Hallauer and Filho, 1988). To conduct a successful breeding initiative, it is essential to comprehend the genetic diversity inherent in traits that contribute to yield, as well as how these traits interact with overall yield. The correlation coefficient can be a valuable tool for pinpointing characteristics that hold minimal or negligible importance within the selection process (Singh *et al*., 2014). Genotypic and phenotypic correlations in rice yield refer to the relationships between different traits or characteristics and their influence on the yield of rice crops. The genotypic correlation examines the degree of association between the genetic factors (genes) responsible for different traits and the resulting yield. It helps plant breeders understand how closely related genetic factors contribute to yield variation (Li *et al.,* 2018). For instance, if there's a strong positive genotypic correlation between traits like grain size and yield, it suggests that these traits tend to be inherited together, making them potential targets for simultaneous improvement through breeding whereas Phenotypic correlation considers the observable traits or characteristics in the plant (phenotype) and how they relate to each other and impact yield. It considers the combined effects of genetics and environmental conditions. For example, if there's a high positive phenotypic correlation between traits like tiller number and yield, it implies that in the field, rice plants with more tillers tend to have higher yields on average. Both genotypic and phenotypic correlations play a crucial role in understanding the complex interactions between various traits and their effects on rice yield (Jayasudha *et al*., 2010).

Path Analysis

The utilization of path coefficient analysis provides a significant approach for recognizing both direct and indirect factors that contribute to interactions. Additionally, it offers a thorough assessment of the specific influences that lead to correlations, while also quantifying the comparative significance of each causal element. Path analysis is used to determine the extent of the contribution made by each individual yield component trait to the ultimate grain yield, encompassing both direct and indirect effects (Nithya *et al.,* 2020).Path coefficient analysis aids in the disentanglement of correlation coefficients into two distinct components: the direct effects, represented by the path coefficient, and the indirect effects, which encompass the influences originating from other variables (Azhmadizadeh*et al.,* 2011). This analytical approach also empowers breeders to arrange genetic attributes in order of their respective contributions (Sreedhar *et al*., 2019).This technique also assists in understanding the complex interplay of factors such as plant growth characteristics, environmental conditions, and agronomic practices, allowing researchers and farmers to prioritize and optimize the management strategies for achieving higher rice yields.

Conclusion

In conclusion, the study of variability parameters such as heritability and genetic advance is crucial for understanding the factors influencing rice yield and yield-related traits. High heritability and significant genetic advance indicate the potential for genetic improvement through selective breeding. These parameters offer valuable insights for plant breeders and researchers in identifying promising genotypes and devising effective breeding strategies to enhance rice productivity and overall crop performance. By considering variability parameters, we can make more informed decisions and foster sustainable agricultural practices aimed at increasing rice yields and addressing food security challenges. The coefficient of variation (CV) serves as a valuable tool for assessing the variability and stability of rice yield and yield-related traits. A higher CV indicates greater variation in the trait within the population, while a lower CV suggests greater uniformity and stability.Studying the CV of rice yield and yield-related traits provides valuable insights for plant breeders and researchers. Incorporating the coefficient of variation in rice breeding programs and research endeavors can contribute to the development of high-yielding, stable, and adaptable rice varieties, ultimately supporting global food security and sustainable agricultural practices.Correlation analysis helps us understand the relationships between different agronomic traits and their impact on rice yield. It allows us to identify which traits are positively or negatively correlated with yield, guiding breeding and management decisions. Moreover, it helps in the early identification of traits that might indirectly affect yield through their influence on other traits.Path analysis takes this a step further by dissecting the causal relationships between traits, distinguishing between direct and indirect effects on yield. This information is invaluable for prioritizing breeding efforts and agricultural interventions, as it highlights the most influential traits and their pathways of influence.Together, these three analytical tools provide a comprehensive framework for rice breeders and farmers to make informed decisions about trait selection, crop management, and resource allocation. By leveraging variability, correlation, and path analysis, we can work towards developing more productive and resilient rice varieties, ultimately contributing to food security and sustainable agriculture.

References

Asante, M.D., Adjah, K.L and Annan-Afful, E. 2019. Assessment of genetic diversity for grain yield and yield component traits in some genotypes of rice (*Oryza sativa* L.). *Journal of Crop Science and Biotechnology*. *22*(2): 123-130.

Ahmadizadeh, M., Nori, A., Shahbazi, H., Aharizad, S. 2011. Correlated response of morpho-physiological traits of grain yield in durum wheat under normal irrigation and drought stress conditions in greenhouse. *African Journal of Biotechnology*. 10(85): 19771–19779.

Bekele, B.D., Rakhi, S., Naveen, G.K., Kundur, P.J and Shashidhar, H.E.2013. Estimation of genetic variability and correlation studies for grain zinc concentrations and yield related traits in selected rice (*Oryza sativa* L.) genotypes. *Asian Journalof Experimental Biol. Science.* 4(3):391-397.

Bose, L.K., Das, S., Pradhan, S.K., Subudhi, H., Singh, S and Singh, O. 2007. Genetic variability of quality characters and grain yield in lowland rice genotypes of Eastern India. *Korean journal of breeding science*. 39(1):1-6.

Chavan, B.R., Dalvi, V.V., Kunkerkar, R.L., Mane, A.V and Gokhale, N.B. 2022. Studies on genetic variability for yield and yield contributing traits in aromatic rice (*Oryza sativa* L.). *The Pharma Innovation Journal*. *11*(2): 1732-1735.

Demeke, B., Dejene, T and Abebe, D. 2023. Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (*Oryza Sativa* L.) genotypes at pawe, northwestern Ethiopia. *Cogent Food & Agriculture*. *9*(1): 2157099.

Dewey, D. R. and Lu, K. H. 1959. Correlation and path coefficient analysis of components of crested wheat grass seed production. *Journal of Agronomy*. 51: 515-18.

Edukondalu, B., Reddy, V.R., Rani, T.S., Kumari, C.A and Soundharya, B. 2017. Studies on variability, heritability, correlation and path analysis for yield, yield attributes in rice (*Oryza sativa* L.). *International journal of current microbiology and applied sciences*. *6*(10): 2369-2376.

Falconer, D.S. 1964. An Introduction to Quantitative Genetics. 2nd ed. Oliver and Boyd Publishing Co. Pvt. Ltd. Edinburgh. 312-324.

Gupta, H., Purushottam, G.Y., Yadav, S.K., Singh, S and Kumar, S. 2022. Genetic variability, heritability and genetic advance for yield and its related traits in rainfed upland rice (*Oryza sativa* L.) genotypes. *The Pharma Innovation Journal*. 11(2): 2520-2524.

Hallauer, A.R and Miranda Filho, J.D. 1988. Quantitative genetics in maize breeding. Ames. Iowa State University Press. 10: 468.

Hasan, M. J., Kulsum, M. U., Mohiuddin, S. J and Zahid-ALRafiq, M. 2019. Genetic interrelationship among yield and its components in rice hybrids. Bangladesh.*Journal of Botany*. 48(4): 1207–1213.

Johanson, H. W., Robinson, H. F and Comstock, R. E. 1955. Estimates of genetic andenvironmental variability in soybean. *Agronomy Journal*. 47 (7): 314- 315.

Jayasudha, S and Sharma, D. 2010. Genetic parameters of variability, correlation and path-coefficient for grain yield and physiological traits in rice (*Oryza sativa* L.) under shallow lowland situation. *Electronic Journal of Plant Breeding*. *1*(5): 1332-1338.

Larik AS, Malik SI, Kakar AA and Naz MA.2000. Assessment of heritability and genetic advance for yield and yield components in *Gossypium hirsutum* L. *Scientific Khyber.* 13: 39-44.

Li, F., Xie, J., Zhu, X., Wang, X., Zhao, Y., Ma, X., Zhang, Z., Rashid, M.A., Zhang, Z., Zhi, L and Zhang, S. 2018. Genetic basis underlying correlations among growth duration and yield traits revealed by GWAS in rice (*Oryza sativa* L.). *Frontiers in plant science*. *9*: 650.

Luo, L.J., Li, Z.K., Mei, H.W., Shu, Q.Y., Tabien, R., Zhong, D.B., Ying, C.S., Stansel, J.W., Khush, G.S and Paterson, A. 2001. Overdominant epistatic loci are the primary genetic basis of inbreeding depression and heterosis in rice. II. Grain yield components. *Genetics*. *158*(4): 1755-1771.

Manivelan, K., Juliet Hepziba, S., Suresh, R., Theradimani, M., Renuka, R and Gnanamalar, R.P. 2022. Inherent variability, correlation and path analysis in lowland rice (*Oryza sativa* L.). *In Biological Forum–An International Journal*. 14 (2): 771-778).

Maurya, R.K., Dwivedi, D.K., Khan, N.A., Giri, S.P. and Dixit, S. 2022. Genetic variability studies for qualitative and quantitative traits in rice (*Oryza sativa* L.). *The Pharma Innovation Journal*, *11*(5): 1140-1143.

Nithya, N., Beena, R., Stephen, R., Abida, P.S., Jayalekshmi, V.G., Viji, M.M and Manju, R.V. 2020. Genetic variability, heritability, correlation coefficient and path analysis of morphophysiological and yield related traits of rice under drought stress. *Chemical Science Review and Letters*. 9(33): 48-54.

Oad, F. C., Samo, M. A., Hassan, Z. U., Pompe, S. C and Oad, N. L. 2002. Correlation and path analysis of quantitative characters of rice ratoon cultivars and advance lines. *International Journal of Agricultural Biology.* 4(2): 204-207.

Oladosu, Y., Rafii, M.Y., Abdullah, N., Magaji, U., Miah, G., Hussin, G and Ramli, A. 2017. Genotype× Environment interaction and stability analyses of yield and yield components of established and mutant rice genotypes tested in multiple locations in Malaysia. *Acta Agriculturae Scandinavica, Section B—Soil & Plant Science*. 67(7): 590-606.

Paikhomba, N., Kumar, A., Chaurasia, A.K and Rai, P.K. 2014. Assessment of genetic parameters for yield and yield components in hybrid rice and parents. *Journal of Rice Research*. 2(1): 117.

Robinson, H. F., Comstock, R. E and Harvey, P. H.1949. Estimates of heritability and the degree of dominance in corn.

Sabesan T, Suresh R, Saravanan K. 2009. Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline lowland of Tamil Nadu. *Electronic Journal of Plant Breeding*. 1: 56-59.

Singh, A.K., Nandan, R and Singh, P.K. 2014. Genetic variability and association analysis in rice Germplasm under rainfed conditions. *Crop Research*. 47(1-3): 7– 11.

Sreedhar, S and Reddy, R.U. 2019. Association studies for yield and its traits in rice (*Oryza sativa* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences*. 8(1): 2337-2342.

Sudeepthi K, Srinivas T, Ravi Kumar BNVSR, Jyothula DPB, Nafeez Umar SK. 2020. Assessment of Genetic Variability, Character Association and Path Analysis for Yield and Yield Component Traits In Rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 11(1):144-148.

Sumanth V, Suresh BG, Ram BJ, Srujana G. Estimation of genetic variability, heritability, and genetic advance for grain yield components in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry.*6(4):1437-1439.

Talekar, S.C., Praveena, M.V and Satish, R.G. 2022. Genetic variability and association studies for grain yield and yield related traits in rice (*Oryza sativa* L.). *International Journal of Plant Sciences*. 17(2): 202-208.

Tiwari DN, Tripathi SR, Tripathi MP, Khatri N, Bastola BR. 2019. Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. *Advances in Agriculture*. 1-9.

Vikas, K., Ram, R.B., Rajvanshi, S. K and Shishupal, D.2015. Study on genetic variability, heritability and genetic advance for yield and yield attributing characters in cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.]. *International Journal of Agricultural Science& Research.* 5 (4): 235-245.

Wright, S.1934. Correlation and causation.*Journal of Agricultural Research.* 20: 557-585.