A review: Genetic analysis of yield and its contributing characters in Rice (*Oryza sativa* L.)

Abstract

Rice is the most important staple food crop of the world because of being the major source of calories of more than half of the total global population. Genetic variability for quantitative traits is the key component of breeding programme for broadening the gene pool of rice and other crops. High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters. The genetic coefficient of variation together with heritability estimate would give the best picture of the amount of advance to be expected from the selection. The amount of genetic advance under selection mainly depends on the amount of genetic variability. In rice, yield is determined by some indirect traits like plant height, growth period, tillering ability, panicle length, seed length, seed setting rate and grains per panicle whereas direct traits like panicle number per plant, filled grains per panicle and 1000-grain-weight.

Keywords: staple food, genetic variability, desirable traits, selection and heritability.

Introduction

Rice (Oryza sativa L.) is one of the most important food grain crops in the world, providing food for more than half of the world's population **(Baroudy *et al*., 2020).** Rice is also one of the most economically viable crop, ranking 2nd next to wheat with 497 million metric tons produced **(IRRI, 2021).** Diallel analysis of earliness, grain yield and related attributes may reveal delightful information about the kind of gene action involved in the expression of a character. Also, conventional breeding between relevant varieties **(Hassanien *et al*, 2020)** may be helpful in specific scenarios to understand the type of gene action involved in the expression of a character. The addition of some natural components with biological activities to rice crops like amino acids **(El-Sobki *et al*., 2021),** peptides, nanoparticles **(Saad *et al*., 2021),** herbal extracts and essential oils may increase gene expression besides breeding. Grain yield is a complex trait and highly influenced by many biotic and abiotic stresses including bacteria, viruses, fungi, water-logging, salinity etc. In any crop breeding programmes, direct selection for yield under complex environments could be misleading and therefore a successful selection will depend upon the information on the genetic variability and association of morpho-agronomic traits with grain yield. Correlation coefficient provides a better understanding of the different traits with grain yield. The study of association among various traits is useful to breeders in selecting genotype possessing groups of desired traits.

Genetic variability in rice:

For any crop improvement it depends on proportions of genetic variability present in base population. Environmental affects impacts on the total observable variations of quantitative traits. Therefore, partitioning of overall variance due to genetic and non-genetic causes becomes necessary for any effective breeding programme. **Divya *et al*., (2018)** noted significant variation for all the traits studied that indicated there is existence of genetic variability for all the traits varying from lower to higher coefficients of variance. The results found that the moderate genotypic and phenotypic coefficients of variance were recorded for number of productive tillers per plant, number of grains per panicle and seed yield per plant. **Mall *et al*., (2005)** studied 35 genotypes of rice evaluated for genetic variability, heritability and genetic advance for yield and its component. Their study revealed highly significant differences among 35 genotypes of rice for all the yield contributing traits. A wide range of variation was observed for mean values of plant height, days to panicle initiation, days to 50 % flowering, number of tillers per plant, number of panicles per plant, number of spikelets per panicle, panicle length (cm), flag leaf area. **Koli *et al*., (2020)** evaluated 40 wild rice germplasm lines for 12 quantitative traits using D^2 analysis in order to study the diversity pattern. The genotypes were grouped into 7 clusters. Maximum number of genotypes (32) were grouped under cluster I followed by cluster IV with 3 genotypes, while clusters II, III, V, VI and VIII, had only one genotype each. **Sangam *et al*., (2011)** evaluated 81 rice genotypes for 13 quantitative characters to examine the nature and magnitude of variability, heritability and genetic advance. Analysis of variance showed that the differences among 81 genotypes were significant for all the characters except flag leaf width.

Estimation of genetic variability, heritability and genetic advance **Rao *et al.*, (2014)** were studied along with character association and path analysis between yield and its contributing traits in 49 rice cultures. Analysis of variance showed the existence of significant differences among genotypes for all the traits under studied. The extent of PCV and GCV was moderate to high for number of grains per panicle, test weight and grain yield. **Adjah *et al.*, (2020)** also studied 100 rice germplasm to assess genetic variability, heritability and correlations for 11 milling and appearance quality traits and grain yield by using 10 × 10 alpha lattice design (ALD) with 3 replications following standard cultivation practices. Analysis of variance revealed significant differences for the traits studied. Poor milling and grain appearance is a common feature of locally produced rice in West Africa **(Adjah *et al.*, 2020)**.

Selection criterion by correlation and path coefficient analysis in rice

Rice is considered as an essential and stable food for about 66.5% of people worldwide, providing almost 21% of energy **(Wogu *et al.*, 2011).** To know about the relationship between quantitative traits, it is important to assess the feasibility of a joint selection of two or more traits instead of selecting the secondary traits as genetic gains for primary traits under consideration **(Ezeaku and Muhammad, 2006).**

For increasing the rice production, the aim of breeding programs is to use more genetic diverse population and also apply effective selection methods to increase yield by its component traits. Identifying the relationship between yield and yield traits through correlation analysis is an essential step **(Akhtar *et al.*, 2011),** but dividing the influence of traits into direct and indirect effects by using path analysis is more essential tool for the selection of yield traits **(Ahmadizadeh *et al*., 2011, Dhavaleshvar *et al.*, 2019).**

Path analysis is a statistical tool that is used for estimation of relationships between prediction variables and response variables by a path chart **(Samonte *et al*., 1998, Esmail, 2001).** Yield being a complex character is associated with its component traits (number of panicle per plant, number of grains per spike, 1000 grain weight etc.) **(Ikeda *et al.*, 2013, Zhou *et al.*, 2018).**

Often this is dependent on its relationship to the grain yield, makes the selection process ineffective. Therefore, **Singh *et al*., (1985)** reported that loading the path parameter helps in segmenting the correlation into direct and indirect effects. Path analysis and correlation coefficient is needed that divides the correlation coefficient into its direct and indirect effect components (**Surek and Beser, 2003)**. Plant breeders use path analysis to identify useful features as selection criteria for improvement of crop **(Milligan *et al*., 1990).**

Further, **Saleh *et al*., (2020)** conducted an experiment at the experimental farm of the Rice Research and Training Center (RRTC), Egypt. The seeds of the 22 rice accessions were grown in randomized complete block design (RCBD) with 3 replication. Direct and indirect path coefficients were estimated by using **GenStat 12, J Nelder (2009),** as described by **(Singh and Chudhary 1977).** They have found a positive correlation of grain yield with traits under study. The short period to heading will provide more time to increase the number of panicle per plant and 1000 grain weight will be improved by increasing of panicle length as well as increasing panicle number per plant. Similar positive correlation was also observed with the results of **Karim *et al*. (2014), Kumar *et al*. (2011), Khush (2013), , Kumar *et al*. (2017), Lakshmi *et al*. (2017), Bhutta *et al.* (2019), Chhangte and Devi, (2019),** and **Panda *et al.* (2019).** Current knowledge about trait relationships helps us to select the suitable genotype for crop improvement **(Gonçalves *et al*., 2017).**

Recent progress on molecular breeding of rice

Molecular breeding of rice for high yield, superior grain quality, and strong environmental adaptability is crucial for feeding the world's rapidly growing population **(Rao *et al.*, 2014).** To meet the security of food supply, it is necessary to increase the crop yield per unit area by 50 % before 2030 **(Cheng and Hu 2008).** High yield is the everlasting theme pursued by rice breeders. Super rice breeding in the model of ideal plant architecture using molecular design is important for future development (**Yao *et al*. 2010).** In the field of Aromatic Rice, some advance studies have been conducted. The aromatic rice cultivars sometimes shows variation in aroma when they are grown in regions other than their normal traditional growing regions **(Sansenya *et al.*, 2018).** Aroma production in *Biriyanicheera* variety is observed to be due to the similar mutation in *BADH2* gene as that of the popular scented rice Basmati (**Veerabhadraswamy *et al*., 2022).**

Increasing grain yield is a major objective in any breeding programs, because of the need to meet the increased demand for rice in future. Some trais like, grain shape, grain number per panicle, plant height, number of tillers, leaf size, and leaf angle, have been associated with improved grain yield. **Seo *et al*.,(2021)** showed that the *OsbHLH079* gene is associated with the control of leaf angle and grain shape via brassino steroid biosynthesis and signaling pathways . **Gull *et al*.,(2019)** focused on grain shape and grain weight, and they estimated the genetic effects of each allelic combination among 7 genes GS2, GS3, GS5, GW5, GS7, SLG7, and GW8 in improving grain length, grain width, grain thickness, and thousand grain weight. **Jiang *et al*.,(2021)** identified a semi-dwarfism gene, *OsCYP96B4*, which affected the content of γ-aminobutyrate (GABA), amino acids, saccharides, and other secondary metabolites in rice plants. **Yu *et al*., (2021)** detected 8 QTLs underlying heterosis in characters, including days to heading, grain yield, and plant height between the 2 rice subspecies *O. sativa* ssp. *indica* and *O. sativa* ssp. *japonica*. **Gao *et al*.,(2021)** identified that the *OsEWL4* gene which is a regulator of tiller number and plant biomass by using targeted mutations of 8 rice *FLW* genes using the **CRISPR/Cas9** analysis. **Fan *et al*., (2021)** estimated over expression and knockdown transformants of the *OsNAR2.1* gene and revealed that changing expression levels of the *OsNAR2.1* gene altered global methylation at the whole genome level and the phenotypes of plant height and grain yield at the plant level. **Zhang *et al*., (2020)** found a large set of genes that are differentially expressed at the shoot apical meristem in response to application of nitrogen, which regulated the number of tillers per plant and panicles in rice plants. These novel technologies are powerful tools to understand the molecular basis of increasing rice yields.

Conclusion

Presence of genetic variability and heritability in a crop species is an important requirement for the improvement of economically important traits like yield in rice. Yield enhancement is the major breeding aim in rice breeding programmes. Knowledge of the nature and magnitude of genetic variation helps plant breeders to develop new and improved cultivars with desirable traits, which include both farmer-preferred traits (high yield potential, large seed, etc.) and breeder-preferred traits (biotic and abiotic resistance and photosensitivity, etc.). From the very beginning of agriculture, natural genetic variability has been exploited within crop species to meet subsistence food requirement Genetic variability of crop plants is the foundation for the sustainable development of new cultivars. So, there is a need to characterize the diverse genetic resources using different statistical tools and utilize them in the breeding programme.

References

Abd El-Aty, M. S., Abo-Youssef, M. I., Galal, A. A., Salama, A. M., Salama, A. A., El-Shehawi, A. M., ... & El-Tahan, A. M. (2021). Genetic behavior of earliness and yield traits of some rice (Oryza sativa L.) genotypes. *Saudi Journal of Biological Sciences*..

Adjah, Kossi Lorimpo, et al. "Genetic variability, heritability and correlations for milling and grain appearance qualities in some accessions of rice (Oryza sativa L.)." *Physiology and molecular biology of plants* 26.6 (2020): 1309-1317.

Akhtar, N., Nazir, M. F., Rabnawaz, A., Mahmood, T., Safdar, M. E., Asif, M., & Rehman, A. (2011). Estimation of heritability, correlation and path coefficient analysis in fine grain rice (Oryza sativa L.). *Journal of Animal and Plant Sciences*, *21*(4).

Baroudy, A. A. E., Ali, A., Mohamed, E. S., Moghanm, F. S., Shokr, M. S., Savin, I., ... & Lasaponara, R. (2020). Modeling land suitability for rice crop using remote sensing and soil quality indicators: the case study of the nile delta. *Sustainability*, *12*(22), 9653.

Bhutta, M. A., Munir, S. A. N. A., Qureshi, M. K., Shahzad, A. N., Aslam, K. A. S. H. I. F., Manzoor, H., & Shabir, G. (2019). Correlation and path analysis of morphological parameters contributing to yield in rice (Oryza sativa) under drought stress. *Pak J Bot*, *51*(1), 73-80.

Cheng, S., & Hu, P. (2008). Development strategy of rice science and technology in China. *Chin J Rice Sci*, *22*, 223-226.

Chhangte, L., & Devi, T. R. (2019). Correlation and path analysis studies in aromatic rice germplasm of North-East region of India. *The pharma Innovation Journal*, *8*(10), 01-04.

Divya, J., Raju, C. D., Rao, L. S., & Aparna, K. (2018). Genetic Variability Studies in genetically diverse rice genotypes. *Int. J. Curr. Microbiol. App. Sci*, *7*(4), 1169-1172.

El-Sobki, A. E., Saad, A. M., El-Saadony, M. T., El-Tahan, A. M., Taha, A. E., Aljuaid, B. S., ... & Salem, R. E. (2021). Fluctuation in amino acids content in Triticum aestivum L. cultivars as an indicator on the impact of post-emergence herbicides in controlling weeds. *Saudi journal of biological sciences*, *28*(11), 6332-6338.

Ezeaku, I. E., & Mohammed, S. G. (2006). Character association and path analysis in grain sorghum. *African Journal of Biotechnology*, *5*(14).

Fan, X., Chen, J., Wu, Y., Teo, C., Xu, G., & Fan, X. (2020). Genetic and global epigenetic modification, which determines the phenotype of transgenic rice?. *International journal of molecular sciences*, *21*(5), 1819.

Gonçalves, D. D. L., Barelli, M. A. A., Oliveira, T. C. D., Santos, P. R. J. D., Silva, C. R. D., Poletine, J. P., & Neves, L. G. (2017). Genetic correlation and path analysis of common bean collected from Caceres Mato Grosso State, Brazil. *Ciência Rural*, *47*(8).

Gao, Q., Li, G., Sun, H., Xu, M., Wang, H., Ji, J., ... & Zhao, X. (2020). Targeted mutagenesis of the rice FW 2.2-like gene family using the CRISPR/Cas9 system reveals OsFWL4 as a regulator of tiller number and plant yield in rice. *International journal of molecular sciences*, *21*(3), 809.

Gull, S., Haider, Z., Gu, H., Raza Khan, R. A., Miao, J., Wenchen, T., ... & Liang, G. (2019). InDel marker based estimation of multi-gene allele contribution and genetic variations for grain size and weight in rice (Oryza sativa L.). *International journal of molecular sciences*, *20*(19), 4824.

Hassanin, A. A., Saad, A. M., Bardisi, E. A., Salama, A., & Sitohy, M. Z. (2020). Transfer of anthocyanin accumulating delila and rosea1 genes from the transgenic tomato micro-tom cultivar to moneymaker cultivar by conventional breeding. *Journal of Agricultural and Food Chemistry*, *68*(39), 10741-10749.

Ikeda, M., Miura, K., Aya, K., Kitano, H., & Matsuoka, M. (2013). Genes offering the potential for designing yield-related traits in rice. *Current opinion in plant biology*, *16*(2), 213-220.

Karim, D., Siddique, M. N. A., Sarkar, U., Hasnat, Z., & Sultana, J. (2014). Phenotypic and genotypic correlation co-efficient of quantitative characters and character association of aromatic rice. *Journal of Bioscience and Agriculture Research*, *1*(1), 34-46.

Khush, G. S. (2013). Strategies for increasing the yield potential of cereals: case of rice as an example. *Plant Breeding*, *132*(5), 433-436.

Koli, G. K., Upadhyay, S., Rathi, S. R., Gupta, S., Kumar, K., Singh, P. K., & Sinha, B. (2020). Genetic diversity analysis for yield and yield attributing traits of wild germplasm in rice. *Journal of Pharmacognosy and Phytochemistry*, *9*(1), 949-951.

Kumar, S., Bhuvaneswari, S., Devi, E. L., Sharma, S. K., Ansari, M. A., Singh, I. M., ... & Prakash, N. A. R. E. N. D. R. A. (2017). Estimation of genetic variability, correlation and path analysis in short duration rice genotypes of Manipur. *Journal of Agri Search*, *4*(2), 112-118.

Mall, A. K., Babu, J. D. P., & Babu, J. S. (2005). Estimation of genetic variability in rice. *Journal of Maharashtra Agricultural Universities (India).*

Milligan, S. B., Gravois, K. A., Bischoff, K. P., & Martin, F. A. (1990). Crop effects on genetic relationships among sugarcane traits. *Crop Science*, *30*(4), 927-931.

Rao, V. T., Mohan, Y. C., Bhadru, D., Bharathi, D., & Venkanna, V. (2014). Genetic Variability and Association Analysis in Rice.

Rao, Y., Yang, Y., Huang, L., Pan, J., Ma, B., Qian, Q., & Zeng, D. (2013). Research progress on cold stress in rice. *Mol Plant Breed*, *11*(3), 443-450.

Saad, A. M., El-Saadony, M. T., El-Tahan, A. M., Sayed, S., Moustafa, M. A., Taha, A. E., ... & Ramadan, M. M. (2021). Polyphenolic extracts from pomegranate and watermelon wastes as substrate to fabricate sustainable silver nanoparticles with larvicidal effect against Spodoptera littoralis. *Saudi Journal of Biological Sciences*, *28*(10), 5674-5683.

PB. Samonte, S. O., Wilson, L. T., & McClung, A. M. (1998). Path analyses of yield and yield-related traits of fifteen diverse rice genotypes. *Crop Science*, *38*(5), 1130-1136.

Saleh, M. M., Salem, K. F., & Elabd, A. B. (2020). Definition of selection criterion using correlation and path coefficient analysis in rice (Oryza sativa L.) genotypes. *Bulletin of the National Research Centre*, *44*(1), 1-6.

Sansenya, S., Hua, Y., & Chumanee, S. (2018). The correlation between 2-acetyl-1-pyrroline content, biological compounds and molecular characterization to the aroma intensities of Thai local rice. *Journal of Oleo Science*, *67*(7), 893-904.

Singh, S. K., Singh, C. M., & Lal, G. M. (2011). Assessment of genetic variability for yield and its component characters in rice (Oryza sativa L.). *Research in Plant Biology*, *1*(4).

Seo, H., Kim, S. H., Lee, B. D., Lim, J. H., Lee, S. J., An, G., & Paek, N. C. (2020). The rice basic Helix–Loop–Helix 79 (OsbHLH079) determines leaf angle and grain shape. *International journal of molecular sciences*, *21*(6), 2090.

Veerabhadraswamy, M., Sindhumole, P., Mathew, D., Shylaja, M. R., Joseph, J., Augustine, R., & James, D. (2022). Molecular analysis of aroma gene (BADH2) in Biriyanicheera: a tropical aromatic rice genotype from Kerala, India. *Molecular Biology Reports*, 1-7.

Wogu, M. D., Omoruyi, M. I., Odeh, H. O., & Guobadia, J. N. (2011). Microbial load in ready-to-eat rice sold in Benin City. *Journal of Microbiology and Antimicrobials*, *3*(2), 29-33.

Yao, S., Chen, T., Zhang, Y., Zhu, Z., Zhao, L., Zhao, Q., ... & Wang, C. (2010). Pyramiding of translucent endosperm mutant gene Wx-mq and rice stripe disease resistance gene Stv-bi by marker-assisted selection in rice (Oryza sativa). *Chinese Journal of Rice Science*, *24*(4), 341-347.

Yu, Y., Zhu, M., Cui, Y., Liu, Y., Li, Z., Jiang, N., ... & Sui, G. (2020). Genome sequence and QTL analyses using backcross recombinant inbred lines (BILs) and BILF1 lines uncover multiple heterosis-related loci. *International Journal of Molecular Sciences*, *21*(3), 780.

Yu, Y., Zhu, M., Cui, Y., Liu, Y., Li, Z., Jiang, N., ... & Sui, G. (2020). Genome sequence and QTL analyses using backcross recombinant inbred lines (BILs) and BILF1 lines uncover multiple heterosis-related loci. *International Journal of Molecular Sciences*, *21*(3), 780.

Zhang, Q., Shen, L., Wang, Z., Hu, G., Ren, D., Hu, J., ... & Qian, Q. (2019). OsCAF1, a CRM domain containing protein, influences chloroplast development. *International journal of molecular sciences*, *20*(18), 4386.

Zhou, Y., Tao, Y., Yuan, Y., Zhang, Y., Miao, J., Zhang, R., ... & Liang, G. (2018). Characterisation of a novel quantitative trait locus, GN4-1, for grain number and yield in rice (Oryza sativa L.). *Theoretical and applied genetics*, *131*(3), 637-648.