RESEARCH ARTICLE

Genetic variability and association studies for grain yield and yield related traits in rice (*Oryza sativa* L.)

■ **S. C. Talekar, M. Vani Praveena and R. G. Satish**

SUMMARY

In this study correlation, path co-efficient analysis, genetic variability, heritability and genetic advance over mean were studied in 100 germplasm lines evaluated along with 4 checks in augmented Block Design at Agriculture Research Station, Mugad, University of Agricultural Sciences, Dharwad during *Kharif* 2020 Analysis of variance showed significant difference among the treatments at 5% probability level. There is a significant correlation observed in a positive direction for grain yield and panicle length. A significantly positive correlation was observed for panicles per square meter with days to 50% flowering and panicle length. Panicle length (0.38) followed by days to 50% flowering (0.15) and 1000 grain weight (0.08) manifested positive direct effects on grain yield while the negative direct effect on yield was shown by panicles per square meter (-0.026). High GCV was observed for grain yield (58.07) while high PCV was observed for grain yield (29.65) and 1000 grain weight (21.54). Heritability for the traits ranged from 60.88% (days to 50% flowering) to 94.76% (grain yield) with high heritability observed for all the five traits studied. High genetic advance over mean was observed for grain yield (116.62) followed by 1000 grain weight (33.29) while medium genetic advance over mean was observed for other traits studied. Although 1000 grain weight showed positive and non-significant correlation the trait manifested a positive direct effect on yield coupled with high PCV, heritability, medium GCV and genetic advance over mean while grain yield itself manifested high variability, heritability, genetic advance over mean and medium GCV suggesting indirect selection for yield via 1000 grain weight and direct selection of superior lines in the germplasm for grain yield will contribute for crop improvement.

Key Words : Association studies, Grain yield, Yield related traits, Rice

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Rice is a major cereal and staple food crop for half of the world's population *i.e.* about four billion people and in India, it is a critical component of

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food security programs (Krishnamurthy *et al.,* 2020). Rice is grown mostly in irrigated and rainfed lowland areas in tropical countries. Irrigated rice systems produce 78% of all rice production and account for 55% of all harvested rice land. The leading rice-producing states are West Bengal, Uttar Pradesh, Punjab, Odisha, Andhra Pradesh, Bihar and Chhattisgarh. It is the staple food for more than 65% of the Indian population contributing approximately 40% to the total food grain production. India grows rice on 43 million hectares with a production of 112 million tons of milled rice and average productivity of 2.6 t ha^{-1} (Pathak *et al.,* 2020). The area under rice has increased by 1.5 times over the years, and production has raised by more than five times. Furthermore, India is the world's largest rice exporter, with 12.5 million metric tons of export, contributing significantly to the Indian economy. With this, India has not only achieved self-sufficiency in rice but also produces a surplus to export. However, the world's population is expected to reach 9.1 billion people by 2050, necessitating a 70% increase in food production (Singh *et al.,* 2021).

Rice, also known as the Global Grain because it is a staple food in over 100 countries around the world, is primarily grown in the wet season in large areas with low productivity due to the non-availability of high yielding varieties with stable performance in different agro-climatic conditions and seasons prevailing in different parts of the country (Yugandhar *et al.,* 2018). To realize increased yield and production potential in rice, it is important to launch a sound breeding program to arrive at developing varieties with high yields suitable for different climatic conditions.

Plant disease and pest outbreaks are becoming more common, resulting in lower crop yields, endangering global food security. Important diseases include sorghum downey mildew (Sharma *et al*., 2010), chickpea dry root rot (Talekar *et al*., 2017 and Talekar *et al*., 2021), chickpea phyllody (Balol *et al*., 2021), groundnut leaf spots (Kolekar *et al*., 2016), pigeonpea wilt (Saxena *et al*., 2012), sunflower necrosis (Sundaresha *et al.*, 2012) in determining grain yield variance among genotypes, genetic variability for disease resistance and yield components is crucial. Understanding the availability of genetic variability for yield and yield contributing characteristics in plant germplasm resources is critical because variability is the cornerstone of any breeding programme. Variability provides a better understanding of the breeding behaviour of various traits and determining important characteristics for selecting the best cultivars. Different genetic parameters like co-efficient of variance (phenotypic co-efficient of variation and genotypic co-efficient of variation), heritability and genetic advance over mean gives a complete view of available variability in the population, which aids in selecting genotypes with desirable traits (Vikas *et al.,* 2015). The statistical measure of how genes influence individual variances observed within a population is known as heritability. Heritability of trait being a good indicator of inheritance of a trait from one generation to the next generation is widely used by breeders in selecting superior genotypes from a diverse populations. Genetic advance under selection is defined as an increase in the mean genotypic value of the selected families over the base population, which explains the degree of gain realized at particular selection pressure. (Ogunniyan and Olakojo, 2015). Thus, the estimates of both heritability and genetic advance together will arrive at valid conclusions in determining gain under selection rather than heritability alone.

Yield being a complex and polygenic trait, apart from variability estimates, association studies also help in selecting the traits which are responsible for increased yields. Correlation explains the mutual relationship of interdependency between two variables and the correlation co-efficient measures the degree of genic and non-genic association between two or more variables, making indirect selection reliable (Hallauer and Filho, 1988). However, correlation estimates alone don't arrive at a true association between two variables since it is occasionally affected by the third variable (Bello *et al.,* 2010). Path analysis is an important statistical technique used along with correlation studies to establish cause and effect relationships between variables and separate direct effects from indirect effects which should be taken care of accordingly during selection to improve yield.

As the knowledge of variability and degree of relationship is important in formulating dynamic breeding programs, the present investigation was taken upto study different variability parameters, correlation and path co-efficients for yield and yield-related traits in rice.

MATERIAL AND METHODS

Details of the experiment layout:

The field experiment was planned with 100 rice germplasm lines at Agriculture Research Station, Mugad, University of Agricultural Sciences, Dharwad, during *Kharif* 2020. A total of 100 germplasm lines of rice and

four checks namely BPT5204, PSB-68, MGD-101 and Siri1253 were drilled sown at a spacing of 20×10 cm in an Augmented Randomized Block Design with 4 blocks. Each block comprised 25 germplasm lines and four checks were repeated in each block. The experiment was grown in rainfed conditions by following appropriate cultural practices.

Data collection:

Data was collected on a plot and plant basis at different agronomic stages of the crop suitable for each individual measured trait. Data related to days to 50% flowering, panicle length (cm), number of panicles per square meter, 1000-grain weight (g), and grain yield (kgha⁻¹) were collected and analyzed to draw valid conclusions.

Data analysis:

Data on grain yield and yield-related traits were analyzed in R software. Analysis of variance and variability was done using R software (version 4.2.0). The association between grain yield and its component traits was calculated using formulas for genotypic correlation co-efficients as suggested by Johanson *et al.,* (1955). The cause and effect relationship in terms of direct and indirect effects was calculated using formulas for path co-efficient analysis as suggested by Wright (1921). The phenotypic and genotypic co-efficient of variation was analyzed using formulas suggested by Singh and Chaudhary (1985); heritability as suggested by Johnson *et al.* (1955); genetic advance as given by Burton, (1952) and genetic a s percent of mean as described by Souza *et al.* (2009).

RESULTS AND DISCUSSION

The results obtained from the present investigation as well as relevant discussion have been summarized under following heads :

Analysis of variance (ANOVA):

Analysis of variance revealed the significance of

blocks ignoring treatment and treatments eliminating blocks for most of the traits studied (data not shown). This suggested the availability of an appreciable amount of genetic variability in the germplasm lines screened for yield and yield-related traits in rice. The availability of genetic variability in the original breeding materials increases the likelihood of creating desired recombinants for crop improvement (Pratap *et al.,* 2012).

Co-efficient of variation, heritability and genetic advance:

Estimates of co-efficient of variation *i.e.* genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability (h^2) and genetic advance over mean were presented in Table 1. Phenotypic and genotypic (PCV and GCV) co-efficient of variation was categorized as 0-10% (low), 10-20% (moderate) and > 20% (high). For all the traits analyzed, the phenotypic co-efficient of variation was found to be higher than the genotypic co-efficient of variation. This indicates the influence of the environment on these traits. Similar results were earlier reported by Gywali *et al.* (2018), and Nithya *et al.* (2020). The difference between PCV and GCV explains the degree of environmental influence on observed traits. In this study least difference was observed between GCV and PCV explaining the minimal influence of the environment on yield and yield-related traits (Beena *et al.,* 2021). The least difference between the genotypic and phenotypic co-efficient of variation was observed for panicle length followed by grain yield. Thus selection based on panicle length and grain yield will bring significant yield enhancement. Similar results were earlier reported by Adhikari *et al.* (2018) and Asante *et al.* (2019). High GCV was observed for grain yield (58.07), while medium GCV was observed for days to 50% flowering (10.18) and 1000 grain weight (18.64). The highest attributes of GCV are important for breeding high-yielding varieties by the selection of superior genotypes followed by hybridization. While the lowest GCV values were observed for panicle length (9.11) and panicles per square meter (7.87). On the other hand,

Table 1: Estimates of genetic variability parameters for yield and yield related traits in rice					
Trait	Mean	PV	GV	GCV	PCV
Days to 50% flowering	99.66	148.04	102.9	10.18	12.21
Panicle length	20.86	4.65	3.61	9.11	10.34
Panicles/sq.m.	280.51	801.11	487.75	7.87	10.09
1000 Grain weight	21.4	21.26	15.92	18.64	21.54
Grain yield	2011	1439020.9	1363642.74	58.07	59.65

highest PCV was observed for grain yield (59.65) and 1000 grain weight (21.54).

To arrive at a conclusion on the degree of heritable variation both heritability and genetic advance need to be analysed. Johnson *et al.* (1955) categorized heritability as <30% (low), 30-60% (moderate) and >60% (high). GAM *i.e.*, genetic advance as per cent of mean was categorized (Johnson *et al.,*1955) into 0-10% (low), 10-20% (moderate) and more than 20% (high). Estimates of heritability and genetic advance over mean were presented in Fig. 1 and 2.
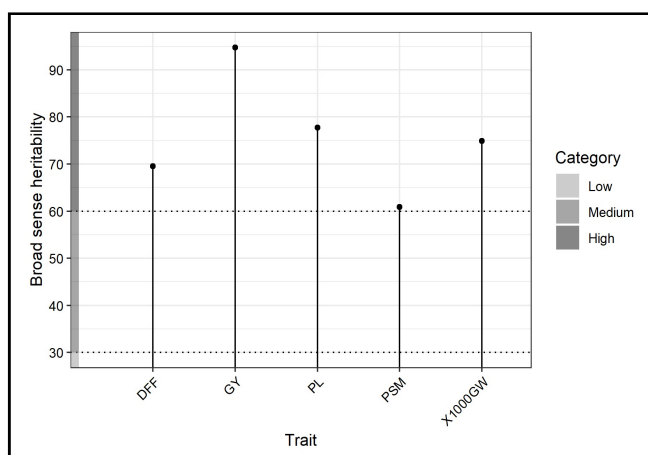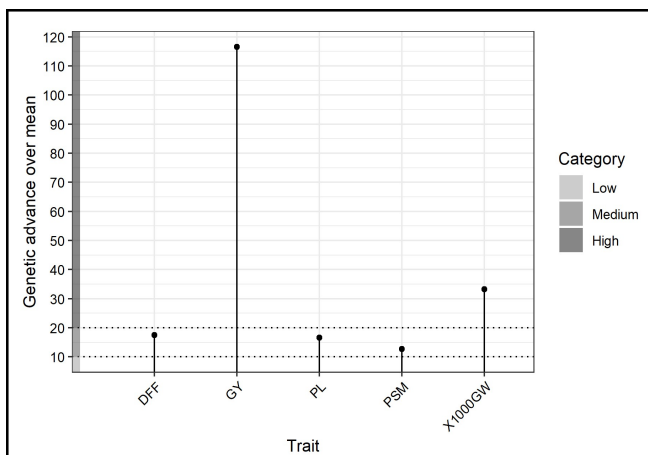

Fig. 1: Broad sense heritability for grain yield and yield related traits in rice

DFF: Days to 50% flowering, PL: Panicle length, PSM: panicles per square meter, X1000GW: 1000 Grain weight and GY: Grain yield

Fig. 2: Genetic advance as percent of mean for grain yield and yield related traits in rice

In this study, heritability ranged from 60.88% (days to 50% flowering) to 94.76% (grain yield). All the five traits under the study showed high heritability indicating

all these traits are least affected by the environment. Although selection for these traits may not be useful as broad sense heritability includes total variation which includes non-additive components along with the additive component. Similar results were reported by Rashid *et al.* (2017) and Tiwari *et al.* (2019). Hence genetic advance over mean need to be worked out. The GAM *i.e.* genetic advance over mean ranged from 12.67 (Panicles per square meter) to 116.62 (grain yield). Highest GAM was observed for grain yield (116.62) followed by 1000 grain weight (33.29), while medium genetic advance over mean was observed for days to 50% flowering (17.51), followed by panicle length (16.57) and panicles per square meter (12.67). These results were in line with Rohit *et al.* (2017), Adhikari *et al.* (2018) and Nithya *et al.,* 2020. High heritability with medium genetic advance over mean was observed for days to 50% flowering, panicle length and panicles per square meter indicating the role of both additive and non-additive gene action (Kishore *et al.,* 2015 and Lakshmi *et al.,* 2019). High heritability with high genetic advance over mean was observed for 1000 grain weight and grain yield which indicates the selection for these will be effective since they are governed by additive gene action.

In this study medium and high GCV, PCV coupled with heritability and genetic advance was observed for 1000 grain weight and grain yield indicating the importance of additive gene action and genetic improvement of yield can be achieved by selection of these traits. Similar findings were reported by Aswin *et al.,* 2021; Singh *et al.,* 2020 and Gebrie *et al.,* 2022.

Correlation estimates:

Out of nine correlation estimates, only three were positive and significant while the other three estimates were negative (Table 2). These balanced estimates reveal a chance of getting a good response to indirect selection for yield-related traits in the evaluated rice germplasm. The measure of the degree of association between the traits revealed a significant and positive correlation for panicles per square meter with days to 50% flowering and panicle length. A significantly positive correlation was observed between grain yield and panicle length. Similar results were reported by Sameera *et al.* (2016); Srijan *et al.* (2016) and Saha *et al.* (2019). A negative correlation was observed between 1000 grain weight and days to 50% flowering, panicle length and panicles per square meter. This suggested that grain weight decreased

Table 2 : Correlation co-efficients among yield and yield attributing traits in rice

Characters	Days to 50% flowering	Panicle length	Panicles per square meter	1000-grain weight	Grain yield
Days to 50% flowering	1				
Panicle length	0.006	1			
Panicles per square meter	0.22*	0.25*	1		
1000-grain weight	-0.14	-0.05	-0.14	1	
Grain yield	0.12	0.38**	0.10	0.026	1

Table 3: Direct and indirect effects among yield attributing traits in rice

	Days to 50% flowering	Panicle length	Panicles per square meter	1000-grain weight	Correlation co-efficients for GY
Days to 50% flowering	0.15	0.01	-0.007	-0.013	0.12
Panicle length	0.004	0.38	-0.006	-0.006	0.38
Panicles per square meter	0.044	0.093	-0.026	-0.011	0.10
1000-grain weight	-0.03	-0.03	0.004	0.08	0.02

Residual effect: 0.83

with an increase in panicle length and the number of panicles per square meter. This negative association between yield traits was also reported by Srijan *et al.* (2016). The highest correlation co-efficients (0.38) were observed between grain yield and panicle length. The results suggested that the selection of genotypes with high panicle length will be effective in increasing grain yield.

Path co-efficient analysis:

Along with correlation co-efficient estimates, path analysis was also done considering yield as a dependent trait and other yield related traits such as days to 50% flowering, panicle length, panicles per square meter, and 1000-grain weight as independent traits to facilitate the selection of genotypes from germplasm to arrive at increased yields. The classification suggested by Lenka and Misra (1973) was used to interpret the path coefficient analysis results. In this study genotypic correlations were used to separate direct effects from indirect effects on grain yield (Table 3). The highest positive direct effect on grain yield was observed for panicle length (0.38) followed by days to 50% flowering (0.15) and 1000-grain weight (0.08). However, panicles per square meter showed a negative direct effect on grain yield. The highest positive indirect effect on grain yield was observed for panicle per square meter through panicle length. Similar results were also reported by Kampe *et al.* (2018) and (Singh *et al.* 2020). Path coefficient of direct effect (0.38) and highest genotypic correlation (0.38) of panicle length was the same value

implying correlation results of panicle length truly explain the relationship between cause factor and effect (Table 3). This suggests the direct selection of genotypes with high panicle length will effectively improve the yield simultaneously (Beena *et al.,* 2021). A high residual effect (0.83) indicates the need to include other important parameters influencing yield.

Conclusion:

Although panicle length showed a significant correlation in the positive direction with grain yield and the highest direct effect on grain yield the trait manifested low GCV, medium PCV, high heritability, and medium genetic advance. Whereas 1000 grain weight displayed a non-significant but positive correlation coupled with the positive direct effect on yield, high PCV, heritability, and genetic advance over mean and medium GCV. On the other hand, grain yield manifested high variability, heritability and GAM. This suggests that indirect selection for yield through 1000-grain weight and direct selection of genotyped with high grain yield will be useful in the breeding programme to achieve yield enhancement in rice.

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