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Genetic Variability Analysis and Trait Association for Resistance Gene Pyramided F_2 Population in Rice (*Oryza sativa* L.)

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ABSTRACT

The current experiment comprised of 186 number of plants of F_2 segregating generation for which genetic variability parameters, correlation and path coefficient analysis were estimated for eight agro-morphological traits. The PCV was recorded higher than the GCV for all the character studied. High GCV coupled with high PCV was exhibited by number of tillers, number of productive tillers, number of filed grains and single plant yield. Higher GCV and PCV estimate provide wider scope of selection for elite segregants. High heritability coupled with high genetic advance was recorded for single plant yield. The presence of high heritability with high genetic advance showed additive effects of the gene and least affected by the environmental condition. Single plant yield has a highly significant and positive correlation with plant height, number of tillers, number of productive tillers, panicle length, number of filled grain per panicle and hundred grain weight. The path coefficient analysis revealed that positive direct effect towards single plant yield was exhibited by number of productive tillers, number of filled grain per panicle and hundred grain weight.

Key words: *Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), Heritability (h^2), Genetic advance (GA) and Correlation.*

INTRODUCTION

Rice being the prime cereals crop sustaining two thirds of the world's population. Asia is the biggest rice producer and consumer, accounting for 90 per cent of the world's production and consumption of rice. It is grown in all the continents, occupying 159 million hectare area and producing 683 million tonnes (equivalent to 456 million tons of milled rice)[21]. Presently India has about 433.88 lakh hectare of area under rice with an annual production of 104.32 million ton (GOI 2016-17). It is estimated that India needs to produce 120 million tons of rice by 2030 to feed its projected one and half billion plus population by then[2]. Biotic stress is the major constraint in Rice production and productivity and accounting for a loss of 1-85%[36].

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The average annual yield loss due to gall midge in India is US$ 80 million[948].Rice blast causes 10% - 30% of harvest losses to global rice yield by forming serious epidemics all over the rice growing regions in the world. The yield losses of 20 - 30% from BLB have been reported and can increase up to 80%[26, 31]. Genetic variability is an important parameters for crop improvement and mostly depends on its presence in base population[1]. Segregating population is the essence for improvement of plant traits by adopting various breeding technologies for further improvement[14]. The genotypic coefficient of variation estimates the heritable variability whereas phenotypic coefficient of variation measures the role of environment on genotype. The phenomenon of transmission of characters from parents to subsequent generation is usually measured by heritability[8]. The correlation coefficient measures provide the degree of interrelationship between yield and yield contributing traits and path coefficient measures magnitude of direct and indirect effects of characters on complex dependent characters like yield[24].

MATERIAL AND METHODS

F_2 seed of a cross between pyramided ADT38 (*Gm1+Gm4*) and (B_{95-1} x Tetep) (*Xa21+Pi54*) generated in the gall midge resistance project of the DPMB & B was used as the starting materials for the present study. Kavya and Abhaya are the donors for *Gm1* and *Gm4* genes. B_{95-1} x Tetep is the donors for *Xa21* and *Pi54* genes. The field experiment was carried out at Wet lands, Tamil Nadu Agricultural University, Coimbatore during 2012-2013 growing season. The F_2 seeds of the cross were directly sown in the field with single seeds per hill at spacing of 20 × 20 cm. The standard agronomical practices were followed to establish a good crop and to obtain good harvest. Observations were recorded for a total of 186 plants of F_2 population on individual plant basis. The characters observed for eliciting the information are: days to fifty per cent flowering (DFF), plant height (PH), number of tillers (NT), number of productive tillers (NPT), panicle length (PL), number of filled grains (NFG), hundred grain weight (HGW) and single plant yield (SPY).

Statistical Analysis

The descriptive statistics were estimated for each trait studied with the help of MS – EXCEL and for biometrical calculation GENRES software was used. The standard statistical procedure was adopted for Phenotypic and genotypic coefficient of variation (PCV and GCV)[20], broad sense heritability and genetic advance as percent of mean[20], genotypic correlation coefficient[27] and path coefficient analysis[49, 11].

RESULT AND DISCUSSION

The knowledge on nature and magnitude of genotypic and phenotypic variability present in any crop species plays an eminent role in designing a successful breeding program[4]. The amount of variability present in early segregating generations and the magnitude of genotypic coefficient and phenotypic coefficient of variability should be given much importance[44]. The mean, range, genotypic coefficient of variation (GCV) (%), phenotypic coefficient of variation (PCV) (%), heritability (%) (broad sense) and genetic advance as percent of mean were presented in **Table 1**.

A wide range of variability was observed for all most all the traits under study except for days to 50% flowering and hundred seed weight. The Phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all characters, clearly indicating the environmental influence in expression of these characters. This was in conformity with earlier findings[10]. However large differences were recorded between PCV and GCV for characters viz., number of tillers, number of productive tillers and panicle length. The genotypic coefficient of variation measures the extent of genetic variability present for a trait but does not assess the amount of genetic variation which is heritable[38]. High GCV gives an indication of justifiable variability among the genotype with respect to these characters and therefore provide scope for improvement through selection[33, 45]. High GCV coupled with high PCV was exhibited by number of tillers, number of productive tillers, number of filed grains and single plant yield. Higher GCV and PCV estimate provide wider scope of selection for elite segregants[5]. Similar results were in obtained for single plant yield[47], number of filled grain per panicle[47], number of productive tillers[35, 43]. Low GCV estimate coupled with low PCV was recorded for days to 50% flowering, whereas low GCV coupled with moderate PCV was exhibited by panicle length and hundred seed weight. The low GCV estimate gives an indication of less variability among lines in F_2 population. Low GCV for panicle length[30, 22] as revealed from earlier reports.

Heritability of a trait is important in determining its response to selection. Genetic improvement of genotypes for quantitative traits requires reliable estimate of heritability for designing an efficient breeding program. The knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character into subsequent generations[37, 46]. High heritability estimate was recorded for days to 50% flowering (75.37), plant height (77.40), number of filled grain (95.55) and single plant yield (92.10). However moderate heritability estimate was recorded for number of tillers (50.25), number of productive tillers (45.16) and hundred seed weight (49.50). For panicle length (13.66) low estimate of heritability was recorded.

Genetic advance as percentage of mean is more reliable index for understanding the effectiveness of selection in improving the traits because its estimated value is derived by involvement of heritability, phenotypic standard deviation and intensity of selection[40]. Thus genetic advance as percentage of mean along with heritability provides clear picture regarding the influences positively the effectiveness of selection for improving the plant characters. Estimation of heritability along with genetic gain is usually more useful in predicting the resultant effect from selecting the best individual. High heritability coupled with high genetic advance was recorded for single plant yield. Similar findings was reported for single plant yield[3, 13]. Moderate heritability coupled with high genetic advance was recorded for number of tillers, number of productive tillers and hundred seed weight. Moderate to high heritability and genetic advance percent of mean could be explained by additive gene action and their improvement could be achieved through mass selection[32, 23]. High heritability coupled with low genetic advance percent of mean was recorded for days to 50% flowering, plant height and number of filled grain per panicle. This type of results were also reported earlier for days to 50% flowering and number of filled grain per panicle[12, 34]. It is the indication of predominance of epistasis and dominant gene action (non-additive gene action) and selection for such traits may not be rewarding in early generation. Low heritability coupled with low genetic advance as percent of mean was recorded for panicle length clearly indicating high environmental influence and selection would be ineffective[29].

Yield is a complex character and composed of several components among which some affect the yield directly while others contribute indirectly. The study of interrelationship among quantitative traits is important for assessing the degree and direction of association between a pair of characters. It will be useful for simultaneous improvement of correlated traits through selection. Genotypic correlation plays a key role in the development and execution of suitable breeding programs[39]. The data obtained from genotypic correlation study was mentioned in **Table 2**. Correlation studies revealed that single plant yield has a highly significant and positive correlation with plant height (r = 0.322**), number of tillers (r = 0.486**), number of productive tillers (r = 0.570**), panicle length (r = 0.190**), number of filled grain per panicle (r = 0.375**) and hundred rain weight (r = 0.234**). These results suggest that selection to improve rice yield directed by phenotype of these traits may be effective[32]. Similar results were in line up with earlier reports[19, 28, 6, 7, 42]. However single plant yield was negatively non-significantly associated with days to 50% flowering.

The path coefficient measures the magnitude of direct and indirect effects of characters on complex dependent characters like yield and thus enable the breeders to judge best about the important component characters during selection. The result of various causes influencing single plant yield (direct and indirect effect) are shown in **Table 3**. The path coefficient analysis revealed that positive direct effect was exhibited by number of productive tillers, number of filled grain per panicle and hundred grain weight towards single plant yield. Hence, selection of the above traits would result in improvement of grain yield in rice. Similar finding were in accordance with earlier reports for hundred seed weight[41, 18], number of productive tillers[16], number of filled grain per panicle[17, 15].

The reported ratings of the direct and indirect effect ranging from 0.30-1.00 as high and above 1.00 as very high[25] were used for classification of effect. In this study the values of the direct and positive effect for the above characters were ranging from 0.19 – 1.08. Hence, the contribution of the above characters to single plant yield is evidently very high hence, they can be potentially help for direct selection for increased yield.

Table 1. Variability parameters of F_2 segregating generation for different yield and yield contributing traits

Characters	RANGE	MEAN	PCV	GCV	$h^2_{(bs)}$ (in %)	GA (%) of mean
DFF (days)	85-93	88.18	2.47	2.14	75.37	1.83
PH (cm)	36-86	67.85	13.75	12.10	77.40	4.95
NT (no.)	3-20	7.06	45.57	32.30	50.25	22.08
NPT (no.)	2-18	6.11	50.47	33.92	45.16	23.01
PL (cm)	8-23	16.86	18.79	6.94	13.66	2.86
NFG (no.)	45-182	109.85	31.28	30.58	95.55	4.82
HGW (gm)	1.2-2.2	1.53	12.47	8.77	49.50	24.55
SPY (gm)	2.98-40.31	9.75	57.43	55.12	92.10	24.42

Days to fifty per cent flowering (DFF), plant height (PH), number of tillers (NT), number of productive tillers (NPT), panicle length (PL), number of filled grains (NFG), hundred grain weight (HGW) and single plant yield (SPY), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) (h^2), Genetic advance (GA).

Table 2. Genotypic correlation between different pair of traits in F_2 segregating generation

	DFF	PH	NT	NPT	PL	NFG	HGW	SPY
DFF	1.000	-0.132	0.055	0.030	-0.196**	-0.062	-0.073	-0.061
PH		1.000	0.194**	0.202**	0.612**	0.176*	0.299**	0.322**
NT			1.000	0.931**	0.157*	-0.379**	0.101	0.486**
NPT				1.000	0.161*	-0.403**	0.146*	0.570**
PL					1.000	0.105	0.188*	0.190**
NFG						1.000	-0.108	0.375**
HGW							1.000	0.234**
SPY								1.000

**** Significant at 1% level, * Significant at 5% level**

Days to fifty per cent flowering (DFF), plant height (PH), number of tillers (NT), number of productive tillers (NPT), panicle length (PL), number of filled grains (NFG), hundred grain weight (HGW) and single plant yield (SPY).

Table 3. Path analysis showing direct and indirect effects of different traits on single plant yield in F_2 segregating generations

	DFF	PH	NT	NPT	PL	NFG	HGW	SPY
DFF	**-0.033**	0.001	-0.014	0.033	0.013	-0.046	-0.014	-0.061
PH	0.004	**-0.001**	-0.049	0.220	-0.039	0.131	0.057	0.322
NT	-0.002	-0.000	**-0.254**	1.015	-0.010	-0.282	0.019	0.486
NPT	-0.001	-0.000	-0.236	**1.089**	-0.010	-0.299	0.028	0.570
PL	0.006	-0.000	-0.039	0.175	**-0.065**	0.078	0.036	0.190
NFG	0.002	-0.000	0.096	-0.439	-0.007	**0.744**	-0.021	0.375
HGW	0.002	-0.000	-0.026	0.159	-0.012	-0.080	**0.191**	0.234

Residual effect: 0.4351, Diagonal values indicate the direct effects

Days to fifty per cent flowering (DFF), plant height (PH), number of tillers (NT), number of productive tillers (NPT), panicle length (PL), number of filled grains (NFG), hundred grain weight (HGW) and single plant yield (SPY).

REFERENCES

1. Adebisi, M.A., Ariyo, O.J. and Kehinde, O.B., Variation and correlation studies in quantitative characteristics in soybean. Proc. Annual conference Agril. Society Nigeria. University of Agriculture, Abeokuta. **pp.** 121-125 (2001).
2. Adhya, T. K., Vision 2030. Central Rice Research Institute, Indian Council of Agricultural Research, Bhubaneswar, India. (2011).
3. Ahmad, F., Hanafi, M.M., Hakim, M.A., Rafii, M.Y., Arolu, I.W. and Akmar Abdullah, S.N., Genetic Divergence and Heritability of 42 Coloured Upland Rice Genotypes (Oryza sativa) as Revealed by Microsatellites Marker and AgroMorphological Traits. *PLoS ONE,* **10(9):** 138246 (2015).
4. Allard, R.W., Principles of plant breeding. John Wiley and Sons. Inc., U.S.A. **pp.** 485 (1960).
5. Ameenal, M., Shalini, T., Govintharaj, P., Manonmani, S. and Robin, S., Assessment of parental genetic variability in rice. *Int. J. Agri. Sci.,* **8(54):** 2917-2919 (2016).
6. Augustina, U.A., Iwunor, O.P., and Ijeoma, O.R., Heritability and character correlation among some rice genotypes for yield and yield components. *J. Plant Breed. Genet.,* **01(02):** 73-84 (2013).
7. Baloch, A.W., Bhatti, S.M., Baloch, M., Jogi, Q.D. and Kandhro, M.N., Correlation analysis of various metric traits with grain yield and heritability estimation. *Pak. J. Agri. Agril. Engg. Vet. Sci.,* **32(2):** 136–142 (2016).
8. Bello, O.B, Ige, S.A., Azeez, M.A., Afolabi, M.S., Abdulmaliq, S.Y. and Mahamood, J., Heritability and Genetic Advance for Grain Yield and its Component Characters in Maize (*Zea mays* L.). *Intl. J. Plant Res.,* **2:** 138-145 (2012).
9. Bentur, J. S., Pasalu, I. C., Sharma, N. P., Rao, U. P. and Mishra, B., Gall midge resistance in rice: Current status in India and future strategies. DRR Research Paper Series 01/2003. Directorate of Rice Research, Rajendranagar, Hyderabad, **pp.** 20 (2003).

10. Bhadru, D., Tirumala, R.V., Chandra, M.Y. and Bharathi, D., Genetic variability and diversity studies in yield and its component traits in rice (Oryza sativa L.). SABRAO *J. Breed. & Genet.,* **44 (1):** 129-137 (2012).
11. Dewey, D.R. and Lu, K.H., A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.,* **57:** 515-18 (1959).
12. Divya, B., Robin, S., Rabindran, R. and John Joel A., Molecular and morphological characterisation pf back cross generations for yield and blast resistance in Rice. *J. Rice Res.,* **4:** 169 (2016).
13. Govintharaj, P., Shalini, T., Manonmani, S. and Robin, S., Genetic parameters studies on bacterial blight resistance genes introgressed segregating population in Rice. *World Scientific News,* **59:** 85-96 (2016).
14. Govintharaj, P., Tannidi, S., Swaminathan, M. And Sabariappan, R., Estimates of genetic variability, heritability and genetic advance for Blast resistance gene introgressed segregating population in Rice. *Int. J. Curr. Microbiol. App. Sci.,* **5(12):** 672-677 (2016).
15. Gunasekaran, K., Sivakami, R., Sabariappan, R., Ponnaiah, G., Nachimuthu, V.V. and Pandian, B.A., Assesment of genetic variability, correlation and path coefficient analysis for morphological and quality traits in rice (Oryza sativa L.). *Agric. Sci. Digest,* **37(4):** 251-256 (2017).
16. Harsha, I.D., Kumar, S. and Talha, M., Assessment of Genetic Variability and Inter-Character Association Studies in Rice Genotypes (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci.,* **6(9):** 2041-2046 (2017).
17. Hossain, S., Maksudul Haque, M. D. and Rahman, J., Genetic variability, correlation and path coefficient analysis of morphological traits in some extinct local aman rice (Oryza sativa L). *J. Rice Res.,* **3:** 158 (2015).
18. Islam, M.A., Raffi, S.A., Hossain, M.A. and Hasan, A.K., Character association and path analysis of grain yield and yield related traits in some promising early to medium duration rice advanced lines. *Intl. J. Expt. Agric.,* **5(1):** 8-12 (2015).
19. Jayasudha, S., and Sharma, D., Genetic parameters of variability, correlation and path-coefficient for grain yield and physiological traits in rice (*Oryza sativa* L.) under shallow lowland situation. *Elect. J. Plant Breed.,* **1:** 33-38 (2010).
20. Johnson, H.W., Robinson, M.F. and Comstock, R.E., Estimation of genetic variability and environmental variability in soybean. *Agron. J.,* **47:** 314-318 (1955).
21. Kahani, F and Hittalmani, S., Genetic Analysis and Traits Association in F_2 Intervarietal Populations in Rice Under Aerobic Condition. *J. Rice Res.,* **3:** 152 (2015).
22. Kalaimaghal, R., Studies on genetic variability of grain iron and zinc content in F_2, F_3 generation of rice (Oryza sativa L.). M.Sc. (Ag.) Thesis, Tamil Nadu Agricultural University, Coimbatore. (2011).
23. Khatun, T., Hanafi, M.M. Yusop, M.R. and Wong, M.Y., Genetic Variation, Heritability, and Diversity Analysis of Upland Rice (Oryza sativa L.) Genotypes Based on Quantitative Traits. *BioMed. Res. Int.,* 1-7. (2015).
24. Laxuman, P., Salimath, M., Shashidhar, H. E., Mohankumar, H. D., Patil, S. S., Vamadevaiah, H. M. and Janagoudar, B. S., Character association and path coefficient analysis among the backcross inbred lines derived from Indica x Nerica cross for productivity traits in rice (*Oryza sativa* L.). *Karnataka J. Agric. Sci.,* **24(5):** 563-565 (2011).
25. Lenka, D. and Mishra, B., Path coefficient analysis of yield in rice varieties. *Indian J. Agric. Sci*.**, 43:** 376-379 (1973).
26. Mew, T. W., Vera Cruz, C. M. and Medalla, E. S., Changes in the race frequency of *Xanthomonas oryza pv. oryzae* in response to the planting of rice

cultivars in the Philippines. *Plant Dis.,* **76:** 10291032 (1993).

27. Miller, D.A., Williams, J.C.I., Robinson, H.F. and Comstock, K.B., Estimate of genotypic and environmental variances and covariance in upland cotton and their implication in selection. *Agro. J.,* **50:** 126-31 (1985).
28. Minnie, C. M., Reddy, T. D., and Raju, C. S., Correlation and path analysis for yield and its components in rice (*Oryza sativa* L.). *Journal of Research ANGRAU,* **41(1):** 132-134 (2013).
29. Nandarajan, N. and Gunasekaran, M., Quantitative Genetics and Biometrical Techniques in Plant Breeding. Kalyani Publishers, Ludhiana, **pp.** 258 (2005).
30. Nandeshwar, B.C., Pal, S., Senapati, B.K. and De, D.K., Genetic variability and character association among biometrical traits in F_2 generation of some rice crosses. *Elect. J. Plant Breed.,* **1(4):** 758-763 (2010).
31. Noh, T.H., Lee, D.K., Park, J.C., Shim, H.K., Choi, M.Y., Kang, M.H., and Kim, J. D., Effect of bacterial leaf blight occurrence on rice yield and grain quality in different rice growth stage. *Res. Plant Dis.,* **13:** 20–23 (2007).
32. Ogunbayo, S.A., Sie, M., Ojo, D.K., Sanni, K.A. and Akinwale, M.G., Genetic variation and heritability of yield and related traits in promising rice genotypes (*Oryza sativa* L). *J. Plant breed. Crop Sci.,* **6:** 153-159 (2014).
33. Pandey, P. and Anurag, P.J., Estimation of genetic parameters in indigenous rice. *AAB Bioflux,* **2(1):** 79-84 (2010).
34. Prabhu, S.M., Ganesan, N.M., Jeyaprakash, P., Selvakumar, R., and Prabhakaran, N.K., Assessment of Genetic Variability Studies among the Backcross Populations in Rice [*Oryza sativa* (L.)], *Int. J. Pure App. Biosci.,* **5(4):** 368-372 (2017).
35. Purusothaman, R., Genetic analysis for high iron and zinc content in rice (*Oryza sativa* L.) grains. M.Sc. (Ag.) Thesis, Tamil Nadu Agricultural University, Coimbatore (2010).
36. Rola, A. C. and Widawsky, D. A., Impact of rice research. Proc. International Conference on Impact of Rice Research. TDRI., IRRI. **pp.** 135-158 (1998).
37. Sabesan, T., Suresh, R. and Saravanan, K., Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamil Nadu. *Elect. J. Plant Breed.,* **1:** 56-59 (2009).
38. Sala, M. And Shanthi, P., Variability, heritability and genetic advance studies in F2 population of Rice (Oryza sativa L.). *Int. J. Forestry & Crop Improv.,* **7(1):** 57-60 (2016).
39. Selvaraj, C. I., Nagarajan, P., Thiyagarajan, K., Bharathi, M., and Rabindran, R., Genetic parameters of variability, correlation and path coefficient studies for grain yield and other yield Attributes among rice blast disease resistant genotypes of rice (*Oryza sativa* L.). *Afric. J. Biotechnol.***,** **10:** 3322-3334 (2011b).
40. Sinha, S. and Wagh, P., Genetic studies and divergence analysis for yield, physiological traits and oil content in Linseed. *Res. J. Agri. Sci.,* **4:** 168-75 (2013).
41. Solanki, A. and Tiwari, J. K., Genetic variability analysis for various yield attributing and quality traits in rice (*Oryza Sativa* L.). *The Bioscan,* **8(4):** 1403–1407 (2013).
42. Sravan, T., Jaiswal, H. K., Waza, S. A., and Priyanka, K., Analysis of variability and character association in indigenous aromatic rice (*Oryza Sativa* L.). *Elect. J. Plant Breed.,* 159–164 (2016).
43. Subbaiah, P.V., Sekhar, M.R., Reddy, K.H.P. and Reddy, N.P.E., Variability and genetic parameters for grain yield and its components and kernel quality attributes in CMS based rice hybrids (Oryza sativa L.). *Int. J. Appl. Biol. &Pharm. Technol.,* **2(3):** 603-609 (2011).
44. Subramanian, S. and Menon, M. P., Genotypic and phenotypic variability in

rice. *Madras Agric. J.,* **60:** 1093-1096 (1973).

45. Tiwari, D. K., Pandey, P., Tripathi, S., Giri, S. P. and Dwivedi, J. L., Studies on genetic variability for yield components in rice (*Oryza sativa* L.) *AAB Bioflux,* **3(1):** 2-15 (2011).
46. Ullah, M.Z., Bashar, M.K., Bhuiyan, M.S.R., Khalequzzaman, M. and Hasan, M.J., Interrelationship and Cause-effect Analysis among Morpho-physiological traits in Birouin Rice of Bangladesh. *Int. J. Plant Breed. Genet.,* **5:** 246-254 (2011).
47. Vanishree, S., Swapna, K., Ch., Damodar Raju, Ch., Srendar Raju, and Sreedhar, M., Genetic variability and selection criteria in rice. *J. Biological & Scient. Opinion,* **1(4):** 203-206 (2013).
48. Widowsky, D. A. and O’Toole, J. C., Prioritizing rice research agenda for eastern India. In: Rice research in Asia: progress and priorities **pp.** 109–129 (1996).
49. Wright, S., Correlation and causation. *J. Agri. Sci.,* **20:** 557-87 (1921).