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Estimation of Variability, Correlation Coefficient and Path Analysis in Improved Restorer Lines of Rice (*Oryza sativa* L.)

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Authors' contributions

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

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ABSTRACT

The present investigation was conducted to estimate genetic variability parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA) along with correlations and path coefficients from data collected on 40 F_4 - F_5 population derived from a cross between aerobic restorer AR 9-18 and blast resistant donor MSM 1212 possessing *Pi54*. Analysis of variance indicated significant differences among the genotypes for all the characters studied. Moderate GCV and PCV was observed for number of productive tillers per plant, number of grains per panicle, per day productivity and single plant yield. High heritability coupled with high genetic advance as percent of mean were observed for number

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of productive tillers per plant, number of grains per panicle, per day productivity and single plant yield, whereas high heritability coupled with moderate genetic advance as percent of mean were observed for panicle length, spikelet fertility, thousand grain weight and plant height. Grain yield per plant showed positive correlation with per day productivity, days to 50% flowering, panicle length, number of productive tillers per plant, thousand grain weight and spikelet fertility, while, negative association with number of grains per panicle and plant height. The trait per day productivity had highest direct effect on single plant yield followed by days to 50% flowering, panicle length, number of productive tillers per plant, thousand grain weight, spikelet fertility (%). Hence, per day productivity and number of productive tillers per plant are identified as key traits for developing high yielding genotypes of rice for future breeding programme.

Keywords: PCV; GCV; correlation coefficient; path analysis; rice.

1. INTRODUCTION

“Rice (*Oryza sativa* L.) is the staple food for more than 1.25 billion people in most parts of India. An increase in rice production is necessary to bring self-sufficiency in the country to feed the burgeoning population” [1]. Rice hybrids have yield superiority of about 15–20 % over the best commercial inbred varieties [2] and large-scale adoption of hybrid rice production is one of the feasible options to meet the food security challenges in India [3]. However, the major problems in hybrid rice breeding are the limited number of parental lines with specific desirable traits. Therefore, improving parental lines must be an integral part of hybrid rice breeding programmes. A population with a high degree of variability allows selection to generate a variety with desirable characteristics. “Planning and execution of any breeding program for improvement on quantitative traits depends on magnitude of genetic variability. Therefore, success on plant breeding activities entirely depends on the existence of genetic variability with respect to desired traits and selection skill of plant breeder” [4]. “Variability, expected genetic advances and heritability of the traits are therefore key basis for genetic improvement of the trait. Correlation and path analysis establish the extent of association between yield and its components and also bring out relative importance of their direct and indirect effects, thus giving an obvious understanding of their association with grain yield. Ultimately, this kind of analysis could help the breeder to design his selection strategies to improve grain yield” [5]. In the light of the above scenario, the present investigation conducted to identify the most important characters for breeding programme by exploiting the genetic variability parameters, heritability, genetic advance as percent of mean, correlation coefficient and path analysis in restorer lines of rice.

2. MATERIALS AND METHODS

The research was carried out at ICAR-Research Farm, Indian Institute of Rice Research (IIRR), Hyderabad, Telangana during the *khari*, 2021. For the present genetic study, the experimental material consists of 40 F₄-F₅ population derived from a cross between aerobic restorer, AR 9-18 and blast resistant donor, MSM 1212 possessing *Pi54*. The experiment was conducted using randomized complete block design with two replications. Thirty days old seedlings of F₄-F₅ population along with check were transplanted with 15 x 20 cm spacing between the plants and rows. Phenotypic data was recorded for nine yield and its attributing traits *viz.*, days to 50 % flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), spikelet fertility (%), number of grains per panicle, thousand grain weight (g), per day productivity (kg/ha/day) and single plant yield (g) on all the forty F₄-F₅ population and check based on flowering duration and maturity. During the experiment for raising a healthy nursery and main crop recommended cultural practices and crop protection measures were taken up.

Analysis of variance (ANOVA) for the randomized complete block design was computed using the method of Panse and Sukhatme [6], genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed using the method of Burton and Dewane [7]. Variation ranges were classified as high (> 20%), moderate (10-20%), or low (< 10%) as proposed by Sivasubramanian and Madhavamenon [8]. Broad sense heritability (h^2 (bs)) was estimated as the ratio of genotypic variance to total variance, categorized as high (> 60%), moderate (30-60%), or low (0-30%) based on Robinson et al. [9]. Genetic advance was calculated and categorized as high (> 20%), moderate (10-20%), or low (< 10%) following

Johnson et al. guidelines [10]. Simple correlations were computed using Weber and Moorthy's formula [11], and path analysis was computed using the method suggested by Dewey and Lu [12].

3. RESULTS AND DISCUSSION

The analysis of variance carried out for the single plant yield and its attributing traits. The variations among the treatments were highly significant for all the characters under study indicating the existence of considerable genetic variation in the experimental material. The analysis of variance was calculated using the method of Panse and Sukhatme [6] and presented in Table 1.

“To uncover the role of environmental effect on different traits GCV and PCV values are vital” [13]. “For all the traits studied it was observed that PCV values in comparison with GCV values were slightly higher which indicates that the expression of traits was influenced less by the environmental factors” [13]. Moderate PCV and GCV were recorded for number of productive tillers per hill, number of grains per panicle, per day productivity and single plant yield. Similar results of moderate PCV and GCV was reported by Dhanwani et al. [14], Yadav et al. [15], Lingaiah et al. [16] for number of productive tillers per plant and number of grains per panicle, Yadav et al. [15] and Sudeepthi et al. [17] for single plant yield.

The traits viz., days to 50 percent flowering, panicle length, plant height, spikelet fertility, thousand grain weight recorded low levels of PCV and GCV, which suggest that these traits exhibited less variability so, the selection may not be fruitful based on these traits. Similar results were given by Sravan et al. [18], Yadav et al. [15] for thousand grain weight, days to 50 percent flowering, panicle length, spikelet fertility, Savitha and Usha Kumari [19], Sala and Shanthi [20], Singh and Varma [21], Abhilash et al. [22] for plant height.

All the studied traits exhibited high heritability. The traits viz., number of productive tillers per plant, number of grains per panicle, single plant yield and per day productivity recorded high heritability with high genetic advance, which favours additive gene action. Earlier researchers, Savitha and Usha Kumari [19], Ali et al. [23], Pradeep et al. [24], Subbulakshmi and Muthuswamy [25], reported similar findings for

productive tiller number per plant, number of grains per panicle and single plant yield.

The traits viz., panicle length, spikelet fertility and thousand grain weight and plant height showed high heritability but genetic advance was moderate which limits further improvement through direct selection. Panwar and Mathur [26] reported similar findings for spikelet fertility, panicle length, thousand grain weight and Nath et al. [27] reported similar findings with plant height.

Correlation analysis provides information regarding nature and degree of relationship among various traits and decides the component traits, on the basis of which traits can be chosen to improve grain yield genetically. In this study, correlations between yield and its related traits namely days to 50 % flowering, plant height, number of productive tillers per plant, panicle length, spikelet fertility, number of grains per panicle, thousand grain weight, per day productivity and single plant yield were computed [Bhargava et al., 2021]. Correlation coefficient results were represented in Table 3 which was done by considering single plant yield as dependent variable.

Thousand grain weight exhibited positive and significant correlation with spikelet fertility, per day productivity, panicle length and single plant yield. Similar results were reported by Prasad et al. [24] for single plant yield, Gautam et al. [28] and Tripathi et al. [29] with number of productive tillers per plant and number of grains per panicle, Ghazy et al. [30] with panicle length. Days to 50 percent flowering exhibited negative and significant correlation with per day productivity. Plant height exhibited negative and significant correlation with number of grains per panicle, similar results were reported by Muthuvijayaragavan and Murugan [31]. Number of productive tillers per plant exhibited significant positive correlation with single plant yield and per day productivity, similar results were reported by Saha et al. [32] Kiruthikadevi et al. [33]. Panicle length showed positive and significant correlation with thousand grain weight, per day productivity and single plant yield. Similar results were reported by Prasad et al. [24]. Spikelet fertility exhibited positive and significant correlation with number of grains per panicle and thousand grain weight. Similar results were reported by Tripathi et al. [29]. Per day productivity revealed positive and significant correlation with thousand grain weight, number of grains per panicle, number of

productive tillers per plant, panicle length and single plant yield and negative significant correlation with days to 50% flowering. Similar results were reported by Bhadru et al. [34] with single plant yield and days to 50 % flowering. Thousand grain weight, number of productive tillers per plant, panicle length, per day productivity and number of grains per panicle exhibited significant and positive association with single plant yield. This suggests that ultimate increase in yield may be due to improvement of these traits. Similar results were reported by Touhiduzzaman et al. [35] with days to 50 % flowering, Shrivatsav et al. [36] with plant height, number of grains per panicle and panicle length, Padmaja et al. [37] with number of productive tillers per plant and thousand grain weight, Parimala et al. [38] with spikelet fertility and Bhadru et al. [34] with per day productivity.

“Path coefficient analysis explains the direct and indirect causes of association using other attributes by dividing the correlations for explaining the cause-and effect relationship clearly” [39]. Table 4 depicts the path coefficient

analysis estimates for yield and its attributing traits. Per day productivity exerted highest positive direct effect on plant yield followed by days to 50% flowering, panicle length, number of productive tillers per plant, thousand grain weight, spikelet fertility, indicates yield improvement is directly associated with these traits. Similar results of direct positive effect on plant yield were reported by Padmaja et al. [37] with number of productive tillers per plant and panicle length, Kalaiselvan et al. [40] with thousand grain weight, spikelet fertility and days to 50% flowering.

Negative direct effect on single plant yield was exhibited by plant height and number of grains per panicle. Similar results of negative direct results were reported by Shrivatsav et al. [41]. At phenotypic level the residual effect was 0.19. The trait per day productivity exhibited highest positive direct effect among all the yield attributing traits [42,43]. Hence, it can be considered as major contributor to plant yield. Phenotypical path diagram for plant yield was represented in Fig. 3.

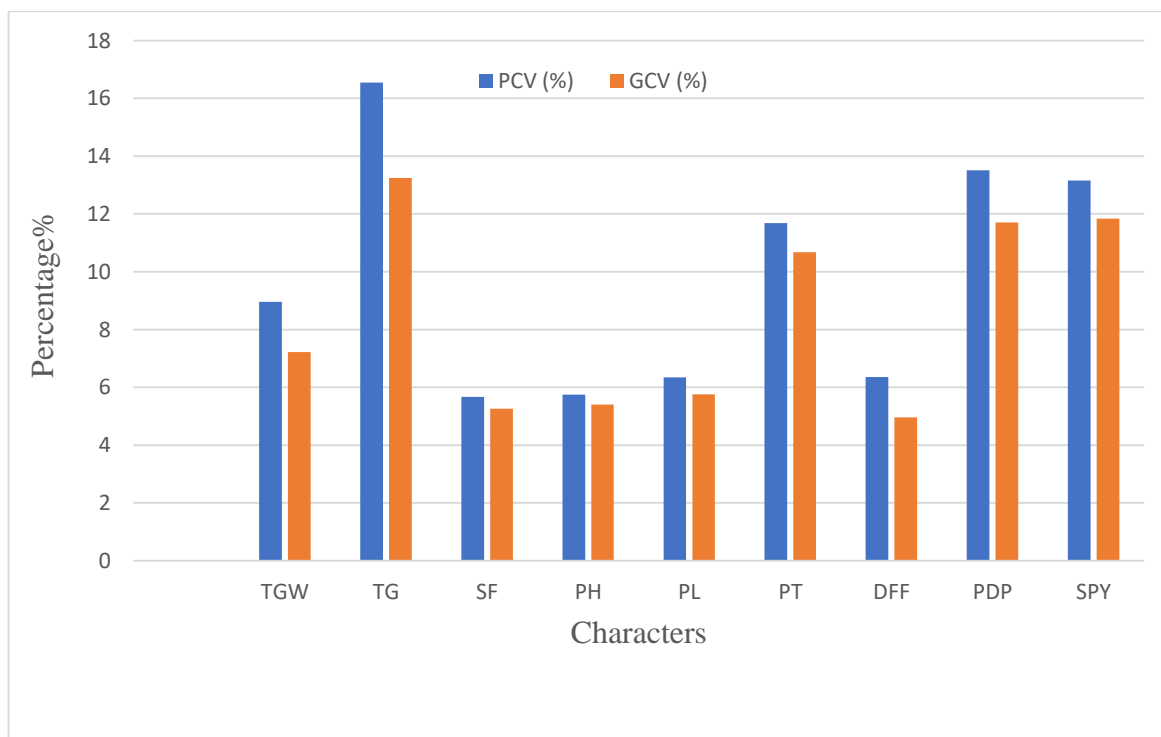


Fig. 1. Graphical representation of PCV and GCV for yield contributing traits
DFF- Days to 50% flowering, **PH-** Plant height (cm), **PT-**Number of productive tillers per plant, **PL-**Panicle length (cm), **TG-**Number of grains, **SF-**Spikelet fertility (%), **TGW-** Thousand grain weight (g), **PDP-**Per day productivity, **SPY-** Single plant yield (g)

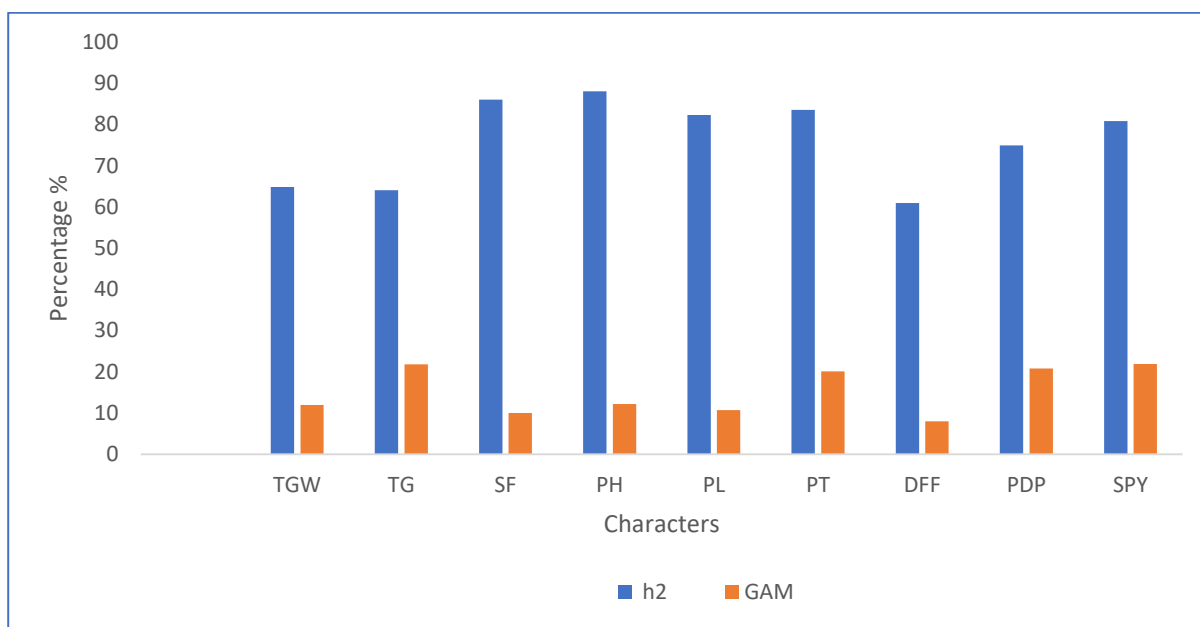


Fig. 2. Graphical representation of heritability in broad sense (h^2) and genetic advance as per cent of mean (GAM) (5%). for yield contributing traits

DFF- Days to 50% flowering, *PH*- Plant height (cm), *PT*-Number of productive tillers per plant, *PL*-Panicle length (cm), *TG*-Number of grains, *SF*-Spikelet fertility (%), *TGW*- Thousand grain weight (g), *PDP*-Per day productivity, *SPY*- Single plant yield (g)

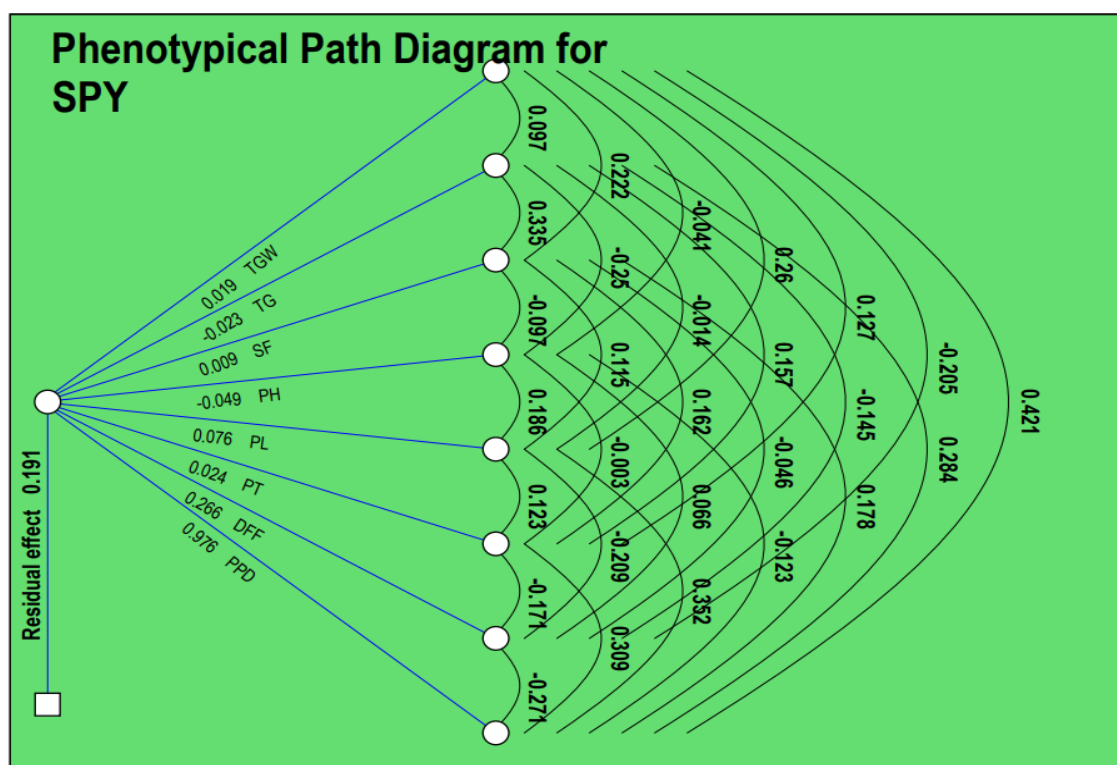


Fig. 3. Phenotypical path diagram for yield related traits

DFF- Days to 50% flowering, *PH*- Plant height (cm), *PT*-Number of productive tillers per plant, *PL*-Panicle length (cm), *TG*-Number of grains per panicle, *SF*-Spikelet fertility (%), *TGW*- Thousand grain weight (g), *PPD*-Per day productivity, *SPY*- Single plant yield (g).

Table 1. Analysis of variance for yield & yield attributing traits in F₄-F₅ population of AR 9-18 × MSM 1212

| Source of variation | D.F | Mean sum of squares | | | | | | | | |
|---------------------|-----|---------------------|----------|---------|---------|---------|----------|---------|------------|-----------|
| | | TGW | TG | SF | PH | PL | PT | DFF | PDP | SPY |
| Replication | 2 | 0.2325 | 796.53 | 0.248 | 0.144 | 4.145 | 0.0959 | 55.04 | 0.000048 | 0.1110 |
| Treatment | 42 | 5.811** | 1198.0** | 41.19** | 85.48** | 3.706** | 1.7163** | 74.32** | 0.001487** | 23.5851** |
| Error | 84 | 1.2387 | 262.26 | 3.083 | 5.430 | 0.358 | 0.1531 | 17.99 | 0.000233 | 2.491 |

DFF- Days to 50% flowering, *PH*- Plant height (cm), *PT*-Number of productive tillers per plant, *PL*-Panicle length (cm), *TG*-Number of grains per panicle, *SF*-Spikelet fertility (%), *TGW*- Thousand grain weight (g), *PDP*-Per day productivity, *SPY*- Single plant yield (g).

Table 2. Genetic variability parameters for yield and related traits in the F₄-F₅ population of AR 9-18 × MSM 1212

| Traits | General mean | Range | | PCV (%) | GCV (%) | Heritability in broad sense (h ²) (%) | Genetic Advance as percent of mean (at 5%) |
|--------|--------------|---------|---------|---------|---------|---|--|
| | | Minimum | maximum | | | | |
| TGW | 23.98 | 16.04 | 20.94 | 8.96 | 7.22 | 64.86 | 11.97 |
| TG | 162.30 | 112.00 | 231.00 | 16.54 | 13.24 | 64.08 | 21.84 |
| SF | 82.88 | 72.77 | 92.01 | 5.67 | 5.26 | 86.08 | 10.06 |
| PH | 117.15 | 101.83 | 128.50 | 5.75 | 5.40 | 88.06 | 12.23 |
| PL | 22.43 | 18.33 | 25.86 | 6.35 | 5.76 | 82.37 | 10.78 |
| PT | 8.27 | 6.00 | 10.00 | 11.68 | 10.68 | 83.62 | 20.13 |
| DFF | 106.78 | 88.00 | 121.0 | 6.36 | 4.96 | 61.01 | 7.99 |
| PDP | 0.20 | 0.11 | 0.26 | 13.51 | 11.70 | 75.00 | 20.87 |
| SPY | 27.42 | 15.33 | 33.56 | 13.16 | 11.84 | 80.89 | 21.93 |

DFF- Days to 50% flowering, *PH*- Plant height (cm), *PT*-Number of productive tillers per plant, *PL*-Panicle length (cm), *TG*-Number of grains per panicle, *SF*-Spikelet fertility (%), *TGW*- Thousand grain weight (g), *PDP*-Per day productivity, *SPY*- Single plant yield (g).

Table 3. Correlation analysis among yield and related traits in F₄-F₅ population of AR 9-18 x MSM 1212

| Traits | TGW | TG | SF | PH | PL | PT | DFF | PPD | SPY |
|--------|------|--------|-----------|-----------|---------|---------|---------|-------------|------------|
| TGW | 1 ** | 0.0973 | 0.2220 * | -0.0410 | 0.2602* | 0.1274 | -0.2053 | 0.42051 *** | 0.3993*** |
| TG | | 1 ** | 0.3353 ** | -0.2503 * | -0.0140 | 0.1570 | -0.1453 | 0.2836 ** | 0.2353 * |
| SF | | | 1 ** | -0.0966 | 0.1146 | 0.1619 | -0.0460 | 0.1778 | 0.1842 |
| PH | | | | 1 ** | 0.1864 | -0.0030 | 0.0660 | -0.1229 | -0.1329 |
| PL | | | | | 1 ** | 0.1229 | -0.2089 | 0.3522** | 0.3645*** |
| PT | | | | | | 1 ** | -0.1709 | 0.3092 ** | 0.2906 ** |
| DFF | | | | | | | 1 ** | -0.2705 * | -0.0224 |
| PPD | | | | | | | | 1 ** | 0.94735*** |
| SPY | | | | | | | | | 1 ** |

DFF- Days to 50% flowering, *PH*- Plant height (cm), *PT*-Number of productive tillers per plant, *PL*-Panicle length (cm), *TG*-Number of grains per panicle, *SF*-Spikelet fertility (%), *TGW*- Thousand grain weight (g), *PDP*-Per day productivity, *SPY*- Single plant yield (g).

Table 4. Phenotypic path coefficient analysis representing direct and indirect effects on single plant yield by its related traits in F₄-F₅ population of AR 9-18 x MSM 1212

| Traits | TGW | TG | SF | PH | PL | PT | DFF | PPD | SPY |
|--------|---------------|----------------|---------------|----------------|---------------|---------------|---------------|---------------|---------|
| TGW | 0.0188 | 0.0018 | 0.0042 | -0.0008 | 0.0049 | 0.0024 | -0.0039 | 0.0079 | 0.3993 |
| TG | -0.0022 | -0.0225 | -0.0075 | 0.0056 | 0.0003 | -0.0035 | 0.0033 | -0.0064 | 0.2354 |
| SF | 0.0020 | 0.0030 | 0.0089 | -0.0009 | 0.0010 | 0.0014 | -0.0004 | 0.0016 | 0.1842 |
| PH | 0.0020 | 0.0122 | 0.0047 | -0.0487 | -0.0091 | 0.0001 | -0.0032 | 0.0060 | -0.1330 |
| PL | 0.0198 | -0.0011 | 0.0087 | 0.0142 | 0.0763 | 0.0094 | -0.0159 | 0.0269 | 0.3645 |
| PT | 0.0031 | 0.0038 | 0.0040 | -0.0001 | 0.0030 | 0.0245 | -0.0042 | 0.0076 | 0.2906 |
| DFF | -0.0546 | -0.0387 | -0.0122 | 0.0176 | -0.0555 | -0.0454 | 0.2659 | -0.0719 | -0.0224 |
| PPD | 0.4103 | 0.2767 | 0.1735 | -0.1200 | 0.3437 | 0.3018 | -0.2639 | 0.9757 | 0.9474 |

Direct effects are represented in bold values; Residual effect: 0.191

DFF- Days to 50% flowering, *PH*- Plant height (cm), *PT*-Number of productive tillers per plant, *PL*-Panicle length (cm), *TG*-Number of grains per panicle, *SF*-Spikelet fertility (%), *TGW*- Thousand grain weight (g), *PDP*-Per day productivity, *SPY*- Single plant yield (g)

4. CONCLUSION

Analysis of variance revealed significant differences among the treatments for all the characters under study indicating the existence of considerable genetic variation in the experimental material. Moderate PCV and GCV were recorded for number of productive tillers per plant, number of grains per panicle, per day productivity and single plant yield which signifies fair level of selection in these characters. Number of productive tillers per plant, number of grains per panicle, per day productivity and single plant yield showed high heritability with high genetic advance as per cent of mean which signifies predominance of additive gene action in their genetic control. So, for improvement of these traits simple selection would be productive. Analysis of correlation and path coefficient together revealed that among the yield traits studied, per day productivity and number of productive tillers per plant were considered as most critical ones as they exhibited higher correlation coefficients and direct positive effects in association to plant yield.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Kumar A, Bhowmick PK, Singh VJ, Malik M, Gupta AK, Seth R et al. Marker-assisted identification of restorer gene (s) in iso-cytoplasmic restorer lines of WA cytoplasm in rice and assessment of their fertility restoration potential across environments. *Physiol Mol Biol Plants*. 2017;23(4):891-909.
2. Virmani SS. Hybrid rice. *Adv Agron*. 1996;57:377-462.
3. Pranathi K, Viraktamath BC, Neeraja CN, Balachandran SM, Hari Prasad AS, Koteswara Rao P et al. Development and validation of candidate gene-specific markers for the major fertility restorer genes, Rf4 and Rf3 in rice. *Mol Breed*. 2016;36:1-14.

4. Adhikari BN, Joshi BP, Shrestha J, Bhatta NR. Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (*Oryza sativa* L.). *J Agric Nat Resour*. 2018;1(1):149-60.
5. Babu VR, Shreya K, Dangji KS, Usharani G, Shankar AS. Correlation and path analysis studies in popular rice hybrids of India. *Int J Sci Res Publ*. 2012;2(3):1-5.
6. Panse VG, Sukhatme PV. *Statistical Methods for Agricultural Workers*. Indian Council of Agricultural Research Publication. 1985;87-89.
7. Burton GW, Devane EH. Estimating heritability in tall tissue (*Festula arundnacea* L.) from replicated clonal material. *Agron J*. 1953;45(10):478-81.
8. Sivasubramanian S, Madhavamenon P. Genetic analysis of quantitative characters in rice through diallel crosses. *Madras Agric J*. 1973;60:1097-8.
9. Robinson FA, Comstock RE, Harvey PH. Estimation of heritability and degree of dominance in corn. *Agron J*. 1949;41:353-9.
10. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybeans. *Agron J*. 1955;47(7):314-8.
11. Weber CR, Moorthy BR. Heritability and non-heritability relationships and variability of oil content and agronomic characters in the F2 generation of soybean crosses. *Agron J*. 1952;44(4):202-9.
12. Dewey DR, Lu KH. A correlation and path analysis of components of crested wheat grass seed production. *Agron J*. 1959;51:513-4.
13. Akinwale MG, Gregorio G, Nwilene F, Akinyele BO, Ogunbayo SA, Odiyi AC. Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *Afr J Plant Sci*. 2011;5(3):207-12.
14. Dhanwani RK, Sarawgi AK, Solanki A, Tiwari JK 2013. Genetic variability analysis for various yield attributing and quality traits in rice (*O. sativa* L.). *The Bioscan*, 8(4):1403-7.
15. Yadav R, Rajpoot P, Verma OP, Singh PK, Singh P, Pathak V. Genetic variability, heritability and genetic advance in Rice (*Oryza sativa* L.) for grain yield and itâ€™s contributing attributes under sodic soil. *J Pharmacogn Phytochem*. 2017;6(5):1294-6.

16. Lingaiah N. Variability studies in F2 population of Rice (*Oryza sativa* L.). Int J Agric Sci, ISSN. 2018;10(9):0975-3710.
17. Sudeepthi K, Srinivas TVSR, Kumar BR, Jyothula DPB, Umar SN. Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). Electron J Plant Breed. 2020;11(01):144-8.
18. Sravan T, Rangare NR, Suresh BG, Kumar SR. Genetic variability and character association in rainfed upland rice (*Oryza sativa* L.). Rice Res. 2012;5(1):2.
19. Savitha P, Usha Kumari R. Assessment of genetic variability and correlation studies among traditional land races and improved cultivars for segregating generations of rice (*Oryza sativa* L.). Int J Sci Nat. 2015;6(2):135-40.
20. Sala M, Shanthi P. Variability, heritability and genetic advance studies in F2 population of rice (*Oryza sativa* L.). Int J For Crop Improv. 2016;7(1):57-60.
21. Singh N, Verma OP. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) under salt stressed soil. J Pharmacogn Phytochem. 2018;7(3):3114-7.
22. Abhilash R, Thirumurugan T, Sassikumar D, Chitra S. Genetic studies in F2 for biometrical traits in Rice (*Oryza sativa* L.). Electron J Plant Breed. 2018;9(3):1067-76.
23. Ali EN, Rajeswari S, Saraswathi R, Jeyaprakash P. Genetic variability and character association for earliness, yield and its contributing traits in F2 population of rice (*Oryza sativa* L.). Electron J Plant Breed. 2018;9(3):1163-9.
24. Prasad KR, Krishna KR, Kumar SS, Senguttuvel P, Rao LS. Screening of lines for restoring fertility genes Rf3 and Rf4 with SSR markers in rice (*Oryza sativa* L.). Int J Pure App Biosci. 2017;5(4):647-50.
25. Subbulakshmi K, Muthuswamy A. Estimation of genetic variability, heritability and correlation studies in F2 and F3 populations for yield and quality traits in rice (*Oryza sativa* L.). Life Sciences Leaflets. 2018;95:1-11.
26. Panwar LL, Mathur SS. Variability studies in segregating populations of Rice (*Oryza sativa* L.). Annals Agric Res. 2007;28(1).
27. Nath S, Kole PC. Genetic variability and yield analysis in rice. Electron J Plant Breed. 2021;12(1):253-8.
28. Gautam D, Kandel BP, Adhikari BB. Performance of rice genotypes in western mid hill of Nepal. J Plant Breed Genet. 2018;6(3):111-6.
29. Tripathi N, Verma OP, Singh PK, Rajpoot P. Studies on correlation and path coefficient analysis for yield and its components in rice (*Oryza sativa* L.) under salt affected soil. J Pharmacogn Phytochem. 2018;7(3):1626-9.
30. Ghazy MI, Salem KFM, Sallam A. Utilization of genetic diversity and marker-trait to improve drought tolerance in rice (*Oryza sativa* L.). Mol Biol Rep. 2021;48(1):157-70.
31. Muthuvijayaragavan R, Murugan E. Association analysis of F2 generation in rice (*Oryza sativa* L.) under salinity condition. Electron J Plant Breed. 2020;11(1):283-9.
32. Saha SR, Hassan L, Haque MA, Islam MM, Rasel M. Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces. J Bangladesh Agric Univ. 2019;17(1):26-32.
33. Kiruthikadevi U, Banumathy S, Arunachalam P, Renuka R, Thirumurugan T. Correlation, path analysis and stress indices studies of saltol introgressed lines of rice for salinity tolerance. Electron J Plant Breed. 2020;11(1):230-7.
34. Bhadru D, Reddy DL, Ramesha MS. Correlation and path coefficient analysis of yield and yield contributing traits in rice hybrids and their parental lines. Electron J Plant Breed. 2011;2(1):112-6.
35. Touhiduzzaman SR, Asif M, Mehraj H, Uddin AJ. Correlation and genetic distance on sixteen rice varieties grown under SRI. Adv Plants Agric Res. 2016;3(3):95-9.
36. Shrivastav SP, Verma OP, Singh V, Lal K. Interrelationships among yield and its contributing traits in rice (*Oryza sativa* L.) under sodic soil. Electron J Plant Breed. 2020;11(4):1044-52.
37. Padmaja D, Radhika K, Rao LV, Padma V. Studies on variability, heritability and genetic advance for quantitative characters in rice (*Oryza sativa* L.). Indian J Plant Genet Resour. 2008;21(3):196-8.
38. Parimala K, Devi KR. Estimation of variability and genetic parameters in indica and japonica genotypes of rice (*Oryza sativa* L.). Int J Curr Microbiol Appl Sci. 2019;8(3):1138-42.
39. Wright S. Correlation and causation. J Agric Res. 1921;20:557-85.

40. Kalaiselvan S, Subramanian A, Thirumurugan T, Rajanbabu V. Genetic variability and association studies in F2 population of rice under sodicity. Electron J Plant Breed. 2019;10(2):601-13.
41. 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.). J Pharmacogn Phytochem. 2017;6(4): 1437-9.
42. Sala M, Shanthi P. Variability, heritability and genetic advance studies in F2 population of rice (*Oryza sativa* L.). Int J For Crop Improv. 2016;7(1):57-60.
43. Bhargava K, Shivani D, Pushpavalli RM, Beulah SP, P. Senguttuvel Genetic variability, correlation and path coefficient analysis in segregating population of rice. Electron J Plant Breed. 2021;12(2):549-55.

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