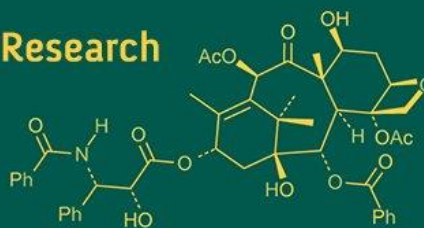
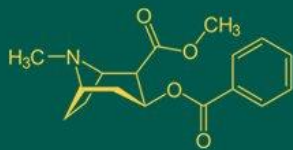


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Margam Bharath Kumar

(1) Professor Jayashankar
Telangana Agricultural
University, Rajendranagar,
Hyderabad, Telangana, India
(2) ICAR-Indian Institute of
Rice Research, Rajendranagar,
Hyderabad, Telangana, India

B Vidyadhar

Professor Jayashankar
Telangana Agricultural
University, Rajendranagar,
Hyderabad, Telangana, India

R Abdul Fiyaz

ICAR-Indian Institute of Rice
Research, Rajendranagar,
Hyderabad, Telangana, India

Ch. Anuradha

Professor Jayashankar
Telangana Agricultural
University, Rajendranagar,
Hyderabad, Telangana, India

D Srinivasa Chary

Professor Jayashankar
Telangana Agricultural
University, Rajendranagar,
Hyderabad, Telangana, India

Corresponding Author:

Margam Bharath Kumar

(1) Professor Jayashankar
Telangana Agricultural
University, Rajendranagar,
Hyderabad, Telangana, India
(2) ICAR-Indian Institute of
Rice Research, Rajendranagar,
Hyderabad, Telangana, India

Studies on PCV, GCV, heritability and genetic advance in F₂ segregating population of cross KJT-5-4-14 x Dokra-Dokri in rice (*Oryza sativa* L.)

Margam BharathKumar, B Vidyadhar, R Abdul Fiyaz, Ch. Anuradha and D Srinivasa Chary

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Abstract

The present experiment was conducted to study the variability, heritability and genetic advance in F₂ segregating population of cross KJT-5-4-14 x Dokra-Dokri, taken up in augmented design at ICAR-IIRR, Hyderabad during the *Kharif*-2022. Analysis of variance revealed the presence of significant differences for all 11 traits studies indicating the presence of genetic variability among the individuals studied. Higher values of PCV and GCV were observed for panicle weight, number of filled grains, number of unfilled grains, total grains per panicle, spikelet fertility and single plant yield possibility for genetic improvement of these traits through selection. PCV values are higher than GCV values indicating environmental effect on these traits further plant height, panicle weight, number of filled grains, number of unfilled grains, total grains per panicle, spikelet fertility, thousand grain weight and single plant yield recorded high heritability (>60%) associated with high genetic advance as % of mean (>20) resulting in minimum environmental influence on the expression and selection for improvement of such characters could be worthwhile. High heritability coupled with moderate genetic advance as % of mean was observed for panicle length propounding non-additive gene action in their inheritance suggesting heterosis breeding could be useful for improving these traits. Overall high PCV and GCV coupled with high heritability and high genetic advance as % of mean was noticed for panicle weight, number of filled grains, number of unfilled grains, total grains per panicle, spikelet fertility and single plant yield suggesting significant amount of variability with predominance of additive type of gene action. Hence, direct phenotypic selection would be effective for improvement of these traits even in early generations.

Keywords: Variability, F₂ segregating population; heritability, additive gene action, genotype, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV)

1. Introduction

Rice (*Oryza sativa* L.) is an important staple food and a primary dietary intake for over half of the world population. Rice is grown on 45.15 million hectares in India, with an annual production of 123.81 million tons with an average productivity of 2742 kilograms of milled rice per hectare (Ministry of Agriculture, 2023-24) [2]. While India contributes 22% of the global rice supply, its burgeoning populace poses a significant threat to food security by 2050, increasing future rice demand (Khush 2005) [2]. Though Novel rice cultivars have produced higher yields over last few decades they have reached a yield threshold because of narrow genetic base becoming a major bottleneck for further yield improvement besides many biotic and abiotic stresses (Fiyaz *et al.*, 2022) [3]. Identification of untapped potential of wild relatives of crop species having high variability and their utilization in hybridization programs through selection of desirable traits that enhance yield is one of the best feasible solutions for achieving high productivity and nutritional security Ahmed *et al.*, 1998 [4].

Existence of Genetic variability among yield attributes is mandatory during selection for the successful yield enhancement through breeding. Presence of high segregation and recombination in segregating populations can be taken as advantage for selection of superior progenies Priyanka *et al.*, 2019 [5]. Presence of low genetic difference between Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) indicate low genetic difference and high environmental effects large differences Tuhina-Khatun *et al.*,

2015^[6]. More precise genetic gain under selection may be obtained from Heritability estimates along with genetic advance Johnson *et al.*, 1955^[7]. Third- and fourth-degree statistics i.e., skewness and kurtosis in segregating generations can help in better understanding of genetics of the traits Savitha *et al.*, 2015^[8]. Hence, the current study was conducted to assess variability, heritability, and genetic progress as a percentage of the mean in F₂ segregating generations, which might be beneficial in selection and future yield enhancement.

2. Materials and Methods

The experiment was carried out at Indian Council of Agricultural Research-Indian Institute of Rice Research (ICAR-IIRR), Rajendranagar, Hyderabad, during *kharif* 2022. The experimental trial was laid out in ICAR-IIRR Rajendranagar Farm using Augmented Randomized Complete Block Design (ARCB) consisting of 92 F₂ segregating population derived from cross KJT-5-4-14 x Dokra-Dokri having high test weight. The experimental area contains a total of four blocks. Prior determining individuals in each block, two checks were initially randomized. Each block was contained 23 F₂'S and 2 checks as reported earlier Bharath *et al.* 2023^[9]. Thirty days old seedlings were transplanted in the main field with a spacing of 20 x 15 cm. All cultural practices and plant protection measures were taken to ensure uniform and healthy crop stand. Eleven traits, namely, Plant Height (cm), Panicle length (PL) (cm), Total Number of Tillers per plant (TNT), No. of Productive Tillers per plant (NPT), Panicle weight (PW), No. of filled grains per panicle (NFG), No. of unfilled grains per panicle (NUFG), Total No. of grains per panicle (TGP), Spikelet fertility (SF) (%), 1000 grain weight (TGW)(gm), and Single plant yield (SPY) (gm) were recorded in every individual F₂ plant.

2.1 Statistical analysis

The augmented ANOVA analysis was carried out in R studio (version 3.5.2) using augmented RCBD package

developed by Aravind *et al.*, 2019^[10] (<https://aravind-j.github.io/augmentedRCBD/>). The genetic variability parameters, namely, Genotypic and Phenotypic Coefficient of Variation were calculated as per formula outlined by Singh and Chaudhary (1977)^[11] and classified as described by Sivasubramanian and Madhava Menon (1973)^[12] while estimates of Heritability was calculated using the formula given by Allard 1960^[13] and genetic advance as percentage of mean was calculated by adopting the formula given by Johnson *et al.*, 1955^[7].

3. Results and Discussion

3.1 Mean performance

The ANOVA analysis revealed that variance due to treatment (ignoring blocks) was highly significant for all the characters except total number of tillers per plant (TNT) and productive tillers (NPT) revealing that F₂ segregating population under study had enough variation showing the inherent genetic differences between the individuals given in Table-1. The Plant height had a range of variance 87.12 cm to 194.63 cm, with an average of 148.83 cm which is in agreement with Gupta *et al.*, 2023^[14]. The average panicle length in the F₂ population studied was noticed to be 27.70 cm, the lowest panicle length was 21.56 cm and the highest was 31.81 cm, similar results were observed by Manojkumar *et al.*, 2022^[15]. Total number of tillers per plant ranged from 7.12 to 16.50 with an average of 11.05 whereas the average number of productive tillers per plant was 9.85, with a range of 6.62 to 15.13. The average spikelet fertility was 73.89 per cent, with the lowest spikelet fertility value being 31.16 per cent and the greatest spikelet fertility value being 97.73 per cent. The average TGW was 26.22 gm, with the lowest and the highest of 13.93 and 39.85 g respectively. Similar variation in F₂ was reported by Khandappagol *et al.*,^[16]. Single plant yield had a mean value of 27.01 g with minimum and maximum of 10.81 and 67.40 g respectively which is in agreement with the reports of Manojkumar *et al.*,^[15].

Table 1: Analysis of variance for 11 characters of F₂ segregating population

Source	Treatment (Ignoring Blocks)	Check	Test	Test vs. Check	Block (eliminating Treatments)	Std Error	Std. Deviation	CV	Residuals
Df	93	1	91	1	3				3
PH	812.74 *	7750.13 **	741.64 *	345.35 *	23.79	2.86	27.68	3.88	33.13
PL	4.87 *	57.78 **	4.35 *	0.15	1.03	0.23	2.19	1.92	0.28
TNT	4.62	28.12 *	3.33	98.46 **	0.12	0.19	1.83	13.92	2.46
NPT	4.05	15.12 *	3.07	82.22 **	0.46	0.20	1.91	12.02	1.46
PW	3.56 **	11.19 **	3.52 **	0.16	0.10	0.19	1.85	4.95	0.07
NFG	4152.84 **	13203.13 **	4046.72 **	4759.36 **	209.12	6.72	65.18	6.73	138.13
NUFG	1197.82 *	60.50	1220.40 *	280.54	88.83	3.60	34.90	13.05	56.17
TGP	3854.95 *	11476.13 **	3783.58 *	2728.88 *	261.12	6.47	62.71	6.04	196.46
SF	254.81 **	152.59 *	256.83 **	173.00 *	12.37	1.66	16.07	3.99	8.78
TGW	27.86 **	1342.92 **	13.68 **	3.39 *	0.31	0.43	4.19	2.00	0.28
SPY	193.60 *	147.06 *	182.09 *	1286.97 **	2.31	1.37	13.32	12.06	11.23

Significant values are as follows: ns- Non-significant, * Significant at 5%, ** Significant at 1%;

PH – Plant height (cm); PL – Panicle length (cm); TNT- Total number of tillers; NPT-Number of productive tillers; PW-Panicle weight (g); NFG-Number of filled grains; NUGF- No. of Unfilled grains; TGP- Total grains per panicle; SF – Spikelet fertility (%); TGW- Thousand grain weight (g) and SPY- Single plant yield (g).

3.2 PCV and GCV

The development of a plant characteristic is greatly influenced by genetic variability and heritability. Prior

knowledge of population variability estimates and the heritable elements of a trait are helpful tools in any breeding programme. It would be more challenging to enhance a

character through selection unless a significant amount of the variation is heritable. Breeding would benefit from knowledge of the character's heritability apart from its phenotypic and genotypic coefficient of variation. In order to compare the variability seen across various traits, the coefficient of variation expressed at the phenotypic and genotypic levels was used.

The results of genotypic (GCV) and phenotypic (PCV) coefficients of variation are presented in Table 2 and Fig. 1 that varied from high to moderate. For all traits higher PCV value was observed compared to GCV value, indicating the effect of environment. Greater difference between PCV and GCV values was recorded in Total number of tillers (TNT) followed by number of productive tillers (NPT) indicating higher influence of environment on these traits, resulting in low heritability values. However, panicle weight, total grains per panicle, spikelet fertility and thousand grain weight recorded minimum variation between GCV and PCV values, indicating lesser influence of environment resulting in high heritability values. Similar results were reported by

Vijayakumari *et al.*^[17] for panicle weight and Gupta *et al.*^[14] for thousand grain weight. Higher values of PCV and GCV were observed for panicle weight, number of filled grains, number of unfilled grains, total grains per panicle, and single plant yield. These results were consistent with Dileep Kumar *et al.*,^[18] Sravani *et al.*,^[19] for above traits; Borah *et al.*,^[20] Manojkumar *et al.*,^[15] for filled grains and total grains per panicle; Kujur *et al.*,^[21] Abdul Fiyaz *et al.*,^[22] for single plant yield suggesting possibility of yield improvement through selection of these traits. Moderate values of PCV and GCV were observed for plant height, number of productive tillers and TGW. Similar results were observed by Sravani *et al.*,^[19] for above three traits; vijayakumari *et al.*,^[17] for spikelet fertility; Abdul Fiyaz *et al.*,^[22] and Faysal *et al.*,^[23] for TGW suggesting greater influence of genetic factors on these traits and relatively less influence of the environment. Low values of PCV and GCV were observed for panicle length similar findings were obtained by Gnaneswari *et al.*,^[24] Yumkhaibam *et al.*^[25]

Table 2: Magnitude of variability, heritability and genetic advance for different characters of F₂ segregating population during *khari*, 2022.

Trait	Mean	Min	Max	GCV (%)	PCV (%)	h^2 (%)	GA (%)	GAM (at 50%)
PH	148.83	87.12	194.63	17.88	18.30	95.53	53.67	36.06
PL	27.70	21.56	31.81	7.28	7.53	93.53	4.02	14.52
TNT	11.05	7.12	16.50	8.45	16.52	26.15	0.98	8.91
NPT	9.85	6.62	15.13	12.90	17.79	52.55	1.90	19.29
PW	5.29	1.37	8.83	35.10	35.45	98.06	3.79	71.70
NFG	173.24	36.63	300.13	36.09	36.72	96.59	126.76	73.17
NUFG	57.79	4.75	163.75	59.04	60.45	95.40	68.75	118.96
TGP	231.03	72.38	358.88	25.92	26.62	94.81	120.31	52.07
SF	73.89	31.16	97.73	21.31	21.69	96.58	31.93	43.21
TGW	26.22	13.93	39.85	13.96	14.10	97.99	7.48	28.51
SPY	27.01	10.81	67.40	48.40	49.97	93.83	26.12	96.73

GCV - Genotypic coefficient of variation; PCV - Phenotypic coefficient of variation; h^2 - Heritability; GA - Genetic advance; GAM- Genetic advance as percent of mean; PH - Plant height (cm); PL - Panicle length (cm); TNT- Total number of tillers; NPT-Number of productive tillers; PW-Panicle weight (g); NFG-Number of filled grains; NUGF- No. of Unfilled grains; TGP- Total grains per panicle; SF - Spikelet fertility (%); TGW- Thousand grain weight (g) and SPY- Single plant yield (g).

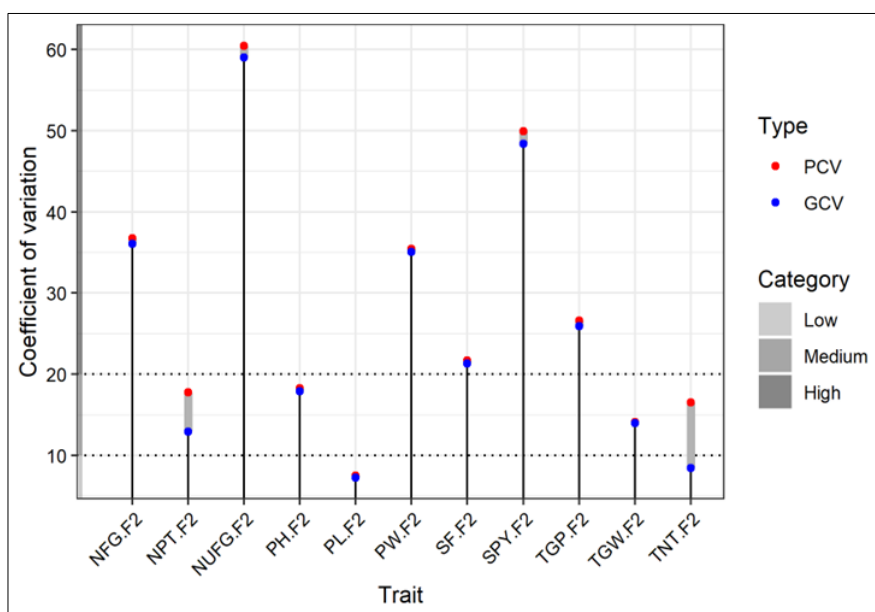


Fig 1: Phenotypic and Genotypic coefficients of variation for different traits in F₂ Population of Rice

3.3 Heritability (h^2) and Genetic Advance (GA)

When heritability along with genetic advance are followed greater degree of accuracy in predicting the genetic gain under selection is possible than heritability estimates alone.

However, it is not necessary that a character showing high heritability will also exhibit high genetic advance Johnson *et al.*^[7].

The traits plant height, panicle weight, number of filled grains, number of unfilled grains, total grains per panicle, spikelet fertility, thousand grain weight and single plant yield recorded high heritability ($>60\%$) associated with high genetic advance as % of mean (>20) presented in Table 2 and Fig. 2,3. Similar results were obtained by Dileep Kumar *et al.*,^[18] Sravani *et al.*,^[19] vijayakumari *et al.*,^[17] for above traits; Manoj kumar *et al.*,^[15] for panicle length, number of filled grains per panicle, total grains per panicle and test weight; Gupta *et al.*,^[14] for plant height, single plant yield; Abdul Fiyaz *et al.*,^[22] for total grains per panicle and test weight resulting in minimum environmental influence on the expression and selection for improvement of such characters could be worthwhile. High heritability coupled with moderate genetic advance as % of mean was observed for panicle length earlier reported by Lakshmi *et al.*,^[26] Gupta *et al.*,^[14] Borah *et al.*,^[20] showing greater role of non-additive gene action in their inheritance

suggesting heterosis breeding for improving these traits. Moderate heritability and genetic advance as % of mean was observed for number of productive tillers per plant which is in conformity with the results of Singh *et al.*,^[27] indicating the presence of both additive and non-additive gene effects and considerable effect of the environment. Overall high GCV and PCV coupled with high heritability and high genetic advance as % of mean was recorded for panicle weight, number of filled grains, number of unfilled grains, total grains per panicle, and single plant yield. Similar findings were reported by Bharath *et al.*, 2023^[9], Shivani *et al.*,^[28] Bagudam *et al.*,^[29] Manojkumar *et al.*,^[15] for filled grains per panicle, total grains per panicle; Bhargava *et al.*,^[30] for total grains per panicle suggesting significant amount of variability with predominance of additive type of gene action. Hence, direct phenotypic selection would be effective for improvement of these traits even in early generations.

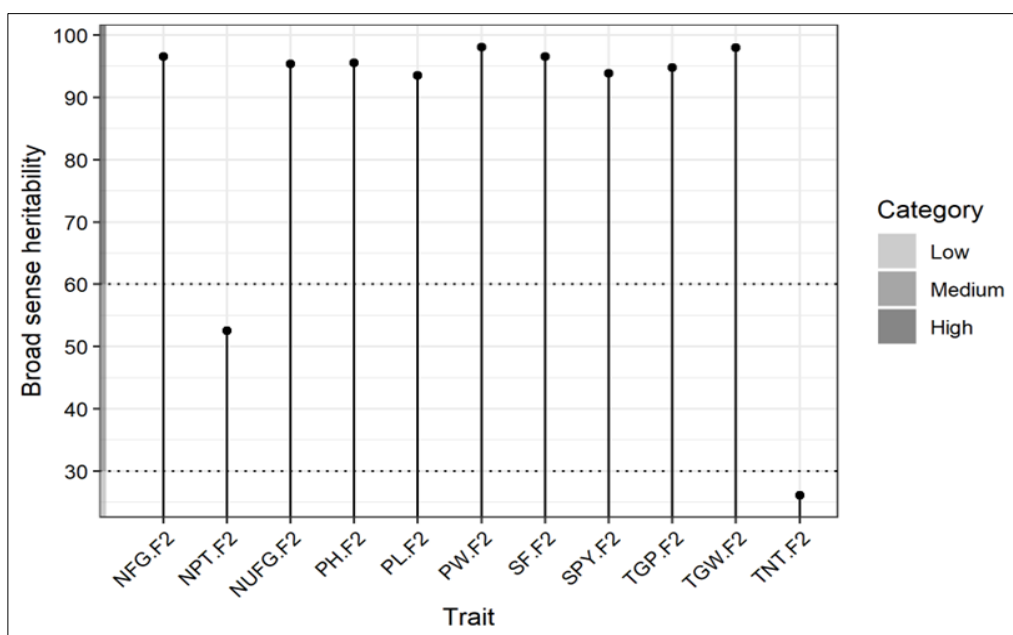


Fig 2: Heritability (h^2) for different traits in F_2 Population of Rice

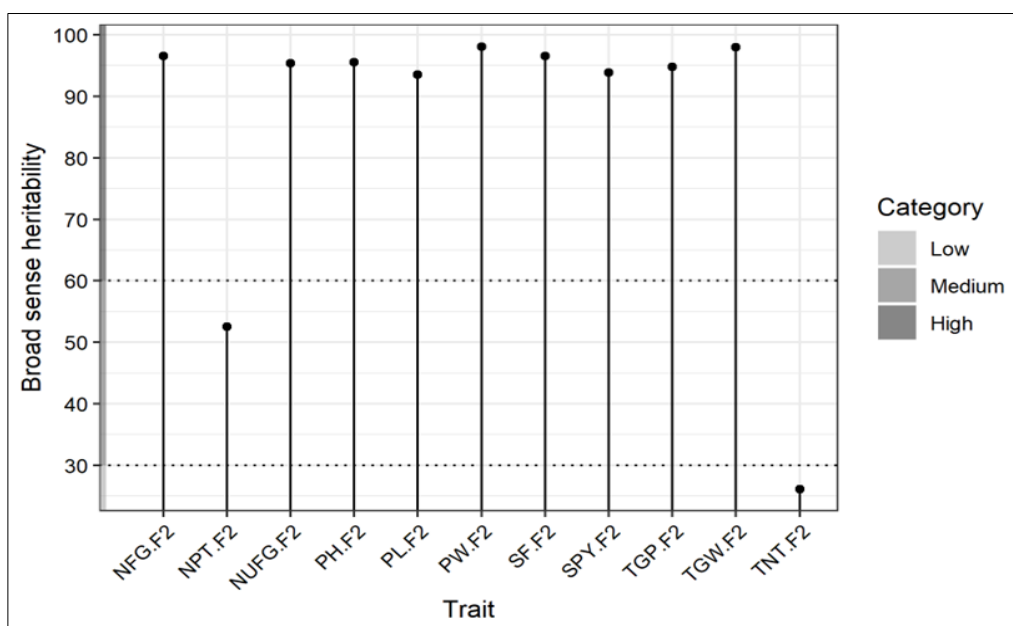


Fig 3: Genetic advance over mean for different traits in F_2 Population of Rice

4. Conclusion

Overall, the study found that the F₂ segregating population had enough diversity, which could be efficiently managed using proper breeding procedures and programs to generate superior varieties. Most characteristics had high GCV, PCV, heritability, and genetic progress, showing that additive gene action predominated and that direct phenotypic selection may be done even in early generations.

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6. Competing Interests

Authors have declared that no competing interests exist.

7. References

- Ministry of Agriculture and Farmers Welfare. Agricultural Statistics at a Glance: Rice-Major states-Area, production and yield along with coverage under irrigation. Department of Agriculture Cooperation and Farmers Welfare, Directorate of Economics and Statistics, Government of India; c2024.
- Khush GS. What it will take to feed 5.0 billion rice consumers in 2030. *Plant Molecular Biology*. 2005;59(1):1-6.
- Fiyaz RA, Shivani D, Chaithanya K, Mounika K, Chiranjeevi M, Laha GS, Sundaram RM. Genetic improvement of rice for bacterial blight resistance: Present status and future prospects. *Rice Science*. 2022;29(2):118-132.
- Ahmed MI, Siddiq EA. Rice. In: Banga SS, Banga SK, editors. *Hybrid cultivar development*. New Delhi: Narosa Publishing House; c1998. p. 221-256.
- Priyanka A, Gnanamalar R, Banumathy S, Senthil N, Hemalatha G. Genetic variability and frequency distribution studies in F₂ segregating generation of rice. *Electronic Journal of Plant Breeding*. 2019;10(3):988-994.
- Tuhina-Khatun M, Hanafi MM, Yusop RM, Wong M, Salleh FM, Ferdous J. Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. *BioMed Research International*; c2015.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability of soybeans. *Agronomy Journal*. 1955;47:314-318.
- Savitha P, Usha Kumara R. Genetic variability studies in F₂ and F₃ segregating generations for yield and its components in rice (*Oryza sativa* L.). *Indian Journal of Science and Technology*. 2015;8(17).
- Bharath M, Vidyadhar B, Anuradha C, Chary K, Fiyaz RA. Genetic variability, heritability and genetic advance in F₂ segregating population of cross RNR-15048 x Dokra-Dokri in rice (*Oryza sativa* L.). *International Journal of Environment and Climate Change*. 2023;13(12):965-972.
- Aravind J, Mukesh Sankar S, Wankhede DP, Kaur V. Augmented RCBD analysis of augmented randomised complete block designs. R package version 0.1.7. 2023.
- Singh RK, Chaudhary BD. *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani Publishers; c1977. p. 215-218.
- Sivasubramanian S, Madhava Menon P. Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*. 1973;60(9-13):1093-1096.
- Allard RW. *Principles of Plant Breeding*. 2nd ed. New York: John Wiley and Sons Inc; c1960. p. 485.
- Gupta P, Parikh M, Tandekar K. Genetic variability assessment in accessions of rice (*Oryza sativa* L.). 2023;12(3):4721-4725.
- Manojkumar D, Srinivas T, Rao LS, Suneetha Y, Sundaram RM, Kumari VP. Study of genetic variability and trait associations in F₂ population of YH3 x AKDRMS 21-54 intra-specific cross of rice. *The Pharma Innovation Journal*. 2022;11(9):1735-1742.
- Khandappagol M, Rajanna MP, Savita SK. Variability and frequency distribution studies in F₂ population of two crosses involving traditional varieties of rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*. 2019;8(1):1630-1634.
- Vijayakumari M, Pillai MA, Senguttuvel P, Saravanan S, Sheela J. Assessment of genetic variability and correlation studies in direct seeded aerobic rice ecosystem. 2022;11(8):398-403.
- Dileep Kumar GD, Abdul Fiyaz R, Viswanatha KP, Subbarao LV, Chimote VP, Raghuwanshi KS, Amolic VL, Chaithanya K, Shivani D, Bharat Kumar, Rapaka Percy VS, Sathwik B, Sundaram RM. Assessment of genetic variability parameters among the F₂ population of a cross between Jaya × isogenic line of MTU1010 for yield and its component traits in rice. *Journal of Rice Research*. 2022;15(2):118-122.
- Sravani B, Anuradha C, Sundaram RM, Supriya K, Gandhi N, Fiyaz RA. Genetic variability, heritability and genetic advance in 3K rice (*Oryza sativa* L.) genotypes. *International Journal of Environment and Climate Change*. 2022;12(11):2259-2265.
- Borah N, Pratim P, Behera BV, Sarma RN. Genetic variability, heritability and genetic advance of aromatic rice for yield and its components. *Biol Forum-Int J*. 2023;15(5):1516-1522.
- Kujur VK, Abhinav Sao MK, Tiwari A. Genetic variability, heritability and association analyses for yield and related characters in rice germplasm (*Oryza sativa* L.). *The Pharma Innovation Journal*. 2023;12(4):2236-2240.
- Abdul Fiyaz R, Ramya KT, Chikkalingaiah AB, Gireesh C, RS K. Genetic variability, correlation and path coefficient analysis studies in rice (*Oryza sativa* L.) under alkaline soil condition. *Electronic Journal of Plant Breeding*. 2011;2(4):531-537.
- Faysal ASM, Ali L, Azam MG, Sarker U, Ercisli S, Golokhvast KS, Marc RA. Genetic variability, character association, and path coefficient analysis in transplant Aman rice genotypes. *Plants*. 2022;11(21):2952.
- Gnaneswari VM, Krishnan V, Anandhan T, Vengadessan V, Nadaradja S, Tamilzharasi M. Assessment of genetic variability and diversity analysis in medium duration rice accessions. *Electronic Journal of Plant Breeding*. 2023;14(1):329-335.
- Yumkhaibam RS, Ram M, Mehendi S, Prakash S. Assessment of genetic variability for yield and yield

- contributing traits in rice (*Oryza sativa* L.). 2023;12(6):1816-1820.
26. Lakshmi MS, Suneetha Y, Srinivas T. Genetic variability, correlation and path analysis for grain yield and yield components in rice genotypes. Journal of Pharmacognosy and Phytochemistry. 2021;10(1):1369-1372.
27. Singh SK, Singh CM, Lal GM. Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). Research in Plant Biology. 2011;1(4):73-76.
28. Shivani D, Cheralu C, Neeraja CN, Shankar VG. Genetic variability studies in Swarna x Type 3 RIL population of rice (*Oryza sativa* L.). International Journal of Pure and Applied Bioscience. 2018;6(2):384-392.
29. Bagudam R, Eswari KB, Badri J, Rao PR. Correlation and path analysis for yield and its component traits in NPT core set of rice (*Oryza sativa* L.). International Journal of Current Microbiology and Applied Sciences. 2018;7(9):97-108.
30. Bhargava K, Shivani D, Pushpavalli SNCVL, Sundaram RM, Beulah P, Senguttuvel P. Genetic variability, correlation and path coefficient analysis in segregating population of rice. Electronic Journal of Plant Breeding. 2021;12(2):549-555.