



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(4): 2231-2235
© 2023 TPI

www.thepharmajournal.com

Received: 20-01-2023

Accepted: 23-02-2023

Ashish Kumar Banjare
Department of Genetics and
Plant Breeding, CoA, IGKV,
Raipur, Chhattisgarh, India

Ravindra Kumar Verma
Department of Genetics and
Plant Breeding, CoA, IGKV,
Raipur, Chhattisgarh, India

Rajeev Shrivastava,
Department of Genetics and
Plant Breeding, CoA, IGKV,
Raipur, Chhattisgarh, India

SB Verulker
Department of Genetics and
Plant Breeding, CoA, IGKV,
Raipur, Chhattisgarh, India

Ravi R Saxena
Department of Genetics and
Plant Breeding, CoA, IGKV,
Raipur, Chhattisgarh, India

Vipin Kumar Pandey
Department of Genetics and
Plant Breeding, CoA, IGKV,
Raipur, Chhattisgarh, India

Vishal Kumar Gupta
Department of Genetics and
Plant Breeding, CoA, IGKV,
Raipur, Chhattisgarh, India

Namita Singh
Department of Genetics and
Plant Breeding, CoA, IGKV,
Raipur, Chhattisgarh, India

Corresponding Author:
Ashish Kumar Banjare
Department of Genetics and
Plant Breeding, CoA, IGKV,
Raipur, Chhattisgarh, India

Study of genetic variability in some elite rice (*Oryza sativa* L.) germplasm accessions

Ashish Kumar Banjare, Ravindra Kumar Verma, Rajeev Shrivastava, SB Verulker, Ravi R Saxena, Vipin Kumar Pandey, Vishal Kumar Gupta and Namita Singh

Abstract

The experiment was conducted at research cum industrial farm Department of Genetics and Plant Breeding, College of Agriculture, Raipur during, *Kharif* season 2018 in Augmented Randomized Complete Block Design in three replication. The experimental materials, consisting of 120 rice germplasm with 5 check varieties. The objective of this work was to assess the magnitude of variability among genetic parameters. The genetic variability analysis in Rice for fourteen characters under study. The present study revealed sufficient genetic variability for various qualitative and quantitative traits. Thus, the various analysis carried out had shown wide variability among the rice germplasm for various traits. The wide range of variability observed for the traits evaluated may be attributed to the diverse genetic background of the accessions studied and these could be used for selection of the germplasm for development of new varieties. The results reported in present investigation indicating that the low level of environmental factors interruption in either expression of various traits or low genotypes sensitivity to environmental conditions and traits were highly governed by role of genetic control because very low difference between PCV and GCV. The traits generally resulted from the interaction between environmental and genetic components where the high heritability coupled with moderate genetic advance as percent of mean was recorded. Furthermore, it was found that the environmental factors do not play noticeable influences in the phenotypic expression. Thus, indicating selection based on these characters would be rewarding for yield improvement in Rice.

Keywords: *Oryza sativa* L., genetic variability, heritability, GCV, PCV

Introduction

Rice (*Oryza sativa* L.) is a self-pollinated cereal crop belonging to the family *Gramineae* and having chromosome number $2n=24$. The genus *Oryza* is known to consist of two cultivated species i.e., Asian rice (*O. sativa*, $2n=24$) and African rice (*O. glaberrima*, $2n=24$) and 22 wild species. The genus *Oryza* is originated in the Gondwanaland continents (Chang, 1976). India ranks first in rice area and second in rice production, after China.

Globally, total area coverage under *kharif* rice during 2018-19 is estimated at 437.9 lakh hectares with production of rice during 2018-19 are estimated at a record 116 million tonnes. Production of rice has increased by 3.66 million tonnes as compare of during 2017-18. (Anonymous, 2019-20).

Chhattisgarh is eminent by the name "Rice Bowl of India" because maximum area is covered under rice cultivation. During 2021-22 totals estimated area of rice around 3.89 million hectares than the production of 7.25 million metric tonnes and productivity 3438 kg / hectares (Anonymous, 2021-22) [2, 3].

Variability refers to the presence of differences among the individuals of plant population. The estimates of variability help the plant breeder in selection of elite genotypes from diverse genetic population. Selection is also effective there is significant amount of genetic variability among the individuals in the population. (Singh and Narayanam, 2007) [17]. Selection for various yield contributing characters, which are naturally polygenic inherited and majorly influenced by environment. So due to less impression of direct selection for yield, more efforts should be over indirect selection for yield components. Genetic traits such as genotypic coefficient of variability, heritability and genetic advance provide precise estimate of genetic variation of quantitative traits (Yadav and Dalal, 1972, Khorgade and Pillai, 1994., Khan *et al.*, 2000) [21, 14, 13]. The progress in breeding for such characters is determined by the magnitude and nature of interactions between their genotypic and phenotypic variability under varying

conditions of soil and climate. Hence, partitioning the overall variability into its heritable and non-heritable components with the help of genetic parameters such as genetic coefficient of variation, heritability and genetic advance constitutes an important step in plant breeding programme.

Material and Methods

An experiment comprised of 120 rice germplasm accessions with 5 check varieties (Table-1) was conducted at research cum industrial farm Department of Genetics and Plant Breeding, College of Agriculture, Raipur during, *Kharif* season 2018 in Augmented Randomized Complete Block Design in three replication recommended package of practices were applied to raise the normal crop. The experimental materials, consisting of 120 rice germplasm with 5 check varieties. Observations were recorded on five randomly selected plants from each genotype, on 14 characters *viz.* Flag leaf length, flag leaf width, days to 50% flowering, plant height, number of total tillers per plant, number of effective tillers per plant, panicle length, number of grains per panicle, number of filled grains per panicle, number of unfilled grains per panicle, spikelet sterility percentage, spikelet fertility percentage, 100 grain weight and grain yield per plant. The mean data were utilized to calculate variability parameters *viz.* range, genotypic and phenotypic coefficient of variation. The statistical analysis for genetic variability was done as per the procedure of Cochran and Cox (1957)^[7], Heritability in broad sense by Hanson *et al.*, (1956) and genetic advance by Johnson *et al.*, (1955)^[11] and calculation of mean values for all the qualitative traits was estimated by using software R Studio, R package augmented RCBD developed by Arvind *et al.*, (2021)^[4].

Results and Discussion

Analysis of variance

Analysis of variance (ANOVA) showed presence of high significant variation among the germplasm accessions for all the traits with respect to seed yield and its components in Rice. This is an indication of existence of sufficient variability for the traits (Table-3).

Genetic variability parameters

The experimental materials, consisting of 120 rice germplasm but the investigation was carried out on a set of 116 rice germplasm since four rice germplasm accessions were not germinated. In augmented design the check varieties taken were Poornima, Mahamaya, Swarna, Indira Sugandhit Dhan-1 and Indira Aerobic-1. The 116 rice germplasm with five check varieties were tested and characterized for 14 different quantitative traits. Analysis of variance (ANOVA) showed presence of high significant variation among the germplasm accessions for all the traits. ANOVA for all the traits revealed highly significant differences and variability among the checks and germplasm. Furthermore the germplasm and checks interaction also revealed highly significant differences excluding normalized difference panicle length and seed yield/plant for check varieties. In case of adjusted blocks the quantitative traits such as filled grains/panicle, plant height, spikelet fertility, spikelet sterility and unfilled grains/panicle reported the insignificant difference upon the analysis (Table 3).

Coefficient of variation

In the present investigation the magnitude of variability among the different characters of rice germplasm were estimated with open source software program R Studio. During investigation of magnitude of variability, the error variance components, environment (E), error mean square for genotype (G) and G x E were used. The various variability parameters were studied *viz.* phenotypic variance (PV), genetic variance (GV) phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2), genetic advance (GA), genetic advance as percentage of mean (GAM) for different characters have been presented. (Table 2)

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV)

In present investigation it was found that the genotypic coefficient of variation (GVC) is slightly lower than the phenotypic coefficient of variation (PVC) for the various traits studied in experiment (Table 2). Indicating that the low level of environmental factors interruption in either expression of various traits or low genotypes sensitivity to environmental conditions and traits were highly governed by role of genetic control because very low difference between PCV and GCV. Similar findings were reported by (Karim *et al.*, 2007, Sravan *et al.*, 2012)^[12, 18]. Furthermore, it was found that the environmental factors do not play noticeable influences in the phenotypic expression as previous works suggesting the same (Ubarhande *et al.*, 2009, Pandey and Anurag, 2010, Seyoum *et al.*, 2012)^[20, 15, 16].

Genotypic coefficient of variation (GCV)

The highest GCV of 76.19% was observed for unfilled grains per panicle (UG) followed by 46.57%, 36.79%, 35.92%, 35.81%, 33.13%, 26.83% and 26.09% GCV found in spikelet sterility% (SS), seed yield per plant (SY), number of grains per panicle (NG), filled grains per panicle (FG), flag leaf width (FLW), number of effective tillers per plant (NE) and numbers of tillers per plant (NT) respectively. However lowest GCV was recorded from flag leaf length (FLL- 5.75%) and days to 50% flowering (D50- 9.14%). (Table 2) (Fig.1).

Phenotypic coefficient of variation (PCV)

highest phenotypic coefficient of variation (PCV) was observed in unfilled grains per panicle (UG- 77.12%) followed by 48.03%, 37.38%, 36.12%, 36.04%, 33.58%, 27.20%, 26.41% and 20.23% for spikelet sterility% (SS), seed yield per plant (SY), number of grains per panicle (NG), filled grains per panicle (FG), flag leaf width (FLW), number of effective tillers per plant (NE), numbers of tillers per plant (NT) and 100 seed weight (100S) respectively. The result showed that lowest PCV of 9.2% and 7.3% was observed in days to 50% flowering (D50) and flag leaf length (FLL) respectively which is similar to result found in case of GCV (Table 2) (Fig. 1).

Heritability (h^2)

The heritability (h^2) estimate varied from 62.07% to 98.94% where highest heritability of 98.94% was recorded from number of grains per panicle (NG) and lowest heritability of 62.07% was observed in flag leaf length (FLL). Similarly, high heritability also found in other traits such as days to 50% flowering (D50- 98.63%), plant height (PH- 96.42%), filled

grains per panicle (FG- 98.73%), unfilled grains per panicle (UG- 97.61%), spikelet fertility% (SF- 94.07%), spikelet sterility% (SS- 94.03%), flag leaf width (FLW- 97.37%), numbers of tillers per plant (NT- 97.61%), number of effective tillers per plant (NE- 97.24%), panicle length (PL- 71.06%), 100 seed weight (100S- 89.04%) and seed yield per plant (SY- 96.88%). In last decades the high degree of heritability for various traits such as plant height (PH), filled grains per panicle (FG), unfilled grains per panicle (UG), number of grains per panicle (NG), spikelet fertility (SF), panicle length (PL), 100 seed weight (100S) and seed yield per plant (SY). Similar findings were reported by (Karim *et al.*, 2007, Seyoum *et al.*, 2012 and Sravan *et al.*, 2012) [12, 16, 18]. (Table 2) (Fig. 2).

Genetic advance as percentage of mean (GAM)

The genetic advance as percentage of mean (GAM) showed that the highest of 155.3 was observed in unfilled grains per panicle (UG) followed by 93.16 in spikelet sterility% (SS), 74.71 in seed yield per plant (SY), 73.72 in number of grains

per panicle (NG), 73.40 in filled grains per panicle (FG), 67.45 in flag leaf width (FLW), 54.57 in number of effective tillers per plant (NE), 53.17 in numbers of tillers per plant (NT), 37.17 in 100 seed weight (100S), 31.53 in plant height (PH) and 21.47 in spikelet fertility% (SF). GAM was found very low in flag leaf length (FLL-9.34) whereas, medium GAM present in days to 50% flowering (D50-18.73) and panicle length (PL-19.23) (Table 2) (Fig. 3).

In the present study, filled grains per panicle, unfilled grains per panicle, number of grains per panicle, spikelet fertility, spikelet sterility, flag leaf width, numbers of tillers per plant, number of effective tillers per plant, 100 seed weight, plant height and seed yield per plant showed higher heritability combined with high genetic advance as percent of mean (GAM) (Table 2). This findings suggesting that the expression of traits due to additive gene action therefore the selection can be successful in breeding programme. Similar findings were reported by (Suman *et al.*, 2005, Bekele *et al.*, 2013, Hossain and Rahman, 2015) [19, 5, 10].

Table 1: List of germplasm accessions with checks used for quantitative and qualitative characters study.

1	CGR10101	26	CGR14455	51	CGR15550	76	CGR13956	101	CGR1624
2	CGR10135	27	CGR14459	52	CGR15614	77	CGR14454	102	CGR1642
3	CGR10140	28	CGR14507	53	CGR15735	78	CGR14633	103	CGR1748
4	CGR10324	29	CGR14516	54	CGR15939	79	CGR14643	104	CGR1795
5	CGR10334	30	CGR14540	55	CGR15999	80	CGR14893	105	CGR1815
6	CGR10405	31	CGR14563	56	CGR16026	81	CGR15069	106	CGR1871
7	CGR10705	32	CGR14565	57	CGR16236	82	CGR15383	107	CGR1874
8	CGR10855	33	CGR14583	58	CGR16269	83	CGR3	108	CGR1899
9	CGR11032	34	CGR14589	59	CGR16336	84	CGR482	109	CGR1909
10	CGR11357	35	CGR14617	60	CGR16877	85	CGR551	110	CGR1927
11	CGR11471	36	CGR14824	61	CGR16985	86	CGR576	111	CGR1928
12	CGR11561	37	CGR14959	62	CGR17028	87	CGR731	112	CGR1943
13	CGR12036	38	CGR14961	63	CGR17112	88	CGR754	113	CGR1944
14	CGR12153	39	CGR14982	64	CGR17358	89	CGR760	114	CGR1963
15	CGR13015	40	CGR14998	65	CGR17448	90	CGR877	115	CGR20096
16	CGR13104	41	CGR14999	66	CGR10291	91	CGR896	116	CGR20097
17	CGR13105	42	CGR15000	67	CGR10330	92	CGR898	117	CGR20098
18	CGR13178	43	CGR15024	68	CGR11167	93	CGR941	118	CGR20102
19	CGR14173	44	CGR15039	69	CGR11992	94	CGR942	119	CGR20104
20	CGR14178	45	CGR15041	70	CGR12031	95	CGR948	120	CGR20105
21	CGR14181	46	CGR15146	71	CGR12526	96	CGR978	CH	Poornima
22	CGR14202	47	CGR15256	72	CGR12756	97	CGR1157	CH	Mahamaya
23	CGR14242	48	CGR15452	73	CGR13098	98	CGR1174	CH	Swarna
24	CGR14411	49	CGR15484	74	CGR13124	99	CGR1180	CH	Indira Sugandhit Dhan -1
25	CGR14432	50	CGR15514	75	CGR13151	100	CGR1588	CH	Indira Aerobic - 1

Table 2: Estimation of means, variance components, phenotypic coefficient of variations (PCV), genotypic coefficient of variations (GCV), broad sense heritability (hBS), genetic advance (GA) and genetic advance as percent of mean (GAM) of various traits of rice germplasm

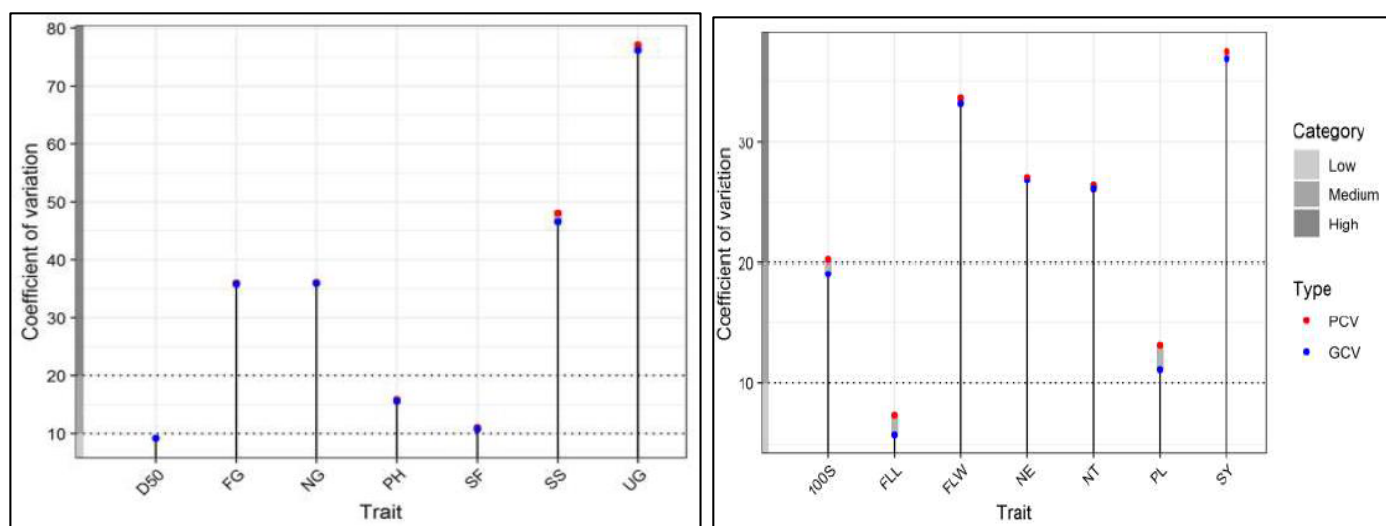
Trait	Mean	PV	GV	EV	GCV	GCV. category	PCV	PCV. category	ECV	hBS	hBS. category	GA	GAM	GAM. category
D50	97.77	80.98	79.88	1.11	9.14	Low	9.2	Low	1.08	98.63	High	18.31	18.73	Medium
PH	134.69	455.85	439.54	16.31	15.57	Medium	15.85	Medium	3	96.42	High	42.47	31.53	High
FG	135.97	2401.07	2370.51	30.56	35.81	High	36.04	High	4.07	98.73	High	99.8	73.4	High
UG	32.21	617.12	602.39	14.73	76.19	High	77.12	High	11.91	97.61	High	50.03	155.3	High
NG	168.18	3689.23	3650.15	39.08	35.92	High	36.12	High	3.72	98.94	High	123.98	73.72	High
SF	81.28	80.81	76.02	4.79	10.73	Medium	11.06	Medium	2.69	94.07	High	17.45	21.47	High
SS	18.72	80.81	75.99	4.83	46.57	High	48.03	High	11.74	94.03	High	17.44	93.16	High

D50 = days to 50% flowering, PH = plant height, FG = filled grains per panicle, UG = unfilled grains per panicle, NG = number of grains per panicle, SF = spikelet fertility and SS = spikelet sterility

Table 3: Analysis of variance for the tested quantitative traits

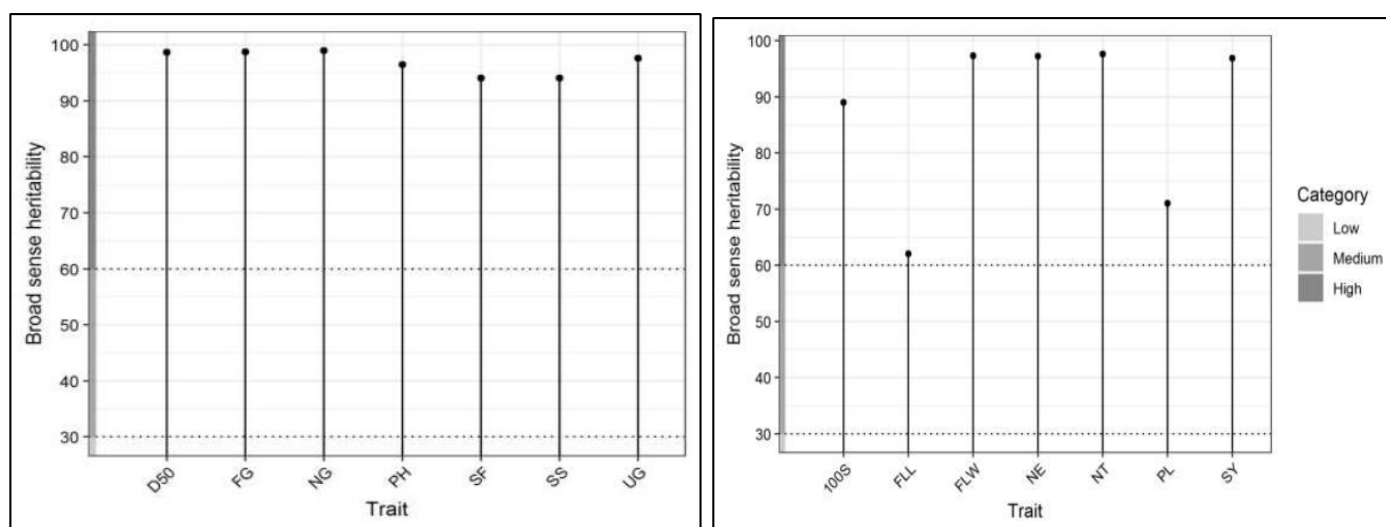
Source	Df	Days to 50% flowering (days)	Filled grains/panicle	Number of grains/panicle	Plant height (cm)	Spikelet fertility (%)	Spikelet sterility (%)	Unfilled grains/panicle
Germplasm (G) with Check (C)	120	90.44 **	2383.46 **	3596.06 **	752.77 **	86.68 **	86.69 **	618.82 **
Check (C)	4	371.17 **	2370.59 **	1672.54 **	742.72 **	160.47 **	161.5 **	333.74 **
Germplasm (G) vs. Check (C)	1	54.95 **	409.41 **	575.18 **	3438.72 **	465.96 **	463.82 **	1955.14 **
Germplasm (G)	115	80.98 **	2401.07 **	3689.23 **	455.85 **	80.81 **	80.81 **	617.12 **
Adjusted Block (B)	3	37.65 **	100.17 ns	234.46 **	17.26 ns	10.21 ns	10.18 ns	43.7 ns
Residuals	12	1.11	30.56	39.08	16.31	4.79	4.83	14.73
Source	Df	100 seed weight (g)	Flag leaf length	Flag leaf width	No. of effective tillers/plant	Numbers of tillers/plant	Panicle length (cm)	Seed yield/plant (g/plant)
Germplasm (G) with Check (C)	120	0.29 **	21.73 **	0.37 **	4.74 **	5.11 **	10.04 **	63.58 **
Check (C)	4	1.37 **	170.56 **	0.09 **	2.74 **	2.74 **	20.98 **	70.07 **
Germplasm (G) vs. Check (C)	1	0.21 *	977.4 **	2.11 **	13.76 **	12.17 **	7.29 ns	0.38 ns
Germplasm (G)	115	0.25 **	8.24 *	0.36 **	4.73 **	5.13 **	9.69 **	63.9 **
Adjusted Block (B)	3	0.32 **	52.23 **	0.05 *	0.88 **	1.22 **	17.7 **	25.25 **
Residuals	12	0.03	3.13	0.01	0.13	0.12	2.8	1.99

ns, non-significant, * significant at $p \leq 0.05$, ** significant at $p \leq 0.01$



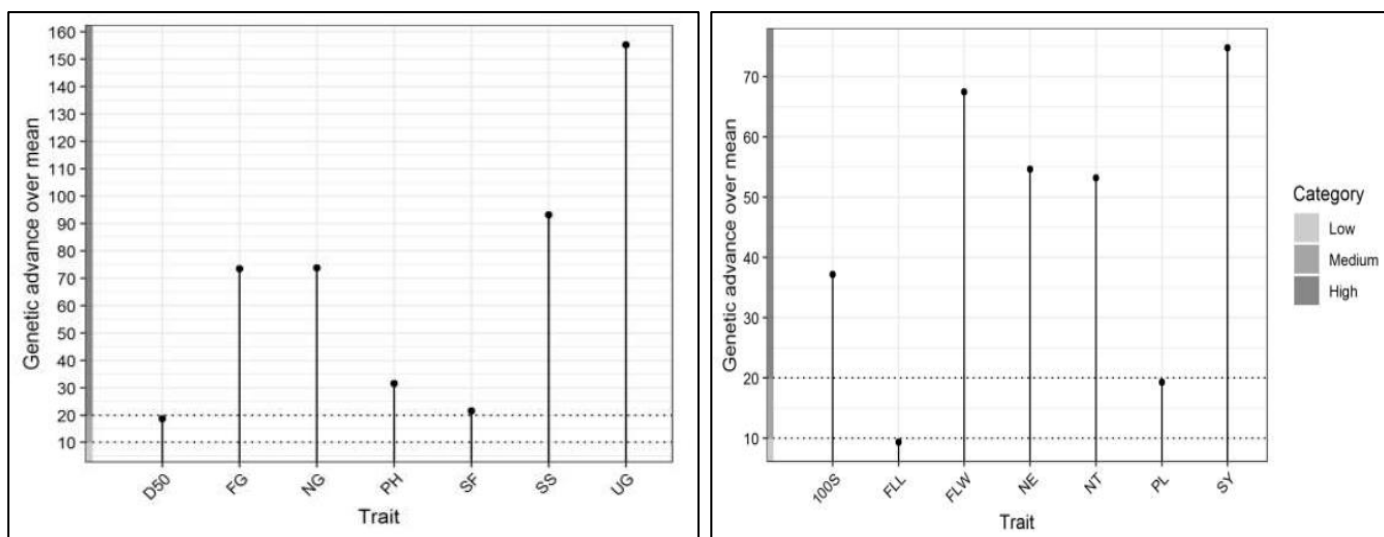
D50 = days to 50% flowering, PH = plant height, FG = filled grains per panicle, UG = unfilled grains per panicle, NG = number of grains per panicle, SF = spikelet fertility, SS = spikelet sterility, FLL = flag leaf length, FLW = flag leaf width, NT = numbers of tillers per plant, NE = number of effective tillers per plant, PL = panicle length, 100S = 100 seed weight and SY = seed yield per plant

Fig 1: Phenotypic coefficient of variations (PCV) and genotypic coefficient of variations (GCV) of various traits of rice germplasm



D50 = days to 50% flowering, PH = plant height, FG = filled grains per panicle, UG = unfilled grains per panicle, NG = number of grains per panicle, SF = spikelet fertility, SS = spikelet sterility, FLL = flag leaf length, FLW = flag leaf width, NT = numbers of tillers per plant, NE = number of effective tillers per plant, PL = panicle length, 100S = 100 seed weight and SY = seed yield per plant

Fig 2: Broad sense heritability (hBS) of various traits of rice germplasm



D50 = days to 50% flowering, PH = plant height, FG = filled grains per panicle, UG = unfilled grains per panicle, NG = number of grains per panicle, SF = spikelet fertility, SS = spikelet sterility, FLL = flag leaf length, FLW = flag leaf width, NT = numbers of tillers per plant, NE = number of effective tillers per plant, PL = panicle length, 100S = 100 seed weight and SY = seed yield per plant

Fig 3: Genetic advance as percent of mean (GAM) of various traits of rice germplasm accessions

Acknowledgements

The first authors wish to acknowledge Department of Genetics & Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.), for providing education and research programme. I would like to give my sincerest thanks to my major advisor Dr. Rajeev Shrivastava and my co-advisor Dr. Ravindra Kumar Verma, member Dr. S. B. Verulkar, and Dr. R. R. Saxena sir and non-teaching staff. Now I sincerely thank each and every faculty members of Department of Genetics and Plant Breeding, IGKV, Raipur (C.G.), for teaching and supporting.

References

- Anonymous (a). Annual Report. Department of Agriculture and Farmers Welfare, Ministry of Agriculture, Government of India, New Delhi; c2020. p. 4.
- Anonymous (b). Annual Report. Department of Agriculture and Farmers Welfare, Ministry of Agriculture, Government of India, New Delhi; c2022. p. 4.
- Anonymous (c). Krishi Digidarshika. Directorate of extension services. IGKV, Raipur (C.G.); c2022.
- Aravind J, Mukesh Sankar S, Wankhede DP, Kaur V. Augmented RCBD: Analysis of Augmented Randomised Complete Block Designs. R package version 0.1.4.9000; c2021. <https://aravindj.github.io/augmentedRCBD/>
<https://cran.r-project.org/package=augmentedRCBD>.
- Bekele BD, Rakhi SG, Naveen Kundur P, Shashidhar H. Estimation of genetic variability and correlation studies for grain zinc concentrations and yield related traits in selected rice (*Oryza sativa* L.) genotypes. Asian J of Experimental Bio. Sci., 2013;4:345-351.
- Chang TT. The origin, evolution, cultivation, dissemination and diversification of Asian and African rice. Euphytica. c1976;25:435-441.
- Chocharan WG, Cox GM. Experimental designs. Asia Publication House, Bombay, London, New York; c1957. p. 148-181.
- De Candolle A. Origin of cultivated plants. London; c1886. p.468.
- Hanson WD, Robinson HF, Comstock RE. Biometrical studies of yield in segregating population Korean Lespandez. Agron. J. 1956;48:268-272.
- Hossain S, Haque M, Rahman J. Genetic variability, correlation and path coefficient analysis of morphological traits in some extinct local Aman rice (*Oryza sativa* L.). Rice Res. Open Access; c2015.
- Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlation in soybean and their implications in selection. J of Agron; c1955. p. 477- 483.
- Karim D, Sarkar U, Siddique M, Miah MK, Hasnat M. Variability and genetic parameter analysis in aromatic rice. Int. J Sus. Crop Prod., 2007;2:15-18.
- Khan NI, Din F, Khan MN, Shahid MTH. Correlation and path coefficient analysis in Linseed. J of Agril. Res., 2000;36:83-87.
- Khorgade PW, Pillai B. Genetic variability studies in linseed. Agril. Sci. of Digest. 1994;14(1):54-56.
- Pandey P, Anurag PJ. Estimation of genetic parameters in indigenous rice. Adva. in Agri. & Bot. 2010;2:79-84.
- Seyoum M, Alamerew S, Alamerew, Bante K. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). J of Plant Sci. 2012;7(1):13-22.
- Singh P, Narayanam SS. Biometrical Techniques in Plant Breeding, Kalyani Pub; c2007. p. 56-57.
- Sravan T, Rangare N, Suresh B, Kumar S. Genetic variability and character association in rainfed upland rice (*Oryza sativa* L.). J of Rice Res., 2012;5:24-29.
- Suman A, Shankar V, Rao L, Sreedhar N. Variability, heritability and genetic advance in rice (*Oryza sativa* L.). Crop Research-Hisar. 2005;30:211.
- Ubarhande V, Prasad R, Singh R, Singh S, Agrawal R. Variability and diversity studies in rain-fed rice (*Oryza sativa* L.). Ind. J Plant Genet. Resour., 2009;22(2):134-137.
- Yadav TP, Dalal JL. Genetic variability and correlation studies in Linseed (*Linum usitatissimum* L.). Haryana Agril. Uni. J. Res. 1972;9:182-184.