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Studies on genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.)

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Abstract

The analysis of genetic variability was done for forty-six rice genotypes in the student instructional farm during Kharif 2023-24 at Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya. The experiment was conducted in a randomized block design (RBD) with 3 replications. In general, phenotypic coefficients of variation (PCV) estimates were higher than genotypic coefficients of variation (GCV) estimates for all the studied characters in all genotypes displaying the influence of environment effect on the studied characters. The higher estimates of PCV and GCV were observed for productive tillers per plant. High value of PCV was also recorded for 1000-grain weight. High value of broad sense heritability were recorded for days to 50 % flowering (95.34), number of fertile spikelets per panicle (93.81), days to maturity (93.11), number of spikelets per panicle (87.79), flag leaf area (83.09), plant height (83.02). High heritability coupled with high genetic advance was observed for number of fertile spikelets per panicle, number of spikelets per panicle, flag leaf area and days to 50% flowering, indicate the lesser influence of environment in expression of these traits and prevalence of additive gene action in their inheritance hence, amenable of simple selection.

Keywords: PCV, GCV, heritability, genetic advance

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Introduction:

Rice (*Oryza sativa* L.) is the most important staple and cereal component that sustains two-thirds of the world's population, and the chief livelihood of human beings abundantly relies on rice due to its sovereignty, nutritive properties, and energy value (Burlando and Cornara, 2014). It is a self-pollinated cereal crop belonging to the family Poaceae with the chromosome number $2n = 24$ (Kumar *et al.*, 2020). Rice provides 50–80% of daily calorie intake among the poor class of society. More than 90% of the world's rice is produced and consumed in Asia (Khush, 2005). The two cultivated rice species are *Oryza sativa*, widely grown in Asia and other countries; and *Oryza glaberrima*, grown in Africa only. The cultivated Asian rice species, *O. sativa*, is composed of two subspecies, *indica* and *japonica*. The genetic diversity of japonica type is considered lower than that of *indica* type (Glaszmann, 1987; Zhang *et al.*, 1992). New Rice for Africa (NERICA) was developed by interspecific cross (*O. sativa* and *O. glaberrima*) (Jones *et al.*, 1997). Genetic variability refers to the diversity present within a population due to genetic differences among individuals. It is essential for the selection and breeding of crops like rice to develop improved varieties with desirable traits. Khaliq *et al.* (2016) have estimated genetic variability in rice populations to understand the range of variation present for various traits. GCV measures the extent of genetic variation present in a population relative to the population mean. It helps plant breeders to understand the inherent genetic variability for specific traits. Studies such as Khaliq *et al.* (2016) have estimated GCV in rice populations to assess the genetic diversity for various agronomic traits. PCV measures the total variation observed in a trait within a population, including both genetic and environmental components. It is useful for evaluating the overall phenotypic variability of traits in rice. Research by Pandey & Reddy (2011) has assessed PCV in sorghum genotypes under different stress conditions to understand phenotypic variation. Heritability is the proportion of phenotypic variation in a trait that is attributable to genetic variation. It indicates the degree to which offspring resemble their parents for a particular trait. In rice breeding, estimating heritability helps in predicting the response to selection. Khaliq *et al.* (2016) estimated heritability in an F₂ population of rice to understand the genetic basis of traits. Genetic advance refers to the increase in the mean value of a trait achieved through selection in a breeding population over one generation. It provides an indication of the potential progress that can be made through selection for specific traits. Studies like Kumar & Bhowmick (2020) have used genetic advance to identify promising traits for rice improvement.

Rice is a major source of food for more than 2.7 billion people on a daily basis and

is planted on about one-tenth of the earth's arable land. It is the single largest source of food energy for more than half of the world's population. A 100 g of rice provides 345.0 kcal, 78.2 g of carbohydrates and 6.8 g of protein. inclusive of considerable amount of recommended Zinc and Niacin. Rice protein is biologically richest as its digestibility is very high (88%). The world's population is projected (based on medium fertility) to grow from 7.7 billion in 2019 to 8.5 billion in 2030 (10% increase), and further to 9.7 billion in 2050 (26%) and to 10.9 billion in 2100 (42%) (Bin Rahman, A. R., & Zhang, J. (2023)). Besides its important significance, it is rich in genetic diversity in the form of thousands of land races and progenitor species (Nagaraju *et al.* 2002). Globally, India stands first in rice area and second in rice production, after China. It contributes about 40 to 43% of total food grain production and is playing a vital role in the food and livelihood security system. In India area, production and productivity of rice is about 45.01 million hectares during 2021-2022 with production of 122.27 million tones and productivity 27.11 qnt/hac. (World Agricultural Production, 2022). Rice constitutes a significant portion of the daily diet particularly in developing countries of Asia, supplying 50-80% of the daily caloric intake, proteins, minerals and vitamins etc. The annual global rice production of 513.02 million tones was produced area of 158 million hectares in 2021-2022. Rice Production last year was 508.84 million tons. This year's 513.02 estimated millions of tons could represent an increase of 4.18 million tons or 0.82% in rice production around the globe. (USDA 2022).

The knowledge about genetic variability can help to know if these variations are heritable or non-heritable. The magnitude of variation due to heritable component is very important because, it would be a guide for selection of parents for crop improvement (Dutta *et al.* 2013). Therefore, selection for high yield requires knowledge about genetic variability and good understanding of correlation between yield and yield components regarding to the genetic material that is on hand. Genetic variability for agronomic traits is the key component of breeding program for broadening the gene pool of rice (Dutta *et al.* 2013). The success of breeding program depends upon the quantum of genetic variability available for exploitation and the extent to which the desirable characters are heritable (Tiwari *et al.* 2011). The existence of variability is essential for improvement of genetic material. Selection is also effective when there is significant amount of genetic variability among the individuals in breeding materials.

Materials and Methods

The experiment was conducted in the Student Instructional farm of ANDUA&T, Kumarganj, Ayodhya during *Kharif* 2023-24. The site is located between latitude of 26⁰

32°38' north and longitudes of 81° 49'40" east, on an altitude of 131 meters above the mean sea level. The seeds of rice genotype were sown in nursery bed. The present experimental materials are consisting ten germplasm lines having the viz., Sabarmati, IET 18517, Heera, Ferni, Moti Farm, Paudhan, Binni, IET 18933, Bhadani III and Dudhia used as lines and three promising rice varieties viz., NDR 359, WGL-32100 and NDR 2064 were used as testers, three checks (Sarju 52, NDR 9930111 and BPT 5204) were the experimental materials of this study. The crosses will be made into "line x tester" mating design (Kempthorne, 1957) to produce 30 crosses. After 22 days, single seedling per hill was transplanted with 20 cm row to row and 15 cm plant to plant spacing in Randomized Block Design (RBD) with three replications. Observations were recorded on Days to 50% flowering, days to maturity, plant height (cm), productive tillers per plant, panicle length (cm), flag leaf area (cm²), The number of spikelets per panicle, Number of fertile spikelet per panicles, spikelet fertility (%), biological yield per plant (g), harvest index (%), 1000-grain weight (g), grain yield per plant (g). Estimation of genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV) was done according to the formula given by Burton and De Vane (1953).

3. Results and Discussion

3.1 Variability Parameters analysis

Analysis of variance revealed highly significant and exploitable variability among all the genotypes for thirteen characters (Table 1). Greater variability in the initial breeding materials ensures better chances of producing desired recombinants for improvement of the crop. This suggests the presence of variation among the genotypes for all these traits. The phenotypic (PCV) and genotypic (GCV) coefficient of variation for the thirteen characters (Table 2). In general, the magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits. The high estimates of genotypic and phenotypic coefficient of variation (>20%) were recorded for productive tillers per plant (20.05 and 23.44). High value of PCV was also recorded for 1000-grain weight (20.45) but its GCV shows moderate value (17.02), number of fertile spikelets per panicle (17.33 and 17.89), flag leaf area (15.03 and 10.49), grain yield per plant (13.74 and 17.36), number of spikelets per panicle (13.36 and 14.26) and days to 50% flowering (10.39 and 10.64) respectively. Moderate value of PCV was also recorded for panicle length (13.38), harvest index (11.24) and biological yield per (10.17) but its GCV value recorded low. Rest traits viz., plant height, days to maturity and spikelet fertility showed low estimates (<10%) of GCV and PCV.

Table 1: Analysis of variance for 13 characters in rice genotypes in Kharif 2023-24

S. No.	Characters	Source of variations		
		Replications	Treatments	Error
	Degree of freedom	2	32	64
1.	Day to 50% flowering	9.85	251.52**	4.14
2.	Day to maturity	3.84	222.71**	6.14
3.	Plant height (cm2)	18.98	255.88*	15.86
4.	Productive tillers per plant	13.48	19.75**	1.40
5.	Panicle length (cm)	18.78	30.25**	5.09
6.	Flag leaf area (cm2)	10.68	64.21**	9.04
7.	Number of spikelets per panicle	28.13	1081.12**	76.64
8.	Number of fertile spikelets per panicle	2.81	1524.18**	51.16
9.	Spikelet fertility (%)	13.10	95.30*	13.39
10.	1000-seed weight (g)	1.62	45.15**	5.72
11.	Biological yield per plant (g)	24.24	83.15**	8.00
12.	Harvest index (%)	21.04	42.80*	16.18
13.	Grain yield/plant (g)	3.53	48.90*	6.81

*, ** significant at 5 and 1% probability levels, respectively

Table 2: Estimates of mean, range, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense (h^2b) and genetic advance in percent of mean (GA %) for 13 characters in rice genotypes under *Kharif 2023-24*.

S. No.	Characters	Mean	Range		Coefficient of Variation		h^2b (%)	GA	GA % Mean
			Min	Max	GCV (%)	PCV (%)			
1.	Day to 50% flowering	90.93	74.56	119.00	10.39	10.64	95.34	19.00	20.90
2.	Day to Maturity	121.91	103.00	148.00	7.45	7.72	93.11	18.05	14.81
3.	Plant height (cm)	123.57	92.34	149.72	7.12	7.81	83.02	16.51	13.36
4.	Productive tillers per plant	10.59	6.00	16.50	20.05	23.44	73.18	3.74	35.34
5.	Panicle length (cm ²)	25.46	16.54	33.52	9.96	13.38	55.40	3.89	15.27
6.	Flag leaf area (cm ²)	27.14	16.31	36.18	15.03	16.49	83.09	7.66	28.22
7.	Number of spikelets per panicle	174.72	122.49	269.20	13.36	14.26	87.79	45.07	25.80
8.	Number of fertile spikelets per panicle	145.40	100.40	238.69	17.33	17.89	93.81	50.27	34.58
9.	Spikelet fertility (%)	82.98	65.90	95.01	5.46	7.07	59.66	7.21	8.69
10.	1000-grain weight (g)	19.62	10.20	26.54	17.02	20.45	69.23	5.72	29.17
11.	Biological yield per plant (g)	54.25	45.56	66.84	8.52	10.17	70.27	7.99	14.72
12.	Harvest index (%)	43.96	28.31	49.99	6.19	11.24	30.31	3.08	7.02
13.	Grain yield/plant (g)	23.92	14.23	33.21	13.74	17.36	62.66	5.36	22.41

3.2. Heritability and genetic advance parameters analysis

High estimates of broad sense heritability (>75%) were recorded for days to 50 % flowering (95.34), number of fertile spikelets per panicle (93.81), days to maturity (93.11), number of spikelets per panicle (87.79), flag leaf area (83.09), plant height (83.02). The moderate estimates of heritability (50-75%) were recorded for productive tillers/plant (73.18), biological yield per plant (70.27), 1000-grain weight (69.23). grain yield/plant (62.66), spikelet fertility (59.66) and panicle length (27.12). The trait possessed low estimates of heritability (<50%) in broad sense for harvest index (30.31). The genetic advance in per cent of mean under field condition. The high genetic advance in percent of mean (>20%) was recorded for productive tillers per plant (35.34), number of fertile spikelets per panicle (34.58), 1000-seed weight (29.17), flag leaf area (28.22), number of spikelets per panicle (25.8), grain yield/plant (22.41) and day to 50% flowering (20.9). While, day to maturity (14.81), biological yield/plant (14.72) and plant height (13.36) had moderate estimates (10-20%) of heritability. Rest traits i.e., spikelet fertility (8.69), harvest index (7.02) were possessed low (<10%) estimates of heritability in the environment. Highest variance due to genotypes along with phenotypes were observed for number of fertile spikelets per panicle (634.85 and 676.72) followed by number of spikelets per panicle (545.29 and 621.14) and plant height (137.72 and 149.08). The estimate of heritability alone is not very much useful on predicting resultant effect for selecting the best individual because it includes the effect of both additive gene as well as non-additive gene. High genetic advance only occurs due to additive gene action (Panse and Shukhatme 1967). So, heritability coupled with genetic advance would be more useful than heritability alone.

High heritability along with high genetic advance was observed for the characters number of fertile spikelets per panicle, number of spikelets per panicle, flag leaf area and days to 50% flowering indicating that these characters are largely controlled by additive gene action, which indicates that improvement in these characters is possible through mass selection and progeny selection. Similar study was done by Chandramohan *et al.* (2016)^[1]. High heritability coupled with moderate genetic advance values was recorded for days to maturity suggested the role of both additive and non-additive gene effects in their inheritance, therefore, adoption of breeding procedures which could exploit both the gene actions would be a prospective approach (Krishna *et al.* 2008 and Patil and Sarawgi, 2005)^[5, 8].

The traits that showed high heritability coupled with high genetic advance are under the

control of additive gene action (Panse and Sukhatme, 1957) and can be improved through simple or progeny selection methods, while the characters which showed high heritability coupled with moderate or low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding (Samadhia, 2005) [16]. In the present study high heritability associated with high genetic advance for yield attributing characters was in accordance with the Parimala and Devi (2019) and Saha *et al.* (2019).

Conclusion

From the present study, it can conclude that, there is adequate genetic variability present in the material studied. Highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for productive tillers per plant and 1000-grain weight indicating that these characters could be used as selection for crop improvement. High heritability along with high genetic advance was observed for number of fertile spikelets per panicle, number of spikelets per panicle, flag leaf area and days to 50% flowering indicating that these characters are largely controlled by additive gene action and these characters can be improved by the mass selection and progeny selection. Therefore, the results suggest that the number of fertile spikelets per panicle, number of spikelets per panicle and days to 50% flowering are important yield contributing traits and selection based on these traits would be most effective.

References:

- Bin Rahman, A. R., & Zhang, J. (2023).** Trends in rice research: 2030 and beyond. *Food and Energy Security*, 12(2), e390.
- Burlando, B., & Cornara, L. (2014).** Therapeutic properties of rice constituents and derivatives (*Oryza sativa L.*): A review update. *Trends in food science & technology*, 40(1), 82-98.
- Burton GW, De Vane EM (1953).** Estimating heritability in all foscue (*Festuca arundica*) for replicated clonal material. *Agron. J*, 1; 45:478-487.
- Chandramohan Y, Srinivas B, Thippeswamy S, Padmaja, D (2016).** Diversity and variability analysis for yield parameters in rice (*Oryza sativa L.*) genotypes. *Indian J Agric. Res.*; 50(6):609-613.
- Chandramohan, Y., Srinivas, B., Thippeswamy, S., & Padmaja, D. (2016).** Diversity and

variability analysis for yield parameters in rice (*Oryza sativa* L.) genotypes. *Indian Journal of Agricultural Research*, 50(6), 609-613.

Chaudary P, Mishra DK, Koutu GK (2013). Genetic variation, association and path coefficient analysis for grain yield and its components in RILs derived population of rice. *Journal of progressive agriculture*.; 4(2):54-56.

Datta, S., & Das, L. (2013). Characterization and genetic variability analysis in *Capsicum annum* L. germplasm.

Dutta P, Dutta PN, Borua PK (2013). Morphological Traits as Selection Indices in Rice: A Statistical View. *Univ. J Agric. Res.* 2013; 1(3):85-96.

Glaszmann, J. C. (1987). Isozymes and classification of Asian rice varieties. *Theoretical and Applied genetics*, 74, 21-30.

Gopalan C, Rama Sastri BV, Balasubramanian S (2007). Nutritive Value of Indian Foods. National Institute of Nutrition (NIN), ICMR, India.

Hanson CH, Robinson HF, Comstock RE (1956). Biometrical studies of yield in segregating population of Korean Lespedeza *Agron. J*; 48:268-271.

Johnson HW, Robinson HP, Comstock RE (1955). Estimates of genetic and environment variability in Soybeans. *Agron. J*; 47:314-318.

Jones, M. P., Dingkuhn, M., Aluko/snm>, G. K., & Semon, M. (1997). Interspecific *Oryza sativa* L. x *O. glaberrima* Steud. progenies in upland rice improvement. *Euphytica*, 94, 237-246.

Khaliq, I., Irshad, A., & Hussain, M. (2016). Estimation of genetic variability, heritability, genetic advance and correlation analysis in F2 population of rice (*Oryza sativa* L.). *Pure and Applied Biology*, 5(2), 394-400.

Krishna L, Raju CD, Raju CS (2008). Genetic variability and correlation in yield and grain quality characters of rice germplasm. *The Andhra Agric. J*; 55:276-279.

Kumar, R., & Bhowmick, M. K. (2020). Path analysis for identifying important morphological and yield contributing traits in rice (*Oryza sativa* L.) under different

planting methods. *International Journal of Agriculture, Environment and BioResearch*, 5(2), 166-175.

Kumar, S. R., & Arumugam, T. (2013). Variability, heritability and genetic advance for fruit yield, quality and pest and disease incidence in eggplant. *Vegetable Science*, 40(1), 111-113.

Nagaraju, J., Kathirvel, M., Kumar, R. R., Siddiq, E. A., & Hasnain, S. E. (2002). Genetic analysis of traditional and evolved Basmati and non-Basmati rice varieties by using fluorescence-based ISSR-PCR and SSR markers. *Proceedings of the National Academy of sciences*, 99(9), 5836-5841.

Pandey, V., & Reddy, B. V. S. (2011). Grain yield and physiological traits of sorghum (*Sorghum bicolor* (L.) Moench) genotypes as influenced by timing and severity of water-deficit stress. *Crop and Pasture Science*, 62(9), 726-738.

Panse VG, Shukhatme PV. Statistical Methods for agricultural workers (1967). 2nd Edn. ICAR, New Delhi, 152-157.

Patil PV, Sarawgi AK 2005). Studies on genetic variability, correlation and path analysis in traditional aromatic rice accessions. *Ann. Plant. Physiology*; 19:92-95.

Tiwari R, Suresh BG, Mishra VK, Kumar A 2011). Genetic variability and character association in direct seeded upland rice (*Oryza sativa* L.). *Environment and Ecology*; 29(4A):2132-2135.

Tiwari, D. K., Pandey, P., Tripathi, S., Giri, S. P., & Dwivedi, J. L. (2011). Studies on genetic variability for yield components in rice (*Oryza sativa* L.). *Advances in Agriculture & Botany*, 3(1), 76-81.

Vanisree S, Swapna K, Raju CD, Raju CS, Sreedhar M (2013). Genetic variability and selection criteria in rice. *J Bio. Res. and Sci Opin.*; 1:342-346.

Zhang, Q., Maroof, M. S., Lu, T. Y., & Shen, B. Z. (1992). Genetic diversity and differentiation of indica and japonica rice detected by RFLP analysis. *Theoretical and Applied Genetics*, 83, 495-499.