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Research Note

Variability, heritability and genetic advance for yield and its component traits in NPT core set of rice (*Oryza sativa* L.)

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Abstract

Presence of adequate genetic variability and its critical analysis are needed for initiating any crop improvement programme and for adopting appropriate selection techniques. An investigation was carried out to know the extent of genetic variability present in forty six genotypes of rice during *kharif* 2017. Analysis of variance revealed highly significant differences for all the 12 characters, indicating the presence of genetic variability among the genotypes. The magnitude of PCV was slightly higher than GCV for the traits *viz.,* plant height, number of tillers per plant, number of panicles, panicle weight, grain number, test weight, single plant yield, plot yield and biomass, indicating less influence of environmental factors on the expression of traits and the possibility for genetic improvement through direct selection for these traits. The estimates of PCV and GCV were moderate for the traits *viz.,* days to 50% flowering, panicle length and harvest index, indicating the influence of environment rather than the genotype alone. The heritability and genetic advance estimates were moderate for panicle length and high for all the other traits *viz.,* days to 50% flowering, plant height, number of tillers per plant, number of panicles, panicle length, panicle weight, grain number, test weight, single plant yield, plot yield, biomass and harvest index, indicating the influence of additive gene action, as such selection would likely be effective for improvement of these traits.

Keywords
Rice, variability, heritability, genetic advance

Rice is the most important human food crop in the world for direct feeding more number of people than any other crop. It is the staple food for over half the global population. Despite the age old human issues about balancing population and food supplies, the world population is anticipated to still grow, presumably reaching 9-11 billion sometimes during 2030- 2050. With the current trends of population growth and agricultural production, the demand for food in most parts of world will double by the year 2025 and nearly triple by 2050. Crop yield improvement is of prime importance to fulfill the demands owing to constant increase in population. Grain yield is a complex character which is influenced by several quantitative traits, governed by polygenes. The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding programme. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone.

Variability in genotypes for yield and its component traits forms the essential factor to be considered while making selection. A critical assessment of genetic variability present in the germplasm of crop and its estimation is a pre-requisite for successful exploitation and improvement of yield through breeding. Heritability is the measure of transmission of characters from generation to generation and the estimates of heritability will be of immense help to the breeder in selecting superior individuals for a desired trait for successful utilization in the breeding programme. Genetic advance measures the difference between the mean genotypic values of selected population and the original population from which these were selected. Johnson *et al.* (1955) suggested that heritability estimates along with genetic advance would be more useful in predicting genetic gain under selection than heritability estimates alone. Keeping in view the above perspectives, the present investigation is carried out with the objective of estimating the genetic variability for yield, yield contributing character, heritability and genetic advance which would help in selection and further improvement of rice genotypes.

Forty six (46) rice genotypes comprising NPT (New Plant Type) core set (Jyothi *et al.*, 2018) of tropical *japonica* accessions, *indica* land races along with checks were evaluated for yield and component traits during *Kharif* 2017 in Randomized Block Design (RBD) with three replications at ICAR-Indian Institute of Rice Research (ICAR-IIRR), Ramachandrapuram farm, ICRISAT campus, Hyderabad. Thirty days old seedlings were transplanted by adopting a spacing of 15 cm between plants and 20 cm between rows. Recommended agronomic and plant protection measures for raising a healthy nursery and main crop were taken up during the experiment.

Observations were recorded on five randomly selected plants in each genotype in each replication for twelve quantitative traits *viz.*, days to fifty percent flowering (DFF), plant height (PH) (cm), tillers per plant (TN), number of panicles (PN), panicle length (PL) (cm), panicle weight (PW) (g), grain number (GN), thousand grain weight (TW) (g), single plant yield (SPY) (g), plot yield (PY) (kg m^{-2}), biomass (BM) (g) and harvest index (HI) (%). The mean of five plants for each metric trait was considered for statistical analysis using WINDOSTAT software version 9.2. The analysis of variance (ANOVA) was done on the basis of model described by Cochran and Cox (1950) for randomized complete block design. The genotypic and phenotype variances were calculated as per the formulae proposed by Burton and Devane, 1953. Heritability in broad sense (h^2) was calculated by the formula given by Lush, 1949 as suggested by Johnson *et al.* (1955). From the heritability estimates, the genetic advance (GA) was calculated by the formula given by Johnson *et al.* (1955).

Analysis of variance revealed highly significant differences among the 46 genotypes for all the 12 characters (Table 1) indicating the presence of adequate amount of genetic variability among the genotypes assessed. It also indicates the representativeness of the NPT core set (Jyothi *et al.*, 2018) capturing maximum variability available among sub species of *O. sativa*. The genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean were estimated for forty six genotypes and the details are furnished in table 2. The graphical representation of variability parameters is depicted in Fig 1 and Fig 2.

The present investigation revealed that the estimates of PCV were slightly higher than GCV for all the characters studied indicating less influence of environmental factors on the expression of traits. As the characters were less influenced by the environment, the traits can be used for selection. The magnitude of PCV and GCV estimates were moderate for three traits *viz.*, days to 50% flowering, panicle length and harvest index. Similar such observations were made by Mishu *et al*. (2016) for days to 50% flowering and panicle length in six aromatic rice varieties and by Muthuramu and Sakthivel (2016) for harvest index, in 23 rice cultivars under upland rice ecosystem, which indicates the need for improvement of base population through intermating followed by recurrent selection or selection could be postponed for these characters until advanced generations to increase the gene flow and to fix favourable alleles. High estimates of GCV and PCV were observed for plant height, number of tillers per plant, number of panicles, panicle weight, grain number, test weight, single plant yield, plot yield and biomass. Similar findings were reported by Singh *et al.* (2013) for plant height in 11 genotypes of exotic germplasm of upland rice and Gangashetty *et al.* (2013) for plant height, number of tillers per plant and panicle weight in 42 local non-basmati aromatic genotypes of rice. High estimates of GCV and PCV for panicle weight were reported by Awaneet and Senapati (2013) in 33 lines of advanced generation lines obtained from the cross of Sabita/Samba Mahsuri and Sanghera *et al*. (2013) in fourteen cold tolerant local red rice ecotypes. For grain yield per plot, the results are in agreement with Aditya and Anuradha (2013) in eighteen rainfed upland rice genotypes and Muthuramu and Sakthivel (2016) in 23 advance rice cultivars under upland rice ecosystem.Such similar observations for grain yield per plant were in conformity with Alam *et al.* (2014) in 76 bangladesh landraces of rice, Rathor *et al.* (2014) in 40 rice germplasm and local rice land races and Kumar *et al*. (2015) in 25 rice hybrids. Neha *et al.* (2014) reported high GCV and PCV estimates for grain yield per plant and number of tiller per plant in 45 exotic upland rice germplasm under rainfed ecosystem.

Thirumala Rao *et al.* (2014) reported similar estimates for number of grains per panicle, test weight and grain yield in forty nine rice genotypes. For the number of filled grains per panicle and yield per plant, high estimates for GCV and PCV were reported by Khatun *et al.* (2015) in forty-three upland rice genotypes and Devi *et al.* (2016) in 27 genotypes of rice. Harsha *et al.* (2017) reported similar results for the number of panicles per plant, yield per plant and test weight in 29 lines of rice genotypes which included basmati and non-basmati types. Prabhu *et al.* (2017) had reported for high estimates of PCV and GCV for grain yield per plant, number of grains per panicle and number of panicles per plant in four BC_1F_2 backcrossing populations of rice cultures. Similar findings were reported for biomass by Patel *et al*. (2014) in 44 diverse upland rice genotypes under rainfed condition. In similar to our findings, the above reported observations for high GCV and PCV estimates in different set of genotypes including early segregating and advanced generation for important yield component traits, does indicate the possibility for genetic improvement through direct selection for these traits.

Heritability measures the contribution of genetic variability to the phenotypic variability and is a good index of the transmission of characters from parents to their offspring. The estimates of heritability can be utilized for prediction of genetic gain, which indicates the genetic improvement that would result from selection of best individuals. Genetic advance (GA) is the measure of genetic gain under selection. Heritability estimates along with genetic advance are normally more helpful in predicting the genetic gain under selection than heritability estimates alone.

Moderate heritability coupled with moderate genetic advance for panicle length was reported earlier by Bisne *et al.* (2009) in 44 genotypes (Four CMS lines, eight promising rice varieties and thirty-two hybrids) of rice and Neha *et al.* (2017) in 22 exotic upland rice germplasm, indicated that this trait was heritable and could be potentially improved by selective breeding.

High heritability coupled with high genetic advance estimates were recorded for all the other traits *viz.*, days to 50% flowering, plant height, number of tillers per plant, number of panicles, panicle weight, grain number, test weight, single plant yield, plot yield, biomass and harvest index. These results are in conformity with Neha *et al.* (2014) for plant height and days to 50% flowering in 45 exotic upland rice germplasm under rainfed ecosystem and Alam *et al.* (2014) for number of grains per panicle in 76 bangladesh landraces of rice. Similar findings were reported by Rathor *et al.* (2014) for test weight in 40 rice germplasm and Kumar *et al*. (2015) for grain yield per hill in 25 rice hybrids.

Devi *et al.* (2016) had reported high heritability and GA for effective tillers, plant height, grains per panicle, test weight and yield per plant in 27 genotypes of rice. Konate *et al.* (2016) reported similar findings for biomass, days to 50% flowering, plant height, number of panicles and yield per plant in 20 genotypes consisting of 17 F_5 inbred lines. Also the results were in conformity with Mishu *et al.* (2016) for test weight in six aromatic rice varieties and, Harsha *et al.* (2017) for test weight and days to 50% flowering in 29 lines of rice genotypes which included basmati and non-basmati types. Such estimates were reported by Rashmi *et al.* (2017) for days to 50% flowering and panicle weight in 65 rice germplasms.. Srujana *et al.* (2017) for grain yield, number of panicles, and tillers per hill in 29 rice genotypes from IRRI, which support the present findings. This indicates that there was low environmental influence on the expression of these characters and hence one can practice selection.

The genetic architecture of grain yield is based on the overall net effect produced by various yield components interacting with one another. The present investigation revealed that there is adequate genetic variability present in the material studied. Among all the characters, days to 50% flowering, plant height, number of tillers per plant, number of panicles, panicle weight, grain number, test weight, single plant yield, plot yield, biomass and harvest index recorded high heritability as well as high genetic advance, indicating the presence of considerable variation and additive gene effects. Hence, improvement of these characters could be effective through phenotypic selection.

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Table 1. Analysis of variance for yield and its component traits among rice genotypes

Source of variation	d.f	DFF	PH	TN	PN	PL	PW	GN	TW	SPY	PY	BM	HI
Replication	2	9.94	106	0.27	0.36	19.14	0.01	37.27	3.1	0.19	0.0003	1832	1.46
Treatment	45	693*	2397*	31.45*	25.43*	37.55*	8*	15120*	77.01*	67.93*	0.41*	913556*	214*
Error	90	3.29	36.6	2.05	2.37	3.31	0.02	121	1.28	0.83	0.002	3735	1.15

*Significance at 5% level
DFF- Days to 50% flowering, PH- Plant height, TN- Tillers per plant, PN- number of panicles or productive tillers per plant, PL- Panicle length, PW- Panicle weight, GN- Grain number, TW- Test weight, SPY- Single plant yield, PY- Plot yield, BM- Biomass, HI- Harvest index.

Table 2. Variability parameters in rice genotypes.

S.No	Characters	General mean	Range	Coefficient of variation (%)		Heritability in broad sence (h^2) %	Gen. Adv as percent of mean (at 5%)
				PCV (%)	GCV (%)		
1	Days to 50% flowering	101.23	60-124	15.09	14.98	98.6	30.64
2	Plant height (cm)	123.84	68.17-183	23.17	22.65	95.6	45.61
3	Tillers number	11.18	5-18	30.79	28	82.7	52.44
4	Panicle number	10.14	5-17	31.28	27.35	76.4	49.26
5	Panicle length (cm)	27.79	15-35	15.82	10.85	47.1	15.33
6	Panicle weight (g)	5.04	2.77-10.10	32.47	32.36	99.4	66.46
7	Grain number	232.75	129-396	30.75	30.38	97.6	61.83
8	Test weight (g)	23.12	12.9-34.17	22.27	21.73	95.2	43.67
9	Single plant yield (g)	18.08	8-30.5	26.62	26.14	96.4	52.88
10	Plot yield (kg m^{-2})	1.18	0.54-2.08	31.72	31.44	98.2	64.19
11	Biomass (g)	1672	314-3213	33.12	32.9	98.8	67.39
12	Harvest index (%)	44.06	21.46-66.48	19.29	19.14	98.4	39.11

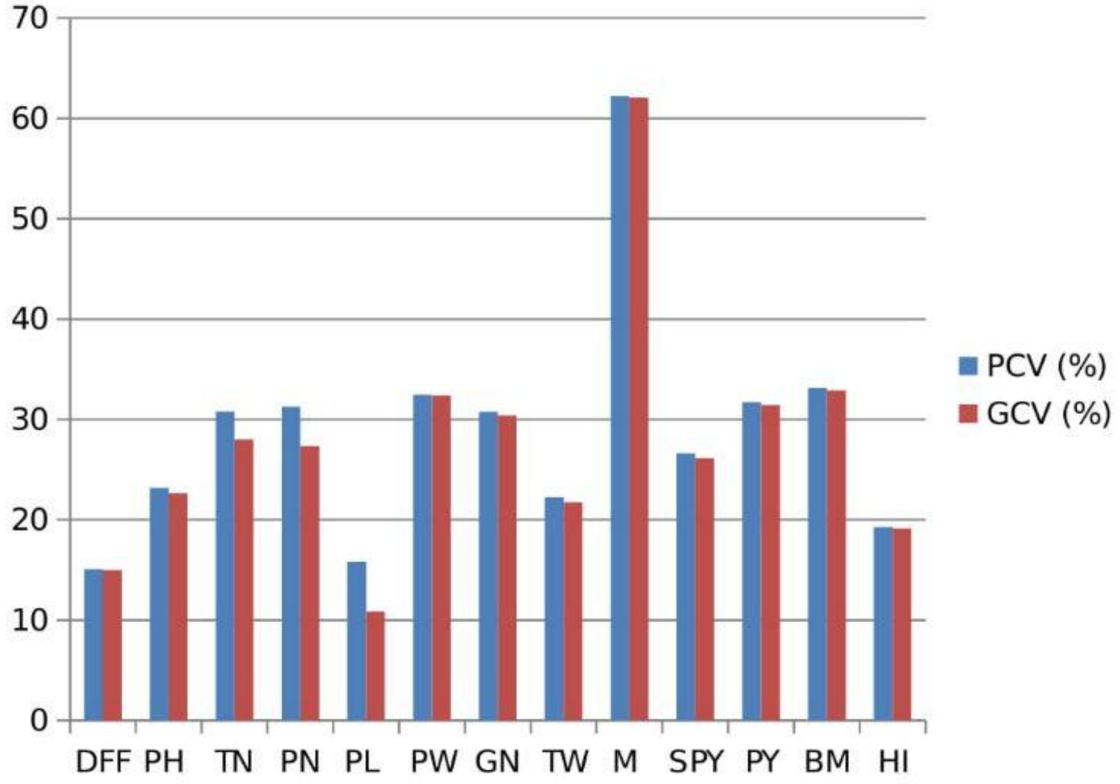

Fig. 1. Graphical representation of PCV and GCV

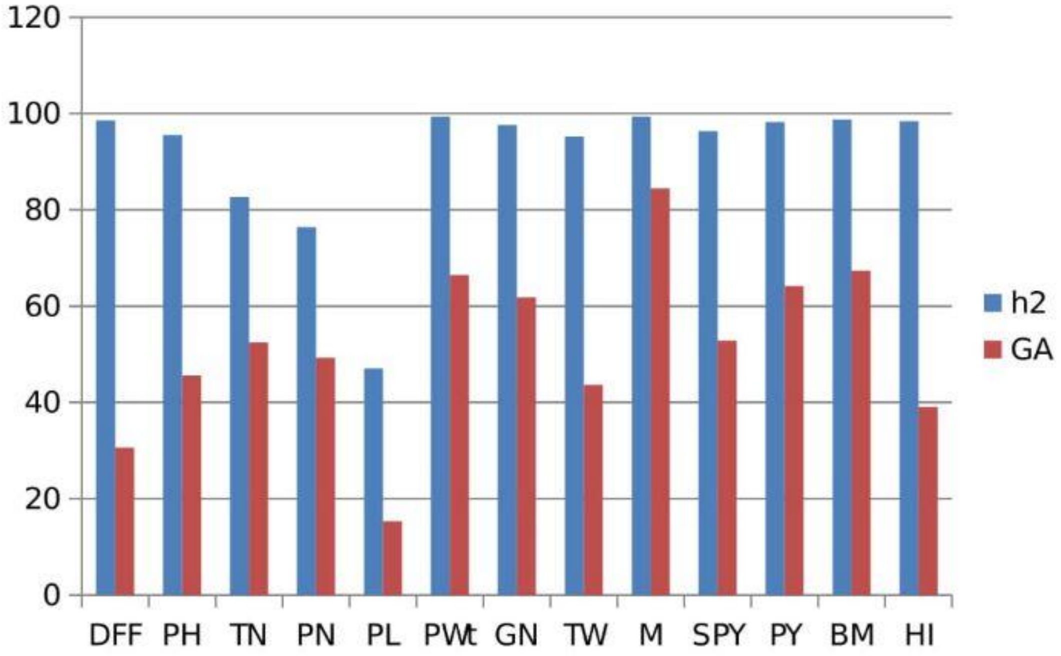

Fig. 2. Graphical representation of heritability (broad sense) and genetic advance as per cent of mean (5%)