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Genetic variability studies in traditional rice landraces of India

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Abstract

Rice is the predominantly consumed food across the globe and there is an urgent need to increase its production and productivity to feed the increasing population. Landraces and germplasm harbor tremendous amount of genetic variation that can be utilized to develop better varieties. Keeping this in view the current work has been carried out in 48 germplasm lines to estimate genetic variability, heritability, genetic advance and correlation between associated traits at the ICAR-Indian Institute of Rice Research (ICAR-IIRR) during Rabi 2021-2022. Six of the ten traits showed high values of PCV and GCV viz. number of productive tillers, panicle weight, number of filled grains, test weight and single plant yield revealing lesser influence of environment on these traits. Plant height and panicle length had moderate GCV and PCV, number of tillers had high PCV and moderate GCV while days to 50% flowering had low GCV and PCV. Values of Heritability (except for number of tillers and single plant yield) and genetic advance as percent of mean were high for all the traits indicating that selection would be effective and rewarding. Days to 50% flowering had high positive correlation with number of tillers. Single plant yield most strongly correlated with panicle weight followed by number of filled grains per panicle, number of productive tillers and test weight indicating that yield can be improved by selection for the above associated traits. The knowledge of the above estimates will be useful to fully exploit the potential genetic variation available in the population.

Keywords: Genetic variability, heritability, genetic advance

Introduction

Rice (*Oryza sativa* L.) is one of the most important food crops, contributing around twenty-one percent of daily calorie intake in Asian countries. The production across the world and India is 517.00 million tonnes and 127.93 tonnes respectively. With the rising population, shrinking arable land and stagnated productivity of rice, there is an immediate need in improvement of rice in terms of production and productivity shrinking, it is expected that millions of people would starve in future, so it's necessary to increase rice production and productivity. Genetic variation is prerequisite and keystone for improvement of any crop. Traditional Landraces have tremendous amount of genetic variation that can be utilized in the breeding programs. Genotypic and phenotypic coefficient of variation estimates the amount of inherent genetic variation and variation in crops due to external environmental influences in addition to genetic variation. Heritability determines the probability of inheriting the trait to the next generation. Furthermore, estimates of genetic heritability combined with genetic advance would improve the efficiency of selection in breeding programs. Correlation analysis between traits and direct and indirect effects of different traits on grain yield would help in direct or indirect selection of traits that influence improvement in yield. Keeping this in view, the present study was carried out to study the genetic variability in rice landraces collected across India.

Materials and Methods

A total of 48 rice landraces of which 24 were collected from ICAR-Indian Institute of Rice Research (ICAR-IIRR) and 24 from TNAU AC & RI, Killikulam were evaluated for genetic variability studies during Rabi season 2022 in the experimental farm of ICAR-IIRR, Hyderabad. The design used was completely randomized block design for 48 genotypes. Variation studies were done for different traits that include Days for 50% flowering, Panicle weight, No. of filled grains and unfilled grains, test weight, Plant height, panicle length, no of tillers and productive tillers, and grain yield per plant.

The traits were estimated for Genotypic and Phenotypic coefficient of variation (GCV & PCV), Heritability and Genetic advance and correlation studies.

Statistical analysis

The collected data was analysed using Statistical Analysis System software (SAS). Analysis of Variance was done as suggested by Panse and Sukhatme (1957) [17]. GCV and PCV,

heritability, and genetic advance as percent of mean parameters were estimated following the formula suggested by Burton *et al.*, (1953) [18].

Results and Discussion

The Analysis of variance of various yield attributed traits is presented in table 1.

Table 1: ANOVA table for variation in 10 yield attributing characters among 48 genotypes

Source of variation	df	DF	PH	PL	NT	NPT	PW	NFG	NUFG	TW	SPY
Replication	2	6.58	69.09	1.31	6.76	3.15	0.06	499.22	12.84	7.13	44.05
treatment	47	312.48	825.65	30.72	21.17	25.40	1.78	4127.74	1022.20	67.43	161.98
Error	94	0.57	13.55	2.31	4.86	3.75	0.14	422.58	110.17	0.03	39.52

Range of Variability

Highest range of variability was observed in number of filled grains (33-251), followed by number of unfilled grains (1-103) and least range of variability was observed in number of tillers (6-21). Other traits such as days to 50% flowering ranged from 85 to 123 days, 76 to 140 cm for plant height, 16 to 34.5 cm for panicle length, 3 to 22 for number of productive tillers, 1.02 gm to 4.65 gm for panicle weight, 8.36 gm to 29.49 gm for test weight 6.39gm to 51.37gm for single plant yield.

Genetic Variability Parameters

GCV (Genotypic coefficient of variation) and PCV (Phenotypic coefficient of variation) values were high for number of productive tillers (24.28 & 29.93) panicle weight (28.66 & 32.11), number of filled grains (31.48 & 36.47) number of unfilled grains (76.03 & 88.75) test weight (22.76 & 22.78) single plant yield (27.13 & 38.06) indicating that the

influence of environment on the observed variation of traits is low. Similar results were obtained by Rao *et al.* (2020) [15] Sudeepthi *et al.* (2020a) [11] for productive tillers, Parimala *et al.* (2020) [19], Nath and Kole (2021) [7] for test weight, Singh *et al.* (2020) [15] Nath and Kole (2021) [7] for single plant yield, and Nayak *et al.* (2016) [13] for number of filled grains per panicle GCV and PCV values were moderate for plant height (15.02 & 15.39) and panicle length (12.64 & 14.10). Similar results were concluded by Singh *et al.* (2020) [15], Nath and Kole (2021) [7]. GCV values were moderate (18.00) & PCV values were high (24.79) for number of tillers. GCV and PCV values were low for days to 50% flowering (9.92 & 9.94) indicate there is a greater influence of environment on the variation that is observed. Similar results for Days to 50% flowering were obtained by Hossain *et al.* (2015) [10] Chandramohan *et al.* (2016) [5]. The GCV and PCV values of the above traits have been presented in Figure 1.

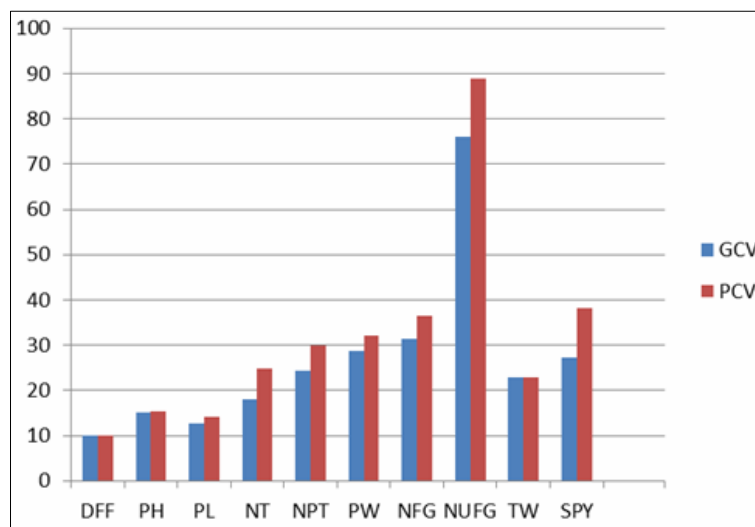


Fig 1: Genotypic and phenotypic coefficient of variation among the 48 genotypes

Heritability and Genetic Advance

Heritability and genetic advance as percent of mean were high for days to 50% flowering (99.45 & 20.38), plant height (95.23 & 30.20), panicle length (80.36 & 23.35), number of productive tillers (65.81 & 40.58), panicle weight (79.64 & 52.69), number of filled grains (74.50 & 55.98), number of unfilled grains (73.39 & 134.19) and test weight (99.86 & 45.86).

Similar results were confirmed by, Rao *et al.* (2020) [16] Singh *et al.* (2020) [15] for panicle length, Rao *et al.* (2020) [16] Sudeepthi *et al.* (2020) [11] for productive tillers per plant,

Nayak *et al.* (2016) [13] for number of filled grains per panicle and test weight, plant height and days to 50% flowering. This indicates that these traits are governed by additive gene action and the selection will be effective and rewarding. Moderate heritability and high genetic advance as percent of mean values were observed for number of tillers (52.77 & 26.95) and single plant yield (50.80 & 39.38). Similar results were concluded by Manickavelu *et al.* (2006) [9]. This also indicates that these traits are governed by additive gene action and the selection will be effective and rewarding. The Heritability and Genetic advance values of the above traits have been presented in Figure 2.

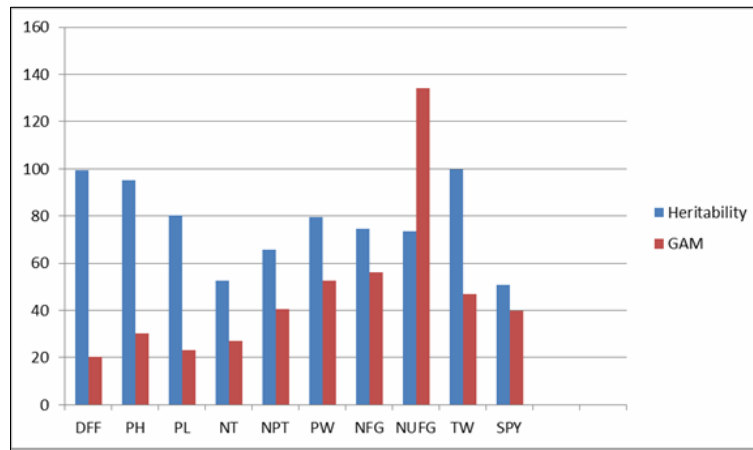


Fig 2: Heritability and genetic advance among the 48 genotypes

Correlation Analysis (Genotypic and Phenotypic Level)

Days to 50% flowering has a significant positive correlation with number of productive tillers (0.189*) and number of filled grains (0.174**) at genotypic level and number of tillers (0.312**, 0.226**), number of unfilled grains (0.324*, 0.28**) at both genotypic and phenotypic levels. Improvement in days to 50% flowering may lead to increase number of productive tillers (0.189*) and number of filled grains (0.174**) at genotypic level and number of tillers number of filled grains at both genotypic and phenotypic levels increase in number of productive tillers and number of unfilled grains at genotypic level.

Plant height has a significant positive correlation with Number of tillers at genotypic level (0.192*) and panicle length (0.56**, 0.485**) and number of unfilled grains (0.279**, 0.228**) and negative correlation with single plant yield (-0.316**, -0.216**) at both genotypic and phenotypic levels. Similar results were obtained by Saha *et al.* (2019)^[6] for correlation between panicle length and by Nath and Kole (2021)^[7] for single plant yield. Increase in plant height would may also lead to increase number of tillers at genotypic level and number of unfilled grains, panicle length at genotypic and phenotypic levels but may not increase single plant yield since it is negatively correlated at both genotypic and phenotypic levels. Panicle length has a significant negative correlation with single plant yield (-0.301**, 0.211*). Increase in panicle length may increase not increase single plant yield since it is negatively correlated at both genotypic and phenotypic levels.

Number of tillers has a significant positive correlation with number of filled grains (0.452**, 0.321**), number of unfilled grains (0.363**, 0.253**) and number of productive tillers (0.73**, 0.806**) panicle length (0.186*) and has negative correlation with test weight (-0.561**, -0.405**). Increase in number of tillers may also lead to increase days to 50% flowering, number of filled grains number of productive tillers panicle length but may not increase test weight since it is negatively correlated at both genotypic and phenotypic levels. Number of productive tillers has a significant positive correlation with number of filled grains (0.394**, 0.31**) number of unfilled grains (0.248**, 0.194*) and single plant yield (0.274**, 0.88*) and has negative correlation with test weight (-0.371**, -0.299**). Increase in number of productive tillers may also lead to increase in number of filled grains number of unfilled grains and single plant yield but may not increase test weight since it is negatively correlated at both genotypic and phenotypic levels.

Panicle weight has a significant positive correlation with

number of filled grains (0.58**, 0.637**), test weight (0.341**, 0.302**) and single plant yield (0.632**, 0.435**) Increase in number of Panicle weight may also lead to increase, number of filled grains test weight and single plant yield correlated at both genotypic and phenotypic levels.

Number of filled grains has a significant positive correlation with single plant yield (0.322**, 0.243**) number of unfilled grains (0.312**, 0.217**) and significant negative correlation with test weight (-0.48**, -0.389**). Similar results were obtained by Saha *et al.* (2019)^[6]. Increase in Number of filled grains may also lead to number of unfilled grains and single plant yield but may not increase test weight since it is negatively correlated at both genotypic and phenotypic levels. Number of unfilled grains has a significant negative correlation with test weight (-0.213**, -0.182*). Increase in Number of unfilled grains may not increase test weight since it is negatively correlated at both genotypic and phenotypic levels. Test weight has a significant positive correlation with and single plant yield (0.255**, 0.184*). Similar results were obtained by Devi *et al.* (2019)^[8]. Increase in test weight may also lead to single plant yield.

Conclusion

The analysis of the above data concludes that most of the traits having high PCV and GCV suggest that a lesser amount of environmental effect is present with a significant amount of variation. Lower levels of PCV and GCV indicate higher effect of environmental effects Higher or moderate values of heritability and higher values of genetic advance as per cent of mean were observed for all the traits under study, indicating that these traits were governed by additive gene action and hence direct selection of these traits would be rewarding and would be effective. Strong correlation of panicle weight, test weight, number of filled grains per panicle, and number of productive tillers with single plant yield reveal that yield can be improved by direct selection of these characters for developing good varieties in the future.

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