Studies on PCV, GCV, heritability, and genetic advance in rice genotypes for yield and yield components

ABSTRACT

The present experiment was carried out in twelve genotypes including IRRI introgression lines and a *Japonica* cultivar to analyse the genetic variability, heritability, and genetic advance for fourteen characters in rice. Significant differences were observed among the genotypes. All the traits under study recorded a high phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV) indicating the presence of environment controlling the traits. But, the less difference between PCV and GCV implies that the involvement had a negligible role in the trait expression. High PCV and GCV were observed for the character's plant height, ~~the~~ number of productive tillers, 1000 grain weight, L/B ratio, protein content, phenol content, and reducing sugar, representing that these characters in genotypes are contributed by additive gene action and the direct selection will improve the trait easily. Among the traits studied, high heritability and genetic advance were obtained for plant height, number of days to 50% flowering, panicle length, number of grains per panicle, grain breadth, L/B ratio, protein content, phenol content, and ascorbic acid, representing that these characters are predominant in additive gene action.

Keywords: *Rice, Genetic advance, Genotypic coefficient of variation (GCV), Heritability, Phenotypic coefficient of variation (PCV)*

1. INTRODUCTION

One of the most important cereal crops in the world, rice provides a significant percentage of the world's population with a staple diet [1]. Continuous attempts are being made to enhance rice~~'s~~ productivity and yield-related factors in order to fulfil the rising demand for grain and maintain food security. The inherent potential of rice genotypes, the heritability of characteristics, and the possibility for genetic advancement are all determined through genetic research [2]. The present study examines research on, the phenotypic coefficient of variation (PCV), genotypic ~~genomic~~ coefficient of variation (GCV), heritability and genetic advance in rice genotypes with an emphasis on the effects these factors have on yield and yield-related variables.

The variability of attributes within and between various rice genotypes is measured statistically using the terms phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). While GCV quantifies the genetic variability underlying a trait, PCV assesses the amount of variation that is seen in that trait [3].

The amount of phenotypic variation in a characteristic that may be attributable to genetic factors is estimated by heritability. High heritability suggests that genetic diversity significantly influences how a characteristic manifests, making it simpler to select for and enhance the trait. Low heritability, on the other hand, indicates that environmental influences have a stronger impact on trait expression [4].

Genetic advance examines the enhancement that can be made to a characteristic *via*., breeding programs and calculates the probable gain through selection. It stands for the variance between the mean performance of chosen individuals and the population as a whole [5].

2. MATERIALS AND METHODS

The experiment was conducted in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during the year 2022.

2.1 Plant materials

The rice genotypes Jyothi, Manu Ratna, White Ponni, Wayrarem, Vandana, PTB-33, PTB-21, IRRI introgression lines IR7103-121-15-B and IR65482-7-216-1-2, *japonica* variety Kinandang Patong, breeding line RP2068-18-3-5 and APO were employed in the study.

2.2 Experimental design

A randomized block design with twelve treatments and three replications was the experimental design followed in the present study.

2.3 Data collection

The morphological observations *viz.,* plant height (cm), number of days to 50% flowering, number of tillers, number of productive tillers, panicle length (cm), number of grains per panicle, grain weight (g), grain length (cm), LB ratio, protein content (g/100g), phenol content (mg/100g), ascorbic acid (mg/100g), reducing sugar (g/100g) were recorded from the twelve rice genotypes.

2.4 Data analysis

The morphological observations recorded were subjected to the calculation of the following genetic parameters;

Genetic Components of Variance

Phenotypic and genotypic components of variance were estimated for each character by equating the expected value of mean squares (MS) to the respective variance components [6].

i. Genotypic Variance (V_G), $V_G=\frac{\mathrm{MST-MSE}}{\mathrm{r}}$

ii. Environmental Variance (V_E), $V_E=MSE$

iii. Phenotypic Variance (V_P), $V_P= V_G+ V_E$

Coefficient of Variation

Genotypic, Phenotypic, and Environmental Coefficient of Variation were estimated from V_P, V_G, and V_E, expressed in percentage for each trait.

i. Genotypic coefficient of variation, $GCV=\frac{\sqrt{VG}}{X}\times 100$

ii. Phenotypic coefficient of variation, $PCV=\frac{\sqrt{VP}}{X}\times 100$

iii. Environmental coefficient of variation, $ECV=\frac{\sqrt{VE}}{X}\times 100$

Where, X= Grand mean

Following are the categories for the range of variation [7],

i. High: >20 percent

ii. Medium: 10-20 percent

iii. Low: <10 percent

Broad Sense Heritability

Ratio of genotypic variance to the total observed variance in the population and calculation expressed in percentage.

~~H~~$h^2=\frac{\mathrm{VG}}{\mathrm{VP}}\times 100$

Range of Heritability estimation [8] is,

i. High: >60 percent

ii. Medium: 30-60 percent

iii. Low: <30 percent

Genetic Advance

The expected genetic gain or improvement in the next generation by selecting a superior genotype under a certain amount of selection pressure. Genetic advance was estimated by using the formula [9].

GA= Kh~~H~~$^2\sqrt{VP}$

Where K= selection differential, At 5% selection intensity K=2.06,

H^2= Heritability, V_p= Phenotypic variance

Genetic Advance as Percent of Mean

GAM= GA/X ×100

Where, GA= Genetic Advance, X= Grand Mean

Ranges of genetic advance are [8],

i. High= >20 percent

ii. Medium= 10-20 percent

iii. Low= 10 percent

3. RESULTS AND DISCUSSION

The genetic parameters PCV, GCV, heritability, and genetic advance were estimated using the morphological observations on twelve genotypes of rice (Table 1).

Plant height
The plant height showed high PCV (29.095%), GCV (27.406%), heritability (88.7%), and genetic advance as per the mean (53.178%).

Number of days to 50% flowering
Moderate PCV (19.491%) and GCV (18.876%) with high heritability (93.8%) and genetic advance as per the mean (37.658%) were observed in the character.

Number of productive tillers
The trait showed high PCV (38.378%) and GCV (22.952%), moderate heritability (35.8%), and high genetic advance as per the mean (28.276%).

Culm thickness

The moderate PCV (12.489%) and GCV (10.555%), high heritability (71.4%), and moderate genetic advance as per the mean (18.377%) were observed for the culm thickness.

Panicle length
Moderate PCV (13.980%) and GCV (13.320%), high heritability (90.8%), and genetic advance as per the mean (26.142%) were observed for the panicle length.

Number of grains per panicle
The PCV (19.730%) and GCV (19.360%) were moderate, and heritability (96.3%) and genetic advance as per the mean (39.133%) were high for the number of grains per panicle.

1000 grain weight

The high PCV (26.546%), GCV (25.779%), heritability (94.3%), and genetic advance as per the mean (51.571%) were observed for 1000 grain weight.

Grain length

The grain length showed low PCV (7.886%) and GCV (7.024%), high heritability (79.3%), and moderate genetic advance as per the mean (12.887%).

Grain breadth

Moderate PCV (16.716%), GCV (16.059%), high heritability (92.3%), and genetic advance (31.789%) were recorded for grain breadth.

LB ratio

The LB ratio showed high PCV (21.874%), GCV (20.857%), heritability (90.9%), and genetic advance as per the mean (40.969%).

Protein content (g/100g)

The protein content showed high PCV (21.874%), GCV (20.857%), heritability (90.9%), and genetic advance as per the mean (40.969%).

Phenol content (mg/100g)

The phenol content showed high PCV (31.803%), GCV (30.128%), heritability (89.7%) and genetic advance as per the mean (58.794%).

Ascorbic acid (mg/100g)

The ascorbic acid content recorded moderate PCV (18.224%), GCV (17.894%), high heritability (96.4%), and high genetic advance as per the mean (36.195%).

Reducing sugar (g/100g)

The reducing sugar recorded high PCV (43.989%), GCV (40.492%), heritability (84.7%), and genetic advance as per the mean (76.783%).

The coefficient of variation measures the estimates of genetic variability present in the population. All the traits under study recorded a high phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV) indicating the presence of environment controlling the traits. But, the less difference between PCV and GCV implies that the involvement had a negligible role in the trait expression (Figure 1). The narrow gap between PCV and GCV in the traits of rice was reported [2,10,11]. High PCV and GCV were observed for the character's plant height, the number of productive tillers, 1000 grain weight, L/B ratio, protein content, phenol content, and reducing sugar, representing that these characters in genotypes are contributed by additive gene action and the direct selection will improve the trait easily. The same findings were reported for plant height [10], the number of tillers [2, 12], protein content [13], phenolic content [10,11], and reducing sugar [14] in rice genotypes. High PCV and GCV in the L/B ratio and 1000 grain weight were reported [15]. Moderate PCV and GCV were recorded for the character's number of days to 50% flowering, culm thickness, panicle length, number of grains per panicle, grain breadth, and ascorbic acid, indicating the scope for selection, and these traits were moderately contributed by the genetic constitution of rice genotypes. Similar results were obtained for panicle length, number of grains per panicle [16] [17], culm thickness [17], and grain breadth, for the number of days to 50% flowering, panicle length [18]. Low PCV and GCV were reported.~~ in the~~ The character grain length, in which direct selection of these traits will not be effective for crop improvement. The same results were reported in the study on local rice germplasms [19].

The heritable amount of genetic variation present in a trait is estimated using the measures of heritability. Heritability estimations serve as a predictive tool for expressing the accuracy of phenotypic value. Genetic advancement is a helpful indicator of the advancement that may be anticipated as a result of applying selection to the relevant population. So, both heritability and genetic advance helps in the effective selection of a trait. A more accurate estimate of selection value would result from the combination of heritability and genetic advancement [8]. Among the traits studied, high heritability and genetic advance were obtained for plant height, number of days to 50% flowering, panicle length, number of grains per panicle, grain breadth, L/B ratio, protein content, phenol content, and ascorbic acid, representing that these characters are predominant in additive gene action (Figure 2). Similar findings were earlier reported for panicle length, grain breadth, and L/B ratio, number of grains per panicle, the number of days to 50% flowering, grain breadth, phenol, and plant height, days to 50% flowering, plant height, panicle length, grains per panicle, grain breadth, L/B ratio, protein content, and total phenol content [17] [18].

Table 1. Genetic parameters studied for yield and yield-related traits

Characters	Genotypic variance	Phenotypic variance	Environmental variance	PCV	GCV	Heritability (%)	Genetic Advance (%)
Plant Height (cm)	852.300	960.612	108.312	29.095	27.406	88.7	53.178
Number of days to 50% flowering	297.656	317.356	19.700	19.491	18.876	93.8	37.658
Number of productive tillers	1.652	4.617	2.967	38.378	22.952	35.8	28.276
Culm thickness (mm)	0.005	0.007	0.002	12.489	10.555	71.4	18.377
Panicle length	8.930	9.838	0.908	13.980	13.320	90.8	26.142
Number of grains per panicle	559.675	581.275	21.600	19.730	19.360	96.3	39.133
1000 grain weight	33.361	35.376	2.015	26.546	25.779	94.3	51.571
Grain length	0.311	0.392	0.081	7.886	7.024	79.3	12.887
Grain breadth	0.180	0.195	0.015	16.716	16.059	92.3	31.783
L/B ratio	0.282	0.306	0.024	21.874	20.857	90.9	40.969
Protein content	3.716	4.087	0.371	21.874	20.857	90.9	40.969
Phenol content	0.009	0.010	0.001	31.803	30.128	89.7	58.794
Ascorbic acid	34.613	35.900	1.287	18.224	17.894	96.4	36.195
Reducing sugar	0.194	0.229	0.035	43.989	40.492	84.7	76.783

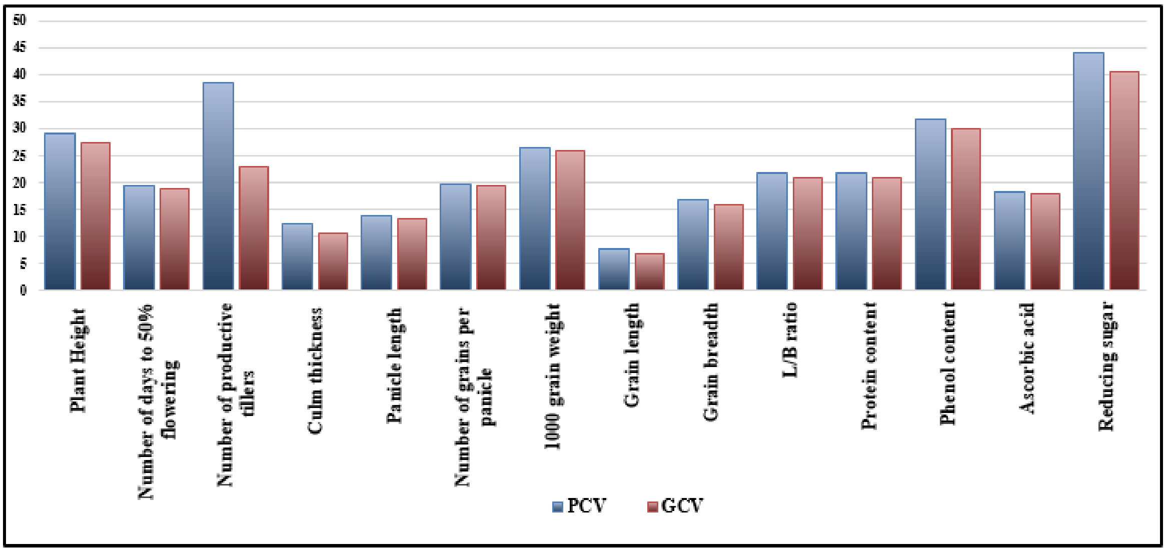

Figure 1. PCV and GCV of yield and yield-related traits in rice genotypes

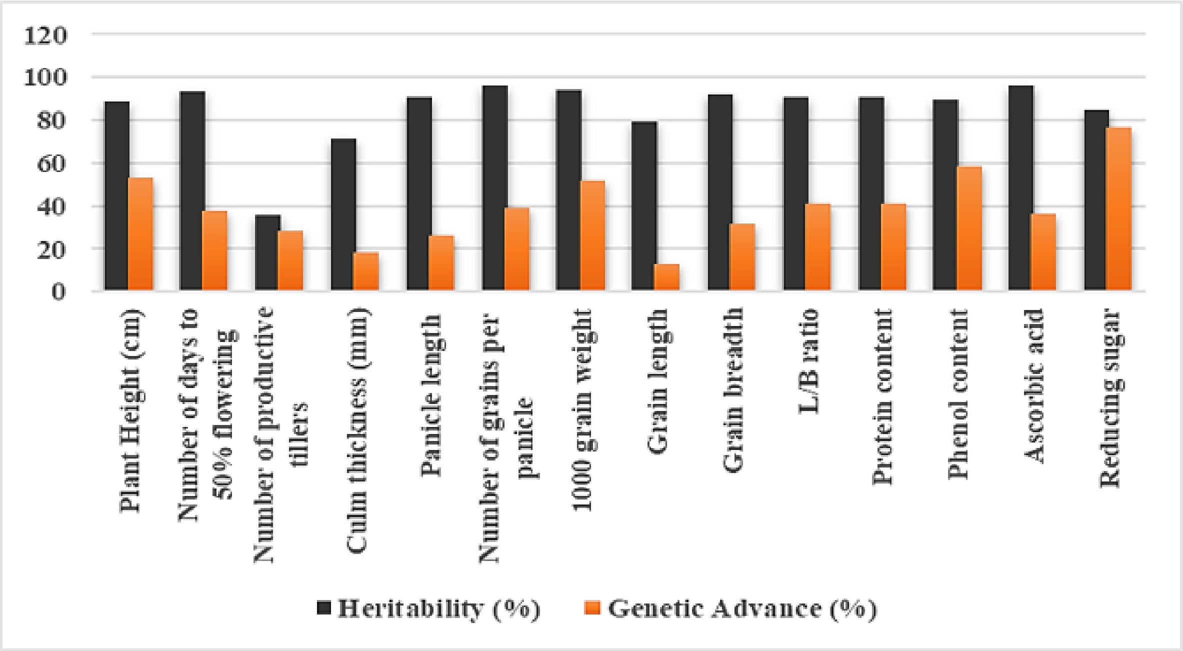

Figure 2. Heritability and genetic advance of yield and yield-related traits in rice genotypes

4. CONCLUSION

All the traits under study recorded a high phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV) indicating the presence of environment controlling the traits. But, the less difference between PCV and GCV implies that the involvement had a negligible role in the trait expression. High PCV and GCV were observed for the character's plant height, the number of productive tillers, 1000 grain weight, L/B ratio, protein content, phenol content, and reducing sugar, representing that these characters in genotypes are contributed by additive gene action and the direct selection will improve the trait easily. Among the traits studied, high heritability and genetic advance were obtained for plant height, number of days to 50% flowering, panicle length, number of grains per panicle, grain breadth, L/B ratio, protein content, phenol content, and ascorbic acid, representing that these characters are predominant in additive gene action.

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