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Research Article

Studies on Genetic Variability, Correlation and Path Coefficient Analysis in F_2 Derivatives of Co 51 × VGD 1 for Yield and Yield Component Traits in Rice (*Oryza Sativa* L.)

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Abstract

Rice is one of the most important staple food crops worldwide, and increasing its productivity is essential to meet the growing demand for food. Genetic variability and the identification of important yield-contributing traits play a crucial role in developing high-yielding rice varieties. The present study was undertaken to assess the genetic variability, heritability, genetic advance, correlation, and path coefficient of six quantitative traits in the F_2 segregating population derived from the cross CO 51 × VGD 1. Genetic parameters, including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability, and genetic advance as a percentage of the mean (GAM), were estimated to understand the nature and extent of genetic variation among the segregants. Among the traits evaluated, the number of productive tillers per plant and single plant yield exhibited high GCV and PCV, coupled with high heritability and genetic advance as a percentage of the mean, suggesting the predominance of additive gene effects and the potential for effective selection. Correlation analysis revealed a significant positive association between the number of productive tillers per plant and single plant yield. Furthermore, path coefficient analysis indicated a strong positive direct effect of productive tillers per plant on single plant yield. These findings suggest that the number of productive tillers per plant is an important yield-contributing trait and can serve as a reliable selection criterion for improving grain yield in rice. Overall, the study highlights the potential of the CO 51 × VGD 1 F_2 population as a useful genetic resource for selecting superior segregants and developing high-yielding rice varieties.

Keywords

Genetic Parameters, Selection, Additive Gene Action, F_2 Segregant

1. Introduction

Rice is the world's second most consumed cereal crop after wheat, providing over 20% of global caloric intake [1]. Asia, often termed the world's "Rice Bowl," accounts for more than 90% of global rice production and consumption (Patel et al., 2018). In India, rice dominates food grain production, covering approximately 41.27 million hectares and yielding 137 million tonnes in 2023–2024 [2]. However, to satisfy the growing global demand by 2050, production must reach nearly 810 Mt [3]. As developing nations achieve self-sufficiency and transition to exporting surplus grain, consumer preferences have shifted toward higher grain quality. Given the diverse demographics and cultural preferences across Asia

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and the rest of the world, defining universal quality attributes remains a challenge [4]. Addressing these demands requires yield enhancement through genetic improvement, which basically relies on understanding and exploiting genetic variability [5].

Heritability estimates the degree to which a trait of interest is transmitted to offspring during breeding cycles. Combined high genetic advance and high heritability enables rapid and effective selection for desired traits within a population [6]. Developing new varieties with improved economic attributes requires a thorough understanding of the relationships between grain yield and its yield-contributing components. Traits that exhibit high heritability and a positive correlation with yield serve as the most critical criteria for effective selection. Because these components can influence yield either directly or indirectly, analyzing inter-trait correlations is essential for simultaneous character improvement [7]. Furthermore, partitioning overall correlations into direct and indirect effects via path analysis clarifies the causal relationships between yield (the dependent variable) and its contributing traits (independent variables) [8]. Since segregating generations display high genetic segregation and recombination, they represent an ideal stage to impose selection [9]. Accordingly, the present investigation was undertaken to evaluate the variability, correlations, and cause-and-effect relationships governing grain yield.

2. Materials and Methods

The present investigation was conducted during 2019 at the Research Farm, Department of Plant Breeding and Genetics, Agricultural College and Research Institute (AC&RI), Madurai. The experimental material comprised F_2 segregants derived from the cross CO 51 ×VGD 1. CO 51 is a high-yielding variety (6,623 kg/ha) characterized by white, medium slender grains with high milling and head rice recovery. The male parent, VGD 1, features short slender grains with a mild aroma. A total of 350 F_2 segregants were raised, and 25-day-old seedlings were transplanted at a spacing of 20 ×20 cm under standard agronomic practices and crop protection measures. Out of the population, 150 individual plants were randomly selected to evaluate six quantitative traits: plant height (cm), number of productive tillers per plant, panicle length (cm), number of filled grains per panicle, hundred-grain weight (g), and single plant yield (g). Genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated according to Burton (1952). Broad-sense heritability (h^2) and genetic advance as a percentage of the mean (GAM) were calculated following Johnson et al. (1955). Phenotypic and genotypic correlation coefficients were determined using the formula proposed by Goulden (1952), and path coefficient analysis was conducted to partition the correlations into direct and indirect effects as outlined by Dewey and Lu (1959).

3. Results and Discussion

The present study revealed substantial variability among the F_2 segregants for all six quantitative traits evaluated. The mean performance recorded for the traits was 102.50 cm for plant height, 24.02 for number of productive tillers per plant, 24.92 cm for panicle length, 143.27 for number of filled grains per panicle, 1.38 g for hundred-grain weight, and 21.06 g for single plant yield. Wide range values were observed across the population: plant height ranged from 74.50 to 124.10 cm, productive tillers per plant from 13.00 to 34.00, panicle length from 14.20 to 34.20 cm, filled grains per panicle from 104.00 to 226.00, hundred-grain weight from 0.91 to 2.24 g, and single plant yield from 9.20 to 41.10 g.

Table 1. *Mean, range and estimates of genetic parameters for six traits in the F_2 generation of cross CO 51 × VGD 1.*

Characters	Mean	Range		PCV (%)	GCV (%)	h^2 in broad sense (%)	GA as% mean
		Min	Max				
Plant height (cm)	102.50	74.50	124.10	13.93	13.29	91.01	26.12
Number of productive tillers per plant	24.02	13.00	34.00	23.23	21.61	86.53	41.42
Panicle length (cm)	24.92	14.20	34.20	9.76	7.33	60.01	11.70
Number of filled grains per panicle	143.27	104.00	226.00	11.13	10.83	95.16	40.81
Hundred grain grain weight (g)	1.38	0.91	2.24	21.91	20.64	88.70	10.05
Single plant yield (g)	21.06	9.20	41.10	43.30	41.93	93.79	83.66

PCV = Phenotypic coefficient of variance; GCV = Genotypic coefficient of variance; h^2 = Heritability; GA - Genetic advance.

Among the six quantitative traits studied, high phenotypic and genotypic coefficients of variation (PCV and GCV) were

recorded for single plant yield (43.30% and 41.93%), number of productive tillers per plant (23.23% and 21.61%), and hundred-grain weight (21.91% and 20.64%). Similar trends were reported by Ray et al [10] for productive tillers per plant in the F_3 generation, as well as Ray et al [10] for hundred-grain weight and single plant yield in the F_4 generation. Moderate PCV and GCV values were exhibited by plant height (13.93% and 13.29%) and number of filled grains per panicle (11.13% and 10.83%), aligning with the findings of Tohid et al [11]. Conversely, low PCV and GCV estimates were observed for panicle length (9.46% and 7.33%), which accords with the results of Parari et al [12] in the F_2 generation. For all traits, PCV estimates were consistently higher than GCV estimates, indicating the influence of environmental factors on trait expression.

Heritability reflects the degree to which a trait is transmitted to subsequent generations during genetic segregation. To avoid over- or underestimating heritability due to seasonal and environmental interactions (i.e., season × generation effects), parents and offspring were evaluated under identical seasonal conditions. High heritability coupled with high genetic advance as a percentage of the mean (GAM) was recorded for single plant yield (93.79% and 83.66%), number of productive tillers per plant (86.53% and 41.42%), number of filled grains per panicle (95.16% and 40.81%), and plant height (91.00% and 26.12%). These observations agree with the findings of Khandappagol et al [13] and Priyanka et al [14]. On the other hand, hundred-grain weight (88.70% and 10.05%) and panicle length (60.00% and 11.70%) exhibited high heritability combined with moderate GAM, which is in agreement with earlier reports by Parari et al [12] and Vignesh et al [16].

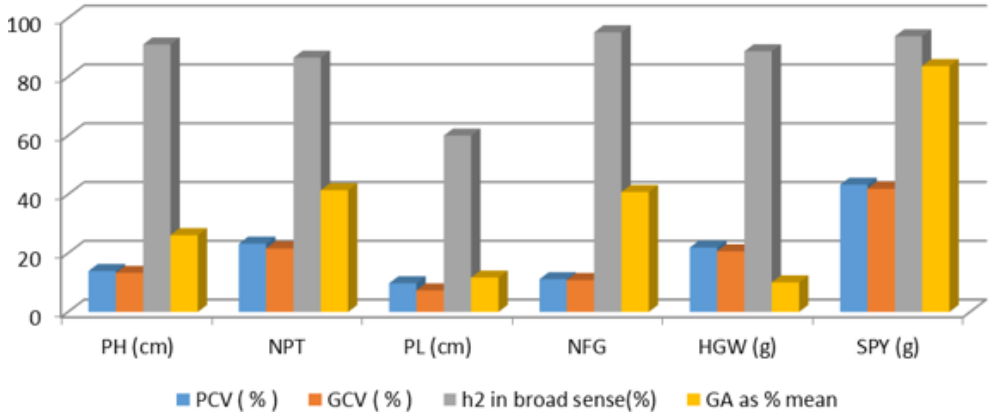


Figure 1. *PCV, GCV, Heritability and Genetic Advance as per cent mean for six quantitative traits in F_2 generation of the Cross CO 51 × VGD 1.*

PH - Plant height NFG - Number of filled grains per panicle; PL - Panicle length HGW - Hundred grain weight; NPT - Number of productive tillers per plant SPY - single plant yield.

Correlation analysis reveals the interrelationships between single plant yield and its component traits, serving as a fundamental basis for effective selection. In the present study, single plant yield exhibited a highly significant positive correlation with the number of productive tillers per plant (r = 0.614), panicle length (r = 0.345), and the number of filled grains per panicle (r = 0.184). These findings align with earlier reports by Bhutta et al. (2019) and Asante et al. (2019) for productive tillers per plant and panicle length, as well as Sarkar et al [17] for filled grains per panicle.

Plant height recorded a significant positive inter-correlation with panicle length (r = 0.431), consistent with the findings of Perves et al [18]. The number of productive tillers per plant also displayed significant positive inter-correlations with panicle length (r = 0.372), number of filled grains per panicle (r = 0.228), and hundred-grain weight (r = 0.177). A similar trend was observed by Agarwal et al [19] for panicle length and filled grains per panicle, and by Nanda et al [20] for hundred-grain weight.

Table 2. *Correlation coefficients among grain yield and yield components in F_2 generation of the Cross CO 51 × VGD 1.*

Characters	PH	NPT	PL	NFG	HGW	SPY
PH	1.000	- 0.075	0.431**	- 0.128	- 0.107	- 0.061
NPT		1.000	0.372**	0.228**	0.177*	0.614**

Characters	PH	NPT	PL	NFG	HGW	SPY
PL			1.000	0.080	0.053	0.345**
NFG				1.000	- 0.026	0.184*
HGW					1.000	0.093
SPY						1.000

*, ** Significant at P=0.05 and P=0.01

Path coefficient analysis was used to partition the correlations of five yield-contributing traits into direct and indirect effects on single plant yield. Productive tillers per plant exerted a high positive direct effect on yield (0.571), consistent with Manojkumar et al [21]. Panicle length showed a moderate indirect effect on yield through productive tillers per plant (0.213), supporting the results of Haleem et al [15]. Additionally, filled grains per panicle (0.131) and hundred-grain weight (0.101) exhibited low positive indirect effects on yield via productive tillers per plant.

Table 3. *Direct (diagonal) and indirect effects of six quantitative traits in F_2 generation of the Cross CO 51 × VGD 1.*

Characters	PH	NPT	PL	NFG	HGW	SPY
PH	0.069	-0.043	0.043	-0.007	0.005	0.016
NPT	-0.005	0.571	0.037	0.012	-0.008	0.614**
PL	0.030	0.213	0.099	0.004	-0.003	0.345**
NFG	-0.009	0.131	0.008	0.054	0.001	0.184*
HGW	-0.007	0.101	0.005	-0.001	-0.005	0.093

*Significant at 5% level ** Significant at 1% level Residual effect= 0.775
PH - Plant height NFG - Number of filled grains per panicle
PL - Panicle length HGW - Hundred grain weight
NPT - Number of productive tillers per plant SPY - single plant yield

4. Conclusion

The present investigation reveals that nearly all evaluated traits exhibited high GCV and PCV values, indicating substantial genetic variation within the selected cross. The close correspondence between GCV and PCV values across traits underscores a minimal environmental influence on phenotypic expression. Notably, the number of productive tillers per plant demonstrated a significant positive direct correlation with single plant yield, alongside positive indirect effects through the number of filled grains per panicle and hundred-grain weight. Given its high heritability coupled with high genetic advance, significant positive correlation, and strong direct contribution to single plant yield, the number of productive tillers per plant serves as an effective and reliable criterion for early-generation selection.

Abbreviations

F_2	Second Filial Generation
GCV	Genotypic Coefficient of Variation
PCV	Phenotypic Coefficient of Variation
h^2	Broad-Sense Heritability
GAM	Genetic Advance as Percentage of Mean
SPY	Single Plant Yield
PH	Plant Height
NPT	Number of Productive Tillers per Plant
PL	Panicle Length
NFGP	Number of Filled Grains per Panicle
HGW	Hundred-Grain Weight
cm	Centimetre
g	Gram
kg	Kilogram
ha	Hectare
Mt	Million Tonnes

Author Contributions

R. Sathishkumar: Conceptualization, Data curation, Formal Analysis, Investigation, Methodology, Writing – original draft, Writing – review & editing

R. P. Gnanamalar: Conceptualization, Formal Analysis, Investigation, Resources, Writing – review & editing

Conflicts of Interest

The authors declare no conflict of interests.

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