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Pushpanjali Kushawaha

Department of Genetics and Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Pooran Chand

Department of Genetics and Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Anjali

Department of Genetics and Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Nirdesh Kumar Chaudhary

Department of Genetics and Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Shiva Mohan

Department of Genetics and Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Corresponding Author:

Pushpanjali Kushawaha

Department of Genetics and Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Assessment of gene action for yield and its contributing traits in rice (*Oryza sativa* L.)

Pushpanjali Kushawaha, Pooran Chand, Anjali, Nirdesh Kumar Chaudhary and Shiva Mohan

Abstract

A total 55 genotype comprising ten parents and their forty-five crosses were presented to study the genetic components and their magnitude effects through diallel mating design. Gene action is a principle, measures of allelic interactions for traits that express the nature of phenotypic behavior, and leads to perfect selection of traits. This study was aimed to measure the allelic interactions of genes responsible for different quantitative traits which have strong association with yield and its contributing characters in rice. The estimates of additive component of genetic variation were highly significant for most of the traits, viz. grains per panicle, spikelet's per panicle, days to 50% flowering, days to maturity, plant height, gel consistency, harvest-index, biological yield per plant, hulling percentage, 1000-grain weight, kernel length after cooking, panicle length, and L/B ratio; except grain yield per plant. Dominance and epistatic interactions played a role in the inheritance of yield and grain quality characters in rice. It can be categorically stated reciprocal recurrent selection or diallel selective mating system are the need of the hour to modify e genetic architecture of rice for attaining higher yields with desirable properties.

Keywords: Rice, gene action, additive, non-additive, dominance, narrow-sense heritability

Introduction

Rice (*Oryza sativa* L.) is a member of the Poaceae family and the genus *Oryza*. It is native to Southeast Asia. Rice is a C₃ plant that has a short day, is hydrophilic, and is self-pollinated. Rice comes in two cultivated varieties and twenty-two wild varieties, with the cultivated varieties being *Oryza sativa* and *Oryza glaberrima*. *Oryza glaberrima* has been cultivated in West Africa for over 3500 years, while *Oryza sativa* is farmed all over the world. With approximately 1, 32,000 rice accessions kept in the International Rice Gene Banks as of December 2019, the International Rice Research Institute (IRRI) in the Philippines has the biggest collection of rice cultivars (IRRI, 2019). The tagline for the 2004 International Year of Rice was "Rice is Life," emphasizing the significance of rice.

Combining ability analysis provides information on additive and non-additive variances (*i.e.*, dominance and epistasis) which are important to decide the proper parents for hybridization to produce superior hybrids. The choice of parents particularly for heterosis breeding should be based on combining ability test and *per se* performance. Performances *per se* do not necessarily reveal which parents are good or poor combiners. To surmount this difficulty, it is necessary to gather information on the nature of gene actions. Non-additive gene types of activities are unreliable to correct, whereas additive gene types of actions or complementary epistatic gene interactions are reliable. There are numerous methods for determining the genetic make-up of cultivars. The ability to synthesize genotypes is dependent on a thorough understanding of the nature and quantity of gene action involved in agronomically relevant trait inheritance, as well as the selection of suitable parents and breeding methodology. A successful breeding programme requires the identification of donor parents for significant features, the assessment of genetic diversity in available germplasm, and an understanding of character connections.

Materials and Methods

Forty-five rice genotypes were grown in a randomized block design with three replications during *Kharif*, 2019-20 and 2020-21 at the technology park of Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut. Each genotype was sown in a 3 meter long row with 20 centimeter row spacing and 10 centimeter plant spacing.

The data were recorded on five competitive plants taken from each replication for days to 50% flowering along with days to maturity, plant height at maturity (cm), panicle length (cm), spikelet's per panicle, grains per panicle, 1000-grain weight (g), biological yield per plant (g), harvest-index (%), gel

consistency (mm), hulling percentage, L/B ratio, kernel length after cooking (mm) and grain yield per plant (g). The genetic components of variation were calculated by the methods suggested by Jinks and Hayman (1953), Hayman (1954) and Aksel and Johnson (1963)^[4, 1].

Table 1: Estimates of genetic components and their magnitude for 14 characters in rice

Component s	Days to 50% Flowering	Days to maturity	Plant height (cm)	Panicle length (cm)	Spikelet's per panicle	Grains per panicle.	1000-grain weight (g).	Biological yield per plant (g)	Harvest index (%)	Gel consistency (mm)	Hulling %	L/B ratio	Kernel length after cooking (mm)	Grain yield per plant (g)
D	56.30**	49.13**	13.40**	0.94**	66.04**	113.23**	2.28**	10.22**	14.41**	16.83**	9.38**	0.07**	2.26**	0.73
SE±	3.85	0.79	1.71	0.21	2.88	5.28	0.21	6.06	2.77	0.30	0.68	0.01	0.04	0.98
F	-19.31**	1.72	0.64	-0.39	-23.59**	126.78**	0.54	18.09	19.00**	8.92**	8.39**	0.01	0.76**	1.24
SE±	8.89	1.82	3.95	0.48	6.64	12.18	0.49	13.97	6.38	0.70	1.57	0.02	0.09	2.27
H ₁	53.29**	-0.56	14.87**	2.51**	20.27**	73.44**	2.65**	53.81**	46.70**	4.99**	6.92**	0.02	0.20**	12.23*
SE±	8.20	1.68	3.65	0.44	6.12	11.24	0.45	12.89	5.89	0.64	1.45	0.01	0.09	2.09
H ₂	45.52**	1.85	9.83**	2.44**	13.40**	37.99**	2.05**	34.28**	25.70**	3.65**	4.14**	0.02*	0.18**	9.43**
SE±	6.97	1.42	3.10	0.37	5.20	9.55	0.39	10.96	5.00	0.55	1.23	0.01	0.07	1.78
h ²	133.95**	52.04**	23.39**	17.37**	111.49**	229.00**	10.41**	58.97**	0.00	16.24**	18.15**	0.05**	1.25**	14.17*
SE±	4.67	0.95	2.07	0.25	3.48	6.39	0.26	7.33	3.35	0.37	0.82	0.01	0.05	1.19
E	3.70**	6.27**	3.55**	0.32**	7.83**	7.42**	0.38**	1.17	1.69	0.31	0.93**	0.01	0.18**	0.27
SE±	1.16	0.24	0.52	0.06	0.87	1.59	0.06	1.83	0.83	0.09	0.21	0.00	0.01	0.30
SQRT(H ₁ /d)	0.97	-	1.05	1.64	0.55	0.81	1.08	2.29	1.80	0.54	0.86	0.55	0.30	4.10
H ₂ /4H ₁	0.21	-0.82	0.17	0.24	0.17	0.13	0.19	0.16	0.14	0.18	0.15	0.22	0.23	0.19
KD/KR	0.70	-	1.05	0.77	0.51	5.56	1.24	2.26	2.16	2.90	3.17	1.44	3.60	1.52
h ² /H ₂	2.94	28.14	2.38	7.12	8.32	6.03	5.08	1.72	0.00	4.44	4.38	2.75	6.87	1.50
r	0.155	0.669	-0.463	-0.965	-0.764	-0.857	-0.887	-0.859	0.528	-0.873	-0.941	-0.609	-0.790	-0.252
Heritability (ns)	39.17	68.02	32.21	18.14	46.61	126.05	38.52	20.16	29.42	119.40	80.63	60.12	93.45	5.64

*, ** significant at 5% and 1% level, respectively

(D=Additive variance, F=Mean of covariance of additive and dominance effects over all arrays, H₁=Dominance variance, H₂=Proportion of positive and negative gene, h=Net dominance effect, E= Environmental component variation, sqrt(H₁/d)=Average degree of dominance, H₂/4H₁=Proportion of dominant gene with positive and negative effect, (KD/KR)=Ratio of dominant and recessive genes, h²/H₂=Number of gene groups, SE±=Significant error).

Results and Discussion

Estimates of genetic components and their magnitude

The estimates of components of genetic variations and its proportional contribution *viz.* variance component due to additive gene effects (D), variance component due to dominance deviation (H₁), estimate of dominance genetic variance due to proportion of positive and negative genes (H₂), net dominance effect (h²), mean of covariance of additive and dominance effects over all arrays (F), environmental component of variation (E), Average degree of dominance, proportion of dominant gene with positive and negative effect, the ratio of dominance and recessive genes, proportion of genes/gene blocks exhibiting dominance, narrow sense heritability of diallel matings are given in the estimates of additive component of genetic variation (D) were highly significant for most of the traits, *viz.* grains per panicle, spikelet's per panicle, days to 50% flowering, days to maturity, plant height, gel consistency, harvest-index, biological yield per plant, hulling percentage, 1000-grain weight, kernel length after cooking, panicle length, and L/B ratio; except grain yield per plant.

The estimates of dominance components (H₁, and H₂) were highly significant for the traits, *viz.* grains per panicle, biological yield per plant, days to 50% flowering, harvest-index, spikelet's per panicle, plant height, grain yield per plant, hulling percentage, gel consistency, 1000-grain weight,

panicle length, and kernel length after cooking except days to maturity and L/B ratio.

In general, estimates of dominance components (H₁, and H₂) were higher than additive component (D) for plant height, panicle length, 1000-grain weight, biological yield per plant, harvest-index, and grain yield per plant, while the remaining traits, *viz.* days to 50% flowering, days to maturity, spikelet's per panicle, grains per panicle, gel consistency, hulling percentage, L/B ratio, and kernel length after cooking showed higher additive variance than dominance variance.

The estimates of net dominance effect, *i.e.*, h², were positive and significant for grains per panicle, days to 50% flowering, spikelet's per panicle, biological yield per plant, days to maturity, plant height, hulling percentage, panicle length, gel consistency, grain yield per plant, 1000-grain weight, kernel length after cooking, and L/B ratio, while nil for harvest-index.

The estimates of mean of covariance of additive and dominance effect over all arrays (F) were significant and positive for grains per panicle, harvest-index, gel consistency, hulling percentage, and kernel length after cooking, signifying that these traits were controlled by excess of positive genes.

The estimates of average degree of dominance (H₁/D)^{1/2} were higher than the unity for most of the traits, suggesting the presence of over-dominance type of intra-allelic interactions. The estimates were higher to unity for plant height, panicle

length, 1000-grain weight, biological yield per plant, harvest-index, and grain yield per plant, suggesting complete to over-dominance for the trait. While remaining traits average degree of dominance were observed less than unity.

The proportion of dominant gene with positive and negative effects ($H_2/4H_1$) was found close to the expected value of 0.25 for most of the traits, suggesting nearly symmetrical distribution of positive and negative alleles at loci showing dominance for the traits, except for the days to maturity.

The ratio of dominance to recessive genes, *i.e.*, KD/KR was greater than unity for all the traits except days to 50% flowering, panicle length, and spikelet's per panicle suggesting presence of an excess of dominant genes in parental lines. However, days to 50% flowering, panicle length, and spikelet's per panicle indicating an excess of recessive genes for these traits.

The ratio of number of genes/genes blocks exhibiting dominance (h^2/H_2) Estimated range from 0.00 (harvest-index) to 28.14 (days to maturity) for various traits, which indicated that at least one to two genes or group of genes showing dominance were present for different traits. The result indicates that most of the traits were controlled by two gene or gene groups exhibiting dominance, except for the harvest-index.

The estimate of narrow sense heritability were observed for grains per panicle (126.05), followed by gel consistency (119.40), kernel length after cooking (93.45), hulling percentage (80.63), days to maturity (68.02), L/B ratio (60.12), spikelet's per panicle (46.61), days to 50% flowering (39.17), 1000-grain weight (38.52), plant height (32.21), harvest-index (29.42), biological yield per plant (20.16), panicle length (18.14), and grain yield per plant (5.64).

The non-additive gene effects may also be exploited to some extent for improving the characters by resorting to breeding methods such as biparental mating followed by recurrent selection and population improvement methods as suggested by Redden and Jensen (1974)^[9].

Nagaraju *et al.* (2015), Vennila *et al.* (2017), Thirumalai *et al.* (2018), Parimala *et al.* (2018), Kirubha *et al.* (2019), Vange *et al.* (2020), Ganapati *et al.* (2020) and Gaballah *et al.* (2022)^[7, 12, 10, 8, 6, 11, 3, 2] have also presented similar kind of results in their findings.

Conclusion

The estimates of additive component of genetic variation were highly significant for grains per panicle, spikelet's per panicle, days to 50% flowering, days to maturity, plant height, gel consistency, harvest-index, biological yield per plant, hulling percentage, 1000-grain weight, kernel length after cooking, panicle length, and L/B ratio.

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