International Journal of Multidisciplinary Research and Development
www.allsubjectjournal.com
Online ISSN: 2349-4182, Print ISSN: 2349-5979
Received: 11-05-2021, Accepted: 26-05-2021, Published: 10-06-2021
Volume 8, Issue 6, 2021, Page No. 10-12

Genetic analysis for quantitative traits in rice (*Oryza Sativa* L.)

KK Barhate, DN Borole, VV Bhavsar, SS Sahane
Botany Section, College of Agriculture, Dhule, Maharashtra, India

Abstract

The magnitude of dominance and dominance x dominance gene effects was recorded higher than additive gene effects for most of the character studied. Duplicate epitasis was observed for the character like plant height, Panicle length, productive tillers per plant, number of seeds per plant and days to 50% flowering in almost majority of crosses, while complimentary epitasis was observed for most of the cross combinations in test weight except KMR-1-41 x VL-311320 and seed yield except Indrayani x KJT-2.Additive and additive x additive gene effect were more effective than dominance in the charecters and crosses are improved by simple selection method. Significant epistastic gene effects coupled with duplicate epitasis indicating that the effective selection and transgressive segregents could be obtained in subsequent generations. The selection in such a case has to be postponed until virtual homozygocity is attended.

Keywords: genetic studies, inheritance, gene action, five generation model, rice, *Oryza sativa* L

Introduction

The success of plant breeding programme depends to a greater extent on the knowledge of the genetic architecture of the population and selection of appropriate breeding method for the improvement of traits of interest. It is essential to estimate the various types of gene action for the selection of appropriate breeding procedure to improve the quantitative and qualitative characters.

The choice of breeding methods for genetic improvement of a crop depends upon the nature and magnitude of genetic variability present. It is usually not directly measurable. One can measure only the phenotypic expression of genetic values as modified by the environment. This partitioning has provided a better knowledge for genetic analysis of quantitatively varying traits. The further partitioning of epistatic component into additive × additive, additive × dominance and dominance × dominance. Such partitioning of variability into various components needs variance estimates from a number of specifically related generations. Generations mean analysis as suggested by Hayman (1958) provides all kinds of non-allelic interaction precisely in addition to the additive and dominance gene effects. The magnitude of additive gene effect is particularly useful in the development of pureline varieties. Generation mean analysis is a relatively simple and statistically reliable tool suitable for preliminary estimation of various gene effects. Estimation and interpretation of non-allelic interactions are more progressive with generation mean analysis as it utilizes the first order statistics which are less compounded with each other when compared with variance estimates. Intermating of selected segregants and postponement of selection to later generation might be suggested to break undesirable linkages in order to improve yield.

Keeping in view the above aspects in present study, generation mean analysis for yield contributing traits in rice was undertaken to find out gene effects controlling in four crosses.

Materials and Methods

The eight genetically diverse parents *viz*. Indrayani, KJT-2, Phule Samruddhi, NLR-20104, VDN-11-37-1-1-1, CB-06-555, KMR-1-41 and VL-311320 were used for present study. Five different generations were obtained and these five generations of four crosses were evaluated in RBD with three replications.

The nature and magnitude of gene effects were estimated for yield and yield components *viz*., days to 50 % flowering, plant height, tillers per plant, panicle length, seeds per panicle, 1000 grain weight and seed yield per plant.

All recommended agronomic practices were carried out as and when required. Total dose of fertilizer applied during crop duration was 100 kg N, 50 kg P_2O_5 and 50 kg K_2O per hectare. Nitrogen was applied in three split doses of 40, 30 and 30 kg N per hectare at paddling i.e. transplanting, 35-40 days after transplanting and 60 days i.e. panicle stage, respectively. Total dose of P_2O_5 and K_2O were applied at the time of transplanting.

The analysis of variance was done as suggested by Panse and Sukhatme (1985) this analysis is based on five populations, P_1, P_2, F_1, F_2, and F_3. Hayman (1958) developed the five parameter model for the estimation of various components of genetic variance.

Results and Discussions

The estimates of major gene effects (m and d) and digenic interactions (h, i and l) studied for different characters in the three crosses are presented in table 1

The parameter ‘m’ was significant in all the cross combinations and all the characters studied.

Table 1: Gene action for different characters in Rice.

Sr. No.	Characters	Crosses	Generation mean					Gene Action
			m	d	h	I	l	
1	Days to 50% flowering	Indrayani X KJT-2	102.67**	-4.00**	-2.67**	7.66**	-16.00**	Complimentary
		Phule Samruddhi X NLR-20104	100.33**	-2.67	0.22	4.89**	-25.78**	Duplicate
		VDN-11-37-1-1-1 X CB-06-555	98.67**	-2.50	0.00	4.83**	-26.67**	Duplicate
		KMR-1-41 X VL-311320	100.67**	-2.67	0.67	6.00**	-24.00**	Duplicate
2	Plant height	Indrayani X KJT-2	92.42**	1.03	0.12	0.36	-3.51**	Duplicate
		Phule Samruddhi X NLR-20104	96.17**	-1.86	1.00**	-0.13	-4.00**	Duplicate
		VDN-11-37-1-1-1 X CB-06-555	101.68*	-0.53	10.97	10.43**	-37.47**	Duplicate
		KMR-1-41 X VL-311320	99.87**	-1.00	5.51**	3.91**	-40.36**	Duplicate
3	Productive Tillers per plant	Indrayani X KJT-2	16.92**	1.07	3.48**	1.94	-5.56	Duplicate
		Phule Samruddhi X NLR-20104	16.22**	2.30*	2.92*	-0.44	0.76	Duplicate
		VDN-11-37-1-1-1 X CB-06-555	17.70**	2.50*	7.53**	3.76**	-11.46**	Duplicate
		KMR-1-41 X VL-311320	16.46**	2.30*	7.02**	5.52**	-18.84**	Duplicate
4	Panicle length	Indrayani X KJT-2	20.60**	0.33	1.47	2.13*	-6.40**	Duplicate
		Phule Samruddhi X NLR-20104	19.73**	0.33	-1.96	-2.48*	10.31**	Duplicate
		VDN-11-37-1-1-1 X CB-06-555	20.00**	0.33	7.07**	7.13**	-11.20**	Duplicate
		KMR-1-41 X VL-311320	19.20**	-0.10	6.88**	6.52**	-15.11**	Duplicate

Sr. No.	Characters	Crosses	Generation mean					Gene Action
			m	d	h	i	l	
5	Seeds per panicle	Indrayani X KJT-2	167.33**	-0.11	14.14**	13.70**	-42.96**	Duplicate
		Phule Samruddhi X NLR-20104	162.89**	6.22**	31.04**	26.93**	-10.96**	Duplicate
		VDN-11-37-1-1-1 X CB-06-555	181.33**	4.66**	12.52**	7.63**	-54.82**	Duplicate
		KMR-1-41 X VL-311320	160.44**	5.83**	0.52	-0.76	18.07**	Duplicate
6	1000 grains weight	Indrayani X KJT-2	22.46**	-0.80	1.11	-1.46	8.19**	Complimentary
		Phule Samruddhi X NLR-20104	22.30**	1.17	0.93	-2.17*	9.60**	Complimentary
		VDN-11-37-1-1-1 X CB-06-555	20.60**	1.89	8.22**	5.14**	3.56**	Complimentary
		KMR-1-41 X VL-311320	19.70**	2.07*	5.31**	4.41**	-4.36**	Duplicate
7	Seed yield per plant	Indrayani X KJT-2	68.86**	7.60**	-5.29**	-26.02**	75.91**	Duplicate
		Phule Samruddhi X NLR-20104	69.92**	11.63**	15.25**	-8.17**	32.48**	Complimentary
		VDN-11-37-1-1-1 X CB-06-555	75.90**	16.53**	2.82*	-12.17**	8.09**	Complimentary
		KMR-1-41 X VL-311320	71.88**	11.53**	1.14	-14.06**	13.9**	Complimentary

Days to 50% flowering

As regards the gene effects, all the gene actions m,i, and l were statistically significant indicating presence of all gene actions except for d and h in the cross Phule Samruddhi x NLR-20104, VDN-11-37-1-1-1 X CB-06-555, KMR-1-41 X VL-311320. Dominant gene effect (d) was predominant in all the crosses. Duplicate type of epistasis was also involved in the inheritance of this character in all the crosses except in cross Indrayani x KJT-2.

Plant height

Additive (d), dominance (h) and epistatic gene effects (m, i and l) were significant in all four crosses. The magnitude of additive gene effect (d) was higher than dominance gene effect in the cross Indrayani x KJT -2whilethe magnitude dominance gene effect (h) was higher than additive gene effect in the crosses such as Phule Samruddhi x NLR-20104, VDN-11-37-1-1-1 x CB-06-555 and KMR-1-41 X VL-311320, all the crosses indicating the character was controlled by dominance gene action. All the crosses showed duplicate gene action.

Tillers per plant

Additive (d), dominance (h) and epistatic gene effects (m, i and l) were significant in all four crosses. Dominance (h) gene effect was governed predominantly this trait in all the four combinations. The duplicate type of interaction was observed in all the crosses except Phule Samruddhi x NLR-20104.

Panicle length

Predominance of dominance (h) gene effects was found in all the crosses. Dominance (h) gene effects were important for inheritance of panicle length in all the crosses. Duplicate type of epitasis was found in the all crosses.

Seeds per panicle

Seeds per panicle were governed predominantly by dominance gene effects exceptKMR-1-41 X VL-311320. Additive (d), dominance (h) and all epistatic gene actions (m, i and l) were significant in all three crosses. The duplicate type of epistasis was observed in all crosses except complementary type of interaction was found in the cross KMR-1-41 X VL-311320.

1000 grains weight

Additive gene effect (d) was predominant in the cross Phule Samruddhi x NLR-20104. Predominance of dominance (h) gene effects was found in all crosses except Phule

Samruddhi x NLR-20104. Complementary type of epitasis was observed for all crosses except KMR-1-41 x VL-311320.

Seed yield per plant

Seed yield per plant was predominantly controlled by additive (d) gene effects in all the combinations except Phule Samruddhi x NLR-20104. The epistatic gene effects (i, m and l) were found significant in all four crosses. Complementary type of epistasis was observed for all crosses except in the cross Indrayani x KJT-2.

The magnitude of dominance gene effects was recorded higher than additive gene effects for most of crosses in the traits like days to 50 % flowering, productive tillers per plant, plant height, seeds per panicle, 1000 grain weight and panicle length. The magnitude of dominance and dominance x dominance gene effects was recorded higher than additive gene effects for most of the character studied. Duplicate epitasis was observed for the character like plant height, Panicle length, productive tillers per plant, number of seeds per plant and days to 50% flowering in almost majority of crosses, while complimentary epitasis was observed for most of the cross combinations in test weight except KMR-1-41 x VL-311320 and seed yield except Indrayani x KJT-2. Additive and additive x additive gene effect were more effective than dominance indicating that characters can be improved by simple selection method. Significant epistastic gene effects coupled with duplicate epistasis indicating that the effective selection and transgressive segregants could be obtained in subsequent generations. The selection in such a case has to be postponed until virtual homozygocity is attended. The results were conformity with Sinha *et al* (2006) [17], Singh *et al* (2007) [16], Manickavelu *et al* (2006) [12], Biswas and Haque (2007) [2], Dwivedi, and Pandey (2012) [4], Tiwari *et al* (2012) [18], El-Lattef *et al* (2012) [5], Chamundeswari *et al* (2013) [3], Ghose *et al* (2013) [6], Yadav *et al* (2013) [19], Koli *et al* (2014) [10], Girija *et al* (2015) [7], Savitha and Kumari (2015) [15], Patel (2015) [14], Barhate *et al* (2016) [1] and Kasture *et al* (2016) [9].

Acknowledgements

Authors are duly acknowledged Agricultural Research Station, Vadgaon Maval for providing the facilities to conduct the research trial.

References

1. Barhate KK, Kashid NV, Meena RK. Genetic studies in rice (Oryza sativa, L), Int. Research J. Multidisciplinary Studies,2016:2(5):2454-8499.
2. Biswas PSM, Enamul Haque. Gene action of agronomic traits in rice (*oryza sativa* l.). Bangladesh J. Pl. Breed. Genet,2007:20(2):31-36.
3. Chamundeswari N, Satyanarayana PV, Suryanarayana Y, Reddy RK: Rice; Grain Yield; Inheritance; Generation Mean Analysis; Epistasis; Gene action. Oryza-An Inter J. Rice,2013:50(2):105.
4. Dwivedi DK, Pandey MP. Gene Action and Heterosis for Yield and Associated Traits in Indica and Tropical Japonica Crosses of Rice (*Oryza sativa* L.) Involving Wide Compatibility gene (s): Inter. J. of Plant Breed and Genet,2012:6:140-150.
5. El-Lattef, Asm Abd, Khalifa Aab Abo, El-Gohary Aaa. Inheritance of some quantitative characters under drought conditions in rice (*Oryza sativa* L.). IJBPAS, 2012:1(5):620-635.
6. Ghosh SC, Chandrakar PK, Rastogi NK. Gene action and fertility restoration behavior of the tropical japonica / indica, japonica / indica derived restores in rice (Oryza sativa L.). Indian J. of Gen. and Plant Breed, 2013:73(1):23-28.
7. Girija RM, Satyanarayana PV, Lal AM, Ashok RY, V Srinivasa R. Gene action of elite rice lines for yield and lodging resistance related traits. Res on Crops, 2015:16(4):689-697.
8. Hayman BI. The separation of epistatic from additive and dominance variation in generation mean, Heredity,1956:23:403-409.
9. Kasture AG, Patel VP, Vanave PB. Study of Genetic Components for Yield Attributing Traits in Rice. Oryza sativa L. Trends in Biosciences,2016:8(8):0976-2485.
10. Koli NR, Chandra P, Mahawar RK, Kumhar BL, Punia SS. Detection of epitasis, additive and dominance variation in rice (*Oryza sativa* L.) using triple test cross analysis. Electronic J of Plant Breed,2014:5(4):632-635.
11. Kumar Sanjeev, Singh HB, Sharma JK. Mode of gene action for grain yield, its components and grain quality traits in non-segregating generation (F_1) of rice. Oryza,2008(b):45(2):152-155.
12. Manickavelu A, Nadarajan N, Ganesh SK, Gnanamalar. Genetic analysis of biparental progenies in rice (Oryza sativa L.). Asian J. Plant Sci,2006:5(1):33-36.
13. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. ICAR, New Delhi,1985,137-139.
14. Patel KS. Genetic analysis for yield and its components traits in rice (Oryza sativa L.) Electronic J. Plant Breed, 2015:6(1):19-25.
15. Savitha P, Kumari UR. Gene effects and genetic analysis of indigenous land races and improved cultivars for yield and yield components in rice (*Oryza sativa* L.) International Journal of Agriculture, Environment and Biotechnology Citation: IJAEB, 2015:8(3):489-499.
16. Singh NK, Singh PK, Singh ON, Singh Sanjay, Dwived i JL, Giri SP *et al.* Gene effects and selection parameters in rainfed low land rice. Oryza, 2007:44(4):291-295.
17. Sinha PK, Mandal NP, Prasad C, Prasad K. Genetic analysis for grain yield and its components in upland rice. Oryza,2006:43(1):5-9.
18. Tiwari DK, Panday Pravin, Giri SP, Dwivedi JL. Nature of gene action and combining ability for yield and its related traits in hybrid rice. Oryza- An Int. J. on Rice,2012:48(4):288-296.
19. Yadav HN, Prasad R, Singh SP, Singh RP, Agrawal RK Scaling test, Generation Mean Analysis, Heterosis and inbreeding depression. Oryza-An Int. J. on Rice,2013:50(2):115.