



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.03
TPI 2020; 9(10): 473-477
© 2020 TPI
www.thepharmajournal.com
Received: 04-08-2020
Accepted: 07-09-2020

AG Singh
Department of Genetics and
Plant Breeding, Navsari
Agricultural University, Navsari,
Gujrat, India

PB Patel
Department of Genetics and
Plant Breeding, Navsari
Agricultural University, Navsari,
Gujrat, India

Generation mean analysis for yield and its components in rice (*Oryza Sativa L.*)

AG Singh and PB Patel

Abstract

The experiment was carried out during summer and *kharif* 2018-19 at Main Rice Research Centre, Navsari Agricultural University, Navsari. Six diversified elite lines of rice (IET-24772, IET-24783, GNR-2, GNR-3, GR-11 and GR-15) were used to study five generations (P₁, P₂, F₁, F₂ and F₃) analysis of quantitative and qualitative traits for eleven characters. The results of additive - dominance model from the scaling tests showed that for all eleven characters evaluated in all the three crosses were inadequate, suggested the existence of epistasis interaction in the inheritance of these characters. On the basis of five parameters model, significant main effects *viz.*, mean (m), additive (d) and dominance (h) and two digenic interactions additive x additive (i) and dominance x dominance (l) were recorded for days to flowering in all the three crosses; days to maturity, grain per panicle and amylose content in cross-I (IET-24772 x IET-24783) and cross-II (GNR-2 x GNR-3); plant height, 100 grain weight, L:B ratio and protein content in cross-II (GNR-2 x GNR-3) and cross-III (GR-11 x GR-15); productive tillers per plant and straw yield per plant in cross-I (IET-24772 x IET-24783); for grain yield per plant in cross-I (IET-24772 x IET-24783) and cross-III (GR-11 x GR-15) indicated the involvement of additive, dominance as well as epistasis interaction for controlling these traits. The duplicate epistasis was recorded for days to flowering, days to maturity, productive tillers per plant and 100 grain weight all the three crosses; plant height in cross-I (IET-24772 x IET-24783); grain per panicle and grain yield per plant in cross-I (IET-24772 x IET-24783) and cross-III (GR-11 x GR-15); L:B ratio in cross-II (GNR-2 x GNR-3) and cross-III; straw yield per plant, protein content and amylose content in cross-I (IET-24772 x IET-24783) and cross-II (GNR-2 x GNR-3).

Keywords: Five generation analysis, scaling test, rice, additive dominance model

Introduction

Rice (*Oryza sativa L.*), the most important agronomical crop, occupies the enviable position around the world. Being a major cereal crop, nutritionally it is one of the world's most important staple foods, with greater portion of the world's population dependant on it for a significant proportion of their caloric intake in the rate of 20 per cent daily calories. India is the largest rice cultivator which accounts for almost thirty per cent rice area of the world's. India is the largest rice growing country, while China is the largest producer of rice.

The world population is expected to reach 8.27 billion by 2030 demanding an increased rice production of 771 million tonnes (Badawi, 2014) [2]. Traits which are directly or indirectly related to economic value are prime concerned for plant breeders which helps in the improvement of those such traits that are generally quantitative in nature and controlled by several number of genes each having small effect acting in cumulative manner, such genes are called polygene (Mather, 1943) [1]. The gene action knowledge provides wider prospective in selection of parents for use in hybridization programmes.

Phenotypic performances based on measurements of quantitative traits, generation mean analysis plays important role as one of the quantitative biometric method. For estimating gene effects generation mean analysis provides useful information regarding (additive and dominance) and their digenic (additive x additive and dominance x dominance) interactions in plant breeding for studying inheritance of quantitative traits. It helps us in understanding the performance of the parents used in crosses and potential of crosses to be used either for heterosis exploitation or pedigree selection.

Materials and Methods

Six diversified elite lines of rice (IET-24772, IET-24783, GNR-2, GNR-3, GR-11 and GR-15) comprised as experimental material selected on the basis of their variation in morphological characters.

Corresponding Author:
AG Singh
Department of Genetics and
Plant Breeding, Navsari
Agricultural University, Navsari,
Gujrat India

The three crosses (IET-24772 x IET-24783, GNR-2 x GNR-3 and GR-11 x GR-15) obtained by crossing of six diverse parents during summer-2018 at Main Rice Research Centre, Navsari Agricultural University, Navsari. F₁s were produced during summer-2018. Selfing of F₁s was done in the *kharif*-2018 to get F₂s. F₃s were produced during summer-2019. The evaluation trial was conducted with all five generations of three crosses along with standard check GNR-7 in *kharif*-2019 at Main Rice Research Centre, Navsari Agricultural University, Navsari. Five generations (P₁, P₂, F₁, F₂ and F₃) of each of the three crosses were sown during *kharif*-2019 in compact family block design with three replications. Each three crosses consisting of five generations were randomly allotted to each plot. Each plot consisted of two rows of parents and F₁s, thirty rows of the F₂ and fifteen rows of the F₃ generations of each cross. Twenty plants were planted in each row.

Results and Discussion

All the five generations *viz.*, P₁, P₂, F₁, F₂ and F₃ with their mean values for eleven different characters of all the three crosses *viz.*, cross-I (IET-24772 x IET-24783), cross-II (GNR-2 x GNR-3) and cross-III (GR-11 x GR-15) were first subjected to simple scaling tests (C and D). The adequacy of additive-dominance model was more precisely tested by joint scaling test (Cavalli, 1952) [4] which effectively combines the whole set of simple scaling tests. The application of individual scaling tests C and D of Mather (1949) [3] showed that additive-dominance model was found inadequate for all the eleven traits *viz.*, days to flowering, days to maturity, plant height, productive tillers per plant, grains per panicle, 100 grain weight, grain yield per plant, straw yield per plant, L:B ratio, protein content and amylose content indicated presence of greater amount of epistasis for different characters in most of the crosses (Table 1 to Table 3).

The values for individual scaling tests and estimates of mean (m), additive gene effect (d), dominance gene effect (h) and epistatic interactions *viz.*, additive x additive (i), and dominance x dominance (l) interactions are presented in table 1, 2 and 3 respectively. Presence of epistasis was revealed from the individual scaling tests C and D for all the traits in almost all the crosses. This indicated that the genetic variation could not be described to additive and dominance effect alone but epistasis also plays a major role.

Five parameters model result revealed that in addition to the significance of mean (m), additive (d) dominance (h) effects and the two digenic interactions additive x additive (i) and dominance x dominance (l) were significant for days to flowering in cross-I, cross-II and cross-III; days to maturity, grain per panicle and amylose content in cross-I and cross-II; plant height, 100 grain weight, L:B ratio and protein content in cross-II and cross-III; productive tillers per plant and straw yield per plant in cross-I; and grain yield per plant in cross-I and cross-III. Same results were obtained by Nayak *et al.* (2007) [5], Singh *et al.* (2007) [6], Roy and Senapati (2011) [7], Samak *et al.* (2011) [8], Kiani *et al.* (2013) [9], Montazeri *et al.* (2014) [10], Shahid *et al.* (2014) [11], Patel *et al.* (2015) [12], Rani *et al.* (2015) [13], Sultana *et al.* (2016) [14] and Kumar *et al.* (2017) [15].

The highly significant mean values in all the crosses from the estimation of generation mean analysis showed that the five generation differed from each other and these all studied traits are quantitatively inherited. The additive (d) gene effect found significant and positive in cross-II and cross-III in days to

flowering, cross-II in days to maturity, productive tillers per plant and grain per panicle, cross-I and cross-III in plant height and amylose content (%), cross-I in 100 grain weight, all the three cross in L:B ratio, cross-I and cross-II in protein content (%).

Similarly, significantly negative additive (d) effect were found in cross-I in days to flowering and days to maturity; cross-II in plant height and amylose content; cross-I and cross-III in productive tillers per plant, grain per panicle and grain yield per plant, cross-II and cross-III in 100 grain weight, cross-I and cross-II in straw yield per plant and cross-III in protein content (%). Simple pedigree selection can be employed to exploit additive component of variation. Mass selection in addition to single plant selection helps in changing the frequencies of desirable genes in heterozygous population. Non-fixable (h and l) component together with duplicate type of epistasis interfere with the improvement in the traits so selection is delayed to later generations. Nayak *et al.* (2007) [5], Singh *et al.* (2007) [6], Roy and Senapati (2011) [7], Samak *et al.* (2011) [8], Kiani *et al.* (2013) [9], Montazeri *et al.* (2014) [10], Shahid *et al.* (2014) [11], Patel *et al.* (2015) [12], Rani *et al.* (2015) [13], Sultana *et al.* (2016) [14] and Kumar *et al.* (2017) [15] were agreement with these results.

The hybrid showing positive and significant dominance (h) effects for days to flowering in cross-III, plant height in all the three crosses, productive tillers per plant in cross-III, grain per panicle in cross-II and cross-III, 100 grain weight and L:B ratio cross-II, grain yield per plant in cross-I and cross-II, protein content in cross-III, amylose content in all the three crosses. Same results were obtained by Nayak *et al.* (2007) [5], Singh *et al.* (2007) [6], Roy and Senapati (2011) [7], Samak *et al.* (2011) [8], Rani *et al.* (2015) [13] and Sultana *et al.* (2016) [14].

Significantly negative dominance (h) effect were observed for days to flowering and protein content in cross-I and cross-II, days for maturity in all the three crosses; productive tillers per plant and grain per panicle and straw yield per plant in cross-I; 100 grain weight and grain yield per plant and L:B ratio in cross-III, respectively.

The result shows that dominance effect plays a major role in the expression of most of the characters taken under study as the magnitude of dominance (h) component was higher than that of additive (d) effect. Non-conventional breeding procedure might be adopted for the exploitation of dominance effect (Gamble, 1962) [16].

Considering the contribution of epistasis gene effect, dominance x dominance (l) interaction had enhancing impact as compared to additive x additive (i) in case of days to flowering, productive tillers per plant and grain per panicle in cross-I and cross-II, days to maturity and protein content in all the three crosses, straw yield per plant in cross-I; plant height and grain yield per plant in cross-II and cross-III; 100 grain weight and amylose content in cross-III and L:B ratio in cross-I and cross-III. The positive sign of dominance x dominance (l) component in these crosses indicates their enhancing impact in the expression of that character in all three crosses of rice.

The dominance x dominance (l) effect was recorded to be significantly negative for days to flowering in cross-III; plant height and grain yield per plant in cross-I; productive tillers per plant in cross-III; 100 grain weight and amylose content in cross-I and cross-II; L:B ratio in cross-II respectively.

The additive x additive (i) interaction showed significantly positive value in case of days to flowering in cross-II and

cross-III; days to maturity, grain per panicle, protein content in cross-II; plant height in cross-I and cross-III; grain yield per plant and 100 grain weight in cross-I; L:B ratio and amylose content in all the three crosses. Cyclic method of breeding can be employed in these crosses in which desirable recombinants are selected and intercrossed.

The additive x additive (i) interaction showed significantly negative value in case of days to flowering, days to maturity, and grain per panicle in cross-I; plant height in cross-II; productive tillers per plant and straw yield per plant in cross-I and cross-II; 100 grain weight and grain yield per plant in cross-II and cross-III and protein content in cross-III, respectively.

Estimate of additive (d) and dominance (h) component varied from cross to cross and character to character. The significant additive and additive x additive epistasis in the present study was observed in days to flowering, plant height, 100 grain weight, L:B ratio and amylose content in all the three crosses; days to maturity, productive tillers per plant, grain per panicle and straw yield per plant in cross-I and cross-II; protein content in cross-II and cross-III and grain yield per plant in cross-I and cross-III. Same results were obtained by Nayak *et al.* (2007) [5] for grains per panicle and 100 grain weight; Singh *et al.* (2007) [6], Roy and Senapati (2011) [7], Samak *et al.* (2011) [8], Kiani *et al.* (2013) [9] for grains per panicle and 100 grain weight; Montazeri *et al.* (2014) [10], Shahid *et al.* (2014) [11], Patel *et al.* (2015) [12] for grains per panicle, 100 grain weight, L:B ratio; Rani *et al.* (2015) [13], Sultana *et al.*

(2016) [14] for grains per panicle, 100 grain weight and L:B ratio and Kumar *et al.* (2017) [15] for L:B ratio.

The duplicate epistasis was observed for all the three crosses in days to flowering, days to maturity, productive tillers per plant and 100 grain weight; plant height in cross-I; grain per panicle and grain yield per plant in cross-I and cross-III; L:B ratio in cross-II and cross-III; straw yield per plant, protein content and amylose content in cross-I and cross-II, respectively; respectively. These results are an agreement with Nayak *et al.* (2007) [5], Singh *et al.* (2007) [6], Roy and Senapati (2011) [7], Samak *et al.* (2011) [8], Kiani *et al.* (2013) [9], Montazeri *et al.* (2014) [10], Shahid *et al.* (2014) [11], Patel *et al.* (2015) [12], Rani *et al.* (2015) [13], Sultana *et al.* (2016) and Kumar *et al.* (2017) [15] while Samak *et al.* (2011) [8] for protein content and amylose content.

The similar sign of dominance (h) and dominance x dominance (l) parameter indicates the involvement of complementary epistasis in the expression of a trait. This type of significant epistasis was observed in plant height in cross-II and cross-III; grain per panicle and grain yield per plant in cross-II; L:B ratio in cross-I; protein content and amylose content in cross-III.

In most of the characters main gene effect and duplicate epistasis were involved. This suggests the need of specific breeding procedure such as intermating of most desirable segregants followed by selfing and selecting superior genotypes coupled with progeny testing to exploit the population under study.

Table 1: Estimation of scaling tests and gene effects for days to flowering, days to maturity, plant height (cm) and productive tillers per plant

Crosses	Gene effect											χ^2 at 2 d.f.	Types of epistasis	
	Scaling test		Five parameter model					Three parameter model						
	C	D	M	$[\hat{d}]$	$[\hat{h}]$	$[\hat{i}]$	$[\hat{l}]$	m	$[\hat{d}]$	$[\hat{h}]$				
Days to flowering														
I	3.50*	11.82*	90.73**	-1.88*	-5.47*	-11.06*	11.08*	-	-	-	276.41*	D		
II	1.16	8.12*	99.38**	6.95*	-2.00*	8.67*	9.27*	-	-	-	157.51*	D		
II	9.40*	-6.47*	101.22**	5.55*	8.73*	16.98*	-21.16*	-	-	-	92.29*	D		
Days to maturity														
I	1.13	11.92*	120.90**	-3.11*	-4.27*	-13.99*	14.38*	-	-	-	263.59*	D		
II	2.6*	11.29*	124.55**	5.85*	-2.78*	4.60*	11.59*	-	-	-	340.74*	D		
III	4.2*	10.13*	124.05**	2.85*	-6.07*	-0.35	7.91*	-	-	-	232.85*	D		
Plant height (cm)														
I	0.40	-2.01*	135.32**	1.01*	0.42	3.44*	-3.21*	-	-	-	18.41*	D		
II	-9.60*	-1.81*	117.84**	-4.31*	2.79*	-9.02*	10.37*	-	-	-	215.12*	C		
III	-15.5*	-8.37*	120.48**	2.15*	1.48*	7.29*	9.50*	-	-	-	451.76*	C		
Productive tillers per plant														
I	-1.93*	2.09*	9.10**	-1.28*	-0.97*	-4.28*	5.37*	-	-	-	56.72*	D		
II	-4.70*	1.43	9.13**	0.31*	-0.35	-1.10*	8.17*	-	-	-	176.44*	D		
III	3.13*	-0.88*	9.63**	-0.76*	1.34*	-0.42	-5.35*	-	-	-	61.40*	D		

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

Table 2: Estimation of scaling tests and gene effects for grain per panicle, 100 grain weight (g), grain yield per plant (g) and straw yield per plant (g)

Crosses	Gene effect											χ^2 at 2 d.f.	Types of epistasis	
	Scaling test		Five parameter model					Three parameter model						
	C	D	M	$[\hat{d}]$	$[\hat{h}]$	$[\hat{i}]$	$[\hat{l}]$	m	$[\hat{d}]$	$[\hat{h}]$				
Grain per panicle														
I	1.16	48.44*	245.16**	-20.88*	-10.92*	-73.87*	63.04*	-	-	-	157.40*	D		
II	-75.13*	-19.64*	232.50**	25.33*	23.94*	51.24*	73.97*	-	-	-	307.40*	C		
II	-18.83*	-29.70*	245.70**	-8.20*	19.42*	0.26	-14.49	-	-	-	61.18*	D		
100 grain weight (g)														
I	0.34*	-0.02	2.42**	0.09*	0.06	0.26*	-0.49*	-	-	-	36.73*	D		
II	0.86*	-0.13*	2.39**	-0.78*	0.11*	-1.33*	-1.31*	-	-	-	408.84*	D		
III	0.30*	1.44*	1.88**	-0.23*	-0.72*	-1.37*	1.52*	-	-	-	626.43*	D		

Grain yield per plant (g)												
I	1.62*	-3.93*	15.88**	-0.90*	3.41*	1.08*	-7.41*	-	-	-	91.61*	D
II	-2.76*	2.10*	16.31**	0.07	1.93*	-1.71*	6.48*	-	-	-	168.46*	C
III	-1.08*	1.94*	16.94**	-1.60*	-0.88*	-4.69*	4.03*	-	-	-	42.84*	D
Straw yield per plant (g)												
I	0.52	6.83*	23.80**	-1.80*	-2.73*	-8.08*	8.41*	-	-	-	73.93*	D
II	2.34*	4.00*	24.58**	-1.45*	-0.16	-5.18*	2.21	-	-	-	42.82*	D
III	-	-	-	-	-	-	-	-	-	-	-	-

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

Table 3: Estimation of scaling tests and gene effects for L:B ratio, protein content (%) and amylose content (%)

Crosses	Gene effect											χ^2 at 2 d.f.	Types of epistasis
	Scaling test		Five parameter model					Three parameter model					
	C	D	M	$[\hat{d}]$	$[\hat{h}]$	$[\hat{i}]$	$[\hat{l}]$	m	$[\hat{c}]$	$[\hat{h}]$			
L:B ratio													
I	-0.23*	0.01	2.82**	0.09*	0.02	0.14*	0.33*	-	-	-	45.66*	C	
II	-0.21*	-0.33*	2.80**	0.13*	0.24*	0.45*	-0.15*	-	-	-	318.60*	D	
III	-0.16*	0.18*	2.83**	0.12*	-0.06*	0.09*	0.47*	-	-	-	84.35*	D	
Protein content (%)													
I	-0.73*	0.27*	8.93**	0.10*	-0.27*	-0.10	1.34*	-	-	-	81.30*	D	
II	-1.93*	-0.41*	5.22**	1.12*	-1.19*	2.19*	2.01*	-	-	-	123.03*	D	
III	-2.31*	-0.94*	5.60**	-0.53*	0.30*	-0.82*	1.82*	-	-	-	155.61*	C	
Amylose content (%)													
I	-2.30*	-3.75*	23.21**	0.53*	2.28*	3.17*	-1.93*	-	-	-	154.63*	D	
II	3.32*	-3.39*	24.35**	-0.35*	3.08*	2.10*	-8.96*	-	-	-	209.39*	D	
III	-3.55*	-1.05*	24.84**	1.07*	0.09	2.26*	3.33*	-	-	-	29.99*	C	

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

Conclusion

Types of gene action can be employed to decide the expression for exploiting various characters under study. Different characters in the same cross or same character in different crosses shows different type and magnitude of gene effects which is necessary for handling of individual cross in segregating populations. In the present investigation, non-allelic (epistasis) interaction played significant role in determining the expression of various characters which are studied. Thus, high volume crossing like biparental and diallel selective mating systems of breeding methods takes care of additive and non-additive gene action which seems more promising for various characters for their improvement under the present investigation.

Pedigree method of selection is one of the most appropriate methods of breeding for the improvement of the characters which are controlled by additive gene effect. Heterosis breeding or hybridization followed by cyclic method of breeding can exploit both additive and non-additive gene effects for improvements of different characters.

References

- Mather K. Polygenic inheritance and natural selection. *Biol. Rev* 1943;18: 32-64.
- Badawi AT. Rice - based production systems for food security and poverty alleviation in the near East and North Africa: New Challenges and Technological Opportunities FAO Rice Conference Rome, Italy 2014.
- Mather K. Biometrical Genetics. Dover Publication, Inc., New work 1949.
- Cavalli LL. An analysis of linkage of quantitative inheritance. In: Quantitative inheritance (Eds. E. C. R. Reeve and C. H. Wedelington). HMSO, London 1952, pp.135-144.
- Nayak AR, Chaudhury D, Reddy JN. Genetics of yield and yield components in scented rice. *Oryza* 2007;44(3):227-230.
- Singh NK, Singh PK, Singh ON, Singh S, Dwivedi JL, Giri SP, *et al.* Gene effects and selection parameters in rainfed low land rice. *Oryza* 2007;44(4):291-295.
- Roy SK, Senapati BK. Estimation of genetic components for grain yield and quality traits of rice. *Oryza* 2011;48(1):22-30.
- Samak N, Hittalmani S, Biradar H. Exploratory studies on genetic variability and genetic control for protein and micronutrient content in F₄ and F₅ generation of rice. *Asian J Pl. Sci.* 2011;10(7):376-379.
- Kiani SH, Kazemitabar SK, Babaeian Jelodar NA, Ranjbar GA. Genetic evaluation of quantitative traits of rice (*Oryza sativa* L.) using generation mean analysis. *Int. J Agric. Crop Sci* 2013;5(19):2329-2336.
- Montazeri Z, Jelodar NB, Bagheri B. Genetic dissection of some important agronomic traits in rice using line x tester method. *Int. J Advanced Biol. Sci. and Biomed. Res* 2014;2(1):181-191.
- Shahid MQ, Liu G, Li J, Naeem M, Liu XD. Heterosis and gene action study of agronomic traits in diploid and autotetraploid rice. *Acta Agril. Scandinavica Section B- Soil and Pl. Sci* 2014;61:23-32.
- Patel VJ, Mistry PM, Chaudhari MH, Dave VD. Combining Ability Analysis in Rice (*Oryza sativa* L.). *Trends in Biosciences* 2015;8(1):82-87.
- Rani PJ, Satyanarayana PV, Chamundeswari N, Ahamed ML, Rani MG. Studies on genetic control of quality traits in rice (*Oryza sativa* L.) using six parameter model of generation mean analysis. *Electronic J Pl. Breeding* 2015;6(3):658-662.
- Sultana R, Ansari NA, Ramesha MS, Shankar AS, Murali Krishna K. Generation mean analysis of quantitative traits in restorer lines of rice (*Oryza sativa* L.). *Asian J of Bio. Science* 2016;11(1):151-161.
- Kumar PS, Saravanan K, Sabesan T. Generation mean analysis for yield and grain quality characters in rice (*Oryza sativa* L.). *Plant Archives* 2017;17(1):557 -560.

16. Gamble EE. Gene effects in corn (*Zea mays* L.). Separation and relative importance of gene effects for yield. Can. J Pl. Sci 1962;42:339-348.
17. Mather K, Jinks JL. Biometrical genetics: the study of continuous variation. Chapman and Hall, London 2nd Ed 1971.