



GENERATION MEAN ANALYSIS FOR YIELD AND GRAIN QUALITY CHARACTERS IN RICE (*ORYZA SATIVA* L.)

P. Satheesh Kumar*, K. Saravanan and T. Sabesan

Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar – 608 002 (Tamil Nadu), India.

Abstract

An investigation was carried out to study the genetics of yield and grain quality characters using generation mean analysis in rice. Seven characters *viz.*, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant were observed in P₁, P₂, F₁, F₂ and F₃ generation of two crosses *viz.*, AURC 22 × IR 64 and AURC 22 × TRY 1 (Five parameter model). Mean analysis revealed that, among the parents, AURC 22 was found to be good performer for kernel length and grain yield per plant.

The cross AURC 22 × TRY 1 exhibited high *per se* performance for grain length, grain breadth, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant. Generation mean analysis revealed that the characters *viz.*, the grain length, grain breadth, kernel breadth and grain yield per plant were predominantly controlled by additive gene effects followed by additive × additive interaction effects. Hence, simple pedigree breeding procedure is suggested for improvement of these characters.

Key words : Generation mean analysis, gene action, rice, *Oryza sativa*.

Introduction

Rice is the most widely consumed staple food for a major part of the world's population, especially in Asia. Around 11 per cent of the arable land is occupied by rice with a total production of 600 million ton representing 21 per cent of the entire calorie supply (Guimaraes, 2009). The UN/FAO forecasts that global food production will need to increase by over 40 per cent by 2030 and 70 per cent by 2050 (FAO, 2009). India occupies the world's largest area under rice with 42.5 million ha and is the second highest producer with 106.65 million tones (2013-14) followed by China, contributing 21 per cent of global rice production. It has a vital role in the food and livelihood security of the country. However, productivity of rice is only 2.54 tonnes ha⁻¹ as against the global average productivity of 3.28 tonnes ha⁻¹ (Anonymous, 2015). Considering the current growth rate in population, the supply projection falls short of expected demand of 121.6 m tons by the year 2030, and 137.3 m tons by the year 2050. This is far below the current growth rate of production (0.36%) in comparison to population growth rate of 1.63 per cent (Anonymous, 2013). In order to achieve this target, the productivity of rice has to be

brought to the level of 3.3 tons ha⁻¹, from the present scenario. The irrigated rice has a share of 70 per cent of total rice production in Indian sub-continent, although it has a share of about 50 per cent of total rice area (Singh, 2009). In this context, increasing its genetic potential for higher yield of the cultures would be the key for meeting world rice requirements. To achieve the target yield level, rice varieties with a yield advantage of about 20 per cent over widely grown varieties must be developed with higher yield potential. Information on genetic parameters of yield and its component characters can help in deciding an appropriate breeding methods. Therefore, gene effects governing yield and quality related traits in two crosses of rice (*Oryza sativa* L.) were estimated following Mather (1949), Hayman (1958) and Cavalli (1952).

Materials and Methods

The five generations namely P₁, P₂, F₁, F₂ and F₃ of two crosses namely, AURC 22 × IR 64 and AURC 22 × TRY 1 were raised in RBD, replicated thrice during December 2013 at Plant Breeding Farm, Faculty of Agriculture, Annamalai University. A spacing of 20 cm between rows and 15 cm between plants was followed. Data from 60 plants in P₁, P₂ and F₁ generations, 600 plants in F₂ generations, 300 plants in F₃ generations were

*Author for correspondence : E-mail: pnsathishkumar@gmail.com

recorded for both the crosses for seven characters namely, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant. The biometrical techniques to detect and estimate the additive (d), dominance (h) and genetic interactions *viz.*, additive \times additive (i), dominance \times dominance (l) from five generations have been analysed according to Mather (1949), Hayman (1958) and Jinks and Jones (1958) using Windostat.

Results and Discussion

The prime objective of hybridization between any two parents is to combine the desirable characters dispersed among them to compensate deficiencies found in one parent by the other. The progenies of these crosses will throw all possible combinations to promote yield. Therefore, the parents selected should inherit the characters to their progenies. The choice of parent was based on the general principle that the parents under selection should have a high *per se* performance for the desirable traits. For a systematic breeding programme, it is necessary to identify the parents which can be the exploited for genetic improvement through hybrid progenies. For which, the breeders are in absolute need of high mean value which is considered as a main criterion for effective selection forever.

Among the parents studied in the present investigation, AURC 22 showed promise for grain yield

per plant and kernel length. IR 64 recorded high grain length, grain L/B ratio and kernel L/B ratio. TRY 1 recorded high grain breadth and kernel breadth. Among the hybrids, the F₁ of AURC 22 \times TRY 1 showed high grain yield per plant, grain length, grain breadth, kernel length, kernel breadth and kernel L/B ratio. The present investigation revealed that the parent AURC 22 and TRY 1 contributed their expression of characters to their progenies (table 1).

The scaling test indicated either C or D significantly deviated from zero for all the characters in both crosses. In cross AURC 22 \times TRY 1 both C and D significantly for grain length, grain breadth, kernel breadth, kernel L/B ratio and grain yield per plant indicating the presence of epistatic interactions. Five parameter model fitted for separating epistasis.

The estimate of gene effects revealed additive gene effects (d) for grain length, grain breadth, kernel breadth and grain yield per plant in the cross AURC 22 \times TRY 1. Similar results were obtained by earlier workers (Singh *et al.*, 2007; Muhammad Yussouf Saleem *et al.*, 2009; Gnanamalar and Vivekanandan, 2013). Dominance gene effects (h) were significant and positive for grain length, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant in the cross AURC 22 \times IR 64 and dominance gene effects (h) were significant and positive for kernel length in the cross AURC 22 \times TRY 1 (table 2).

Table 1 : Mean \pm SE performance of five generations for yield and yield components characters.

Characters	Crosses	P ₁	P ₂	F ₁	F ₂	F ₃
Grain length (mm)	1	9.03 \pm 0.35	9.11 \pm 0.32	8.53 \pm 0.12	7.99 \pm 0.04	7.86 \pm 0.04
	2	9.03 \pm 0.35	8.03 \pm 0.12	8.63 \pm 0.13	8.58 \pm 0.04	8.64 \pm 0.03
Grain breadth (mm)	1	3.00 \pm 0.15	2.04 \pm 0.09	2.52 \pm 0.09	2.41 \pm 0.08	2.49 \pm 0.02
	2	3.00 \pm 0.15	3.06 \pm 0.11	3.02 \pm 0.08	3.05 \pm 0.01	3.10 \pm 0.07
Grain L/B ratio	1	3.02 \pm 0.15	4.46 \pm 0.22	3.42 \pm 0.12	3.51 \pm 0.01	3.58 \pm 0.02
	2	3.02 \pm 0.15	2.62 \pm 0.12	2.83 \pm 0.08	2.76 \pm 0.01	2.80 \pm 0.01
Kernel length (mm)	1	6.94 \pm 0.22	5.96 \pm 0.20	6.41 \pm 0.23	6.50 \pm 0.03	6.42 \pm 0.03
	2	6.94 \pm 0.22	5.81 \pm 0.27	6.54 \pm 0.16	5.97 \pm 0.03	6.06 \pm 0.03
Kernel breadth (mm)	1	2.42 \pm 0.10	1.53 \pm 0.04	2.03 \pm 0.05	1.84 \pm 0.01	1.72 \pm 0.08
	2	2.42 \pm 0.10	2.43 \pm 0.02	2.11 \pm 0.06	2.15 \pm 0.03	2.19 \pm 0.03
Kernel L/B ratio	1	2.86 \pm 0.12	3.91 \pm 0.10	3.09 \pm 0.08	2.87 \pm 0.01	2.72 \pm 0.02
	2	2.86 \pm 0.12	2.38 \pm 0.12	3.19 \pm 0.06	3.15 \pm 0.01	3.20 \pm 0.01
Grain yield per plant (g)	1	32.71 \pm 0.75	21.51 \pm 0.74	32.23 \pm 0.37	29.63 \pm 6.11	27.53 \pm 0.10
	2	32.71 \pm 0.75	22.58 \pm 0.68	33.17 \pm 0.38	33.52 \pm 0.17	34.49 \pm 0.14

Cross 1 : AURC 22/IR 64

Cross 2 : AURC 22/TRY 1

Table 2 : Scaling test and gene effects for yield and yield components characters in rice.

Genetic parameters	Grain length		Grain breadth		Grain L/B ratio	
	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2
C	-3.44±0.56*	0.20±0.48*	-0.44±0.25*	0.10±0.26*	-0.28±0.37*	-0.26±0.26*
D	-2.68±0.51*	0.34±0.41*	0.10±0.18*	0.24 0.35*	-0.18±0.27	0.04±0.21
Gene effects						
(m)	7.99±0.04*	8.58±0.04*	2.41±0.08*	3.05±0.01*	3.51±0.01*	2.76±0.01*
(d)	-0.04±0.23	0.50±0.18*	-0.03±0.09	0.48±0.09*	-0.72±0.13*	0.20±0.09
(h)	0.77±0.16*	-0.19±0.16*	-0.14±0.06*	-0.15±0.20*	-0.24±0.10*	-0.06±0.08*
(i)	1.13±0.45*	0.80±0.43*	0.82±0.19*	0.20±0.24*	-1.36±0.23*	0.33±0.19
(l)	1.01±0.52	0.18±0.53	0.77±0.23*	0.18±0.47	0.13±0.37	0.40 0.27*
	C	D	D	D	D	D

* - Significant at 5 per cent level

Cross 1 : AURC 22/IR 64

D – Duplicate

** - Significant at 1 per cent level

Cross 2 : AURC 22/TRY 1

C – Complementary

Table 2 : Scaling test and gene effects for yield and yield components characters in rice.

Genetic parameters	Kernel length		Kernel breadth		Kernel L/B ratio		Grain yield per plant	
	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2
C	0.28±0.57*	-1.95±0.49	-0.65±0.15	-0.45±0.17*	-1.67±0.24*	1.18±0.22*	-0.16±1.36*	12.45±1.46*
D	-0.22±0.33*	-0.45±0.38*	-0.75±0.11*	-0.37±0.10*	-1.63±0.17*	1.26±0.18*	-3.36±1.15*	15.63±1.22*
Gene effects								
(m)	6.50±0.03*	5.97±0.03*	1.84±0.02*	2.15±0.03*	2.87±0.01*	3.15±0.01*	29.63±0.10*	33.52±0.17*
(d)	0.49±0.15	0.56±0.18	0.05±0.05	0.46±0.05*	-0.52±0.07*	0.24±0.08	5.60±0.52*	5.06±0.50*
(h)	0.15±0.18*	0.14±0.15*	0.44±0.04*	-0.13±0.04	0.61±0.07*	-0.17±0.05*	7.33±0.42*	-2.82±0.58*
(i)	1.17±0.33	1.10±0.32	1.28±0.12*	0.18±0.12*	-0.24±0.16*	-0.16±0.16	13.41±1.01*	1.78±1.08*
(l)	-0.66±0.69	2.00±0.52	-0.13±0.15*	0.10±0.17	0.05±0.26*	0.10±0.20	-4.26±1.42*	4.24±1.92
	D	C	D	D	C	D	D	D

* - Significant at 5 per cent level

Cross 1 : AURC 22/IR 64

D – Duplicate

** - Significant at 1 per cent level

Cross 2 : AURC 22/TRY 1

C – Complementary

Among the epistatic effects, additive × additive were found positive and significant for the characters grain length, grain breadth, kernel breadth and grain yield per plant in both crosses of AURC 22 × IR 64 and AURC 22 × TRY 1. Similar results were obtained by Sabesan (2005), Thirugnanakumar *et al.* (2007), Mahalingam and Nadarajan (2010) and Chamundeswari *et al.* (2013).

The cross AURC 22 × IR 64 showed negative and significant additive × additive effect for grain L/B ratio and kernel L/B ratio. While the same cross observed positive and significant dominance × dominance effect for grain breadth and kernel L/B ratio.

Among seven characters studied, grain breadth, grain L/B ratio, kernel breadth and grain yield per plant showed opposite signs of (h) and (l) indicating duplicate type of epistasis in both crosses. The traits grain length and kernel L/B ratio showed complementary type of gene

interaction as same signs of (h) and (l) in the cross AURC 22 × IR 64.

The same signs of (h) and (l) are exhibited in the cross AURC 22 × TRY 1 for kernel length. The cross AURC 22 × IR 64 showed duplicate gene action for kernel length whereas the cross AURC 22 × TRY 1 showed duplicate gene action for grain length and kernel L/B ratio. This is in concurrence with the earlier reports by Nayak *et al.* (2007), Gnanamalar and Vivekanandan (2013) and Yadav *et al.* (2013) indicating the presence of duplicate gene action for grain breadth, grain L/B ratio, kernel breadth and grain yield per plant. From the foregoing discussion, it is concluded that the most important yield contributing traits as well as yield *per se* were governed by predominantly additive gene action followed by additive × additive type of interaction. Grain yield per plant along with quality characters *viz.*, grain length, grain

breadth and kernel breadth were controlled by additive effect and additive \times additive interaction effects in the cross AURC 22 \times TRY 1. Hence, simple pedigree breeding produce can be used for improvement of these traits in rice.

References

- Anonymous (2013). Vision 2050, Central Rice Research Institute, Indian Council of Agricultural Research, Cuttack (Odisha), 753 006, India.
- Anonymous (2015). *IIRR Vision 2050*. Indian Institute of Rice Research. Indian Council of Agricultural Research. www.icar-iirr.org. pp. 01.
- Cavalli, L. L. (1952). In: *Quantitative Inheritance* (ed. E.C.R. Rieve and C.H. Wadigton) HMSO, London, pp. 135-144.
- Chamundeswari, N., P. V. Sathyanarayana, Y. Suryanarayana and K. Raja Reddy (2013). Studies on inheritance of yield and yield components in rice. *Oryza*, **50(2)** : 105-109.
- Food and Agricultural Organization (2009). *FAO STAT database FAO*, Rome, www.Faostat.org.
- Gnanamalar, R. P. and P. Vivekanandan (2013). Genetic architecture of grain quality characters in rice (*Oryza sativa* L.). *European J. Expt. Biol.*, **3(2)** : 275-279.
- Guimaraes, E. P. (2009). "Rice breeding", In : Cereals, M.J. Cerena (ed.) pp. 99-126. Springer US, DOI 10.1007/978-0-387-72297-9-2.
- Hayman, B. I. (1958). The separation of epistatic from additive and dominance variation in generation means. *Heredity*, **12** : 371-390.
- Jinks, J. L. and R. M. Jones (1958). Estimation of the components of heterosis. *Genetics*, **43** : 223-234.
- Mahalingam, L. and N. Nadarajan (2010). Genetic analysis of grain quality characteristics of two line rice hybrids. *Electronic J. Plant Breed*, **1(4)** : 983-988.
- Mather, K. (1949). *Biometrical genetics*. Dover Publications, Inc., New York.
- Muhammad, Yussouf Saleem, Javed Iqbal Mirza and Muhammad Abisanul Haq (2009). Triple test cross analysis of some physiomorphological traits in basmati rice (*Oryza sativa* L.). *Pakistan J. Bot.*, **41(5)** : 2411-2418.
- Nayak, A. R., D. Chaudhary and J. N. Reddy (2007). Genetics of yield and yield components in scented rice. *Oryza*, **44(3)** : 227-230.
- Sabesan, T. (2005). Studies on the genetics of quality traits in rice (*Oryza sativa* L.). *Ph.D. Thesis*, Annamalai University, Annamalainagar, India.
- Singh, B. N. (2009). *Varietal diversity of rice in India*. http://ec.europa.eu/agriculture/analysis/external/basmati/rice_in_India_bnsingh_en.pdf. Published on 14.07.2010.
- Singh, N. K., P. K. Singh, O. N. Singh, Sanjay Singh, J. K. Dwivedi, S. P. Giri and T. Tiwari (2007). Gene effects and selection parameters in rainfed low land rice. *Oryza*, **44(4)** : 291-295.
- Thirugnanakumar, S., R. Narasimman, N. Senthil Kumar, R. Eswaran and C. Praveen Sampath Kumar (2007). Gene effects for grain yield and its component characters in rice (*Oryza sativa* L.). *Crop Improv.*, **34(1)** : 19-23.
- Yadav, H. N., R. Prasad, S. P. Singh, R. P. Singh and R. K. Agrawal (2013). Detection of epistasis and gene effects for Quality and yield traits in rice. *Oryza*, **50(2)** : 115-119.