

Genetic Analysis of Some Agro- morphological Traits in Rice (*Oryza sativa* L) using Hayman's Graphical Approach

H P Chaturvedi¹, P Talukdar² and Sapu Changkija¹

¹Department of Genetics and Plant Breeding, Nagaland University, Medziphema- 797106 ²Department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat- 783103

(Received: March 2015; Revised: March 2015; Accepted: April 2015)

Abstract

Graphical analysis of a diallel cross provides useful information on the average degree of dominance, dominance order of the parents and additional information about the relationship among the parents. In the present study over dominance was evident for days to 50% flowering, 50% flowering to maturity, plant height, panicle weight, panicle length, grains per panicle, grain filling percent, length- breadth ratio and yield per plant; partial dominance for effective tillers per plant and 1000 grain weight. The parents were well scattered on the regression line indicating their diverse genetic nature.

Keyword:

Introduction

Rice is the staple food. For more than half of humanity, rice is life. It is estimated that the world's unmilled rice production has to increase by about 65% by 2030 to keep pace with the population growth. Improvement of grain yield is main objective in most of the breeding program (Yan et al. 2002). In rice, grain yield is the result of different yield contributing characters such as panicle number per plant, the filled grain number per panicle and the weight of grain (Yosida, 1983). In the pursuit of rendering a permanent genetic improvement in crop plants, an adequate knowledge of gene action, especially components of genetic variance are necessary. Graphical analysis of a diallel cross provides useful information on the average degree of dominance, dominance order of the parents and additional information about the relationship among the parents. Since local genotypes are valuable with reference to many rare physiological and quantitative traits, therefore, the present investigation was undertaken to study genetic analysis of some agro-morphological traits in rice (*Oryza sativa* L) using Hayman's graphical approach.

Materials and Methods

Six parents (Malong, Mehuru, Teke, Piolee, Ranjit and Bahadur) along with 15 F₁ hybrids (Malong x Mehuru, Malong x Teke, Malong x Piolee, Malong x Ranjit,

Malong x Bahadur, Mehuru x Teke, Mehuru x Piolee, Mehuru x Ranjit, Mehuru x Bahadur, Teke x Piolee, Teke x Ranjit, Teke x Bahadur, Piolee x Ranjit, Piolee x Bahadur and Ranjit x Bahadur) of a 6 x 6 diallel cross (excluding reciprocals) were grown in Randomized Complete Block Design with three replications. Thirty days old single seedling per hill was planted at a spacing of 20 X 15 cm with three-meter length row having three rows in each entry. The experiment was conducted with normal package of practices and need based plant protection measures. Observations were recorded on ten sampled plants of the middle row of each plot avoiding the border rows and border plants for days to 50% flowering, 50% flowering to maturity, effective tillers per plant, plant height, panicle weight, panicle length, grains per panicle, grain filling percent, length- breadth ratio, 1000 grains weight and yield per plant. Data pertaining to the parents and F₁'s of 6 x 6 diallel cross (excluding reciprocals) were analyzed according to Jinks-Hayman's approach for diallel assumptions (Jinks & Hayman, 1953) and graphic analysis based on Hayman's approach (Hayman, 1954 a) was accomplished.

Result & Discussion

Analysis of variance (Table-1) indicated significant variation among the genotypes for all the characters. On further partitioning, it could be seen that parents, crosses as well as parents versus crosses also showed significant variation for the characters. Thus, not only the parents and the crosses differed among themselves

Corresponding authors- e-mail: hpchaturvedi68@gmail.com

**Published by the Indian Society of Genetics, Biotechnology Research and Development
Biotech Bhawan 5 E Nikhil Estate, DPS Road, Shastripuram, Agra 282007
Online management by www.isgbrd.co.in**

but also the crosses as a whole differed significantly from the parents for all the characters.

Graphical analysis of a diallel cross provides useful information on the average degree of dominance, dominance order of the parents and additional information about the relationship among the parents. The regression coefficient ($b = 1.0766 \pm 0.266$) of covariance on the variance for days to 50% flowering did not deviate significantly from unity indicating absence of epistasis. The regression line intercepted the W_r axis below the origin indicating over-dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents. For days to 50% flowering to maturity the regression coefficient ($b = 0.7394 \pm 0.084$) of covariance on the variance did not deviate significantly from unity indicating absence of epistasis. The regression line intercepted the W_r axis below the origin indicating over-dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents. The regression coefficient ($b = 0.6102 \pm 0.853$) of covariance on the variance for effective tillers per plant did not deviate significantly either from zero or from unity indicating absence of epistasis. The regression line intercepted the W_r axis above the origin indicating partial dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents. For plant height the regression coefficient ($b = 0.6537 \pm 0.077$) of covariance on the variance did not deviate significantly from unity indicating absence of epistasis. The regression line intercepted the W_r axis below the origin indicating over-dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents. For panicle weight did not deviate significantly from unity indicating absence of epistasis. The regression line intercepted the W_r axis below the origin indicating over-dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents. For panicle length the regression coefficient ($b = 0.7265 \pm 0.501$) of covariance on the variance did not deviate significantly either from zero or unity indicating absence of epistasis. The regression line intercepted the W_r axis below the origin indicating over-dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents. The regression coefficient ($b = 0.5105 \pm 0.255$) of covariance on the variance for grains per panicle did not deviate significantly either from zero or from unity indicating absence of epistasis. The regression line intercepted the W_r axis above the origin indicating partial dominance. The parental points were scattered on the regression line indicating genetic diversity

among the parents. For grain filling percent the regression coefficient ($b = 0.408 \pm 0.161$) of covariance on the variance did not deviate significantly either from zero or unity indicating absence of epistasis. The regression line intercepted the W_r axis below the origin indicating over-dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents. The regression coefficient ($b = 0.7265 \pm 0.292$) of covariance on the variance for length-breadth ratio did not deviate significantly either from zero or from unity indicating absence of epistasis. The regression line intercepted the W_r axis below the origin indicating over-dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents. The regression coefficient ($b = 0.676 \pm 0.346$) of covariance on the variance for 1000-grain weight did not deviate significantly either from zero or from unity indicating absence of epistasis. The regression line intercepted the W_r axis above the origin indicating partial dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents. For yield per plant the regression coefficient ($b = 0.3840 \pm 0.356$) of covariance on the variance did not deviate significantly either from zero or unity indicating absence of epistasis. The regression line intercepted the W_r axis below the origin indicating over-dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents.

The validity of inference drawn from the results of diallel analysis depends on the fulfillment of six assumptions i.e. diploid segregation, homozygous parents, absence of maternal effects, no multiple allelism, no epistasis and independent distribution of genes among parents. The nature of the crop (diploid segregation) and parents (homozygous) with no reciprocal differences reported fulfilled the first three assumptions. Homogeneity of ($W_r - V_r$) over arrays and non-significant deviation of regression coefficient from unity indicated fulfillment of last three assumptions. The regression of W_r on V_r did not deviate significantly from unity for all the characters except 50% flowering to maturity, plant height and panicle weight. This indicated the absence of epistasis for the other characters and presence of it for the exceptions. Thus, for 50% flowering to maturity, plant height and panicle weight, the present analysis could not reflect any clear cut inference. Kearsey and Jinks (1968) and Daly & Robson (1969) pointed out that in studies of quantitative inheritance complete validity of all the assumptions is unlikely. When a trait exhibits a partial failure of the assumptions, estimates of genetic parameters of that trait are still possible (Hayman, 1954 a).

The regression line intercepted the W_r axis below the origin for the characters days to 50% flowering, panicle length, grains per panicle, grain filling percent, length- breadth ratio and yield per plant indicating over- dominance, where as interception was above the origin for effective tillers per plant and 1000 grain weight indicating partial dominance for inheritance of these two characters. Contradictory results between graphical analysis and component analysis were observed for effective tillers per plant and 1000 grain weight. Graphical analysis indicated partial dominance for effective tillers per plant and 1000 grain weight where as component analysis indicated over-dominance. Baker (1978) clarified that to assume genes to be distributed independently in the parents of a diallel cross was not a realistic assumption. He further stated that there was a general agreement regarding failure of this assumption often leading to overestimation of the average level of dominance as derived from graphical analysis of Hayman. Coughtrey and Mathur (1970) in their theoretical consideration and the computer simulation of Feyt (1976) showed that Hayman's test for epistasis is reliable only if genes are distributed independently in the parents of diallel. Hayman (1954a) himself pointed out that the estimate of the average degree of dominance may be increased or decreased by lack of independence of genes in the parents. Hence, perturbation of the W_r - V_r graph may be caused by epistasis and / or correlation between genes. The parents were observed to be well scattered on the regression line indicating their diverse genetic nature. Being close to origin parents found to possess

most dominant genes were Malong for days to 50% flowering; Mehuru, Teke, Poilee and Bahadur for 50% flowering to maturity; Malong, Poilee, Ranjit & Bahadur for plant height; Teke and Bahadur for panicle weight; Poilee for panicle length; Poilee and Bahadur for grain filling percent; Mehuru and Teke for length- breadth ratio and Teke, Ranlit & Bahadur for 1000 grain weight. Out of these parents Bahadur, Teke and Poilee possess dominant genes for six, four and three characters respectively. Parents located in the middle portion of the graph found to possess more or less equal number of dominant and recessive genes. Those were Mehuru, Teke, Poilee and Bahadur for days to 50% flowering; Ranjit for 50% flowering to maturity; Teke and Bahadur for effective tillers per plant; Mehuru for plant height; Mehuru, Ranjit and Poilee for panicle weight; Malong, Ranjit, Mehuru and Bahadur for panicle length; Mehuru, Malong and Teke for grains per panicle; Teke and Ranjit for grain filling percent; Malong, Ranjit and Bahadur for length- breadth ratio; Mehuru and Poilee for 1000 grain weight and Malong and Poilee for yield per plant. Parental points furthestmost from the origin possess most recessive genes. Those were Ranjit for days to 50% flowering; Malong for 50% flowering to maturity; Malong, Mehuru, Poilee, and Ranjit for effective tillers per plant; Teke for plant height and panicle length; Malong for panicle weight; Poilee, Bahadur and Ranjit for grains per panicle; Malong and Mehuru for grain filling percent; Poilee for length- breadth ratio; Malong for 1000 grain weight and Mehuru, Teke, Ranjit and Bahadur for yield per plant.

Table- 1. Analysis of variance for different characters of the genotypes

Sources of Variation	Degree Of Freedom	MEAN SQUARES										
		Days to 50% Flowering	50% Flowering To Maturity	Effective Tillers Per Plant	Plant Height	Panicle Weight	Panicle Length	Grains Per Panicle	Grain Filling Percent	Length-Breadth Ratio	1000 Grains Weight	Yield Per Plant
Replication	2	83.539	1.539	2.671	19.634	0.040	3.676	100.492	2.423	0.011	2.090	2.062
Genotype	20	327.696**	41.249**	16.781**	1046.882**	6.763**	7.017**	2797.711**	211.903**	0.288**	27.799**	293.427**
Parent	5	669.12**	78.76**	4.84**	1578.23**	1.85**	13.34*	371.29*	166.91**	0.292**	30.27**	106.28**
Cross	14	186.56**	9.97**	11.71**	83.79**	1.31**	4.94**	1737.25**	92.87**	0.215**	27.14**	305.71**
Parent Vs Cross	1	596.48**	291.60**	147.48**	11873.43**	107.67**	4.48**	29776.27**	2103.33**	1.29	24.67**	525.89**
Error	40	6.973	1.189	0.519	7.184	0.067	1.882	65.325	13.505	0.017	1.671	1.267

* Significant at 5% level of probability

** Significant at 1% level of probability

References

1. **Baker, R.J.** 1978. Issues in diallel analysis. *Crop Sci.*, 18: 533-536.
2. **Coughtrey, A. and Mather, K.** 1970. Interaction and gene association and dispersion in diallel crosses where gene frequencies are unequal. *Heredity*, 25: 79-88.
3. **Daly, K. and Robson, D.S.** 1969. Estimation of genetic parameters from hybrid derivative in *Nicotiana*. *Genetics, Princeton*, 62: 201-223.
4. **Feyt, H.** 1976. Etude critique de l'analyse des croisements diallels au moyen de la simulation. *Ann. Amelior. Plantes* 26: 173-193.
5. **Hayman, B.I.** 1954 a. The theory of analysis of diallel crosses. *Genetics*, 39: 789-809.
6. **JINKS, J. L. and B. I. HAYMAN**, 1953. The analysis of diallel crosses. *Maize Genetics News Letter* 27: 48-54.
7. **Kearsey, M.J. and Jinks, J. L.** 1968. A general method of detecting additive, dominance and epistatic variation for material traits. *J. Heredity*, 23: 403-410.
8. **Yan W, Hunt LA, Johnson P, Stewart G, Lu X** 2002, On-farm strip trials vs replicated performance trials for cultivar evaluation. *Crop Science* 42, 385–392
9. **Yoshida S** 1983, Rice. In 'Potential productivity of field crops under different environments'. (Eds WH Smith, SJ Banta) pp. 103–127. (International Rice Research Institute Publishing: Los Ba nos, The Philippines)