ESTIMATES OF GENETIC COMPONENTS IN DIALLEL CROSSES FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN RICE (*ORYZA SATIVA* L.)

N. Chamundeswari, P.V. Satyanarayana, K. Raja Reddy and Y. Suryanarayana
Andhra Pradesh Rice Research Institute, Maruteru, West Godavari District
Andhra Pradesh – 534 122, India

Abstract: An experiment was carried out to study the genetic components for seven yield and yield components in rice using a 7-parent diallel cross excluding reciprocals during *kharif* 2009. The parental genotypes used in the study were BPT 5204, MTU 1010, JGL 3844, NLR 34449, MTU 1081, MTU 1075 and JGL 13595. Hayman's analysis of variance (ANOVA) indicated that the traits plant height at maturity, number of tillers per plant, grain yield per plant, were although influenced by both additive and non additive genetic components, the non additive gene actions was more important in controlling the inheritance of these traits. Only dominance genetic component was significant for number of panicles per plant while only additive component was important for panicle length, 1000 grain weight. In case of days to 50% flowering both additive and non additive gene actions were important but additive component was more predominant. Major role of recessive genes was observed in the expression of the traits days to 50% flowering, panicle length. The value of degree of dominance was more than one for all the traits except days to 50% flowering, panicle length and 1000 grain weight indicating the significance of over dominance. Progeny selection was suggested for improvement of 1000-grain weight and panicle length and for other traits only population improvement methods are ideal.
Keywords: Rice, genetic components, diallel, Hayman's approach, yield and yield components, additive and anon additive.

Introduction

Information about the inheritance of controlling the metric traits are worth prime for planning and executing a breeding strategy leading to their genetic improvement. Gene action in rice has been determined mostly by using diallel method which furnishes information on additive and dominant gene effects. Detailed information concerning the genetic control of the characters under selection is important if plant breeders are to conduct their programme efficiently by the choice of appropriate parents and selection methodology. With this back ground a breeding effort was initiated at APRRI & RARS, Maruteru during 2008 and 2009.

Materials and methods

Seven parents viz., BPT 5204, MTU 1010, JGL 3844, NLR 34449, MTU 1081, MTU 1075 and JGL 13595 were selected based on genetic distance, cluster means and *per se*

performance for use in hybridization. The parents were sown at staggered intervals of 10 days, during *Rabi* 2008-09 to facilitate continuous availability of pollen during crossing. Hybridization was done by employing clipping method and emasculation was carried out in afternoon and pollination in morning of next day. Parents were crossed in a diallel fashion without reciprocals and generated seed of 21 crosses. All twenty-one F_1s and their parents were grown in a randomized complete block design with three replications at APRRI & RARS, Maruteru during Kharif 2009. All the recommended package of practices was followed to raise the crop. Observation were recorded on days to 50% flowering, plant height (cm), number of tillers per plant, number of panicles per plant, panicle length (cm), 1000 grain weight (g) and grain yield (g) per plant in each replication. Data was analyzed using the Hayman's approach (1954a and 1954b) as per Singh and Chaudhary (1995). From the data analysis we obtained: (i) variations due to additive effect (D); (ii) the mean of 'Fr' over the arrays (F), Fr is the covariance of additives and non-additive effects in single array; (iii) components of variation due to the dominance effect of the genes (H1); (iv) calculations to predict the proportion of positive and negative genes in the parents (H2); (v) the dominance effects (as the algebraic sum over all loci in heterozygous phase in all crosses) (h2); (vi) the expected environmental components of variation (E); (vii) the mean degree of dominance ((H1/D)1/2); (viii) the proportion of genes with positive and negative effects in the parents (H2/4H1) and (ix) the proportion of dominant and recessive genes in the parents (Kd/Kr); (x) the number of groups of genes which control the character and exhibit dominance (h2/H2).

Results

1. Days to 50 per cent flowering: Both additive (D) and non-additive components (H_1 and H_2) were found significant, indicating the importance of both additive and non-additive gene actions in controlling the expression of this trait. Major role of recessive genes in the expression of this trait was confirmed by a negative estimate of `F' and a less than one ratio of KD/Kr. The ratio of $H_2/4H_1$ was less than 0.25 suggesting unequal distribution of positive and negative genes (Table1).

2. Plant height at maturity: Significance of additive (D) and dominance (H_1 and H_2) components were noticed for this character indicating role of additive and non additive gene action. The estimate of `F' was positive and significant. Mean degree of dominance was more than one suggesting over dominance for this character (Table 1). The $H_2/4H_1$ ratio was less than 0.25 indicating unequal distribution of genes with positive and negative effects.

KD/Kr ratio was more than one, indicating presence of more dominant genes in controlling the character.

3. Number of tillers per plant: Both additive (D) and non-additive components (H_1 and H_2) were found significant, indicating the importance of both additive and non-additive gene actions in controlling the expression of this trait. The estimate of `F' was not significant but positive. KD/Kr ratio was more than unity suggesting influence of high proportion of dominant genes. The value of degree of dominance was more than one indicating the significance of over dominance. $H_2/4H_1$ ratio was less than 0.25 confirming asymmetrical distribution of genes with positive and negative effects (Table 1).

4. Number of panicles per plant: Only dominance genetic component was found to be significant for this trait. `F' estimate was positive and not significant. KD/Kr ratio was much higher than unity thus indicating presence of dominant genes. Estimate of mean degree of dominance was more than one suggesting over dominance (Table 1). The genes with positive and negative effects were unequally distributed since the $H_2/4H_1$ ratio was less than 0.25.

5. Panicle length: Only additive component (D) was found significant for this character (Table 1). The estimate of `F' was negative and non-significant. KD/Kr ratio was less than one showing major influence of recessive genes in the expression of the trait .Mean degree of dominance was lower than unity suggesting partial dominance. $H_2/4H_1$ recorded a ratio higher than 0.25 indicating equal distribution of genes with positive and negative effects among the parents. h^2/H_2 ratio was more than one, which revealed that at least 1 to 2 gene groups among the genes controlling the character expressed additive effect.

6. 1000 grain weight: The additive component (D) was found significant for 1000 grain weight (Table 1). The estimate of `F' was negative and non-significant. KD/Kr ratio was less than one showing major influence of recessive genes in the expression of the trait. Mean degree of dominance was lower than unity suggesting partial dominance. $H_2/4H_1$ recorded a ratio was less than 0.25 confirming asymmetrical distribution of genes with positive and negative effects.

7. Grain yield per plant: Both D and H_1 and H_2 were found significant. Relative magnitude of dominance component was greater than additive component. The estimate of `F' which indicates distribution of dominant and recessive genes was found to be non significant and positive (Table 1). KD/Kr ratio of more than unity also supported that dominant genes were responsible in the expression of this character. Estimate of degree of dominance was more

than one suggesting the presence of over-dominance. The ratio of $H_2/4H_1$ was 0.231 indicating equal distribution of genes.

Discussion

Genetic component analysis revealed that the traits plant height at maturity, number of tillers per plant, grain yield per plant, were although influenced by both additive and non additive genetic components, the non additive gene actions was more important in controlling the inheritance of these traits. Only dominance genetic component was significant for number of panicles per plant while only additive component was important for panicle length, 1000 grain weight. In case of days to 50% flowering both additive and non additive gene actions were important but additive component was more predominant. Akram *et.al.* (2007) observed predominant additive gene action for tillers per plant, predominant of dominant gene action for panicle length, 1000 grain weight and only non additive gene action for grain yield per plant. Kaushik (1984) and Lakshmi (2009) reported the importance of non additive gene effects in the inheritance of the panicle length and 1000 seed weight which was in contradictory to the present results. Haque *et. al.* (1981) reported major role of additive gene effects in controlling the inheritance of 1000 seed weight which was similar to the present result. As per Raju *et al* (2012) all the components of yield and yield except 1000 grain weight were under the influence of non-additive gene action

Major role of recessive genes was observed in the expression of the traits days to 50% flowering, panicle length which was confirmed by a negative estimate of `F' and a less than one ratio of KD/Kr. The ratio of $H_2/4H_1$ was less than 0.25 for the all the characters except for panicle length suggesting unequal distribution of positive and negative genes.

The value of degree of dominance was more than one for all the traits except days to 50% flowering, panicle length and 1000 grain weight indicating the significance of over dominance. Akram *et.al.* (2007) reported partial dominance for tillers per plant panicle length and grain yield per plant and over dominance for 100 seed weight which opposed the present results.

Conclusion

From the foregoing it may be inferred and concluded that the characters (panicle length, 1000 grain weight.) exhibited additive component may be used for direct phenotypic selection in segregating populations. For the characters exhibiting both additive and non additive type of gene action and over dominance the material can be exploited for heterotic effects and population improvement methods are ideal.

References

[1] Akram M Saif Ullah Ajmal and Muhammad Munir 2007 Inheritance of traits related to seedling vigour and grain yield in rice (Oryza sativa L.). Pakistan Journal of Botany 39(1):37-45.

[2] Haque M M Faridi M N Razzaque C A and Newaz M A 1981 Combining ability for yield and component characters in rice. Indian Journal of Agriucltural Sciences 51(10): 711-714.

[3] Hayman B J 1954a The analysis of variance of diallel table. *Biometrics.* **10:** *235-244.*

[4] Hayman B J 1954b The theory and analysis of diallel crosses. *Genetics* **39:** 789-809.

[5] Kaushik R P 1984 Genetic analysis of yield, quality and physiological components in rice (*Oryza sativa* L.). Ph.D Thesis submitted to Himachal Pradesh Krishi Vishva Vidyalaya, India.

[6] Raju CH S, Krishna L, Raju CH D, Vanisree S., Reddy PN, Reddy BB 2012 Genetic studies of quantitative traits through Hayman's approach in rice. Oryza 48 (4): 314-318.

[7] Singh and Chaudhary BD 1995 Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi.

[8] Lakshmi AD 2009 Study of gene action for grain quality, physiological and yield traits in rice (*Oryza sativa* L.). Ph.D Thesis submitted to Acharya N.G Ranga Agricultural University, Hyderabad.

N. Chamundeswari, P.V. Satyanarayana, K. Raja Reddy and Y. Suryanarayana

Table 1: Estimates of genetic components and other parameters for yield and yield contributing characters in F_1 crosses

Component	Days to 50% flowering	Plant height at maturity (cm)	Number of tillers per plant	Number of panicles per plant	Panicle length (cm)	1000 grain weight (g)	Grain yield/plant (g)
D	98.72** ± 5.42	92.52**±13.20	14.18* *±5.23	6.664±3.683	2.196*±0.258	11.31*±1.693	6.73*±3.16
F	-46.97±12.99	111.81**±31.37	8.91±12.56	2.867±8.835	-2.49±0.619	-2.96±4.061	1.40±7.59
H_1	58.63**±13.05	144.64±31.78	38.13**±12.60	26.910*±8.866	0.335±0.621	6.636±4.076	78.03**±7.62
H_2	41.95**±11.49	93.84**±28.00	32.31**±11.10	23.394**±7.812	0.459±0.547	6.048±3.592	72.09*±6.72
h^2	0.96±7.72	26.49±18.8	19.66**±7.46	16.256*±5.247	1.429*±0.367	-0.421±2.412	328.25*±4.51
E	2.12±1.91	1.45±4.66	1.81±1.85	1.591±1.302	1.206*±0.091	1.444*±0.598	1.797±1.12
Degree of dominance	0.771	1.25	1.64	2.009	0.391	0.766	3.405
$H_2/4H_1$	0.179	0.162	0.212	0.217	0.342	0.228	0.231
KD/Kr	0.528	2.87	1.474	1.240	-0.184	0.708	1.063
h^2/H_2	0.023	0.282	0.608	0.695	3.113	-0.07	5.637

* Significant at 5% level   ** Significant at 1% level