



E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2018; SPI: 2477-2480

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Genetic evaluation of quantitative traits of rice (*Oryza sativa* L.) by generation mean analysis

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Abstract

Information on the inheritance of polygenic traits is worthwhile for planning and executing a breeding strategy leading to their genetic improvement. In order to study mode of gene action in rice for traits related to yield [days to 50 per cent flowering, plant height (cm), number of tillers per plant, length of panicle (cm), grain yield per plant (g), straw yield per plant (g) and harvest index (%)], two varieties of rice (Karjat 2 and Munga) were investigated. Direct and reciprocal crosses have been done between parents Karjat 2 and Munga and back crosses at the Experimental Farm of Agricultural Research Station, Karjat and Plant Biotechnology Centre, College of Agriculture, Dapoli, during *kharif* 2013 to *kharif* 2014. The additive x dominance model was significant for the traits *viz.*, plant height, number of tillers per plant, grain yield per plant and harvest index in cross II, while days to 50 per cent flowering in both crosses. The joint scaling test indicated that non allelic gene interactions additive x additive and dominant x dominant were more prominent and played significant role in inheritance of the several traits studied. The additive x dominant interaction were significant but had lesser preponderance for governing the traits and the duplicate type of epistasis was found for days to 50 per cent flowering, grain yield per plant and straw yield per plant (both crosses) and number of tillers per plant in cross I. More than one major gene group appeared to be involved for the expression of plant height while the remaining traits showed the presence of at least one major group of genes controlling their inheritance.

Keywords: Generation Mean analysis, Gene effect, Quantitative Traits, *Oryza sativa*.

Introduction

Food production is one of the most important issues that currently engaged human society. Main human food is derived from cereal plants which are member of Poaceae family so that wheat and rice are supplying more than 40% human food requirement. At the current rate of population growth in India, estimated rice production should be around 135 to 140 million tonnes by 2020. After wheat, rice is the most important cereal in the world and provides food for more than half of people living on the Earth. More than 80% daily calorie and 75% required protein is obtained from rice in Asia. So it is critical to produce high yield cultivars with high quality by inbreeding methods. Yield is complex character and various morphological and physiological characters contribute to grain yield (Luo *et al.*, 2011). Rice varieties with increased yield potential in adverse conditions as well as in normal conditions have to be developed, in order to sustain the rice production across wide range of environments and over the years. In this regard we need primary information about genetic structure of different traits to attain high yield and quality. Knowing about genetic structure of each trait, such as inheritance method and gene mode of action are necessary because this information make us able to design breeding strategies. The most commonly used mating designs Diallel and Line x Tester provide estimates of additive and dominance/non-additive components of gene effect in relation to whole population studied. However, partitioning of genetic variance into its all the probable components i.e., additive, dominance and all types of epistasis with regard to individual cross is of immense value in formulating an effective and sound breeding programme. Among the common approaches followed to understand the nature of gene effect, generation mean analysis using first degree statistics is an accurate one, and gives detail account of gene effects and quality of the genes carried by the parents. Therefore quantitative genetic method such as generation mean analysis is used. Generation Mean Analysis, aimed at estimation of allelic gene actions and non allelic gene interactions by using the six parameter model. The Mather's 1949 individual scaling tests (Scale A, B, C and D) and Cavalli's joint scaling test were used to detect the presence or absence of the epistatic gene interactions i.e. non allelic gene interactions. Inheritance studies are important both from theoretical and practical point of view. Attempts have been made by different workers to find out the relationship between different genes

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governing different characters in rice and their inheritance pattern to the progeny. They also tried to find out inter-relationship among genes (or linkage). Yields can be improved by eliminating undesirable genes/ traits linked with desirable genes/ trait by breaking the linkages. And there is lot of scope for increment in yield by gene manipulation. This is possible only when the genetic construction of plant is understood. As such it is emphasized that the knowledge of inheritance of various characters in rice is a pre-requisite as in other crop plants. Thus, the present study was carried out to estimate different kinds of gene effects in the inheritance of yield and its related traits through generation mean analysis.

Materials and Methods

The mean value was computed for all the six generations over all replications for each cross. The generation mean analysis was carried out following the methodology of Hayman (1958) using six generations and estimated the gene effects viz., *m* (mean), *d* (additive main effect), *h* (dominance main effect), *i* (additive x additive interaction effect), *j* (additive x dominance interaction effect) and *l* (dominance x dominance interaction effect). Experiment was carried out at the Experimental Farm of Agricultural Research Station, Karjat and Plant Biotechnology Centre, College of Agriculture, Dapoli, from *kharif* 2013 to *kharif* 2014. Two rice cultivars (Karjat 2 and Munga) were selected for hybridization. These cultivars were selected because they had different levels of traits which affect yield. In order to recognition, genetic study and heritability levels of cultivars, two crosses between white and red rice cultivars were made during *kharif* 2013. F_1 s were evaluated during *Rabi* 2013-14 and F_2 seeds of each cross were obtained. The BC_1 and BC_2 crosses were effected during *Rabi* 2013-14. The parents, F_1 s, F_2 s, BC_1 s and BC_2 s were evaluated during *kharif* 2014. The seed of six generations viz., Parents (P1 and P2), F_1 , F_2 , BC_1 and BC_2 of each cross were sown for raised the nursery in open field condition. The seedlings of 21 days old were transplanted in randomized block design replicated thrice. A spacing of 20 cm between rows and 15 cm between plants was adopted in the main field at experimental farm, Agricultural Research Station, Karjat during *kharif* 2014 for evaluation. Recommended package of practices were followed to establish the crop. Data collecting including days to 50 per cent flowering, plant height, number of tillers plant⁻¹, panicle length, grain yield plant⁻¹, straw yield plant⁻¹, and harvest index, was done based on single plant. In quantitative experiments and also study on yield components for parents and first generation, 10 plants from each replication were selected, in addition, 50 and 80 plants were selected for first and second back crossing and second generation, respectively. In order to genetic analysis, simple analysis of variance was used for all traits in both crossing. Mean of observations and standard error was calculated. The scaling tests A, B, C and D were computed and their variances were calculated to test the adequacy of the additive-dominance model in each case using formulae given by Mather (1949). When the interactions found present then the six-parameter model given by Hayman (1958) and Jinks and Jones (1958) were utilized for the estimation. The joint scaling test devised by Cavalli (1952) was used for testing goodness of fit on the basis of chi square test. The significance of the test indicated the presence of the epistatic gene action.

Results and Discussion

Mean performance of the six populations, i.e., P1, P2, F_1 , F_2 ,

BC_1 and BC_2 for all traits studied in the cross I (Karjat 2 x Munga) and cross II (Munga x Karjat 2) is presented in the Table 1. The estimated mean effect (*m*) parameter, which reflects the contribution due to the overall mean plus the locus effects and interaction of the fixed loci, were found to be highly significant for all the traits in the two crosses.

A result of individual scaling tests i.e., A, B, C and D scaling tests is presented in Table 2 and the estimated values of the various types of gene effects viz., *m*, *d*, *h*, *i*, *j* and *l* are presented in Table 3. Results of main effects and interaction effects governing quantitative traits are discussed below each trait wise. The significance of scaling test and joint scaling test revealed that additive dominance model was inadequate for both crosses for days to 50 per cent flowering. Both of the scaling tests were in complete agreement indicating that epistasis was operative in the material under study for this trait. For this character *m*, *d*, and *h* values were significant but 'd' value having negative sign in both crosses. Thus the negative sign 'd' indicating that additive was operative towards the parent that flowers not earlier than the parent. Also results indicated the importance of both additive and non additive gene action besides epistasis in the trait inheritance. The results of the present investigation are in complete agreement with the earlier results obtained by Vanaja (1998), Sobita Devi *et al.* (2006) and Nayak *et al.* (2007). The presence of significant scaling test for plant height was confirmed by joint scaling test indicated the presence of non-allelic gene interactions and the additive dominance model need to be further extended for estimation of epistatic effects of gene action. The higher magnitude of additive gene action controlling plant height were observe in both crosses. Thus, these results are in conformity with reports of Roy and Panwar (1993), Sobita Devi *et al.* (2006). Similarly, the dominant gene action observed significant and additive gene action found non-significant in cross I which indicated the number of tillers per plant were governed by the dominant gene action and additive gene action were absent in cross I. In cross I both 'h' and 'l' components had significant and opposite signs which indicated presence of duplicate type of epistasis. These results were in accordance with Roy and Panwar (1993). The results obtained for significance of scaling and joint scaling tests for panicle length indicated the presence of epistatic gene interaction for panicle length inheritance. The estimates of six parameter model indicated the significance for mean, additive gene action and dominant gene action and higher magnitude of dominant gene action. The positive sign of dominant gene action indicated the dominance towards the parents with lower panicle length and positive and higher 'h' indicated dominance towards the higher panicle length parent while, the absence of significance in 'd' and 'h' were also recorded in Cross I indicating non significant role of additive and dominant gene action. These results are in complete agreement with the results reported by Roy and Panwar (1993), Hasib *et al.* (2002) and Murugan and Ganesan (2006). On the basis of significant individual scaling test and joint scaling test for grain yield per plant, it was observed that the additive and dominant gene action was significant for both crosses, indicating the preponderance of 'd' and 'h' type of gene action. Among epistatic gene action for grain yield per plant, additive x additive and dominance x dominance type of gene interaction was recorded in both crosses while additive x dominant type of interaction were significant in cross II. The higher magnitude of dominant x dominant type of interaction was observed in cross I. The duplicate epistasis for both crosses was envisaged. The

duplicate epistasis for this traits also envisaged by Nayak *et al.* (2007) and Roy and Senapati (2011). Significant scaling test and joint scaling test were recorded in both crosses which indicated the presence of epistatic interaction for straw yield per plant. It was observed that the additive and dominant gene action was significant for cross I indicating the preponderance of 'd' and 'h' type of gene action. Significance of scale D indicate additive x additive (i) type of gene action. These results are in conformity with the results obtained by Divya *et al.* (2014). Among epistatic gene action for straw yield per plant, additive x additive and dominance x dominance type of gene interaction was recorded in both crosses. The higher magnitude of dominance x dominance type of gene interaction was observed in both crosses. The values of dominance (h) and dominance x dominance (l) interaction were in opposite direction for straw yield per plant indicated the interaction was fit into duplicate epistasis model. Devika

(2002), Singh *et al.* (2007) and Divya *et al.* (2014) were also in agreement with the above results. The results obtained for significant of scaling and joint scaling test for harvest index indicated the presence of epistatic gene interaction. The estimate of six parameter model indicated the significance for mean, additive gene action and dominant gene action and showed higher magnitude of dominance gene action. The positive sign of dominant gene action indicated the dominance towards the parent. The positive and higher 'h' indicated dominance towards the higher harvest index of parent while the 'l' type was observed non-significant in both crosses. The harvest index was predominantly governed by additive x dominance interaction effect indicated that inter allelic interaction was present in this trait. The results of the present investigation are in complete agreement with the earlier result obtained by Chauhan (1998) and Kiani *et al.* (2013).

Table 1: Estimates of generation means and standard errors of two crosses for yield traits in rice

| Generation | Days to 50% flowering | | Plant height (cm) | | Number of tillers per plant | |
|------------|-----------------------|---------------|-------------------|---------------|-----------------------------|--------------|
| | Cross I | Cross II | Cross I | Cross II | Cross I | Cross II |
| P1 | 104.400±1.026 | 86.300±0.987 | 101.467±1.101 | 131.533±1.517 | 30.933±1.549 | 22.300±1.157 |
| P2 | 86.300±0.987 | 104.400±1.026 | 131.533±1.517 | 101.467±1.101 | 22.300±1.157 | 30.933±1.549 |
| F1 | 99.733±1.399 | 98.733±2.121 | 129.533±2.083 | 100.067±2.271 | 22.733±1.429 | 33.667±1.802 |
| F2 | 97.903±0.884 | 98.867±0.679 | 118.007±2.558 | 115.853±2.204 | 14.043±0.668 | 15.667±0.860 |
| BC1 | 100.167±1.226 | 98.133±1.272 | 109.533±8.601 | 117.100±2.834 | 29.100±4.812 | 20.667±1.925 |
| BC2 | 98.000±1.486 | 101.400±1.322 | 120.100±7.465 | 112.033±3.552 | 24.167±1.848 | 28.633±2.322 |

| Generation | Length of panicle | | Grain yield per plant | | Straw yield per plant | | Harvest index per plant | |
|------------|-------------------|--------------|-----------------------|--------------|-----------------------|--------------|-------------------------|--------------|
| | Cross I | Cross II | Cross I | Cross II | Cross I | Cross II | Cross I | Cross II |
| P1 | 30.800±0.508 | 29.333±0.721 | 84.300±2.086 | 41.733±2.586 | 92.900±1.566 | 61.500±2.748 | 47.536±0.538 | 40.255±1.088 |
| P2 | 29.333±0.721 | 30.800±0.508 | 41.733±2.586 | 84.300±2.086 | 61.500±2.748 | 92.900±1.566 | 40.255±1.088 | 47.536±0.538 |
| F1 | 29.267±1.303 | 30.133±1.067 | 47.300±2.337 | 84.267±2.876 | 55.800±3.082 | 89.767±5.833 | 45.937±1.679 | 48.585±1.454 |
| F2 | 27.643±0.469 | 27.280±0.368 | 40.428±2.281 | 42.713±2.790 | 58.598±2.922 | 57.647±2.922 | 39.858±0.656 | 40.417±0.674 |
| BC1 | 28.100±1.035 | 28.233±0.878 | 73.850±19.634 | 72.867±6.349 | 78.917±17.651 | 87.283±5.907 | 44.042±2.997 | 45.122±1.510 |
| BC2 | 28.167±1.154 | 29.900±0.735 | 60.783±9.097 | 59.200±8.148 | 77.533±8.662 | 98.667±8.468 | 42.659±2.429 | 36.933±3.687 |

* - Significant at 5% level, ** - Significant at 1% level. [Cross-I - Karjat 2 x Munga] [Cross-II - Munga x Karjat 2]

Table 2: Scaling tests for yield traits in two crosses of rice.

| Parameter | | Cross I | | Cross II | |
|-----------------------------|---|-----------|----------|-----------|----------|
| | | | | | |
| Days to 50% flowering | A | 3.800* | ± 1.734 | -11.233** | ± 1.996 |
| | B | -9.967** | ± 1.980 | 0.333 | ± 2.045 |
| | C | -1.447 | ± 2.730 | -7.300* | ± 3.023 |
| | D | -2.360 | ± 1.510 | -1.800 | ± 1.318 |
| Plant height (cm) | A | 11.933 | ± 10.024 | -2.600 | ± 3.632 |
| | B | 20.867* | ± 8.747 | -22.533** | ± 4.353 |
| | C | 20.040** | ± 6.471 | -30.280** | ± 5.827 |
| | D | 6.380 | ± 7.208 | 2.573 | ± 3.655 |
| Number of tillers per plant | A | -4.533 | ± 5.688 | 14.633** | ± 2.544 |
| | B | -3.300 | ± 2.383 | 7.333* | ± 3.011 |
| | C | 42.527** | ± 2.519 | 57.900** | ± 3.086 |
| | D | -25.180** | ± 3.074 | -17.967** | ± 2.005 |
| Length of panicle | A | 3.867** | ± 1.443 | 3.000* | ± 1.257 |
| | B | 2.267 | ± 1.586 | 1.133 | ± 1.089 |
| | C | 8.093** | ± 1.924 | 11.280** | ± 1.581 |
| | D | -0.980 | ± 1.046 | -3.573** | ± 0.786 |
| Grain yield per plant | A | -16.100 | ± 22.743 | -19.733* | ± 7.664 |
| | B | -32.533** | ± 10.695 | 50.167** | ± 9.630 |
| | C | 58.920** | ± 6.222 | 123.713** | ± 7.499 |
| | D | -53.777** | ± 12.768 | -46.640** | ± 6.779 |
| Straw yield per plant | A | -9.133 | ± 20.479 | -23.300** | ± 7.770 |
| | B | -37.767** | ± 10.282 | -14.667 | ± 10.381 |
| | C | 31.607** | ± 7.845 | 103.347** | ± 9.707 |
| | D | -39.253** | ± 11.843 | -70.657** | ± 6.849 |
| Harvest index per plant | A | 5.389 | ± 3.607 | -1.405 | ± 2.035 |
| | B | 0.874 | ± 3.033 | 22.255** | ± 4.351 |
| | C | 20.231** | ± 2.558 | 23.292** | ± 2.394 |
| | D | -6.984** | ± 2.352 | -1.221 | ± 2.429 |

* - Significant at 5% level, ** - Significant at 1% level.

Table 3: Estimates of gene effects for yield traits in two crosses of rice.

| | M | D | H | I | J | L | Type of epistasis |
|------------------------------------|-----------------------|----------------------|------------------------|------------------------|-----------------------|-------------------------|-------------------|
| Days to 50% flowering | | | | | | | |
| Cross I | 97.903** \pm 0.510 | 2.167 \pm 1.112 | 9.103** \pm 3.152 | 4.720 \pm 3.019 | -13.767** \pm 2.371 | -10.887** \pm 5.220 | Duplicate |
| Cross II | 98.867** \pm 0.392 | -3.267** \pm 1.060 | 6.983** \pm 2.936 | 3.600 \pm 2.637 | 11.567** \pm 2.273 | -14.500** \pm 5.206 | Duplicate |
| Plant height (cm) | | | | | | | |
| Cross I | 118.007** \pm 1.477 | -10.567 \pm 6.575 | 0.273 \pm 14.477 | -12.760 \pm 14.417 | 8.933 \pm 13.195 | 45.560 \pm 27.085 | Complementary |
| Cross II | 115.853** \pm 1.272 | 5.067 \pm 2.623 | -21.580** \pm 7.446 | -5.147 \pm 7.310 | -19.933** \pm 5.357 | -19.987 \pm 12.003 | Complementary |
| Number of tillers per plant | | | | | | | |
| Cross I | 14.043** \pm 0.385 | 4.933 \pm 2.976 | 46.477** \pm 6.228 | 50.360** \pm 6.148 | 1.233 \pm 6.056 | -58.193** \pm 12.167 | Duplicate |
| Cross II | 15.667** \pm 0.497 | -7.967** \pm 1.741 | 42.983** \pm 4.180 | 35.933** \pm 4.009 | -7.300** \pm 3.657 | -13.967 \pm 7.618 | Complementary |
| Length of panicle | | | | | | | |
| Cross I | 27.643** \pm 0.271 | -0.067 \pm 0.895 | 1.160 \pm 2.238 | 1.960 \pm 2.093 | -1.600 \pm 1.861 | 4.173 \pm 4.064 | Complementary |
| Cross II | 27.280** \pm 0.213 | -1.667** \pm 0.661 | 7.213** \pm 1.707 | 7.147** \pm 1.572 | -1.867 \pm 1.417 | -3.013 \pm 3.081 | Complementary |
| Grain yield per plant | | | | | | | |
| Cross I | 40.428** \pm 1.317 | 13.067 \pm 12.493 | 91.837** \pm 25.589 | 107.553** \pm 25.536 | -16.433 \pm 25.060 | -156.187** \pm 50.359 | Duplicate |
| Cross II | 42.713** \pm 1.611 | 13.667** \pm 5.964 | 114.530** \pm 13.693 | 93.280** \pm 13.558 | 69.900** \pm 12.081 | -62.847** \pm 25.007 | Duplicate |
| Straw yield per plant | | | | | | | |
| Cross I | 58.598** \pm 1.687 | 1.383 \pm 11.352 | 57.107** \pm 23.769 | 78.507** \pm 23.685 | -28.633 \pm 22.777 | -125.407** \pm 46.079 | Duplicate |
| Cross II | 57.647** \pm 1.687 | -11.383 \pm 5.961 | 153.880** \pm 14.136 | 141.313** \pm 13.699 | 8.633 \pm 12.061 | -179.280** \pm 25.744 | Duplicate |
| Harvest index per plant | | | | | | | |
| Cross I | 39.858** \pm 0.379 | 1.383 \pm 2.227 | 16.009** \pm 4.816 | 13.968** \pm 4.705 | -4.515 \pm 4.509 | -7.705 \pm 9.268 | Complementary |
| Cross II | 40.417** \pm 0.389 | 8.189** \pm 2.300 | 7.131 \pm 4.942 | 2.442 \pm 4.857 | 23.660** \pm 4.654 | 18.409 \pm 9.508 | Complementary |

*- Significant at 5% level, ** - Significant at 1% level. [Cross-I - Karjat 2 x Munga] [Cross-II - Munga x Karjat 2]

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