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**Research Note**

# Generation mean analysis for yield and grain quality traits in rice (*Oryza sativa* L. )

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## Abstract

Three cross combinations each having $P_1$, $P_2$, $F_1$, $F_2$, $BC_1$ and $BC_2$ were evaluated in Compact Family Block Design with three replications to estimate the genetic parameters. Analysis of variance revealed significant differences among generations in all the characters studied except grain breadth in all the three crosses, and kernel length after cooking in cross III. The significance of scaling tests (A, B, C and D) indicated appreciable amount of epistasis present in different characters of three cross combinations under study, indicating the failure of a simple genetic model to explain the genetic system controlling the traits except grain breadth in all the three cross combinations and grain length/breadth ratio in cross combination II.

**Keywords**
Scaling test, epistasis, generations.

Generation mean analysis is based on quantitative biometric methods which measure phenotypic performance of various quantitative traits in basic experimental breeding generations (parental, filial, backcross and segregation generations). It is a useful technique in plant breeding for estimating main gene effects (additive and dominance) and their digenic (additive x additive, additive x dominance, and dominance x dominance) interactions responsible for inheritance of quantitative traits. It helps in understanding the performance of the parents used in cross combinations and potential of cross combinations to be used either for heterosis or other selection procedures. Considering the fact that grain yield and quality traits of rice are the most important complex traits, their improvement is dire objective of rice breeding programme.

During *Kharif*2015 (*i.e.*, during field evaluation of $F_1$ hybrids and parents) the material for generation mean analysis was generated. Some of the $F_1$ plants of the selected three cross combinations were selfed and some plants were backcrossed with their respective parents to obtain the $F_2$ and backcross ($B_1$ and $B_2$) generations respectively. The $F_1$ plants were protected from outside pollen by bagging with muslin cloth bags just before the $F_1$ plants commence to flower. At maturity each $F_1$ plant was harvested separately, keeping any of the doubtful parentage apart. The $F_1$ plants were threshed individually. Simultaneously, the parents of the selected cross combinations were hybridized to generate enough $F_1$ seed. Selfed seed was also obtained for all the parents. Thus, six basic generations, $P_1$, $P_2$, $F_1$, $F_2$, $B_1$ and $B_2$ were developed for each of the three crosses.

Before any model is fitted to estimate gene actions involved on yield and its components, scaling tests were performed as given by Hayman and Mather(1955). The scaling tests A, B, C and D indicated presence of appreciable amount of epistasis for different characters in all the three crosses. Presence of epistatic gene action for grain yield per plant and its related traits have been reported earlier by Sharma *et al.* (1986), Chauhan e*t al.* (1993), Montazeri *et al.* (2014) and Shahid *et al.* (2014).Analysis of variance for generation means comprising six generations *viz*., $P_1$, $P_2$, $F_1$, $F_2$, $BC_1$ and $BC_2$ was computed for five characters for each and mean sum of squares with their degrees of freedom are presented in Table 1. The mean sum of squares revealed significant differences among the families for all the three cross combinations for all the traits except for grain breadth in cross I (Basmati 564 x Ranbir basmati), grain breadth in cross II (Basmati 370 x Pusa 1460), kernel length after cooking and grain breadth in cross III(Basmati 370 x Basmati 1509.

In present investigation, all the four scaling tests (A,B,C and D) were highly significant for most of the characters under study, indicating inadequacy of additive-dominance model to understand the inheritance of yield and its quality traits. The values of individual scaling tests and estimates of mean, additive gene effect, dominance gene effect and epistatic interactions *viz*, additive x additive,

additive x dominance, and dominance x dominance interaction are presented in Table 2.

For yield per plant, cross I and cross II exhibited significant additive and additive x dominance gene effects and both these crosses indicated complimentary type of epistasis, whereas cross III exhibited additive x additive and additive x dominance gene effect, indicating duplicate type of epistasis. As grain yield is the outcome of interplay of various yield contributing characters, heterosis breeding as well as development of pure line variety through pedigree selection in promising crosses would be more effective. For development of promising inbreds, due weightage should be given for improvement of individual yield contributing characters. Similar findings were reported by Shahid *et al.* (2014).

For grain length, additive gene effect was exhibited by cross I and cross II whereas dominance, additive x additive and additive x dominance gene effect was present in all the three crosses. All the crosses indicated duplicate type of epistasis. Results were in accordance with reports of Roy and Senapati (2011).For grain breadth it was found that the additive-dominance model was adequate as none of the individual scaling test as well as $\chi^2$was also found significant in all the three crosses, so there was absence of non-allelic interactions for expression of the trait. The estimates of gene effects revealed that none of the gene effects was predominantly affected the grain breadth. Similar results were recorded by Kacharabhai (2015).

For grain length/breadth ratio, cross I exhibited additive x additive and additive x dominance gene effect and indicated duplicate type of epistasis, whereas cross III exhibited additive x dominance gene effect and complimentary type of epistasis. For cross II, additive-dominance model was adequate as none of the individual scaling test was found significant. The results are in accordance with the reports of Satheesh *et al.* (2010), and Gnanamalar and Vivekanandan (2013). For kernel length after cooking, cross I exhibited dominance gene effect indicating duplicate epistasis, whereas cross II exhibited dominance as well as dominance x dominance gene effect indicating complimentary epistasis. In Cross III, additive-dominance model was adequate as none of the individual scaling test was found significant. Similar results were found by Bano *et al*. (2017).

From the above study it can be concluded that it would be desirable to follow cyclic method of breeding involving conventional breeding approach of selection of superior recombinants and their *inter se m*ating for the development of elite homozygous recombinants having high quality and high yield.

## References

Bano, D. A., Singh, S. P., and Waza, S. A. (2017). Generation Mean Analysis for Yield and Quality Traits in Aromatic Genotypes of Rice *Oryza sativa* L.). I*nternational journal of pure and applied biosciences*, **5**(6) : 70-878.

Chauhan, V. S., Chauhan, J. S. and Tondon, J. P. (1993). Genetic analysis of grain number, grain weight and grain yield in rice (*Oryza sativa* L.). *Indian Journal of Genetics*,**53**(3): 261-263.

Gnanamalar, R. P., and Vivekanandan, P. (2013). Combining ability analysis of grain quality traits in rice (*Oryza sativa* L.). *Asian Journal of Plant Science and Research*, **3**(2): 145-149.

Hayman, B. and Mather, K. (1955).The description of genic interactions in continuous variation. *Biometrics*.**1**(1), 69-82.

Kacharabhai, P. S. (2015). Research Article Genetic analysis of yield and its components traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*.**(**1), 19-25.

Montazeri, Z., Jelodar, N. B. and Bagheri, B. 2014.Genetic dissection of some important agronomic traits in rice using line x tester method. *International Journal of Advanced Biological Sciences and Biomedical Research*,**2**(1): 181-191.

Roy, S. K. and Senapati, B. K. 2011.Estimation of genetic components for grain yield and quality traits of rice. *Oryza*, **48**(1): 22-30.

Satheesh, K. P., Saravanan, K. and Sabesan, T. 2010. Combining ability for yield & yield contributing characters in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*,**1**(5): 1290-1293

Shahid, M. Q., Liu, G., Li, J., Naeem, M. and Liu, X. D. 2014.Heterosis and gene action study of agronomic traits in diploid and autotetraploid rice. *Acta Agriculture Scandinavica Section B-Soil and Plant Science*,**61**: 23-32.

Sharma, D. K., Shrivastava, M. N. and Shrivastava, P. S. 1986.Nature of gene interaction in the inheritance of grain yield, harvest index and their component characters in rice. *Indian Journal of Agricultural Sciences*,**56**(6): 397-403.

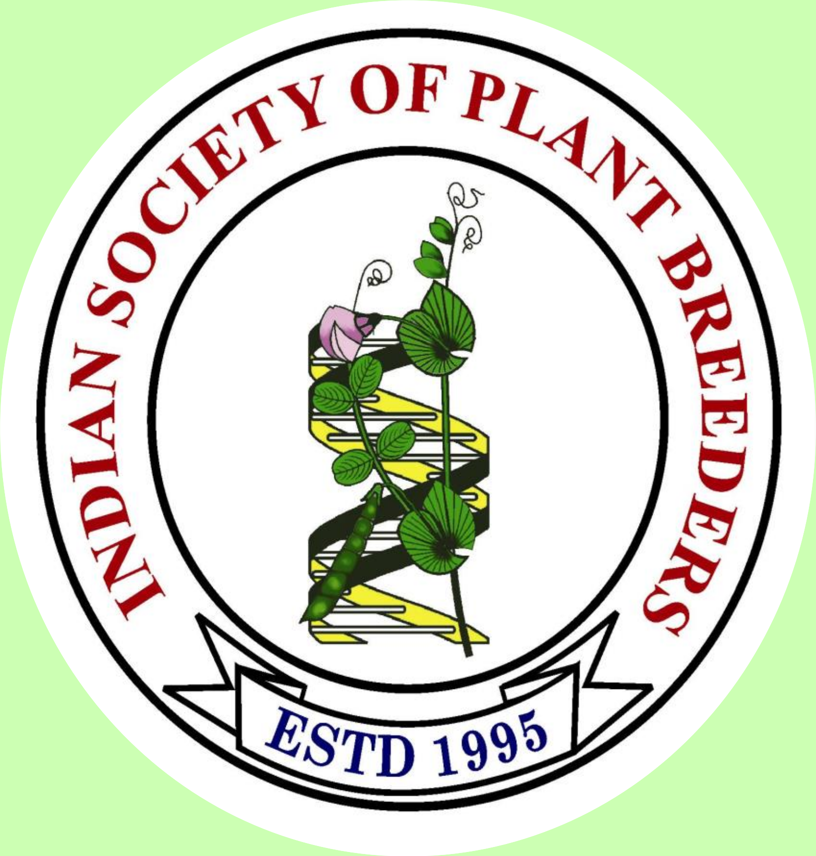
**Table 1. Analysis of variance for three families and their six generations for different characters**

| Source | Df | Mean sum of squares | | | | |
|---|---|---|---|---|---|---|
| | | GYPL | GL | GB | LBR | KLAC |
| **Cross I (Basmati 564 x Ranbir basmati)** | | | | | | |
| **Replications** | 2.00 | 0.01 | 0.05 | 0.01 | 0.05 | 0.1 |
| **Families** | 2.00 | 45.36* | 1.25* | 0.05 | 1.59* | 26.24* |
| **Error** | 4.00 | 0.29 | 0.06 | 0.06 | 0.16 | 0.42 |
| **Cross II (Basmati 370 x Pusa-1460)** | | | | | | |
| **Replications** | 2.00 | 0.47 | 0.05 | 0.02 | 0.2 | 0.2 |
| **Families** | 2.00 | 241.67* | 1.02* | 0.09 | 1.36* | 53.44* |
| **Error** | 4.00 | 1.08 | 0.11 | 0.03 | 0.14 | 1.02 |
| **Cross III (Basmati 370 x Basmati 1509)** | | | | | | |
| **Replications** | 2.00 | 0.08 | 0.07 | 0.02 | 0.09 | 2.86 |
| **Families** | 2.00 | 55.96* | 1.01* | 0.03 | 1.32* | 4.93 |
| **Error** | 4.00 | 0.92 | 0.13 | 0.05 | 0.03 | 1.86 |

*Significant at 5%
**GYPL**: grain yield per plant **GL**: grain length **GB**: grain breadth **LBR**: length breadth ratio **KLAC**: kernel length after cooking

**Table 2. Result of scaling tests and estimates of gene effects in three crosses of rice**

| | Scaling test | | | | Three Parameters Model | | | $X^2$ | Six Parameters Model | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Cross** | **A** | **B** | **C** | **D** | **m** | **[d]** | **[h]** | **(3 *df*)** | *M* | *[d]* | *[h]* | *[i]* | *[j]* | *[l]* |
| **Grain yield per plant (gm)** | | | | | | | | | | | | | | |
| **I** | 5.6** | -7.99** | 0.4 | 1.4 | 20.82** | -1.87* | -3.98 | 1.55 | 20.12** | 4.93** | 1.2 | -2.79 | 6.8** | 5.19 |
| **II** | -13.56** | -19.32** | -15.5** | 8.69** | 38.47** | -0.4 | -54.6** | 6.96 | 23.74** | 2.48 | -4.34 | -17.38** | 2.88 | 50.26** |
| **III** | -0.47 | -12.54** | -17.05** | -2.02 | 16.81** | -0.67 | -1.55 | 1.82 | 18.27** | 5.36** | 7.42 | 4.04 | 6.03** | 8.97 |
| **Grain length (mm)** | | | | | | | | | | | | | | |
| **I** | 1.3** | 1.83** | 0.03 | -1.55** | 3.36** | 0.05 | 9.3** | 0.12 | 6.45** | -0.21* | 3.08** | 3.09** | -0.26 | -6.22** |
| **II** | 0.67** | 0.33* | -1.41** | -1.21** | 4.4** | -0.4** | 6.17** | 0.1 | 6.63** | -0.23* | 2.75** | 2.41** | 0.17 | -3.42** |
| **III** | 0.84** | 0.83** | 0.51 | -0.58** | 5.42** | -0.13 | 4.66** | 0.1 | 7.04** | -0.13 | 1.82** | 1.16** | 0 | -2.83** |
| **Grain breadth (mm)** | | | | | | | | | | | | | | |
| **I** | 0.03 | 0.18 | 0.06 | -0.07 | 1.32** | 0.1 | 0.38 | 0.02 | 1.42** | 0.02 | 0.03 | 0.15 | -0.08 | -0.35 |
| **II** | -0.09 | 0.23 | -0.23 | -0.18 | 1.22** | 0 | 0.63 | 0.04 | 1.41** | -0.16 | 0.13 | 0.37 | -0.16 | -0.51 |
| **III** | -0.08 | 0.07 | -0.06 | -0.03 | 1.45** | -0.04 | -0.04 | 0.02 | 1.42** | -0.11 | -0.08 | 0.05 | -0.08 | -0.05 |
| **Grain length breadth ratio (mm)** | | | | | | | | | | | | | | |
| **I** | 0.95* | 1.21 | -0.35 | -1.25** | 2.62** | -0.38** | 6.48* | 0.21 | 4.69** | -0.51 | 1.82 | 2.5** | -0.13 | -4.66** |
| **II** | 0.97 | -0.05 | 0.75 | -0.09 | 4.33** | -0.05 | 2.21 | 0.18 | 5.16** | 0.45 | 1.11 | 0.17 | 0.51 | -1.09 |
| **III** | -1.32** | -1.25** | -2.39** | 0.09 | 4.75** | 0.01 | -2.02 | 0.19 | 4.43** | -0.02 | 0.72 | -0.17 | -0.04 | 2.74** |
| **Kernal length after cooking (mm)** | | | | | | | | | | | | | | |
| **I** | 3.09** | -0.67 | -0.4 | -1.41 | 16.88** | -2.4** | 10.69 | 0.83 | 20.91** | -0.52 | 5.43* | 2.83 | 1.88 | -5.25 |
| **II** | 1.11 | -6.98** | -6.68** | -0.4 | 20.82** | -2.88** | 0.89 | 1.55 | 22.53** | 1.17 | 5.96* | 0.81 | 4.04** | 5.07 |
| **III** | 1.14 | -1.23 | -0.47 | -0.19 | 21.68** | -1.27 | 0.44 | 0.15 | 21.82** | -0.09 | 0.14 | 0.39 | 1.18 | -0.3 |



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