RESEARCH ARTICLE Indian Journal of Agricultural Research, Volume 59 Issue 9: 1338-1344 (September 2025)

Half Diallel Analysis for Grain Yield and Maturity Duration of Rice (*Oryza sativa* L.) using Hayman and Griffing Method

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10.18805/IJARe.AF-939

ABSTRACT

Background: Six rice genotypes, Namely Rojolele, Pandan Wangi, INPARI 32, INPARI 48, Chakra Buana and M70D, along with their fifteen half diallel crosses, were tested to elucidate the genetic control underlying the inheritance of yield and maturity traits. The research aimed to study genetic variability and yield component characters of six parents of rice genotypes and 15 crossing combinations.

Methods: Twenty-one genotypes, including parents and F1s, were planted using a randomized block design with three replications. The rice grain yield and maturity duration data were utilized for half diallel analysis using the Hayman and Griffing method-2.

Result: The study found that whereas additive gene action controls maturity duration and grain yield per plant features and yield per plant, additive gene action predominates. The study showed that the environment affected the expression of these additive genes and that the additive gene substantially affected the inheritance of these features. Broad-sense heritability (60%) is greater than narrow-sense (12%) of grain yield. Broad-sense and narrow-sense heritability are similarly high (98%, 70%) in maturity duration. This implies that these features can be selected in the early generation using the pedigree technique. Except for grain yield per plant, the general combining ability (GCA) was more critical for maturity duration than the specific combining ability (SCA). According to this result, the research may help rice breeding programs develop early maturity and high grain yield to promote food security.

Key words: Combining ability, Grain yield, Half-diallel, Heritability, Inheritance, Maturity duration.

INTRODUCTION

Rice (*Oryza sativa* L.) is the main cereal crop utilized by humans (El-Hity *et al.,* 2016). It is a major crop that provides staple foods to nearly half of the world's population (Anis *et al.,* 2017). In 2024, the rice cultivation area in Central Java totalled 1.55 million hectares, reflecting a drop of 0.09 million hectares (5.36 per cent) from 2023. In accordance with the cultivated area, rice output in 2024 attained 8.89 million tons of dry milled rice, equivalent to 5.11 million tons of rice for human consumption. Indonesia's national rice production for 2024 was 53.142 million tons (BPS, 2025).

Applying novel alternatives in rice breeding is a potential opportunity to release competitive genotypes in contrast to the conventional method Bassuony and Zsembeli, (2021). However, breeding plants requires a clear understanding of gene action and the ability to combine traits (Hasanalideh *et al.,* 2017). In self-pollinated crops such as rice, these investigations are useful in evaluating the ability of the parental lines, which, when hybridized, would yield superior segregates (Sarawgi *et al.,* 2017). Increasing genetic variability by crossing rice genotypes from different genes is the first step in a rice breeding program. Research that advances our knowledge of plant genetic information also helps breeding operations succeed (Riyanto *et al.,* 2023). Crossing parent plants with high genetic variability can enhance better genetic characteristics (Herwibawa *et al.,* 2014). It is crucial for integrating beneficial alleles and making the required changes (Faysal *et al.,* 2022). The genetic relationship among genotypes from various accessions becomes one of the essential criteria for producing potential heterotic groups (Hussain *et al.,* 2022). By analyzing the combining ability, we can get insight into the relative significance and size of additive and nonadditive gene action types in manifesting the characteristics Zewdu, (2020). In addition, the yield potential of hybrids can be increased by improvement in parental lines. Hence, ensuring greater productivity is of prime factor in any breeding experiment. Traits *viz.*, reduced plant height, moderate tillering habit, large and compact panicles, increased number of grains per panicle, increased thousand kernel weight and higher

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How to cite this article: Mohamad, A.A.M., Suprayogi, Riyanto, A. and Haryanto, T.A.D. (2025). Half Diallel Analysis for Grain Yield and Maturity Duration of Rice (*Oryza sativa* L.) using Hayman and Griffing method. *Indian Journal of Agricultural Research.* **59(9):** 1338-1344. doi: 10.18805/IJARe.AF-939.

Submitted: 25-03-2025 **Accepted:** 09-05-2025 **Online:** 17-06-2025

yield construed significant rice characters for any trait based improvement (Saravanan *et al.,* 2022).

For the plants to develop more effectively in subsequent generations with the desired traits, breeders may select superior plants with high heritability and genetic advancements by considering information about these factors (Kahani and Hittalmani, 2016). A combination of heritability estimates and genetic advance usually are more helpful than heritability estimates alone in predicting the gain under selection (Rattanarat *et al.,* 2020). The diallel analysis is one of the most powerful tools for selecting desirable parents, estimating the GCA of parents and determining the desired crosse s with the high SCA so that heterosis could be utilized and the effect of gene and variance components could be studied (Aditya and Bhartiya, 2017). Applying genetic information to a breeding program, especially the inherited character, which derives from a suitable mating design, is precious (Elmoghazy *et al.,* 2016). Adequate information about heritability, variability and the degree of association among different traits is needed for further yield improvement. It has been proposed that genetic tools be used to establish sustainable solutions to basic crop constraints, but this is difficult due to the large number of variation effects and a lack of adequate evaluation and classification techniques (Hilli and Immadi, 2022).

This research study aims to estimate the genetic parameters of rice maturity duration and grain yield using the half-diallel analysis. It also seeks to investigate the genetic components of the F1 population from the crosses of six parents with different grain yields per plant.

MATERIALS AND METHODS

Location of the experiment

The research was conducted at the Experimental Garden, Department of Agrotechnology, Faculty of Agriculture, Jenderal Soedirman University, Purwokerto, Indonesia, during the growing season 2024 from 15 May to November 2024. The experimental materials in this study are 15 combinations of F1 and six parents.

Plant material

Six genotypes of rice, Rojolele, Pandan Wangi, INPARI 32, INPARI 48, Chakra Buana and M70D, were used as parents in this study. These parents have different maturity duration and high yielding (Table 1). Half-diallel crosses among six parents produced 15 rice F1 genotypes. These parent's Indonesian origin and have various maturity duration and high yielding of rice (Table 1).

Experimental design

The experiment uses a randomized-complete block design with three replications. Seeds of 21 genotypes were grown in a petri dish for one week and then transplanted into polybags. Each polybag consisted of one plant per genotype. Local rice cultivation practices was adopted for rice cultivation and plant protection. The total number of polybags was 63, each containing one plant. Fertilizer applications of 0.4 g N/polybag and 1.0 g N-P-K/polybag were applied twice, *i.e.*, 10 and 20 days after transplanting.

Data collection and analysis

When it matured, panicles were harvested from parents and all generations individually. Panicles were subjected as samples of rice's grain yield and maturity duration.

The varieties, *viz* Rojolele Pandan Wangi, were late maturing, Inpari 32, Inpari 48 medium maturing and Chakra Buana, M70D early maturing. Farmers are growing local rice cultivars in irrigated land, such as Rojolele. However, the local cultivars are late maturing (more than 120 days) and susceptible to pests and disease (Haryanto *et al.,* 2008). Moreover, less current research focuses on developing new high yielding cultivars with early maturity by the cross-breeding program.

Analysis of variance for F1 in half diallel cross for grain yield per plant and maturity of rice followed the statistical model:

$$Y_{ijkl} = m + T_{ij} + b_k + (bT)_{ijk} + e_{ijkl} \quad ....(1)$$

Where,
m = General mean.
T_{ij} = Effect of i x j^{th} genotype.
b_k = Effect of k^{th} block.
$(bT)_{ijk}$ = Interaction effect.
e_{ijkl} = Error effect.

Genetic components of variation

Genetic components of variation were calculated using the following formulas:

$$\text{The regression coefficient of b (Wr, Vr)} = \frac{\text{Cov (Wr, Vr)}}{\text{Var (Vr)}} \quad ....(2)$$

Where,
Wr = Covariance between parents and their offspring.
Vr = Variance of each array.
Cov (Wr, Vr) = Covariance of (Wr, Vr).
Var (Vr) = Variance of Vr.

$$\text{Additive genetic variance (D)} = V_{0L0} - E \quad ....(3)$$

Where,
V_{0L0} = Variance of parents.
E = Environmental variance.

Dominant variance

$$H_1 = V_{0L0} - 4W_{0L01} + 4V_{1L1} - (3n - 2)E/n \quad ....(4)$$

Where V_{0L0} is the variance of parents, W_{0L01} is the covariance between the parents and the array, V_{1L1} is the mean-variance of the array, n is the number of parents and E is the environmental variance.

Proportions of positive or negative genes in the parent

$$H_2 = 4V_{1L1} - 4V_{0L1} - 2E \quad ....(5)$$

V_{1L1} is the mean-variance of the arrays, V_{0L1} is the variance of the mean of arrays and E is the environmental variance.

Mean covariance of additive and dominance

$$F = 2V_{0L0} - 4W_{0L0} - 2(n - 2)E/n \quad ...(6)$$

Where V_{0L0} is the variance of parents, W_{0L0} is the covariance between the parents and the arrays, n is the number of parents and E is the environmental variance.

Dominance effect

$$h^2 = 4(M_{L1} - M_{L0})^2 - 4(n - 1)E/n^2 \quad ...(7)$$

Where $(M_{L1} - M_{L0})^2$ is the difference between the mean of the parents and the mean of their n^2 progeny, n is the number of parents and E is the environmental variance.

Environmental variance.

$$E = 1/r(\text{Error SS} + \text{Rep. SS})/[(r - 1) + (c - 1) \times (r - 1)] \quad ...(8)$$

Where,

Error SS = Sum square of error.

Rep. SS = Sum square of replication.

r = Number of replications.

c = Number of mistakes.

$$\text{Average degree of dominance variance} = (H_1/D)^{1/2} \quad ..(9)$$

Where,

H_1 = Dominance variance.

D = Additive genetic variance.

The proportion of genes with positive and negative effects in the parent = $H_2 / 4H_1$ ....(10)

Where,

H_1 = Dominance variance.

H_2 = Proportion of positive or negative genes in the parent.

The ratio of dominant and recessive gene in the parents =

$$[(4DH_1)^{1/2} + F] / (4DH_1)^{1/2} - F \quad ...(11)$$

Where,

D = Additive genetic variance.

H_1 = Dominance variance.

F = Mean covariance of additive and dominance.

$$\text{Number of gene groups} = h^2/H_2 \quad ....(12)$$

Where h^2 is the dominance effect and H_2 is the proportion of positive or negative genes in the parent.

The coefficient correlation between

$$(Wr + Vr) \text{ and } Yr(r) = \frac{[Cov(Wr+Vr),Yr]}{\sqrt{[Var(Wr+Yr).\ Var(Yr)]}} \quad ....(13)$$

Where (Wr + Vr) is the parental order of dominance, Yr is the parental measurement, Cov(Wr + Vr) is the covariance of (Wr + Vr), Var(Wr + Vr) is the variance of (Wr + Vr) and Var(Yr) is the variance of Yr.

Broad-sense heritability

$$h^2_{bs} = (1 / 2D + 1/2H_1 - 1/2F) / (1/2D + 1/2H_1 - 1/4H_2 - 1/2F + E) \quad ....(14)$$

D is the additive genetic variance, H_1 is the dominance variance, H_2 is the proportion of positive or negative genes in the parent, F is the mean covariance of additive and dominance and E is the environmental variance.

Narrow-sense heritability

$$h^2_{ns} = (1/2D + 1/2H_1 - 1/2H_2 - 1/2F) / (1/2D + 1/2H_1 - 1/2H_2 - 1/2F + E) \quad ...(15)$$

Where D is the additive genetic variance, H_1 is the dominance variance, H_2 is the proportion of positive or negative genes in the parent, F is the mean covariance of additive and dominance and E is the environmental variance.

Combining ability analysis

The statistical model for the analysis variance of combining ability was used as follows:

$$Y_{ij} = m + g_i + g_j + S_{ij} + r_{ij} + \frac{1}{bc}\sum\sum_{eijkl} \quad ....(16)$$

Where Y_{ij} is the mean of i x j^{th} genotype, m is the general mean, g_i is the general combining ability (gca) effect of j^{th} parent, g_j is the general combining ability (gca) effect of j^{th} parent, S_{ij} is the interaction, *i.e.*, SCA effect, r_{ij} is the reciprocal effect and $\frac{1}{bc}\sum\sum_{eijkl}$ is the mean error effect.

$$\text{GCA variance } (g_i) = \frac{1}{2n}\sum (Yi + Yj) - \frac{1}{n^2} Y^2 \quad ....(17)$$

Where Y_i is the mean value of ith genotype cross, Y_j is the mean value of jth genotype selfing, n is the number of parents and Y is the total.

$$\text{SCA variance } (S_{ij}) = \frac{1}{2}(Y_{ij} + Y_{ij}) - \frac{1}{2n}(Y_{i.} + Y_{.i} + Y_{j.} + Y_{.j}) + \frac{1}{n^2}Y \quad ...(18)$$

Where Y_{ij} is the mean of i x j^{th} genotype, Y_{ji} is the mean of j x ith genotype, Y_i. Is the total mean value of ith genotype cross, $Y_{.i}$ is the total mean value of ith genotype selfing, $Y_{j.}$ is the total mean value of jth genotype cross, $Y_{.j}$ is the total mean value of jth genotype selfing, n is the number of parents and Y is the total.

RESULTS AND DISCUSSION

Analysis of variance for genotypes

Analysis of variance showed significant differences among genotypes for grain yield and maturity duration (Table 2). Its significance has also been reported by (Edukondalu *et al*., 2017) and (Akanksha and Jaiswal, 2019). Therefore, notable variations in rice grain yield and maturity duration among genotypes prove they are appropriate for additional genetic research.

Genetic components of variation

Gene interaction

The regression coefficient values of b (Wr, Vr) for grain yield and maturity duration of rice are 0,69 and 1,08. They are not significantly different from one another (Table 3). It is in line with the findings from the previous

research (Singh et al., 2021) for grain yield and maturity duration. The regression coefficient value of b (Wr, Vr) can be used to determine the gene interaction of a trait. According to the t-test, gene interaction is indicated by the value of b (Wr, Vr), which is statistically different from one another, whereas the value of b, which is non-significantly different, shows that there is no gene interaction (Wr, Vr) from one another. This indicates no interactions among the genes in this research for rice maturity duration and grain yield. This means that each gene cannot affect the other and no interaction exists between genes that control grain yield and maturity duration.

Gene distribution in the parents

Using H_2 levels, we can ascertain the genes distribution. According to the findings, there was a substantial difference in the H_2 values for rice grain yield and maturity duration (Table 3). This indicates that the genes determining grain yield and maturity inheritance are not evenly distributed among the parents. Table 3 shows that the values of H_1 are 219,78 and 326,51, while the values of H_2 are 223,10 and 257,30 for grain yield and maturity of rice. It was also reported by (Sharma and Jaiswal, 2021).

The present analysis showed that the values of $H_2/4H_1$ for grain yield and maturity are 0,25 and 0,19 (Table 3).

Dominance level

The dominance effect can be seen from the value of the mean degree of dominance as estimated by $(H_1/D)^{1/2}$. If the value of $(H_1/D)^{1/2}$ is more than 1, it indicates over-dominance. If the value of $(H_1/D)^{1/2}$ between 0 and 1, it indicates partial dominance (Hayman, 1954). Table 3 shows that the value of $(H_1/D)^{1/2}$ of grain yield and rice maturity is more than 1, which is 1,69 and 2,22. It proves that there is over-dominance in these traits. It is similar to Rohman *et al.* (2019) for grain yield.

Dominance effect

The h^2 value indicates the dominance effect. Table 3 shows that the h^2 value significantly differs for grain yield and maturity duration. It was detected during the days from physiological maturity and grain yield, as reported by (El-Satar, 2017).

Environmental variance

Table 3 shows that environmental variance significantly influenced grain yield but did not considerably influence the maturity duration. This proved that the environment has no significant influence on grain yield and maturity expression. Raihan *et al.* (2024) has the identical finding that grain yield per plant and maturity duration for environment was nonsignificant.

Proportion of dominant gene to recessive gene

The Kd/Kr ratio and the F component indicate the ratio of dominant to recessive genes. There are significantly more dominant genes than recessive genes in the parent, as indicated by the positive value of the F component (Mohammed, 2020). The results showed a positive value of the F component. The ratio of Kd/Kr of the grain yield and maturity of rice is 0,99 and 2,44. The grain yield is 0,99, smaller than one, but maturity is 2,44, which is more than one, as shown in Table 3. It indicates that genes in the parent for grain yield and maturity duration of rice are more dominant.

Number of gene groups

The component of h^2/H_2 indicates the number of gene groups that control a trait. The h^2/H_2 values of grain yield are 1,14 and maturity is 1,24. Both are higher than one. It

Table 1: Half Diallel mating design for six varieties of rice.

Variety	Maturity duration (day after duration)	Origin
Rojolele	155	Indonesia
Pandan wangi	150	Indonesia
Inpari 32	104	Indonesia
Inpari 48	110	Indonesia
Chakra buana	102	Indonesia
M70D	91	Indonesia

Table 2: Analysis of variation for rice maturity duration and grain yield per plant for F1 in a half diallel cross.

Source of variation	Degrees of freedom	Mean square	
		Yield per plant (gm)	Maturity duration
Block	2	414,7531 ns	86,1111 ns
Genotype	20	271,8301 *	775,1302**
Error	40	119,2819	7,3278

** Highly significant and *Significant different at the level of 5%; ns = Not significantly different.

Table 3: Estimates of the genetic factors that affect rice maturity duration and grain yield per plant.

Genetic components	Yield per plant (gm)	Maturity duration
b (Wr, Vr)	0,697 ns	1,082 ns
D	30,256 ns	635,3679**
F	-0,288ns	381,0091**
H_1	219,7833**	326,5169**
H_2	223,1023**	257,3053**
h^2	170,6357**	214,0453**
E	45,5811**	3,8765ns
$(H_1/D)^{1/2}$	2,69	0,72
$H_2/4H_1$	0,25	0,19
Kd/Kr	0,99	2,44
h^2/H_2	0,765	0,832
r[(Wr + Vr),Yr]	0,86	0,94
h^2_{bs}	0,60	0,98
h^2_{ns}	0,12	0,70

**Highly significant and *Significant different at the level of 5%; ns = Not significantly different.

Table 4: Value (Wr + Vr) of grain yield per plant and maturity duration of rice.

Cultivars	Grain yield per plant	Maturity duration
Rojolele	254,919	983,044
Pandan Wangi	345,340	697,163
INPARI 32	2,214	207,385
INPARI 48	12,680	77,800
Chakra buana	56,495	67,011
M70D	0,159	190,944

Table 5: Analysis of variation between GCA and combining ability: SCA ratio between rice maturity duration and grain yield per plant.

Source of variance	Degree of freedom	Mean square	
		Grain yield	Maturity
GCA	5	91,39ns	779,99**
SCA	15	90,35*	84,50**
Error	40	39,76	2,442
GCA: SCA ratio		1,011	9,23

**Highly significant and *Significant different at the level of 5%; ns = Not significantly different.

proves the involvement of many genes, or one gene group responsible for their genetic control. As a result, grain yield and maturity are controlled by many groups of genes. A different result was found by Kumar *et al.* (2022) for grain yield and maturity duration.

Direction and order of dominance

A positive value is obtained the correlation of (Wr + Vr) and Yr for rice grain yield and maturity traits (Table 4). M70D is the closest to zero, which means that this parent has the most dominant genes for grain yield. However, the maturity duration is far from zero. It means that the parents have recessive genes. Therefore, the maturity duration in rice is controlled by recessive genes (Agung *et al.,* 2017).

Heritability

The estimation of broad-sense heritability (h^2_{bs}) for grain yield per plant and rice maturity duration are similar to 56,12 % and 99,05%. Whereas, the estimation of narrow-sense heritability (h^2_{ns}) for these traits are 0,29% and 67,29%. It is identical to the result that is reported by Edukondalu *et al.* (2017) and Datta *et al.* (2024) of a high heritability of grain yield and maturity duration.

Heritability is important in quantitative genetics, particularly selective breeding (Salam *et al.,* 2016). The estimated value of broad-sense heritability indicates the relative contribution of genetic factors to the variation of the observed trait (Saha *et al.,* 2019). Grain yield per plant also were had high heritability reported by Riyanto *et al.,* (2021).

Combining ability estimation of grain yield and maturity duration

The estimated effect of GCA regarded as an important indicator of the potential parental genotypes for generating superior-breeding populations. Furthermore, the GCA of the parental lines reveals the average performance of a parent in a series of crosses. The significance of GCA effects in two directions in each character revealed that the parents could transfer the high and low values for a trait. However, increasing and decreasing the value of parental characters would be considered as positive and negative GCA effects. Based on their variation, plant breeders desire to produce high-yielding hybrids with better characteristics than the parents. In plant breeding experiments, diallel analysis is beneficial for estimating GCA and SCA (Yadav *et al.,* 2021). Meanwhile, analysis of combining ability provides an important method for selecting preferred parents and providing the requested information to the nature of gene action which regulates desired traits (Aamer and Ibrahim, 2020).

Guimarães *et al.* (2023) found that the general combining ability (GCA) and the specific combining ability (SCA) were significant. Greater contribution of the SCA, compared to GCA, for the variation among crosses, indicates that non-additive effects were more prevalent for the traits evaluated. The same results were reported by (Dianga *et al.,* 2020) for significant differences of GCA and SCA.

This study demonstrates that general combining ability (GCA) does not significantly affect grain yield, whereas specific combining ability (SCA) does have a significant impact. Conversely, both GCA and SCA significantly influence the maturity duration of rice. The GCA:SCA ratios for grain yield and maturity are greater than one, specifically 1.011 and 9.23 (Table 5), indicating that additive gene action is more predominant than nonadditive gene action in the expression of these traits.

CONCLUSION

The effects of both additive and non-additive gene actions on rice grain yield and maturity duration were verified; the additive gene action had a more significant impact than the non- additive gene action. Broad-sense and narrow-sense heritability values of grain yield and maturity duration were generally high. It highlights how genetics explained most of the observed variances and how effective variety and hybrid selection would be. We consider crossing as the most efficient and suitable method for creating superior rice cultivars based on the variations in GCA/SCA ratios and heredity. To promote food security, this research may help design an efficient rice breeding program that produces high grain yield and early maturity.

ACKNOWLEDGEMENT

The authors thank all the supervisors who contributed to the research and field trial. We also thank the Grant of

Research and Community Services Institute, Jenderal Soedirman University, who supported this research.

Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided but do not accept any liability for any direct or indirect losses resulting from using this content.

Informed consent

All experiment genotype procedures were approved by the Committee of Experimental Plant Breeding Care and Handling Techniques and by the Department of Agrotechnology Committee at the Jenderal Soederman University.

Conflict of interest

The authors declare that they have no competing interests.

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