Jurnal Kultivasi Vol. 23 (2) August 2024
ISSN: 1412-4718, eISSN: 2581-138x

Riyanto A · Oktaviani E · Wulansari NK · Haryanto TAD

Genetic parameters of yield component and yield in M1 rice (*Oryza sativa* L.) generation irradiated with gamma-ray

Abstract. High-yielding varieties are the primary determinant of the success of increasing Indonesia's rice production. Plant breeding for new high-yielding varieties is possible through mutation induction and selecting desired traits. The effectiveness and efficiency of selection require comprehensive genetic parameters. This study aimed to study the genetic diversity, heritability, genetic advance, and relationship between yield components and yield in the M1 generation of mutant rice irradiated with gamma ray. This research used a factorial randomized complete block design, involving gamma irradiation doses of 100 Gy, 150 Gy, and 200 Gy, as the first factor; and the second factor was the rice genotype: UnsoedBDBP, UnsoedBDIU, UnsoedBPIU, UnsoedIUBD, and UnsoedIBP. Each treatment was repeated three times. Results showed that traits with broad genetic variation were tiller number plant^{-1}, grain number panicle^{-1}, and grain yield plant^{-1}. High heritability and genetic advance values were found in plant height, grain number panicle^{-1}, and yield plant^{-1}, indicating that improvement in these traits can be achieved simply through selection methods. Panicle number plant^{-1} and filled grain percentage panicle^{-1} showed a unidirectional relationship and directly affected high values on yield plant^{-1}. Therefore, these traits can be considered selection indicators for breeding high-yielding mutant rice.

Keywords: Genetic parameter · Grain yield · Mutation induction · Rice · Selection.

Submitted: 2 June 2024, Accepted: 27 July 2024, Published: 14 August 2024
DOI: https://doi.org/10.24198/kultivasi.v23i2.55129

Riyanto A[1*] · Oktaviani E[1] · Wulansari NK[1] · Haryanto TAD[1]
[1] Faculty of Agriculture, Jenderal Soedirman University, 5312, Purwokerto, Jawa Tengah, Indonesia
*Correspondence: agus.riyanto0208@unsoed.ac.id

Riyanto A, Oktaviani E, Wulansari NK, Haryanto TAD. 2024. Genetic parameters of yield component and yield in M1 rice (*Oryza sativa* L.) generation irradiated with gamma-ray. Jurnal Kultivasi, 23(2): 187-200.

Introduction

Rice provides an essential dietary component for roughly fifty percent of the world (Singh et al. 2022). On a worldwide scale, it is noteworthy that Indonesia is the third-largest producer of rice (Connor et al. 2021) and the fourth-largest rice consumer (USDA 2023). Rice is considered a basic meal in Indonesia, and it is consumed by over 80% of Indonesia's population and contributes 62.1% to the overall energy intake (Nafisah et al. 2020; Syahri & Somantri 2016). Rice is the primary source of income for many farming households, amounting to approximately 18 million (Haryanto et al. 2011). Furthermore, rice shortages in the domestic market or high rice prices cause political instability (Rosyada et al. 2022). Hence, the Indonesian government must uphold rice production and provide a steady supply to maintain stability in food security.

National rice production amounted to 54.75 million tons (~31.54 million tons of milled rice) in 2022 and 53.98 million tons (~31.10 million tons of milled rice) in 2023 (BPS 2024). These data show that national milled rice production has decreased. Furthermore, with the increase in population, rice consumption will continue to increase. In 2050, Indonesia's population is projected to reach approximately 322 million (Ansari et al. 2023). If the demand for rice is 127.70 kg per capita (Arifin et al. 2019) then Indonesia needs 41.2 million tons of milled rice. Hence, national rice production must be increased.

The Indonesian government strives to meet domestic rice needs by increasing production using high-yielding rice varieties. Highly-yielding varieties significantly augment rice production in Indonesia (Riyanto et al., 2021). High-yielding varieties significantly contribute 56% to the overall growth in national rice production. Furthermore, when these varieties are paired with effective water and fertilizer management practices, their contribution can be further enhanced, reaching up to 75% (Syahri & Somantri 2016). To increase rice production, plant breeding programs to produce high-yielding varieties are very important (Wang et al. 2021).

Mutation induction is one of the supporting tools for developing new varieties (Hernández-Soto et al. 2021) and has produced approximately 3222 mutant varieties (Laskar et al., 2018). Mutation induction is regarded as an alternate method for enhancing genetic diversity, serving as a valuable source of germplasm for plant improvements (Brock, 1971). The purpose of mutation induction is to produce genetic diversity so that it is possible to select plants with desired traits (Muhammad et al., 2021)

Gamma irradiation is a commonly employed physical mutagen to induce mutations (Pérez-Jiménez et al. 2020; Riviello-Flores et al. 2022). Gamma irradiation possesses significant cell and tissue penetration capabilities, which can induce alterations in DNA (Katiyar et al. 2022), resulting in genetic diversity among individuals because DNA controls the phenotype in living organisms (Ishak 2023). Mutation induction using gamma irradiation has proven to change plants' morphological and biochemical characteristics (Saragih et al. 2021). Research that has been conducted shows that gamma irradiation can increase plant yields (Kato et al. 2020).

Selecting mutants with desired traits is the next step in producing new varieties in mutation breeding (Sao et al. 2022). Effective and efficient selection requires comprehensive genetic information for the desired traits. Genetic parameters, including genetic diversity, heritability, and genetic advance, provide significant indicators for choosing the method of selection of desirable traits that might lead to superior mutant development (Sofian et al. 2019). Genetic diversity, heritability, and genetic advance analysis provide valuable insights into the potential benefits that could be achieved in future generations through selective breeding to enhance a certain feature under study (Mahantashivayogayya et al. 2016).

Successful new variety development necessitates a comprehensive knowledge of the genetic diversity of yield components and yields across different genotypes (Oladosu et al. 2014). Mutagenesis can increase genetic diversity. If a trait has wide genetic diversity, the diversity of traits among individuals in the population will also be high, and selection will be easier to obtain the desired traits (Kurniawati et al. 2019). Hence, genetic diversity estimation of yield components and yield among different genotypes holds important value in the strategic development of mutant breeding programs.

The coefficient variability value describes genetic diversity (Choudhary et al. 2018), which

Riyanto A, Oktaviani E, Wulansari NK, Haryanto TAD. 2024. Genetic parameters of yield component and yield in M1 rice (*Oryza sativa* L.) generation irradiated with gamma-ray. Jurnal Kultivasi, 23(2): 187-200.

can be categorized into two distinct measures, i.e., the phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV) (Faysal et al. 2022; Sadimantara et al. 2021). PCV refers to the extent of trait variation observed among different genotypes and is subject to the combined influence of both genetic and environmental factors. Meanwhile, GCV is trait variability between genotypes only influenced by genetic factors (Patel et al. 2021). In selection, traits that have GCV higher than PCV are more desirable.

The environmental impact encompasses both heritable and non-heritable traits estimated by heritability values (Mahantashivayogayya et al. 2016). The estimated heritability value provides insight into the degree to which genetic or environmental factors affect a trait, thus facilitating an evaluation of the degree to which the trait is inherited by future generations (Kartahadimaja et al. 2021). The estimation of the heritability value of a trait is of great significance in the selection of desirable traits. During the initial stages of plant genetic improvement, the development of efficient breeding programs for quantitative traits necessitated the acquisition of dependable estimates of heritability (Chakravarti et al. 2014).

The estimation of selection progress can be more accurately determined by using both heritability estimates and genetic advances instead of relying solely on heritability estimates. Therefore, the primary considerations for plant breeders when developing plant improvement methods are the heritability value and the genetic advance value of desirable traits (Tiwari et al. 2019). Heritability indicates the degree to which genotypic selection can be effective, with its basis often being the phenotypic performance of individuals (Shah et al. 2018). Genetic advance is the disparity between the genotype average value of a selected population and the genotype average value of the initial population from which the genotype was selected (Adhikari et al. 2018). Genetic advance provides information about acquiring expected genetic progress from selecting superior individuals (Anbanandan & Eswaran 2018).

The grain yield is the primary criterion in rice plant breeding for improving new high-yielding varieties. However, grain yield is controlled by polygenic genes and is significantly impacted by environmental factors, hence rendering directly selecting for this feature ineffective (Riadi et al. 2018). Hence, to improve the effectiveness of selection, it is crucial to possess comprehensive knowledge regarding each trait that contributes to rice yield throughout the development of high-yielding varieties (Ata-Ul-Karim et al. 2022).

Correlation and path analysis determine the yield component's contribution to yield. Establishing correlation is essential for developing appropriate selection strategies to enhance genetic improvement in yield (Okasa et al. 2021). Correlation is a method of statistics utilized to quantify the magnitude and orientation of associations between traits (Khomphet et al. 2022; Tsagaye et al. 2022). Nonetheless, correlation analysis provides inconclusive data on how each yield component feature directly or indirectly influences grain yield (Kumari & Parmar 2020). Consequently, it cannot predict selection success (Chavan et al. 2020).

Path analysis is an approach to statistics that partitions the correlation coefficient of yield components and yield into direct and indirect effects. This method is a foundation for identifying and selecting enhanced grain yield (Ashraf et al. 2020; Dewey & Lu 1959). Path analysis coefficients thoroughly comprehend the relevance of various yield components' direct and indirect effects on grain yield (Ratna et al. 2015). Path analysis coefficients assist plant breeders in identifying yield components that might be chosen to enhance grain yield (Muthuramu & Ragavan 2020). Utilizing correlation and path analysis in conjunction provides a more comprehensive understanding of the causal relationship between two distinct traits (Premkumar et al. 2015), making it easier to develop selection methods to increase grain yield in mutant rice. This study aimed to study the genetic diversity, heritability, genetic advance, and relationship between yield components and yield in M_1 generation of mutant rice.

Materials and Methods

Experimental location. The greenhouse of the Faculty of Agriculture, Jenderal Soedirman University, Banyumas, Indonesia, served as the site of experiments. The experimental site was located at coordinates 7°24'28.7"S and 109°15'13.3"N, 110 meters above sea level.

Experimental materials. A gamma-ray irradiated M_1 generation mutant of rice was used as plant material for present work. Rice seeds collected at Plant Breeding and Biotechnology Laboratories were treated with gamma radiation using the facility in the National Nuclear Energy Agency of Indonesia (BATAN),. The gamma-irradiated genotypes were UnsoedBDBP, UnsoedBDIU, UnsoedBPIU, UnsoedIUBD, and UnsoedIBP. After drying to a water content of 12%, the rice seeds from each genotype were put into a ^{60}Co gamma source with an irradiation rate of 510 Gy.h^{-1}. Subsequently, the seedlings underwent 100 Gy, 150 Gy, and 200 Gy of gamma radiation.

Experimental design. This research is a factorial experiment. The first factor was gamma irradiation doses of 100 Gy, 150 Gy, and 200 Gy. The second factor is the rice genotype: UnsoedBDBP, UnsoedBDIU, UnsoedBPIU, UnsoedIUBD, and UnsoedIBP. This research used a randomized complete block design. Each treatment was repeated three times.

Plant cultivation. M_1 generation of mutant rice seeds were grown in germination trays for 2 weeks. Two-week-old seedlings were placed in 35 cm x 40 cm polybags filled with 8 kg of soil. Two rice seedlings are placed in each polybag. Basic fertilizer was applied 10 days before transplanting at 1.21g P_2O_5 per polybag and 0.90g K_2O per polybag. Nitrogen fertilizer at 8.72 g per polybag was applied two and four weeks after planting. Rice plants are maintained according to recommendations for rice cultivation, and plant protection is established until the plants are harvested.

Data collection. Each plant was used as a sample in data collection. The yield component and yield recorded were plant height, tiller number plant^{-1}, panicle number plant^{-1}, heading date, maturity, panicle length, grain number panicle^{-1}, filled grain percentage panicle^{-1}, 1000-grain weight, and grain yield plant^{-1}.

Statistical analysis

Genetic diversity, heritability, and genetic advance. Phenotypic, genotypic, and environmental variance were estimated using analysis of variance as presented in Table 1 (Johnson et al. 1955).

$$\sigma_e^2 = M1 \qquad \ldots\ldots\ldots (1)$$

$$\sigma_{dg}^2 = \sigma_e^2 + r\sigma_{dg}^2 = \frac{M2-M1}{r} \qquad \ldots\ldots\ldots (2)$$

$$\sigma_g^2 = \sigma_e^2 + r\sigma_{dg}^2 + rd\sigma_g^2 = \frac{M3-M1}{rd} \qquad \ldots\ldots\ldots (3)$$

$$\sigma_p^2 = \sigma_g^2 + \frac{\sigma_{dg}^2}{d} + \frac{\sigma_e^2}{rd} \qquad \ldots\ldots\ldots (4)$$

where σ_e^2 is environmental variance, σ_{dg}^2 is irradiation dose x genotype variance, σ_g^2 is genotypic variance, and σ_p^2 is phenotypic variance.

The following formula for PCV and GCV estimation was developed using Singh and Chaudhary (1979) approach:

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} x100\%$$

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} x100\%$$

where σ_p^2 represents the phenotypic variance, σ_g^2 represents the genotypic variance, and $\bar{X}$ represents the population mean value. PCV and GCV were categorized as high if the value exceeded 20%, moderate if the value was between 10% and 20%, and low if the value was below 10%(Sivasubramanian & Menon 1973).

Table 1. Model Analysis of Variant of Irradiation Dose, Genotype, and Irradiation Dose X Genotype Interaction for Yield and Yield Component in M_1 Generation Mutant Rice

Source of variation	Degree of freedom	Sum square	Mean Square	Variance component
Block	r-1	SSr	M5	
Irradiation dose (D)	d-1	SSd	M4	$\sigma_e^2 + r\sigma_{dg}^2 + rg\sigma_d^2$
Genotype (G)	g-1	SSg	M3	$\sigma_e^2 + r\sigma_{dg}^2 + rd\sigma_g^2$
D x G interaction	(d-1) (g-1)	SSdg	M2	$\sigma_e^2 + r\sigma_{dg}^2$
Error	(r-1) (ab-1)	SSe	M1	σ_e^2
Total	rdg-1			

Broad-sense heritability (h^2_{bs}) is calculated using a formula by Burton & DeVane (1953).

$$h^2_{bs} = \frac{\sigma^2_g}{\sigma^2_p} x100\%$$

where h^2_{bs} represents broad-sense heritability, σ^2_p represents phenotypic variance and σ^2_g represents genotypic variance. Broad sense heritability was categorized according to criteria by Stansfield (1991): value > 50% is high, value 50% - 20% is moderate, and value < 20% is low.

The subsequent equation has been used to calculate genetic advance (Johnson et al. 1955).

$$\text{Genetic Advance} = \frac{i \cdot h^2_{bs} \cdot \sigma_p}{\bar{x}} x100$$

where i is the selection intensity, 1.76 at a selection intensity of 10% (Fehr 1991), h^2_{bs} is broad sense heritability, σ_p is phenotypic standard deviation, and $\bar{x}$ is population mean value. According to Begum and Sobhan (1991), genetic advance is categorized as low if it is below 7%, moderate if it falls between 7% and 14%, and high if it exceeds 14%.

Correlation and path analysis among yield component and yield.

The following formula was used for the estimated Pearson correlation coefficient (Miller et al. 1958).

$$r_{p.xy} = \frac{\text{cov.p(x, y)}}{\sqrt{\sigma^2_p(x) \cdot \sigma^2_p(y)}}$$

where $r_{p.xy}$ is the correlation between variable x and variable y, cov.p(xy) is the covariance between variable x and variable y, is the variance of variable x, and is the variance of variable Y.

Variance and covariance are calculated as follows.

$$\sigma^2_p(x) = \frac{\sum_{i=1}^{n}(x_i-\bar{x})^2}{n-1}$$

$$\sigma^2_p(y) = \frac{\sum_{i=1}^{n}(y_i-\bar{y})^2}{n-1}$$

$$cov.p(xy) = \frac{1}{2}\left[\sum xy - \frac{(\sum x)(\sum y)}{n}\right]$$

Using a t-test and the following formula, the significance of coefficient correlation was examined.

$$t_{cal} = r_{p.xy}\sqrt{\frac{n-2}{1-(r_{p.xy})^2}}$$

where "r" and "n" represent the correlation coefficients and the number of pairs of observations, respectively. If the calculated t-value was higher than the critical t-value at a 5% significance level with n – k – 1 of degrees of freedom, where k represents the number of independent variables, then the correlation coefficient was deemed statistically significant.

The determination of both the direct and indirect effects of yield components on yield is achieved with path analysis, which involves the calculation of the following equation (Singh & Chaudhary, 1979).

$$r(x_1Y) = P_{x1y} + r(x_1, x_2)P_{x2y} + \cdots +$$
$$r(x_i, x_n)P_{xiy},\ \text{i = 1, 2, 3, ... n}$$

$\frac{\sigma x_1}{\sigma Y} = 'a'$, path coefficient from x_1 to Y

$\frac{\sigma x_2}{\sigma Y} = 'b'$, path coefficient from x_2 to Y

$\frac{\sigma x_n}{\sigma Y} = 'c'$, path coefficient from x_n to Y

The matrix form of the above equation is as follows.

$$\begin{array}{ccc} \begin{bmatrix} r_{x_1y} \\ r_{x_2y} \\ r_{3y} \end{bmatrix} & = \begin{bmatrix} r_{x_1x_1} & r_{x_1x_2} & r_{x_1x_3} \\ r_{x_2x_1} & r_{x_2x_2} & r_{x_2x_3} \\ r_{x_3x_1} & r_{x_3x_2} & r_{x_3x_3} \end{bmatrix} & \begin{bmatrix} a \\ b \\ c \end{bmatrix} \\ \text{A} & \text{B} & \text{C} \end{array}$$

Path analysis coefficient which shows the direct effect of each independent variable (x) on dependent variable (Y) was calculated by equation C=B^{-1}A, where A is a correlation between independent variable (X) and dependent variable (Y), B is the correlation matrix between independent variables, B^{-1} is inverse of matrix B and C is path analysis coefficient. An indirect effect of the independent variable (X) on a dependent variable (Y) is calculated using the following formula:

$$r(x_1x_2Y) = P_1y.r(x_1x_2)$$
$$r(x_1x_nY) = P_1y.r(x_1x_n)$$

Results and Discussion

Genetic diversity, heritability, and genetic advance. In the present study, the phenotypic variance values of the yield component and yield were greater than the genotypic variance values. Similarly, the PCV value exceeded the GCV value (Table 2). The lowest PCV value was shown by maturity date (5.18%) and the highest was tiller number plant^{-1} (31.50%).

Table 2. Coefficient of variance, phenotypic coefficient of variation, genotypic coefficient of variation, broad sense heritability, and genetic advance of yield and yield component traits in M_1 generation mutant rice.

Traits	σ_p^2	σ_g^2	σ_e^2	PCV	GCV	h_{bs}^2 (%)	GA (%)
PH	166.47	142.26	12.28	12.18	11.26	85.46	18.32
TN	51.39	22.33	28.52	31.50	20.77	43.45	24.09
PN	17.37	3.31	12.62	22.38	9.77	19.06	7.51
HD	8.28	6.79	1.45	5.39	4.88	81.92	7.77
MD	29.68	15.34	12.44	5.18	3.72	51.70	4.71
PL	3.00	1.11	1.29	6.83	4.15	36.99	4.44
GN	1109.61	821.95	247.95	25.51	21.95	74.08	33.26
FGP	36.87	4.27	15.72	7.33	2.49	11.58	1.49
TGW	7.66	0.70	5.96	10.86	3.27	9.07	1.73
GYP	42.24	31.92	1.88	23.64	20.55	75.57	31.44

Note: PH = plant height, TN = tiller number plant^{-1}, PN = panicle number plant^{-1}, HD = heading date, MD = maturity date, PL = panicle length, GN = grain number panicle^{-1}, FGP = filled grain percentage panicle^{-1}, TGW = 1000-grain weight, GYP = grain yield plant^{-1}, ${\sigma_p}^2$ = phenotypic variance, ${\sigma_g}^2$ = genotypic variance, ${\sigma_e}^2$ = environmental variance, ${h_{bs}}^2$ = broad sense heritability, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, and GA = genetic advance.

PCV values of tiller number plant^{-1} (31.50%), panicle number plant^{-1} (22.38%), grain number panicle^{-1} (25.51%), and grain yield plant^{-1} (23.64%) were categorized as high. Plant height exhibited a moderate PCV (12.18%), as did the 1000-grain weight (10.86%). Low PCV values were indicated by heading date (5.39%), maturity date (5.18%), panicle length (6.83%), and filled grain percentage panicle^{-1} (7.33%) (Table 2).

GCV value for the yield component and yield ranged from 2.49% for filled grain percentage panicle^{-1} to 21.95% for grain number panicle^{-1}. The highest GCV values were obtained for tiller number plant^{-1} (20.77%), grain number panicle^{-1} (21.95%), and grain yield plant^{-1} (20.55%). GCV value for plant height was moderate (11.26%). Apart from these traits, the GCV value was categorized as low.

Phenotypic and genetic variations were associated with environmental and genetic effects on trait expression. The observation of greater phenotypic variation than genetic variation suggested that the environment had a significant impact on how a trait is expressed (Ritonga et al. 2018; Tiwari et al. 2019). This investigation revealed that the phenotypic variance was higher than the genetic variance (Table 2). This implied that environmental factors play a role in influencing both the expression of the yield component and yield, in addition to genetic factors.

PCV demonstrated how environment and genetics affect a plant trait's performance (Faysal et al. 2022; Govintharaj et al. 2018). GCV only showed genetic effects on plant trait performance. A PCV value greater than GCV reflected that environmental factors influenced a trait's appearance (Sudeepthi et al. 2020). This study showed that PCV values were higher than GCV values (Table 2). It indicated that environmental factors influence the yield and yield performance of M_1 generation mutant rice.

The comparative value between PCV and GCV described how environmental factors impact trait expression (Adhikari et al. 2018; Faysal et al. 2022). A significant genetic influence on trait expression and a limited environmental influence were reflected in the lower difference between PCV and GCV (Chozin et al. 2017; Kishore et al. 2015). This study showed plant height, heading date, maturity date, grain number panicle^{-1}, and grain yield plant^{-1} had PCV values almost the same as GCV values (Table 2). These findings indicated that genetic factors predominately determine the performance of these traits rather than environmental factors.

PCV and GCV measured genetic diversity within a population (Chavan et al. 2020). The study revealed elevated PCV and GCV values, specifically for tiller number plant^{-1}, grain number panicle^{-1}, and grain yield plant^{-1}. Selection traits with high PCV and GCV values could be a successful strategy. Additionally, the phenotypic appearance of a plant could serve as a reliable indicator of potential genotype selection (Singh, et al. 2011). Furthermore, the high values of PCV and GCV for tiller number plant^{-1}, grain number panicle^{-1}, and grain yield plant^{-1} indicated a broad range of genetic diversity. Populations with broad genetic diversity provided freedom in selection to develop a new variety with the desired trait (Kanaka et al. 2023; Rani et al. 2023). Consequently, there would be freedom in the selection of tiller number plant^{-1}, grain number panicle^{-1}, and grain yield plant^{-1}.

The heritability values ranged from 9.07% for 1000-grain weight to 85.46% for plant height (Table 2). Heritability for plant height (85.46%), heading date (81.92%), maturity date (51.70%), grain number plant-1 (74.08%), and grain yield plant^{-1} (75.57%) was high. Furthermore, moderate heritability was shown by panicle length (36.99%), and low heritability was obtained by panicle number plant^{-1} (19.06%), filled grain percentage panicle^{-1} (11.58%) and 1000-grain weight (9.07 %).

Genetic advances in this study were between 1.49% in filled grain percentage panicle-1 and 33.26% in grain number panicle^{-1} (Table 2). Highly valuable genetic advances were obtained in plant height (18.32%), tiller number plant^{-1} (24.09%), grain number panicle^{-1} (33.26%), and grain yield plant^{-1} (31.44%). Other yield component traits indicated a low genetic advance.

Heritability estimation found that plant height, heading date, maturity date, grain number panicle^{-1}, and grain yield plant^{-1} had high values , and other traits had moderate or low heritability values. Heritability estimation refered to the contribution of genetic components to observed trait variation (Chozin et al. 2017). Genetic factors were the primary controllers of traits with high heritability. simple selection methods can improve these features (Raghavendra and Hittalmani 2016). Therefore, genetic factors significantly impacted plant height, heading date, maturity date, grain number panicle^{-1}, and grain yield plant$^{-1,}$ while environmental factors had a minor influence, as previously discussed.

There was not necessarily a relationship between high heritability and high genetic advantage. Therefore, selecting a trait based on heritability and genetic advance was preferable (Shah et al. 2018; Sundaram et al. 2019). Heritability and genetic advance with high values suggested that additive genes had a greater role in controlling these traits (Dragov et al. 2022; Mandal et al. 2023). This could be used as a guide for choosing an effective selection method for a trait in segregated populations and producing true genotypes in the next generation (Chozin et al. 2017; Govintharaj et al. 2018). Plant height, grain number panicle^{-1}, and grain yield plant^{-1} exhibited high values of heritability and genetic advance in this study, meaning these traits can be improved simply with selection methods. The heading date and maturity date showed high heritability but low genetic advance, suggesting that these traits are influenced by non-additive gene action (Adhikari et al. 2018; Ashe et al. 2023; Islam et al. 2015). Hence, selection for these traits might not be unfavorable (Singh, A. G. et al. 2021).

Correlation and path analysis among yield components and yield. Table 3 displayed the correlation coefficients between yield components and yield. Grain yield plant^{-1} showed a positive correlation with plant height (0.47%), panicle length (0.50%), grain number panicle^{-1} (0.45%), and filled grain percentage panicle^{-1} (0.49%). Apart from these traits, there was no correlation with grain yield plant^{-1}.

The correlation among various yield components was demonstrated in Table 3. Specifically, the 1000-grain weight was found to have a positive correlation with tiller number plant^{-1} (0.32), panicle number plant^{-1} (0.32), and filled grain percentage panicle^{-1} (0.38). However, there was a negative correlation between the 1000-grain weight and grain number panicle^{-1} (-0.46). The grain number panicle^{-1} positively correlated with plant height (0.63) and panicle length (0.36). Nevertheless, there was an important negative correlation between grain number panicle^{-1} and tiller number plant^{-1}. The panicle length exhibited a positive correlation with plant height (0.64) and a negative correlation with tiller number plant^{-1} (-0.34). The maturity date was positively correlated with the heading date (0.70). However, it was negatively associated with tiller number plant^{-1} (-0.35) and panicle number plant^{-1} (-0.34). The data revealed a negative connection between tiller number plant^{-1} (-0.47) and panicle number plant^{-1} (-0.37) with the heading date. An analysis revealed a strong positive connection (0.80) between tiller number plant^{-1} and panicle number plant^{-1}.

Conversely, there was a negative correlation of -0.46 between the tiller number plant^{-1} and plant height.

Path analysis was utilized to disentangle the correlation coefficient of the yield component and yield into direct and indirect effects, as shown in Table 4. The panicle number plant^{-1} (0.57), grain-filled percentage panicle^{-1} (0.48), panicle length (0.34), and grain number panicle^{-1} (0.21) were the yield components that have an impact on the grain yield of plant^{-1}. These characteristics exhibited a clear and beneficial impact on the amount of grain yield plant^{-1}. Other yield components had direct positive or direct negative effects with small values on the grain yield plant^{-1}, including plant height (0.03), tiller number plant^{-1} (-0.35), 1000-grain weight (-0.24), heading date (-0.13), and maturity date (-0.03). Data further showed the traits that had a direct effect with path analysis coefficient values that were the same or higher than correlation coefficient values, namely panicle number plant^{-1} and filled grain percentage plant^{-1}.

Correlation analysis could identify the direction and degree of the relationship among different traits, such as yield components and yield (Balla & Ibrahim 2017; Prakash et al. 2018). The correlation coefficient, which spanned from +1 (positive) to -1 (negative), indicated how symmetrically related the two variables were (Table 3). A positive correlation coefficient indicated that an increase in the value of one variable was accompanied by an increase in the other variable's value. The negative correlation coefficient indicated that as one variable's value rises, the value of another variable falls (Schober & Schwarte 2018). The study found that plant height, panicle length, grain number panicle^{-1}s, and filled grain percentage panicle^{-1} s all had positive correlation coefficient values or a linear relationship with grain yield plant^{-1}.

Table 3. Correlation coefficient of yield components and yield of M$_1$ generation mutant rice.

	PH	TN	PN	DF	DM	PL	GN	FGP	TGW	GYP
PH	1	-0.46 *	-0.27	0.17	0.19	0.64 *	0.63 *	0.10	-0.28	0.47 *
TN		1	0.80 *	-0.47 *	-0.35 *	-0.34 *	-0.50 *	0.13	0.32 *	-0.07
PN			1	-0.37 *	-0.34 *	-0.28	-0.22	0.23	0.32 *	0.23
HD				1	0.70 *	-0.03	0.20	0.19	-0.01	-0.07
MD					1	-0.17	0.29	-0.04	-0.06	-0.19
PL						1	0.36 *	0.14	-0.12	0.50 *
GN							1	-0.06	-0.46 *	0.45 *
FGP								1	0.38 *	0.49 *
TGW									1	-0.13
GYP										1

Note: PH = plant height, TN = tiller number plant^{-1}, PN = panicle number plant^{-1}, HD = heading date, MD = maturity date, PL = panicle length, GN = grain number panicle^{-1}, FGP = filled grain percentage panicle^{-1}, TGW = 1000-grain weight, GYP = grain yield plant^{-1}.

Table 4. Path analysis coefficients of yield components and yields of M$_1$ generation mutant rice.

	Direct effect	Indirect effect								Total effect
		PH	TN	PN	DF	DM	PL	GN	FGP	TGW	
PH	0.03		0.16	-0.15	-0.02	-0.01	0.22	0.13	0.05	0.07	0.47
TN	-0.35	-0.01		0.45	0.06	0.01	-0.12	-0.11	0.06	-0.08	-0.07
PN	0.57	-0.01	-0.28		0.05	0.01	-0.10	-0.05	0.11	-0.08	0.23
HD	-0.13	0.00	0.16	-0.21		-0.02	-0.01	0.04	0.09	0.00	-0.07
MD	-0.03	0.01	0.12	-0.19	-0.09		-0.06	0.06	-0.02	0.01	-0.19
PL	0.34	0.02	0.12	-0.16	0.00	0.00		0.08	0.07	0.03	0.50
GN	0.21	0.02	0.17	-0.13	-0.03	-0.01	0.12		-0.03	0.11	0.45
FGP	0.48	0.00	-0.05	0.13	-0.03	0.00	0.05	-0.01		-0.09	0.49
TGW	-0.24	-0.01	-0.11	0.18	0.00	0.00	-0.04	-0.10	0.18		-0.13

Note: PH = plant height, TN = tiller number plant^{-1}, PN = panicle number plant^{-1}, HD = heading date, MD = maturity date, PL = panicle length, GN = grain number panicle^{-1}, FGP = filled grain percentage panicle^{-1}, TGW = 1000-grain weight, GYP = grain yield plant^{-1}.

The trait selection with a unidirectional relationship could guarantee an increase in both traits (Muthuramu & Ragavan 2020) so that selection was done simultaneously (Archana et al. 2018). This means that selection for plant height, panicle length, grain number panicle^{-1}, and filled grain percentage panicle^{-1} increased grain yield plant^{-1}. However, the selection of plant height needs to be limited because the selection of short plants will reduce grain yield in plant^{-1}. The finding matched the investigation carried out by Riyanto et al. (2021), Jangala et al. (2022), and Thuy et al. (2023).

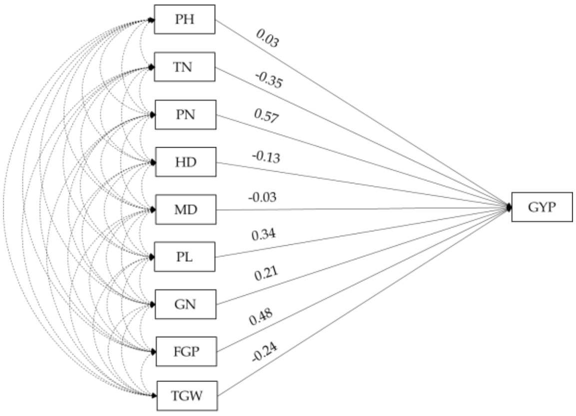

Figure 1. The direct and indirect effects of yield components on yield of M_1 generation mutant rice.

Note: PH = plant height, TN = tiller number plant^{-1}, PN = panicle number plant^{-1}, HD = heading date, MD = maturity date, PL = panicle length, GN = grain number panicle^{-1}, FGP = filled grain percentage panicle^{-1}, TGW = 1000-grain weight, GYP = grain yield plant^{-1}.

The degree and direction of the association between the two characteristics could be determined using the correlation coefficient (Balla & Ibrahim 2017). However, the correlation coefficient could not describe a causal relationship between two variables (Ata-Ul-Karim et al., 2022; Geleta et al., 2019). Path analysis is a method used to elucidate the causal relationship between two traits (Patil & Sahu 2009) and explain one trait's direct or indirect effect against another (Faot et al. 2019; Mulualem et al. 2018). This research found that panicle number plant^{-1}, filled grain percentage panicle^{-1}, panicle length, and grain number panicle^{-1} had a direct and positive effect on yield plant^{-1} (Table 4 and Figure 1), as reported by Huang et al. (2011) and Jangala et al. (2022). This indicated that grain yield plant^{-1} is significantly influenced by these attributes.

When correlation analysis and path analysis were combined, it enabled a more comprehensive comprehension of the cause-and-effect relationships between various pairs of traits (Premkumar et al. 2016). Plant yield could be increased by selecting traits that have a favorable correlation and have a direct positive effect on grain yield plant^{-1} (Muthuramu & Ragavan 2020). This was shown by the panicle number plant^{-1} and the grain-filled percentage plant^{-1}. Based on the correlation coefficient and path coefficient, it was known that these two traits possessed potential as selection indicators for enhancing rice production through mutation induction. The panicle number plant^{-1} as an indicator of selection had been documented (Riyanto et al. 2021; Sudeepthi et al. 2020).

Conclusion

Traits with broad genetic variation were tiller number plant^{-1}, grain number panicle^{-1}, and grain yield plant^{-1}. High heritability and genetic advance values were found in plant height, grain number panicle^{-1}, and yield plant^{-1}, indicating that improvement for these traits can be simply with selection methods. Panicle number plant^{-1} and filled grain percentage panicle^{-1} showed a unidirectional relationship and had a direct effect, with high values on yield plant^{-1}. Therefore, these traits can be considered selection indications for breeding high-yielding mutant rice.

Acknowledgments

The Directorate General of Higher Education, Research, and Technology, Ministry of Education, Culture, Research, and Technology, Republic of Indonesia funded the research. The funding was obtained through the "Regular-Fundamental Research" initiative, with grant numbers 3.50/UN23.35.5/PT.01/VII/2023, 2023.

References

Adhikari BN, Joshi BP, Shrestha J, Bhatta NR. 2018. Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (*Oryza sativa* L.). Journal of Agriculture and Natural Resources, 1: 149–160. https://doi.org/10.3126/janr.v1i1.22230

Anbanandan V, Eswaran R. 2018. Genetic variability studies in rice genotypes. European Journal of Biotechnology and Bioscience, 6: 74–75.

Ansari A, Pranesti A, Telaumbanua M, Alam T, Taryono, Wulandari RA, Nugroho BDA, Supriyanta. 2023. Evaluating the effect of climate change on rice production in Indonesia using multimodelling approach. Heliyon, 9: 1–15. https://doi.org/10.1016/j.heliyon.2023.e19639

Archana RS, Rani MS, Vardhan KMV, Fareeda G. 2018. Correlation and path coefficient analysis for grain yield and yield components in rice (*Oryza sativa* L.). International Journal of Chemical Studies, 6: 189–195. https://doi.org/10.22271/chemi.2020.v8.i2n.8888

Arifin B, Azam N, Martianto D, Karlina L. 2019. The future of Indonesian food consumption. Jurnal Ekonomi Indonesia, 8: 71–102. https://doi.org/10.52813/jei.v8i1.13

Ashe G, Chanyalew S, Tesso B. 2023. Genetic variability , heritability and genetic advance among yield and yield related traits of advanced Tef [*Eragrostis tef* (Zucc .) Trotter] breeding lines, 15: 35. https://doi.org/10.5897/IJGMB2023.0226

Ashraf ATMH, Rahman MM, Hossain MM, Sarker U. 2020. Study of correlation and path analysis in the selected okra genotypes. Asian Research Journal of Agriculture, 12: 1–11. https://doi.org/10.9734/arja/2020/v12i430087

Ata-Ul-Karim ST, Begum H, Lopena V, Borromeo T, Virk P, Hernandez JE, Gregorio GB, Collard BCY, Kato Y. 2022. Genotypic variation of yield-related traits in an irrigated rice breeding program for tropical Asia. Crop and Environment, 1: 173–181. https://doi.org/10.1016/j.crope.2022.08.004

Balla MY, Ibrahim SE. 2017. Genotypic correlation and path coefficient analysis of soybean [*Glycine max* (L.) Merr.] for yield and its components. Agricultural Research and Technology, 7: 3–7. https://doi.org/10.19080/ARTOAJ.2017.07.555715

Begum HA, Sobhan MA. 1991. Genetic variability, heritability and correlation study in *C. capsularis. Bangladesh J. Jute Fibre Res., 16: 113–118.*

BPS. 2024. *Paddy Harvested Area and Production in Indonesia 2023 (Final Figures)*. BPS-Statistics Indonesia, Jakarta.

Brock RD. 1971. The role of induced mutations in plant improvement. Radiation Botany, 11: 181–196. https://doi.org/10.1016/S0033-7560(71)90273-0

Burton GW, DeVane EH. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal, 478–481. https://doi.org/10.2134/agronj1953.00021962004500100005x

Chakravarti SK, Singh S, Kumar H. 2014. Studies on genetic parameters in induced micro-mutation population of aromatic rice (*Oryza sativa* L.) in M_2 and M_3 generations. International Journal of Agricultural and Statistical Sciences, 10: 471–479.

Chavan S, Bhadru D, Swarnalatha V, Mallaiah B. 2020. Studies on genetic parameters, correlation and path analysis for yield and yield attributing traits in sweet corn (*Zea mays* L. *saccharata*). International Journal of Current Microbiology and Applied Sciences, 9: 1725–1734. https://doi.org/10.20546/ijcmas.2020.907.199

Choudhary AK, Haider ZA, Mishra SB, Prasad K, Bhushan S, Kumar S, Choudhary VK, Bhushan M, Prasad JP. 2018. Assessment of genetic variability for yield and yield attributing traits in F2 and F3 population of rice (*Oryza sativa* L.) cross. Current Journal of Applied Science and Technology, 31: 1–5. https://doi.org/10.9734/cjast/2018/45875

Chozin M, Sumardi, Sudjamiko S, Barchia MF. 2017. Genetic variability and traits association analyses on F2 generations for determination of selection criteria in Indonesian inland swamp rice breeding. Australian Journal of Crop Science, 11: 535–541. https://doi.org/10.21475/ajcs.17.11.05.p317

Connor M, de Guia AH, Pustika AB, Sudarmaji, Kobarsih M, Hellin J. 2021. Rice farming in Central Java, Indonesia—adoption of sustainable farming practices, impacts and implications. Agronomy, 11: 1–14. https://doi.org/10.3390/agronomy11050881

Dewey DR, Lu KH. 1959. A correlation and path coefficient analysis components of crested wheat grass seed production. Agronomy Journal, 515–518. https://doi.org/10.2134/agronj1959.00021962005100090002x

Dragov R, Uhr Z, Dimitrov E. 2022. Genetic variability, heritability and genetic advance for important quantitative traits of durum wheat: Part I. Bulgarian Journal of Agricultural Science, 28: 691–698.

Faot MM, Zubaidah S, Kuswantoro H. 2019. Genetic correlation and path analysis of agronomical traits of soybean (Glycine max) lines infected by CpMMV. Biodiversitas, 20: 1496–1503. https://doi.org/10.13057/biodiv/d200602

Faysal ASM, Ali L, Azam MG, Sarker U, Ercisli S, Golokhvast KS, Marc RA. 2022. Genetic variability, character association, and path coefficient analysis in transplant aman rice genotypes. Plants, 11: 1–15. https://doi.org/10.3390/plants11212952

Fehr WR. 1991. *Principles of Cultivar Development: Theory and Technique* (Vol. 1). IOWA, USA: Macmillan Publishing Company. https://doi.org/10.1097/00010694-198805000-00012

Geleta N, Dagnachew L, Zerihun J. 2019. Correlations and path analysis of some quantitative characters in barley (*Hordeum vulgareum* L.) landraces in western Oromia, Ethiopia. African Journal of Plant Science, 13: 34–46. https://doi.org/10.5897/ajps2018.1744

Govintharaj P, Manonmani S, Robin S. 2018. Variability and genetic diversity study in an advanced segregating population of rice with bacterial blight resistance genes introgressed. Ciencia e Agrotecnologia, 42: 291–296. https://doi.org/10.1590/1413-70542018423022317

Haryanto TAD, Suwarto, Riyanto A, Susanti D, Farid N, Kantun IN, Suwarno, Zheng SH. 2011. Variability of grain protein content in improved upland rice genotypes and its response to locations. Electronic Journal of Plant Breeding, 2: 200–208.

Hernández-Soto A, Echeverría-Beirute F, Abdelnour-Esquivel A, Valdez-Melara M, Boch J, Gatica-Arias A. 2021. Rice breeding in the new era: Comparison of useful agronomic traits. Current Plant Biology, 27: 1–15. https://doi.org/10.1016/j.cpb.2021.100211

Huang M, Zou Y, Jiang P, Xia B, Ibrahim M, He-jun A. 2011. Relationship between grain yield and yield components in super hybrid rice. Agricultural Sciences in China, 10: 1537–1544. https://doi.org/10.1016/S1671-2927(11)60149-1

Ishak I. 2023. Genetic variability of mutant rice (*Oryza sativa*) genotype induced by gamma rays. Biodiversitas, 24: 3300–3306. https://doi.org/10.13057/biodiv/d240624

Islam M, Raffi S, Hossain M, Hasan A. 2015. Analysis of genetic variability, heritability and genetic advance for yield and yield associated traits in some promising advanced lines of rice. Progressive Agriculture, 26: 26–31. https://doi.org/10.3329/pa.v26i1.24511

Jangala DJ, Amudha K, Geetha S, Uma D. 2022. Studies on genetic diversity, correlation and path analysis in rice germplasm. Electronic Journal of Plant Breeding, 13: 655–662. https://doi.org/10.37992/2022.1302.081

Johnson HW, Robinson HF, Comstock RE. 1955. Estimates of genetic and environmental variability in soybeans. Agronomy Journal, 47: 314–318. https://doi.org/10.2134/agronj1955.00021962004700070009x

Kanaka KK, Sukhija N, Goli RC, Singh S, Ganguly I, Dixit SP, Dash A, Malik AA. 2023. On the concepts and measures of diversity in the genomics era. Current Plant Biology, 33: 100278. https://doi.org/10.1016/j.cpb.2023.100278

Kartahadimaja J, Utomo SD, Yuliadi E, Salam AK, Warsono, Wahyudi A. 2021. Agronomic characters, genetic and phenotypic diversity coefficients, and heritability of 12 genotypes of rice. Biodiversitas, 22: 1091–1097. https://doi.org/10.13057/biodiv/d220302

Katiyar P, Pandey N, Keshavkant S. 2022. Gamma radiation: A potential tool for abiotic stress mitigation and management of agroecosystem. Plant Stress, 5: 100089. https://doi.org/10.1016/j.stress.2022.100089

Kato H, Li F, Shimizu A. 2020. The selection of gamma-ray irradiated higher yield rice mutants by directed evolution method. Plants, 9: 1–16. https://doi.org/10.3390/plants9081004

Khomphet T, Intana W, Promwee A, Islam SS. 2022. Genetic variability, correlation, and path analysis of Thai commercial melon varieties. International Journal of Agronomy, 2022: 1–6. https://doi.org/10.1155/2022/7877239

Kishore NS, Srinivas T, Nagabhushanam U, Pallavi M, Sameera SK. 2015. Genetic variability, correlation and path analysis for yield and yield components in promising rice (*Oryza sativa* L.) genotypes. SAARC Journal of Agriculture, 13: 99–108. https://doi.org/10.3329/sja.v13i1.24184

Kumari N, Parmar M. 2020. Correlation and path coefficient analysis for grain yield and yield components in rice (*Oryza sativa* L.) under aerobic condition. International Journal of Chemical Studies, 8: 927–930. https://doi.org/10.22271/chemi.2020.v8.i2n.8888

Kurniawati S, Chaniago I, Suliansyah I. 2019. Variability and heritability of Sigah brown rice mutants (M3) in vegetative phase. International Journal of Environment, Agriculture and Biotechnology, 4: 1745–1749. https://doi.org/10.22161/ijeab.46.19

Laskar RA, Chaudhary C, Khan S, Chandra A. 2018. Induction of mutagenized tomato populations for investigation on agronomic traits and mutant phenotyping. Journal of the Saudi Society of Agricultural Sciences, 17: 51–60. https://doi.org/10.1016/j.jssas.2016.01.002

Mahantashivayogayya K, Mahendrakumar, lakkundi BS, Kuchunur PH, Vishwanath J. 2016. Genetic variability studies on rice (*Oryza sativa* L.) mutants for yield and yield components in normal and saline stress soil. Electronic Journal of Plant Breeding, 7: 1162–1168. https://doi.org/10.5958/0975-928X.2016.00162.9

Mandal A, Lal GM, Lavanya GR. 2023. Assessment of genetic variability, correlation and path analysis among rice (*Oryza sativa* L.) landraces genotypes for grain yield characters under irrigated. International Journal of Environment and Climate Change, 13: 55–65. https://doi.org/10.9734/ijecc/2023/v13i102616

Miller PA, Williams JC, Robinson HF. 1958. Estimates of genotypic and environmental covariances in upland cotton and implications in selection. Agronomy Journal, 50: 126–131. https://doi.org/10.2134/agronj1958.00021962005000030004x

Muhammad I, Rafii MY, Nazli MH, Ramlee SI, Harun AR, Oladosu Y. 2021. Determination of lethal (LD) and growth reduction (GR)doses on acute and chronic gamma-irradiated bambara groundnut [Vigna subterranea (L.) Verdc.] varieties. Journal of Radiation Research and Applied Sciences, 14: 133–145. https://doi.org/10.1080/16878507.2021.1883320

Mulualem T, Alamrew S, Tadesse T, Wegary D. 2018. Correlation and path coefficient analysis for agronomical traits of lowland adapted Ethiopian Sorghum genotypes [*Sorghum bicolor* (L.) Moench] genotypes. Greener Journal of Agricultural Sciences, 8: 155–159. https://doi.org/10.15580/gjas.2018.8.060718079

Muthuramu S, Ragavan T. 2020. Genotypic correlation and path coefficient analysis for yield traits in rainfed rice (*Oryza sativa* L.). Journal of Pharmacognosy and Phytochemistry, 9: 1621–1623.

Nafisah, Roza C, Yunani N, Hairmansis A, Rostiati T, Jamil A. 2020. Genetic variabilities of agronomic traits and bacterial leaf blight resistance of high yielding rice varieties. Indonesian Journal of Agricultural Science, 20: 43–54.

Okasa AM, Sjahril R, Riadi M, Mahendradatta M, Sato T, Toriyama K, Ishii K, Hayashi Y, Abe T. 2021. Correlation and path coefficient analysis of grain yield and its components in Toraja land-race aromatic rice mutants induced by heavy ion beam. Asian Journal of Plant Sciences, 20: 406–413. https://doi.org/10.3923/ajps.2021.406.413

Oladosu Y, Rafii MY, Abdullah N, Abdul Malek M, Rahim HA, Hussin G, Abdul Latif M, Kareem I. 2014. Genetic variability and selection criteria in rice mutant lines as revealed by quantitative traits. Scientific World Journal, 2014: 1–12. https://doi.org/10.1155/2014/190531

Patel RRS, Sharma D, Das BK, Mondal S, Sahu PK, Vishwakarma G, Kumar V, Sao R, Khute IK. 2021. Study of coefficient of variation (GCV & PCV), heritability and genetic advance in advanced generation mutant line of rice (*Oryza sativa* L.). The Pharma Innovation Journal, 10: 784–787.

Patil S, Sahu V. 2009. Correlation and path analysis of rice germplasm accessions. International Journal of Plant Sciences, 4: 426–428.

Pérez-Jiménez M, Tallón CI, Pérez-Tornero O. 2020. Inducing mutations in Citrus spp.: Sensitivity of different sources of plant material to gamma radiation. Applied Radiation and Isotopes, 157: 1–7. https://doi.org/10.1016/j.apradiso.2019.109030

Potupureddi G, Balija V, Ballichatla S, Gokulan CG, Awalellu K, Lekkala S, Jallipalli K, Gayathri MG, Mohammad E, Milton M, Arutla S, Burka R, Shankar LG, Phani PA, Venkata SRL, Meenakshi SR, Viraktamath BC, … Madhav MS. 2021. Mutation resource of Samba Mahsuri revealed the presence of high extent of variations among key traits for rice improvement. PLoS ONE, 16: 1–21. https://doi.org/10.1371/journal.pone.0258816

Prakash HP, Verma OP, Chaudhary AK, Amir M. 2018. Correlation and path coefficient analysis in elite germplasm of rice (*Oryza sativa* L.). International Journal of Current Microbiology and Applied Sciences, 7: 177–187. https://doi.org/10.20546/ijcmas.2018.707.400

Premkumar R, Gnanamalar RP, Anandakumar CR. 2015. Correlation and path coefficient analysis among grain yield and kernel characters in rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding, 6: 288–291.

Premkumar R, Gnanamalar RP, Anandakumar CR. 2016. Correlation and path coefficient analysis of grain quality traits in rice (*Oryza sativa* L.). Indian Journal of Agricultural Research, 50: 27–32. https://doi.org/10.18805/ijare.v0iOF.8434

Raghavendra P, Hittalmani S. 2016. Genetic parameters of two BC2F1 populations for development of superior male sterile lines pertaining to morpho-floral traits for aerobic rice (*Oryza sativa* L.). SAARC Journal of Agriculture, 13: 198–213. https://doi.org/10.3329/sja.v13i2.26580

Rani R, Raza G, Tung MH, Rizwan M, Ashfaq H, Shimelis H, Razzaq MK, Arif M. 2023. Genetic diversity and population structure analysis in cultivated soybean (*Glycine max* [L.] Merr.) using SSR and EST-SSR markers. PLoS ONE, 18: 1–19. https://doi.org/10.1371/journal.pone.0286099

Ratna M, Begum S, Husna A, Dey SR, Hossain MS. 2015. Correlation and path coefficients analyses in Basmati rice. Bangladesh Journal of Agricultural Research, 40: 153–161. https://doi.org/10.3329/bjar.v40i1.23768

Riadi M, Sjahril R, Kasim N, Diarjo RH. 2018. Heritability and path coefficient analysis for important characters of yield component related to grain yield in M_4 red rice mutant. In *IOP Conference Series: Earth and Environmental Science* (Vol. 157, hal. 1–5). https://doi.org/10.1088/1755-1315/157/1/012050

Ritonga AW, Chozin MA, Syukur M, Maharijaya A, Sobir. 2018. Short communication: genetic variability, heritability, correlation, and path analysis in tomato (*Solanum lycopersicum*) under shading condition. Biodiversitas, 19: 1527–1531. https://doi.org/10.13057/biodiv/d190445

Riviello-Flores M, Cadena-Iñiguez J, Ruiz-Posadas, LDM Arévalo-Galarza M, Castillo-Juárez I, Soto Hernández M, Castillo-Martínez C. 2022. Use of gamma radiation for the genetic improvement of underutilized plant varieties. Plants, 11: 1–19. https://doi.org/10.3390/plants11091161

Riyanto A, Haryanto TAD, Hidayat P, Suprayogi. 2021. Genetic parameter and analysis of traits interrelationship in F2 rice generation of Inpago Unsoed 1 X Basmati Delta 9. American-Eurasian Journal of Sustainable Agriculture, 15: 15–28. https://doi.org/10.22587/aejsa.2021.15.1.2

Riyanto A, Hidayat P, Suprayogi Y, Haryanto TAD. 2023. Diallel analysis of length and shape of rice using Hayman and Griffing method. Open Agriculture, 8: 1–9. https://doi.org/10.1515/opag-2022-0169

Rosyada A, Putra RE, Gunawan W. 2022. Dynamics of competitiveness and efficiency of rice farming in Java Island, Indonesia. 3BIO: Journal of Biological Science, Technology and Management, 4: 105–119. https://doi.org/10.5614/3bio.2022.4.2.5

Sadimantara GR, Yusuf DN, Febrianti E, Leomo S, Muhidin. 2021. The performance of agronomic traits, genetic variability, and correlation studies for yield and its components in some red rice (*Oryza sativa*) promising lines. Biodiversitas, 22: 3994–4001. https://doi.org/10.13057/biodiv/d220947

Sao R, Sahu PK, Patel RS, Das BK, Jankuloski L, Sharma D. 2022. Genetic improvement in plant architecture, maturity duration and agronomic traits of three traditional rice landraces through gamma ray-based induced mutagenesis. Plants, 11: 1–37. https://doi.org/10.3390/plants11243448

Saragih SHY, Sitanggang KD, Lestari W, Rizal K. 2021. Growth response of labuhanbatu local rice with gamma ray irradiation in M_1 generation. In *IOP Conference Series: Earth and Environmental Science* (Vol. 1012, hal. 2–5). https://doi.org/10.1088/1755-1315/1012/1/012033

Schober P, Schwarte LA. 2018. Correlation coefficients: appropriate use and interpretation. Anesthesia and Analgesia, 126: 1763–1768. https://doi.org/10.1213/ANE.0000000000002864

Shah A, Hassan G, Amin J, Ghani F. 2018. Estimation of genetic parameters and interrelationship among important traits in bread wheat. International Journal of Farming and Allied Sciences, 7: 93–99.

Singh AG, Patel HR, Patel AA, Aditi P, Bhati K, Kajal R. 2021. Assessment of heritability and genetic advance in segregating generation for yield, its components and quality traits in rice (*Oryza sativa* L.). The Pharma Innovation Journal, 10: 271–274. Diambil dari http://www.thepharmajournal.com

Singh KS, Saxena S, Sinam Y, Gautam S, Shantibala Devi GA. 2022. Effect of gamma radiation processing on the quality characteristics of anthocyanin rich ethnic rice cultivars. Applied Food Research, 2: 100081. https://doi.org/10.1016/j.afres.2022.100081

Singh RK, Chaudhary BD. 1979. *Biometrical Methods in Quantitative Genetics Analysis*. New Delhi: Kalyani Publishers.

Singh SK, Singh CM, Lal GM. 2011. Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). Research in Plant Biology, 1: 73–76.

Sivasubramanian S, Menon M. 1973. Heterosis and inbreeding depression in rice. Madras Agricultural Journal, 60: 1139–1144.

Sofian A, Nandariyah, Djoar DW, Sutarno. 2019. Estimation variability, heritability and genetic advance of mutant black rice (M_6). Caraka Tani: J. of Sustainable Agriculture, 34:170–178. https://doi.org/10.20961/carakatani.v34i2.27666

Stansfield WD. 1991. *Schaum's Outline of Theory and Problems of Genetics* (Third). New York: McGraw-Hill Companies.

Sudeepthi K, Srinivas T, Kumar BNVSRR, Jyothula DPB, Umar SN. 2020. Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding, 11: 65–69. https://doi.org/10.37992/2020.1101.026

Sundaram KM, Rajeswari S, Saraswathi R, Jayaprakash P. 2019. Genetic variability studies for yield and its components and quality traits with high iron and zinc content in segregating population of rice (*Oryza sativa* L.). International Journal of Chemical Studies, 7: 800–805.

Syahri, Somantri RU. 2016. The use of improved varieties resistant to pests and diseases to increase national rice production. J. Litbang Pert., 35: 25-36 (In Indonesian).

Thuy NP, Trai NN, Khoa BD, Thao NHX, Phong VT, Thi QVC. 2023. Correlation and path analysis of association among yield, micronutrients, and protein content in rice accessions grown under aerobic condition from Karnataka, India. Plant Breeding and Biotechnology, 11: 117–129. https://doi.org/10.9787/PBB.2023.11.2.117

Tiwari DN, Tripathi SR, Tripathi MP, Khatri N, Bastola BR. 2019. Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. Advances in Agriculture, 2019: 1–9. https://doi.org/10.1101/520338

Tsagaye D, Gadebo A, Aklilu S. 2022. Correlation and path analysis in tomato (Lycopersicon esculentum MILL) genotypes. Ecology and Evolutionary Biology, 7: 46–53. https://doi.org/10.11648/j.eeb.20220703.12

USDA. 2023. *Grain : World Markets and Trade*. New York.

Wang X, Jing ZH, He C, Liu QY, Jia H, Qi JY, Zhang HL. 2021. Breeding rice varieties provides an effective approach to improve productivity and yield sensitivity to climate resources. European Journal of Agronomy, 124: 126239. https://doi.org/10.1016/j.eja.2021.126239