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# Pathway analysis of yield components in several New Plant Type (NPT) rice genotypes

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**Abstract.** *Dulbari, Ahyuni D, Rochman F, Rahmadi R, Priyadi, Subarjo, Budiarti L, Saputra H, Jaya MHIS. 2025. Pathway analysis of yield components in several New Plant Type (NPT) rice genotypes. Biodiversitas 26: 770-777.* Rice is essential for global nutrition, especially in Asia, with increasing production needed to meet rising food demands from population growth. Efforts to increase rice production are carried out through plant breeding programs. Grain weight per panicle is one of the yield components in rice plants that significantly determines production. Despite its importance, its influence in the selection process is not independent, as it is closely associated with other traits, either directly or indirectly. Therefore, this study aimed to determine the relationship between yield components and their direct and indirect effects on grain weight per panicle of several new plant types (NPT) of rice varieties grown in 2 different locations, namely Tanggamus and Lampung Timur. The study procedures were conducted using a Randomized Complete Block Design with 12 genotypes and 3 replications. Genotypes consisted of 10 NRTs, including IPB 3S, IPB 4S, IPB 5R, IPB6R, IPB117-F-7-2-1, IPB 117-F-7-7-1, IPB 117-F-14-4-1, IPB 117-F-15-4-1, IPB 117-F-20-1-1, IPB 117-F-80-2-1. Meanwhile, the 2 control varieties included Ciliwung and Ciherang. The results showed that rice grain weight per panicle significantly correlated with the number of productive tillers, panicle length, number of filled grains per panicle, and percentage of filled grains per panicle. Productive tiller number, panicle length, number of filled grains per panicle, and percentage of filled grains per panicle directly and indirectly affected grain weight per panicle. In addition, the number of filled grains per panicle directly influenced 0.49%.

**Keywords:** Correlation, genotypes, NPT, rice, yield

**Abbreviations**: CV: Coefficient of variant; FGP: Filled grain per panicle; G: Genotype; LP: Length of panicles; LSI: Least significant increases; NFGP: Number of filled grains per panicle; NPT: Number of productive tillers (stems per clump); NPT: New Plant Type; NUFGP: Number of unfilled grains per panicle; W1000: Weight of 1000 seeds; WP: Weight per panicle; PCA: Principal Component Analysis

## INTRODUCTION

Rice (*Oryza sativa* L.) is a staple crop of paramount importance for global nutrition, serving as a primary energy source for many communities in Asia, Africa, and Latin America (Fukagawa and Ziska 2019). It is cultivated extensively, with over 3% of global agricultural land allocated to this crop-approximately 162 million hectares. Global rice production in 2021 reached around 755 million tonnes (FAOSTAT 2021). Indonesia faces significant challenges in food security due to projected population growth, expected to reach 328.93 million by 2050, reflecting an increase of 22.02% since the 2020 Population Census (BPS 2023). This rapid population growth escalates food demand, while agricultural land continues to diminish due to urbanization, making the enhancement of rice production critically important.

The development of high-yielding rice varieties relies on selecting superior genotypes with traits associated with specific yields, as some genotypes demonstrate yields three times higher than traditional varieties, highlighting their productivity potential (Huang et al. 2015). Yield improvements, as noted by Slafer and Andrade (2021), arise from breeding efforts and enhancements in key traits, such as grain weight per panicle-a primary determinant of rice yield. However, the interdependence among yield traits necessitates advanced tools like correlation and path analysis to unravel these complex relationships and enhance selection accuracy. This urgency is particularly evident in New Plant Type (NPT) rice genotypes, strategically designed to achieve superior yield potential while addressing constraints of limited arable land and growing population pressures. Statistical analysis of yield components in these genotypes enables the identification of traits with significant direct and indirect effects, offering critical insights for effective breeding strategies.

Correlation analysis is a valuable tool in agricultural research, measuring the strength and direction of relationships between traits and their impact on productivity. This analysis enables researchers to identify positive or negative associations among traits, predicting how changes in one trait may influence another. For example, correlation analysis has been employed to assess how productivity relates to socio-economic factors such as poverty, revealing both positive and negative associations. Strong correlations allow researchers to predict one trait based on another, thereby supporting trait selection (Hulu and Sinaga 2019).

Path analysis complements correlation analysis by breaking down correlation coefficients into direct and indirect effects, helping breeders understand each trait's contribution to yield (Nithya et al. 2020). It highlights complex interactions among plant traits, environmental conditions, and agricultural practices, aiding in identifying key yield factors (Olivares et al. 2018, 2019; Sreedhar et al. 2019). By comparing regression models from correlation data, path analysis provides deeper insights into trait variability and identifies promising genetic traits for breeding (Elias et al. 2016; Singh et al. 2018), offering critical guidance for enhancing rice productivity.

Insights from path analysis enable breeders to focus on traits with high direct and indirect impacts, further refining the selection process. Recent studies affirm the critical role of path analysis and correlation coefficients in selecting traits that enhance yield, demonstrating their value in yield improvement (Bhandari et al. 2019; Bhor et al. 2020; Thuy et al. 2023; Limbongan 2023). By understanding the direct and indirect effects of yield components, cross-analysis assists breeders in making informed decisions, ultimately supporting the production of high-yielding rice. This research aimed to comprehensively investigate these relationships by examining how yield components influence grain weight per panicle through correlation and path analysis methods. This dual approach will reveal the direct and indirect contributions of each trait, guiding breeders in selecting the most effective traits to enhance rice production to meet the ever-increasing demand.

## MATERIALS AND METHODS

### Study implementation

The study data was taken from 2 locations in Tanggamus and Lampung Timur, Lampung, Indonesia (Figure 1) in 2018. Astronomically, Tanggamus is located between 5°05' North Latitude and 110°15' South Latitude and between 94° 45' and 141° 05' East Longitude, positioned precisely on the equator at 0° latitude (BPS 2024b). Lampung Timur is an area with an average high of around 50 meters of sea surface. Astronomically, Lampung Timur District is located between 105º15’-106º20’ east longitude and 4º37’-5º37’ south latitude (BPS 2024a).

Details research location: (i) Banjarrejo Village, Batanghari District, East Lampung District, with a height of 60 m above sea level, Podzolic soil type Red Yellow, average daily temperature 26.86°C; (ii) Wonorejo Village, District Sumberrejo Tanggamus District with a height of 600 m above sea level, soil type Andosol, with an average daily temperature of 24.15°C. Soil analysis of the two research locations is shown in Table 1.

The report materials were 10 new types of rice genotypes, namely (i) IPB 3S; (ii) IPB 4S; (iii) IPB 5R; (iv) IPB 6R; (v) IPB 117-F-7-2-1; (vi) IPB 117 -F-7-7-1; (vii) IPB 117-F-14-4-1; (viii) IPB 117-F-15-4-1: (ix) IPB 117-F-20-1-1; (x) IPB 117-F-80-2-1, furthermore referred to as G1, G2, G3, G4, G5, G6, G7, G8, G9, G10 and 2 comparison varieties Ciliwung (P1) and Ciherang (P2). The study was arranged using a nested design Randomized Complete Block Design (RCBD) with three replications and fertilization using the type and dose of Urea 300 kg $ha^{-1}$, SP36 200 kg $ha^{-1}$, and KCl 100 kg $ha^{-1}$. Additionally, pest control used pesticides with active ingredients of carbofuran and dimehipo according to recommended doses.

**Table 1.** Soil analysis of the two study locations

| Analysis | Tanggamus | Lampung Timur | Note |
|---|---|---|---|
| pH | 5.12 | 4.42 | |
| N-Total | 0.235 | 0.162 | Kjedhal |
| P-Total | 23.561 | 16.208 | mg/100g |
| P-Tersedia | 11.660 | 6.094 | ppm |
| K-dd | 0.427 | 0.263 | me/100g |
| Na-dd | 0.602 | 0.313 | me/100g |
| Ca-dd | 6.272 | 1.529 | me/100g |
| Al-dd | 14.282 | 5.022 | % |
| C-Organic | 1.135 | 0.892 | % |
| KTK | 17.229 | 8.727 | me/100g |

Source: Politeknik Negeri Lampung Analysis Laboratory 2018

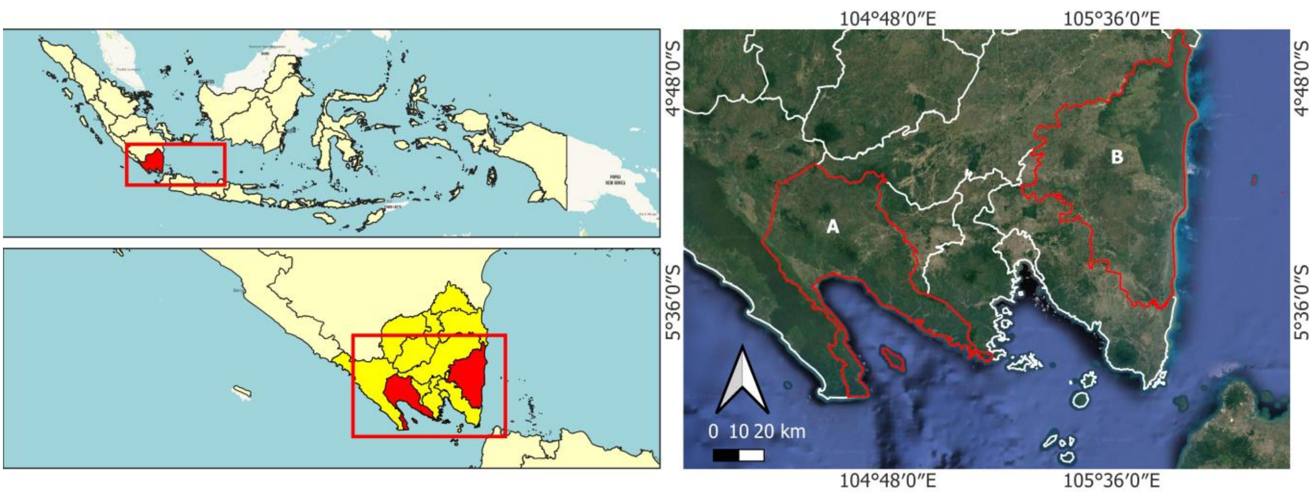

**Figure 1.** Research location. A. Tanggamus District; B. Lampung Timur District, Lampung, Indonesia

Data collection for correlation analysis and path analysis came from rice plants planted in two locations with the following cultivation technology: planting was carried out using seeds aged 21 days after sowing. Seedlings planted 2 cm deep with a spacing of 25 × 25 cm, totaling 3 stems per grove. Essential fertilizer given at planting time consists of 1/3 dose of Urea, an entire dose of SP36, and KCl. Follow-up Urea fertilizer is applied simultaneously when the plants are 3 weeks old after planting, and the second follow-up is 6 weeks old after planting, and fertilization using the type and dose of Urea 300 kg ha$^{-1}$, SP36 200 kg ha$^{-1}$, and KCl 100 kg ha$^{-1}$. Additionally, pest control used pesticides with active ingredients of carbofuran and dimehipo according to recommended doses.

## Data analysis

A combined analysis of variance was carried out to determine genetic diversity. Combined analysis of variance uses the analysis model of two locations in one season as shown in Table 2.

The range of genotype x environment interactions (G×E) was calculated using:

$\sigma^2_p$ : $\sigma^2_g + (\sigma^2_{gl}/l) + (\sigma^2_e/rl)$

$\sigma^2_g$ : $(M_3 - M_2)/rl$

$\sigma^2_{gl}$ : $(M_2 - M_1)/r$

$\sigma^2_e$ : $M_1/rl$

The correlation test was carried out using the simple correlation formula:

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

Where:

$r_{xy}$: Correlation coefficient between characters x and y

cov(x.y) : Variance characters x and y

$o^2(x)$ : Variance character x

$o^2(y)$ : Variance character y

For the difference to be seen, the following equation was used:

$$t = \frac{r_{XY}\sqrt{n-2}}{\sqrt{(1-r^2{}_{XY})}}, \text{ t table} = t\ \alpha, (n\text{-}2)$$

When t arithmetic was more significant than the t table, it meant a real correlation (Figure 2).

The value of Ci (direct effect) can be calculated using the following formula:

$$Ci = Rx^{-1}\,Ry$$

Where:

Rx : Correlation matrix among independent variables; $Rx^{-1}$ : Inverse matrix of Rx

Ci : Vector of path coefficients that indicates the direct effect of each standardized independent variable on the dependent variable

Ry : Vector of correlation coefficients between independent variable Xi (i: 1,2,...,p) and the dependent variable Y

Once the path coefficients Ci have been obtained, several important pieces of information can be derived based on the path analysis method, including (i) The direct effect of the standardized independent variable on the dependent variable Y, as measured by the path coefficient Ci; (ii) The indirect effect of the independent variable Zi on the dependent variable Y, through the independent variable Zj (via the presence of the independent variable Zj in the model), is measured by the magnitude Cj.rij; (iii) The effect of error or residual that cannot be explained by the path analysis model. Effects that cannot be explained by a given model are incorporated as error or residual effects, which are quantified using the formula: $C_s^2 = 1 - \sum C_1\, r_{ij}$ where $C_2 = \sqrt{C_s^2}$

$$\underset{R_x}{\left|\begin{array}{cccc} r_{11} & r_{12} & \dots & r_{1p} \\ r_{21} & r_{22} & \dots & r_{2p} \\ \dots & \dots & \dots & \dots \\ \dots & \dots & \dots & \dots \\ r_{p1} & r_{p2} & \dots & r_{pp} \end{array}\right|} \quad \underset{C_i}{\left|\begin{array}{c} C_1 \\ C_2 \\ \dots \\ \dots \\ C_p \end{array}\right|} = \underset{R_y}{\left|\begin{array}{c} r_{1y} \\ r_{2y} \\ \dots \\ \dots \\ r_{py} \end{array}\right|}$$

**Figure 2.** Path analysis calculation (Singh and Chaudary 1979)

**Table 2.** Combined of variance analysis model for two locations in one season

| Source of variance | Degrees of freedom | Mean of squares | Mean of squares-expectation |
|---|---|---|---|
| Location (L) | l-1 | M5 | $\sigma^2 + g\sigma^2\ r/l + gr\sigma^2\ l$ |
| Replication per location | l(r-1) | M4 | $\sigma^2 + g\sigma^2\ r/l$ |
| Genotype (G) | (g-1) | M3 | $\sigma^2 + r\sigma^2_{gl} + rl\ \sigma^2_g$ |
| Genotype x Location | (g-1)(l-1) | M2 | $\sigma^2 + r\sigma^2_{gl}$ |
| Error | l(g-1)(r-1) | M1 | $\sigma^2$ |

Notes: $(\sigma^2_p)$: Phenotype variance; $(\sigma^2_g)$: Genotypic variance, and dan $(\sigma^2_{gl})$: Interaction variance. The coefficient of genetic variance was estimated based on the genotypic variance $(\sigma^2_g)$

If the correlation value between the causal factor and the effect is nearly equal to the direct effect (with a difference of no more than 0.05), then the coefficient elucidates the actual relationship, and direct selection of that variable will be highly effective (Allard 1960). The determination of characteristics that can serve as effective selection criteria can be observed from the magnitude of the direct effect on the outcome (Ci), the correlation between the characteristic and the outcome (rih), and the difference between the correlation among characteristics and the outcome with the direct effect of those characteristics on the outcome (rih - Ci) < 0.05. If these three conditions are met, then the characteristic is highly effective as a selection criterion for predicting the outcome. The steps for calculating the correlation analysis and its significance were carried out using MINITAB 18 software. Yield component characters correlated with grain weight per panicle were carried out with path analysis to see the direct and indirect effects using R Studio software.

## RESULTS AND DISCUSSION

### Analysis of variance

A variance homogeneity test was carried out at each location before carrying out the combined analysis of variance. The requirement to be able to carry out the combined analysis of variance was that the error range must be homogeneous. The heterogeneity of yield component characters is shown in Table 3, and the results of the combined analysis of variance are presented in Table 4.

Genotype significantly influenced the number of productive tillers, panicle length, filled grains per panicle, unfilled grains per panicle, percentage of filled grains per panicle, the weight of 1000 seeds, and grain weight per panicle. However, against yield, the power character was similar. The location had a very significant effect on the character of the number of productive tillers, the panicle length, the number of filled grains per panicle, the number of unfilled grains per panicle, and the weight of the grain.

The experiment on ten rice genotypes at two locations, Tanggamus and Lampung Timur, showed significant variation in measured yield components, such as the Number of Productive Tillers (NPT), Number of Filled Grains (NFGP), and 1000-grain weight (W1000). Some genotypes demonstrated outstanding performance across various aspects. For instance, genotype G2 exhibited high NFGP and 1000-grain weight at both locations, making it one of the genotypes with superior potential. Genotype G9 also showed promising results in 1000-grain weight, indicating resilience and adaptability in both experimental environments. Meanwhile, some genotypes, like G7, displayed considerable variation between the two locations, suggesting environmental influences on differing yields.

However, even though the average plant growth in Lampung Timur appeared better regarding tiller count and panicle length, the quality of filled grains and grain weight did not consistently exceed those in Tanggamus. This indicates that conditions favorable for vegetative growth do not necessarily lead to higher grain quality. The high coefficient of variation in some yield components, such as the percentage of filled grains and the number of empty grains, suggests the potential for developing more stable genotypes. These results recommend genotypes G2 and G9 for further testing to enhance rice yields under various environmental conditions.

There was no significant effect on the percentage of grain filled per panicle, 1000-grain weight, and yield. The interaction of genotype and location (G×E) significantly affected the character of the number of filled grains per panicle, and the grain weight per panicle showed notable differences. However, no significant differences were observed in the traits of the number of productive tillers, panicle length, number of unfilled grains per panicle, percent of filled grains per panicle, and the weight of 1000. This is to the research results of Kujur et al. (2023). Similar results were reported by Tiwari et al. (2019) and Sudeepthi et al. (2020).

A real interaction in some yield component characters showed a change in response from the same genotype at different locations. Variations in the growing environment did not guarantee that the genotype could grow and be harvested well in all regions within a wide range or vice versa. This was related to the possibility of genotype interactions with the environment in a wide area. The combined average of component characters of genotypes planted in 2 different locations was presented in Table 5.

**Table 3.** Characteristic of genotypic yield components in Tanggamus and Lampung Timur

| **Character** | **Mean square** | | | | | |
|---|---|---|---|---|---|---|
| | **Genotype (G)** | | **Location (E)** | | **Interaction G x E** | |
| The number of productive tillers | 66.69 | ** | 172.98 | ** | 6.69 | ns |
| Panicle length | 21.53 | ** | 33.67 | ** | 2.21 | ns |
| The number of filled grains per panicle | 10001.87 | ** | 59363.09 | ** | 1489.28 | * |
| The number of unfilled grains per panicle | 13.00 | ** | 14.96 | ** | 1.85 | ns |
| Percent of filled grain per panicle | 184.35 | ** | 0.05 | ns | 40.39 | ns |
| Weight of 1000 seeds | 34.13 | ** | 1.64 | ns | 3.06 | ns |
| Grain weight per panicle | 7.79 | ** | 49.86 | * | 1.13 | * |

Notes: NPT: Number of productive tillers (stems per clump); LP: Length of panicles (cm); NFGP: Number of filled grains per panicle (seeds); NUFGP: Number of unfilled grains per panicle (seeds); FGP: Filled grain per panicle (%); W1000: Weight of 1000 seeds (g); WP: Weight per panicle (g); **: Significantly different at 1% level; ab: Different significantly higher than Ciliwung and Ciherang; a: Different significantly higher than Ciliwung (P1); b: Significantly higher than Ciherang (P2) at the 5% level LSI test

**Table 4.** Characteristic of genotypic yield components in Tanggamus and Lampung Timur, Lampung, Indonesia

| **Genotype** | **Yield components characters** | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Tanggamus** | | | | | | | **Lampung Timur** | | | | | | |
| | **NPT** | **LP** | **NFGP** | **NUFGP** | **FGP** | **W1000** | **WP** | **NPT** | **LP** | **NFGP** | **NUFGP** | **FGP** | **W1000** | **WP** |
| G1 | 12.27 | 27.23ab | 203.73ab | 80.72 | 48.20 | 30.89a | 6.62ab | 13.00 | 26.15 | 123.73 | 80.90 | 30.60 | 29.55 | 3.93 |
| G2 | 11.07 | 27.03ab | 242.53ab | 81.78 | 52.47 | 30.98a | 7.91ab | 14.27 | 28.00a | 145.53b | 86.56 | 23.00 | 30.78a | 4.64ab |
| G3 | 12.00 | 28.50ab | 277.60ab | 90.93 | 28.33 | 27.26 | 7.51ab | 13.20 | 29.13ab | 190.87ab | 91.51 | 18.67 | 26.18 | 5.16ab |
| G4 | 13.53 | 26.85ab | 261.40ab | 87.21 | 38.40 | 23.91 | 6.63ab | 16.33 | 30.07ab | 262.47ab | 91.23 | 25.07 | 24.04 | 6.45ab |
| G5 | 12.87 | 26.30ab | 207.33ab | 77.25 | 61.60 | 28.08 | 6.28ab | 14.80 | 27.00 | 168.80ab | 88.30 | 22.07 | 28.68 | 4.78ab |
| G6 | 10.80 | 28.40ab | 241.47ab | 80.39 | 56.67 | 29.05 | 7.35ab | 13.67 | 30.88ab | 182.73ab | 79.43 | 47.87 | 30.23 | 5.76ab |
| G7 | 16.87 | 25.80a | 192.80b | 94.55 | 11.13 | 25.48 | 4.98 | 21.27 | 28.27a | 142.07b | 86.95 | 22.20 | 27.33 | 4.05 |
| G8 | 12.33 | 28.97ab | 251.47ab | 79.43 | 68.33 | 29.30 | 7.84ab | 15.27 | 29.63ab | 162.87ab | 79.00 | 43.73 | 29.37 | 5.13ab |
| G9 | 10.87 | 28.60ab | 235.67ab | 80.44 | 58.00 | 31.11a | 7.19ab | 14.80 | 30.10ab | 145.40 | 72.25 | 56.87 | 34.46ab | 5.37ab |
| G10 | 10.87 | 27.90ab | 228.00ab | 80.57 | 56.47 | 29.74 | 7.19ab | 10.80 | 30.80ab | 179.87 | 77.68 | 54.27 | 30.83a | 5.99ab |
| **P1** | **17.13** | **23.23** | **140.73** | **91.37** | **13.27** | **27.30** | **3.95** | **22.67** | **24.20** | **117.87** | **91.01** | **12.07** | **26.92** | **3.27** |
| **P2** | **16.93** | **24.47** | **131.27** | **89.34** | **16.27** | **30.53** | **4.11** | **24.67** | **25.47** | **102.67** | **89.80** | **11.73** | **28.86** | **3.07** |
| Mean | **13.13** | **26.94** | **217.83** | **84.50** | **42.43** | **28.63** | **6.46** | **16.23** | **28.31** | **160.41** | **84.55** | **30.68** | **28.94** | **4.80** |
| Genotype | ** | ** | ** | ** | ** | ** | ** | ** | ** | ** | ** | ** | ** | ** |
| Coefficient of variant | 13.97 | 3.19 | 12.29 | 6.50 | 19.00 | 4.64 | 13.01 | 11.45 | 5.04 | 11.16 | 5.04 | 17.04 | 5.48 | 10.1 |
| LSI (5%) | 3.89 | 1.82 | 56.85 | 11.65 | 37.59 | 2.82 | 1,79 | 3,94 | 3.03 | 38.01 | 9,04 | 22.65 | 3.37 | 1.03 |

Notes: **:significantly different at 1% level; NPT:Number of productive tillers (stems per clump); LP:Length of panicles (cm); NFGP: Number of filled grains per panicle (seeds); NUFGP: Number of unfilled grains per panicle (seeds); FGP: Filled grain per panicle (%); W1000:weight of 1000 seeds (g); WP:weight per panicle (g); ab: Significantly higher than the control varieties (a) Ciliwung (P1) and (b) Ciherang (P2) on the 5% α LSI test

The coefficient of variant (CV) for all growth characters and yield components was small (< 20%) (Table 5), and this showed that the variation resulting from errors or uncontrollable factors was small. However, the higher the CV value, the lower the accuracy of an experiment. Therefore, yield testing of several lowland rice genotypes that were carried out had a fairly high degree of accuracy in data collection (Liang et al. 2015).

The table presents the characteristics of genotypic yield components from different rice genotypes tested in Tanggamus and Lampung Timur. Key components measured include the number of productive tillers (NPT), panicle length (LP), number of filled and unfilled grains per panicle (NFGP and NUFGP), filled grain percentage (FGP), weight of 1000 grains (W1000), and weight per panicle (WP). Genotypes like G9 showed superior performance in terms of the weight of 1000 grains (32.79g) and filled grain percentage (57.43%), making it a promising candidate for further selection. Other genotypes, such as G6, also demonstrated high NFGP and W1000 values, highlighting their potential for high yield.

The control varieties, P1 (Ciliwung) and P2 (Ciherang) showed high NPT values but had lower numbers of filled grains than some other genotypes, such as G4 and G9. Statistical analysis indicated that several genotypes performed significantly better than the controls, particularly in grain weight and filled grain percentage. These findings suggest that genotypes like G9 and G6 may be suitable for further testing and development in environments similar to those in Tanggamus and Lampung Timur. Thorough discussion represents the causal effect, mainly explaining why and how the research results took place, and not only re-expressing the mentioned results in sentences, not repeating them.

### Correlation analysis

Correlation analysis measures and determines the relationship between two or more variables in a population or data sample. It was used to explain the relationship's strength and direction and whether it was significant. The correlation coefficient ranged from -1 to 1, and the closer it was to 1 or -1, the stronger the relationship between the two variables.

From the combination of Table 5, it was known that several characters correlated with other characters. The character of grain Weight Per Panicle (WP) was significantly associated with the Number Of Productive Tillers (NPT) with a correlation coefficient value (-0.90), which significantly correlated with the Panicle Length (LP) character with a correlation coefficient value (0.93), the Number Of Filled Grain Per Panicle (JGIPM) with a correlation coefficient (0.89), the Number of Empty Grain Per Panicle (NUFGP) character with a correlation coefficient (0.78), and the Percent Grain Filled Per Panicle (NFGP) character with a correlation coefficient (-0.57). WP's character was not correlated with the weight of 1000 seeds, and the plant height and the Number of Productive Tillers (NPT) had a significant and positive correlation with yield (Saito 2014).

Tiwari et al. (2019) reported comparable findings, showing significant positive correlations among yield component traits. Research on trait associations indicated that days to 50% flowering positively correlated with plant height (Tejaswini et al. 2018), panicle length (Umarani et al. 2019), and the total grain count per panicle (Sreedhar and Reddy 2019). Plant height was also positively associated with the number of ear-bearing tillers per plant (Tejaswini et al. 2018) and panicle length (Sreedhar and Reddy 2019). These associations suggest the potential for simultaneous enhancement of these traits through selection. Additionally, a clearer correlation visualization is shown in Figure 3.

**Table 5.** Characteristic of genotypic yield components in Tanggamus and Lampung Timur, Lampung, Indonesia

| **Genotype** | **Parameters** | | | | | | |
|---|---|---|---|---|---|---|---|
| | **NPT** | **LP** | **NFGP** | **NUFGP** | **FGP** | **W1000** | **WP** |
| G1 | 12.63 | 26.69 | 163.73 | 80.81 | 39.40 | 30.22 | 5.27 |
| G2 | 12.67 | 27.52 | 194.03 | 84.17 | 37.73 | 30.88 | 6.28 |
| G3 | 12.60 | 28.82 | 234.23 | 91.22 | 23.50 | 26.72 | 6.34 |
| G4 | 14.93 | 28.46 | 261.93 | 89.22 | 31.73 | 23.97 | 6.54 |
| G5 | 13.83 | 26.65 | 188.07 | 82.77 | 41.83 | 28.38 | 5.53 |
| G6 | 12.23 | 29.64 | 212.10 | 79.91 | 52.27 | 29.64 | 6.56 |
| G7 | 19.07 | 27.03 | 167.43 | 90.75 | 16.67 | 26.41 | 4.52 |
| G8 | 13.80 | 29.30 | 207.17 | 79.22 | 56.03 | 29.33 | 6.49 |
| G9 | 12.83 | 29.35 | 190.53 | 76.35 | 57.43 | 32.79 | 6.28 |
| G10 | 10.83 | 29.35 | 203.93 | 79.12 | 55.37 | 30.28 | 6.59 |
| **P1** | **19.90** | **23.72** | **129.30** | **91.19** | **12.67** | **27.11** | **3,61** |
| **P2** | **20.80** | **24.97** | **116.97** | **89.57** | **14.00** | **29.70** | **3.59** |
| Mean | 14.68 | 27.62 | 189.12 | 84.52 | 36.55 | 28.79 | 5.63 |
| CV (%) | 4.19 | 1.42 | 4.01 | 1.94 | 6.13 | 1.69 | 4.06 |

Notes: NPT: Number of productive tillers (stems per clump); LP: Length of panicles (cm); NFGP: Number of filled grains per panicle (seeds); NUFGP: Number of unfilled grains per panicle (seeds); FGP: Filled grain per panicle (%); W1000: weight of 1000 seeds (g); WP: Weight per panicle (g)

From Figure 3, it is known that the correlation analysis between yield component traits of several new rice genotypes. Positive and negative correlations between traits such as the number of productive tillers (NPT), panicle length (LP), number of filled grains per panicle (NFGP), number of unfilled grains per panicle (NUFGP), and the weight of 1000 seeds (W1000) are depicted with different colors. In panel A, correlations of all traits are shown, with red indicating positive correlations and blue indicating negative ones. Panel B highlights only significant correlations with P values < 0.05, emphasizing the important relationships between traits, by the research results of Singh et al. (2022) and Thuy et al. (2023).

**Path analysis**

Path analysis was carried out with the R Studio application, which was used for multivariate analysis using correlation and principal component analysis. The Pearson correlation coefficient between morphological and agronomic characters was generated using the Corrplot package. The correlation coefficient represented the level of relationship between the 2 characters but could not explain the cause and effect of the relationship. Therefore, a cross-link analysis could be carried out to provide a more meaningful meaning of the correlation coefficient. The Path analysis could show a character's direct and indirect influence on another (Figure 4).

The (Figure 4) illustrates the path analysis results, showing direct and indirect effects between the grain weight per panicle (WP) and several yield component characters. The analyzed traits include the number of productive tillers (X1), panicle length (X2), the number of filled grains per panicle (X3), and the percent of filled grains per panicle (X4). Solid arrows represent direct effects, while dashed arrows indicate indirect effects. Panicle length (X2) and the number of filled grains per panicle (X3) have the most substantial positive direct effects on grain weight per panicle (WP).

The character of the number of productive tillers (NPT) had a direct effect on the character of grain weight per panicle (WP) with a coefficient value of -0.28, the panicle length character (LP) had a direct impact of 0.23, and the character of the number of filled grain per panicle (NFGP) had a direct effect of 0.49. The percentage of Grain Filled Per Panicle (FGP) character caused harm to the WP character, and the panicle length character (LP) had a significant effect on yield (Saito 2014). This was supported by a study by Singh et al. (2020), who reported that grain content and the number of tillers had the most significant direct effect on rice yield. An illustration of direct and indirect influence is shown in Figure 4.

The residual value represented the total unaccounted-for direct effect on characteristics that had yet to be identified. The closer the residual value is to zero, the more effective the cross-sectional analysis was in explaining the causation of the observed correlation values and characteristics and the more complete it was in explaining direct and indirect effects. Based on the analysis results, the residual value in this study was 0.11. This showed that the observed characters were sufficiently representative to determine yield component characteristics' direct and indirect effects on the grain Weight Per Panicle (WP) characteristics. This result is different from the path analysis study conducted by Widyaningtias et al. (2020) on morphological and agronomic characters that determine the voidness of rice panicles with a residual value of 0.39. This shows that the character of production variability observed in the cross section gives an influence of 61%. The residual value, which is approaching 0, indicates that the cross-sectional analysis carried out is very effective in explaining the causal relationship of the observed character correlation value.

**Figure 3.** Correlation between yield component characters of several new rice genotypes a-correlation of all characters. Note: NPT-Number of productive tillers (stems per clump), LP-Length of panicles (cm), NFGP- Number of filled grains per panicle (seeds), NUFGP-Number of unfilled grains per panicle (seeds), FGP-Filled grain per panicle (%), W1000-weight of 1000 seeds (g), WP-weight per panicle (g), b-character correlation with P value <0.05

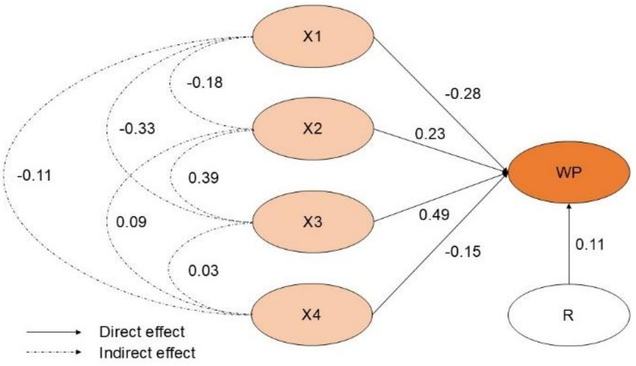

**Figure 4.** Illustration of the direct and indirect effects between the grain weight per panicle character and several yield component characters. Note: X1- Number of productive tillers (NPT), X2- Panicle Length (LP), X3- Number of filled grain per panicle (NFGP), X4-Percent filled grain per panicle, grain weight per panicle (WP)

In conclusion, the results demonstrated a significant correlation between the character of grain weight per panicle and the number of productive tillers, panicle length, number of filled grains per panicle, and percentage of filled grains per panicle. Moreover, the number of productive tillers, panicle length, number of filled grains per panicle, and percentage of filled grains per panicle demonstrated direct and indirect effects on grain weight per panicle. Notably, the number of filled grains per panicle directly impacted 0.49% on the character of grain weight per panicle. This indicates that filled grains per panicle can significantly influence the overall grain weight per panicle and its crucial role in determining yield characteristics.

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