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Performance of Multi-Canopy Rice Combinations Based on Tillering Capacity and Plant Architecture Across Seasons and Nitrogen Levels

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Abstract

The growing challenge of ensuring global food security encourages innovative approaches to rice cultivation. One novel innovation is the multi-canopy cropping system, involving planting 2 rice genotypes with different plant heights at close spacing. This study aimed to evaluate the effect of the tillering capacity of tall rice genotypes and the plant architecture of short genotypes on yield and agronomic traits in a multi-canopy system under different environmental conditions. The genetic materials were 24 combinations of multi-canopy rice genotypes belonging to 3 groups, namely T1-S1, T2-S2, and T3-S3, each consisting of 8 combinations. The T1, T2, T3 groups are the tall genotypes with different tillering ability, namely low, medium, and high; whereas the S1, S2, S3 groups are the short genotypes with different plant architecture, namely green revolution type, dwarf stay-green type, and new plant type. These combinations were evaluated with 4 checks in 4 environments, i.e., 2 planting seasons and 2 nitrogen treatments. The combined analysis involving 3 factors (genotype combination, nitrogen, and season) was performed. The grain yield of all multi-canopy combinations was significantly higher than that of the check varieties in monoculture. Group T3-S3 had a significantly higher average total number of grains than the other groups. Selection based on Multi-trait Genotype-Ideotype Distance Index (MGIDI) at 20% pressure produced the desired selection differential for all selection traits. Four selected lines belonged to the T3-S3 group. The interaction between genotype combination and nitrogen fertilizer was significant for the number of total and productive tillers. This study provides insight for identifying suitable combinations of the tall and short genotypes in breeding multi-canopy rice varieties.

Keywords: crop genetics; cropping systems; genotype and environment interaction; new plant type rice; plant genetic resources

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INTRODUCTION

Rice is one of the most important staple food crops in the world. Asia, the foremost producer and consumer of rice, is encountering substantial challenges that affect the stability of its rice industry. Climate change has elevated temperatures, negatively impacting rice yields and quality (Horie, 2019; Saud et al., 2022; Liu et al., 2024). Enhancing crop yields has emerged as the primary objective in plant breeding, and this study, together with the notion of food barns, is crucial for advancing the Sustainable Development Goals (SDGs).

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Efforts to increase productivity vertically have been widely implemented for vegetables in vertical farming systems (Benke and Tomkins, 2017). The new plant type rice breeding program at the IPB University, Bogor, Indonesia, proposed a novel approach to increase rice yield vertically by a multi-canopy cropping system, and a series of research has been conducted (Widyastuti et al., 2020; Hidayah et al., 2022; Sholehah et al., 2024). The multi-canopy system entails the cultivation of 2 rice genotypes with varying plant heights at reduced planting intervals. The disparity between tall and short rice genotypes will produce tiered panicles, which will facilitate the use of vertical harvesting space and enhance rice yield per unit area. This approach is one of the new complementary technologies for the monoculture system.

Besides genetic factors, suitable environmental conditions are necessary to obtain optimum production. One key element influencing rice yield is the accessibility of fertilizers, particularly nitrogen fertilizer. Urea is a nitrogen source for rice plants and is essential for enhancing agricultural production. Nitrogen is a crucial agronomic component that substantially influences growth metrics, enhancing yields (Liang et al., 2021; Qi et al., 2025). Furthermore, the reaction of rice genotypes to nitrogen fertilizer is crucial in maximizing fertilizer application and enhancing nutrient utilization efficiency in plants. Specific rice genotypes may exhibit varying reactions to nitrogen fertilizer dosage and application technique.

The rice production in 2 distinct seasons, the wet and dry seasons, can substantially influence agricultural productivity and sustainability. Climate change phenomena, uncertain rainfall patterns, and increasingly extreme temperature variations complicate rice farming management. According to some studies, environmental factors indicate that rice planted during the wet season has relatively higher plant growth than upland rice planted during the dry season. This is because during the wet season, plants receive sufficient water, resulting in optimal growth (Sution et al., 2019).

Genetic diversity among rice plants is crucial for different crop improvement programs to overcome varied environmental hurdles. Recent studies have demonstrated that rice genotypes exhibit differential responses under contrasting environmental conditions, particularly under varying water regimes, highlighting significant genotype × environment interactions that affect yield stability and agronomic performance (Habib et al., 2024; Brunet-Loredo et al., 2025). Environmental factors, such as irrigation management, soil conditions, and climatic variability, have been shown to modulate phenotypic expression and productivity, emphasizing the importance of multi-environment evaluation to identify adaptive and resilient genotypes for sustainable rice production.

He et al. (2023) assert that selection is a technique employed to identify genotypes or groups to enhance a population's genetic attributes. Genetic gain, genetic diversity, and heredity affect the selection efficacy. Several studies have explored different aspects of the multi-canopy rice concept. The growth response of short genotypes within structured canopy systems has been evaluated (Widyastuti et al., 2020). The contribution of the flag leaf characteristics of tall genotypes to yield components has also been investigated (Hidayah et al., 2022). Genetic parameters, such as heritability and response to selection in multi-canopy-related traits, have been analyzed (Sholehah et al., 2024). Specific combinations of various short and tall genotypes have been examined (Riswanto, 2025). More recently, preliminary yield evaluation of short genotypes has also been conducted (Listiyanto et al., 2026).

The effect of trait changes in tall plant genotypes on multi-canopy diversification has yet to be well examined. The tall plant genotypes in this study were selected based on the variability in the number of tillers, ranging from a low to high, as this characteristic can determine the intensity of dominance in competition between plants in a multi-canopy planting system. Tillering capacity is an important physiological trait that affects the number of panicles and the yields of rice plants. Meanwhile, short genotype architecture refers to morphological characteristics, such as plant height, leaf type (vertical or horizontal), and canopy shape. Short plant genotypes, densely structured plants, tend to be more efficient at utilizing light in shade and more responsive under stressful conditions (Widyastuti et al., 2020). Therefore, selecting the exemplary short plant architecture is crucial to avoid negative competition with the taller plants above.

This combination of characters in a multi-canopy system is expected to create vertical synergy, where tall plants with good tillering capacity dominate the upper canopy and produce

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many panicles. In contrast, short plants with efficient architecture can still produce optimally under shade. Thus, this system improves vertical space efficiency and increases the possibility of increasing total yield per unit area through genotype-specific interactions in different environments.

However, despite previous studies on multi-canopy rice systems, limited information is available regarding how variations in tillering capacity of tall genotypes interact with contrasting architectural types of short genotypes across different environmental conditions. In particular, the combined effects of these trait-based genotype pairings under varying nitrogen levels and seasonal environments have not been systematically evaluated. This study aimed to examine the effect of combining the tillering capacity of tall rice genotypes with the architecture of short rice genotypes on yield and agronomic traits under multi-canopy conditions across 2 seasons and 2 nitrogen levels.

MATERIALS AND METHOD

Plant materials and experimental sites

The study was conducted at Babakan Experimental Station of IPB University, Bogor, West Java, Indonesia (106°43’ E, 6°33’ S, 201 m above sea level). The first planting season was from September 2023 to January 2024 (wet season), while the second was from March 2024 to July 2024 (dry season). The genetic materials included 24 combinations of tall (T) and short (S) multi-canopy rice genotypes. The tall rice genotypes were categorized by potential tiller number: T1 = low (8 to 13), T2 = medium (14 to 19), and T3 = high (20 to 29); each category comprises 8 genotypes (Table 1). The short rice genotypes, based on architecture, were S1 = green revolution type (semi-dwarf variety with high tillering capacity), S2 = dwarf stay-green type, and S3 = new plant type (Table 1).

The tested groups of combinations of tall and short rice plants were T1-S1 (Z1-Z8), T2-S2 (Z9-Z16), and T3-S3 (Z17-Z24). These 24 combinations were tested with 4 checks, namely T5 (IPB187-F-40 advanced inbred line) and Inpari 32 in multi-canopy (Z25), T5 and Ciherang in multi-canopy (Z26), Inpari 32 in monoculture (Z27), and Ciherang in monoculture (Z28). Two checks of multi-canopy combinations utilizing a relatively good-stature tall genotype (T5) were combined with 2 Green Revolution mega-varieties, Inpari 32 (Z25) and Ciherang (Z26).

The tall genotype T5 was selected as a reference genotype because it had previously been evaluated in a preliminary multi-canopy study and demonstrated stable agronomic performance and suitable plant architecture for a structured canopy system (Listiyanto et al., 2026). Inpari 32 and Ciherang were included as check varieties because of their wide cultivation across diverse environments (Sitaresmi et al., 2025), making them appropriate agronomic benchmarks for evaluating the relative performance of multi-canopy genotype combinations. In addition to these 2 mega-varieties in monoculture, Z27 and Z28 were added as the other 2 checks.

Experimental design and agronomic management practice

The study was performed in 4 environments. Environments 1 and 3 employed fertilizer applications of 200 kg ha^{-1} urea (46% N), 100 kg ha^{-1} SP36 (36% P_2O_5), and 100 kg ha^{-1} KCl (60% K_2O), while environment 2 and 4 utilized fertilizer applications of 75 kg ha^{-1} urea (46% N), 100 kg ha^{-1} SP36 (36% P_2O_5), and 100 kg ha^{-1} KCl (60% K_2O). A randomized complete block design

Table 1. Tall and short rice genotypes evaluated in the multi-canopy system

No.	Tall rice genotypes			Short rice genotypes
	T1	T2	T3	
1	IPB200-F-45	IPB200-F-51	IPB205-F-1	S1: Inpari 32
2	IPB200-F-46	IPB200-F-52	IPB200-F-55	S2: IPB200-F-60
3	IPB200-F-47	IPB203-F-10	IPB200-F-56	S3: IPB200-F-43
4	IPB204-E-12	IPB202-F-3	IPB200-F-57	
5	IPB200-F-48	IPB200-F-53	IPB200-F-58	
6	IPB200-F-49	IPB200-F-54	IPB201-F-17	
7	IPB200-F-50	IPB202-F-4	IPB200-F-59	
8	IPB187-F-40	IPB203-F-11	IPB202-F-5	

Note: A total of 24 combinations of tall and short genotypes belonging to T1-S1, T2-S2, and T3-S3 groups, each comprising 8 combinations, were evaluated in this study

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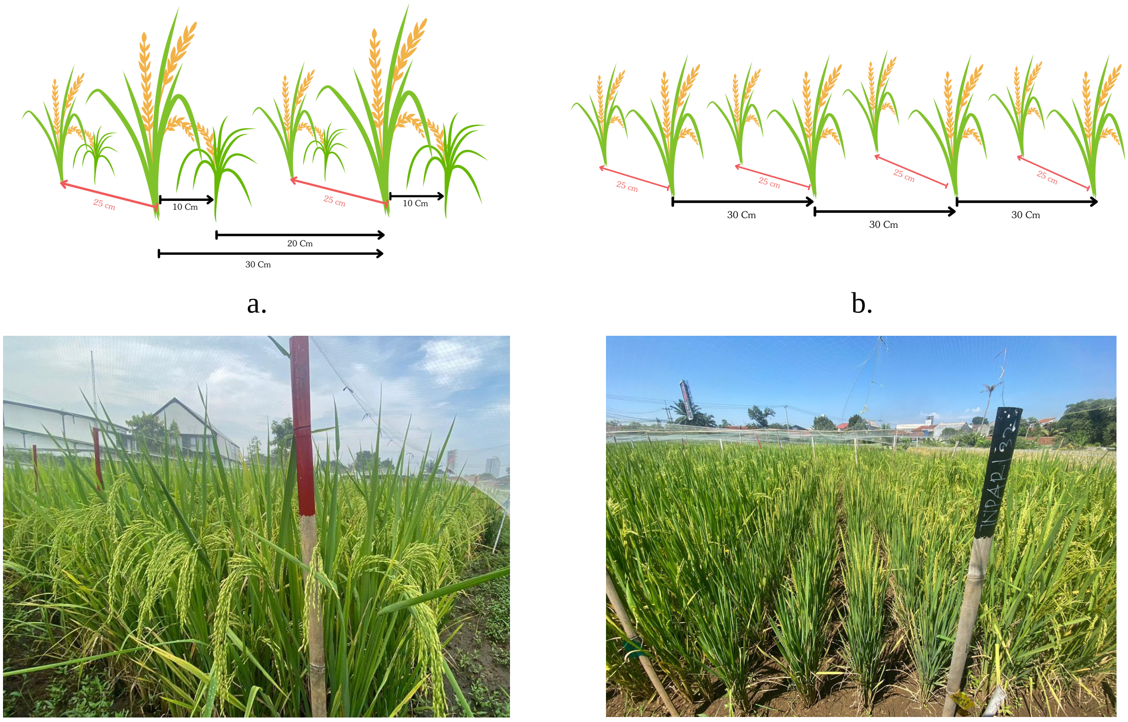

a.

b.

c.

d.

Figure 1. Illustration of multi-canopy (a) and monoculture (b) cropping system in rice, and their appearance in the field: (c) multi-canopy in the generative stage, (d) monoculture in the generative stage

with a single factor and 3 replications was employed in each environment. A total of 28 treatments mentioned in the previous section were evaluated; hence, there were 84 experimental units in each environment. In the multi-canopy system, tall and short genotypes were transplanted in a 1:1 ratio within each experimental unit. The size of an experimental unit was 5.0 m × 1.2 m. A total of 160 plants were established per plot, consisting of 80 tall and 80 short genotype plants. Three sample plants of both short and tall genotypes were collected from each experimental unit.

The preparation of the experimental field includes plowing, followed by harrowing and leveling. Before sowing, the quality seeds were selected by soaking them in water. Selected seeds were then planted in the nursery bed. Transplanting was done when the seedlings were 14 to 16 days after sowing (DAS). The seedlings were planted with a spacing of 30 cm × 25 cm (Figure 1). The separation between tall and low plants in the multi-canopy system was 10 cm. Each planting hill was accommodated with one seedling only. Nitrogen fertilizer application occurs in 2 phases: 1) at 7 days after transplanting (DAT) and 2) at 30 DAT, with each phase receiving one-third and two-thirds of the total urea dosage, respectively. SP-36 and KCl fertilizers were administered once at 7 DAT. Replacement of unviable seedlings was carried out at 7 to 14 DAT. Pest and disease management was conducted according to symptoms and severity seen in the field. Harvesting was performed once 90% of the panicles in a plot had turned yellow, and the grains had hardened, followed by threshing and drying of the grains.

Data observation and statistical analysis

Observations were made on agronomic traits and yield components by sampling 3 plants for each family. In the multi-canopy, grain yield was observed as follows: the tall genotype and the yield of the short genotype were measured, and the sum of these was recorded as the multi-canopy yield. Grain yield was determined from all plants in each plot and adjusted to 14% moisture content using the estimation formula from www.knowledgebank.irri.org (Equation 1).

$$GY = \frac{\left(\frac{10{,}000}{PS} \times GW\right) \times \left(\frac{100\text{-}GMC}{100\text{-}14}\right)}{1{,}000} \qquad (1)$$

Where GY is grain yield (ton ha^{-1}), PS is plot size (m^2), GW is grain weight per plot (kg), GMC is grain moisture content at harvest (%), and 14 is

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for the 14% final adjustment of grain moisture content.

The observed traits were: (1) grain yield, (2) total number of tillers, (3) number of productive tillers, (4) number of filled grains per panicle, (5) total number of grains per panicle, and (6) percent of empty grains per panicle. For multi-canopy combination data, grain yield, total number of tillers, and number of productive tillers were the sums of tall and short genotypes, whereas number of filled grains per panicle, total number of grains per panicle, and percent of empty grains per panicle were the means of the tall and short genotypes. The data analysis encompasses a comprehensive variance assessment from 4 environments, precisely 2 seasons, with 2 nitrogen fertilizer dose levels each season. The experiment was analyzed as a single-factor design, where genotype (multi-canopy combinations) was considered the only treatment factor. Environmental conditions (season and nitrogen level) were treated as separate environments rather than factorial treatment factors.

Analysis of variance (ANOVA) was conducted within each environment and across environments to evaluate genotype effects. Subsequently, the Tukey honestly significant difference (HSD) test was conducted at the 0.05 significance level. Multivariate relationships among traits were assessed using Pearson correlation analysis. Principal component analysis (PCA) was conducted to explore trait associations and identify major components contributing to variation among multi-canopy combinations, and selection via the Multi-trait Genotype-Ideotype Distance Index (MGIDI) method (Olivoto et al., 2021; Olivoto and Nardino, 2021) with 20% pressure. The data analysis software comprises Microsoft Excel 2019, SAS On-Demand for Academics (welcome.oda.sas.com), and RStudio version 2024.12.1, utilizing the packages *readxl*, *ggpubr*, *pheatmap*, and *factoextra*.

RESULTS AND DISCUSSION

Grain yield of genotype combinations in multi-canopy

Table 2 presents the average grain yield values for short genotypes, tall genotypes, and multi-canopy combinations. The short genotypes (Inpari 32, IPB200-F-60, and IPB200-F-43) exhibited considerable variability in average yield across 4 environments, ranging from 1.36 to 2.80 tons ha^{-1}. The tall genotypes had average yields ranging from 2.62 to 4.46 tons ha^{-1}. The highest yield in multi-canopy was shown by the Z2 combination (6.02 tons ha^{-1}). The yield of all multi-canopy rice genotypes exceeded that of the check varieties, Inpari 32 and Ciherang monoculture. In the multi-canopy condition, the tall genotype with the highest average yield was IPB200-F-51 (4.46 tons ha^{-1}), while the short genotype group with the highest average yield was S3 (2.32 tons ha^{-1}), having the new plant type architecture.

The findings of this study demonstrated that the multi-canopy production capacity has risen by 67.4% compared to monoculture. The tall rice genotype has superior productivity relative to the short genotype. Tall genotypes may have an advantage in photosynthetic conditions attributable to their higher stature, enabling enhanced solar absorption that facilitates grain development. Conversely, the short genotype may be more resistant to lodging; however, its yield was generally diminished under suboptimal conditions. Water availability, soil nutrients, and agronomic management influence productivity in each environment. The disparity in yield between tall and short rice genotypes demonstrates the superiority of tall genotypes under optimal environmental circumstances. Rice breeding must incorporate tall plant traits to enhance yield while addressing tolerance to adverse environmental conditions (Liang et al., 2015; Khamid et al., 2023).

Combined analysis of variance across environments

Table 3 presents the findings of the combined analysis of variance for tall and short multi-canopy rice genotypes cultivated throughout 2 planting seasons with 2 nitrogen doses. Traits exhibiting notable differences across seasons include grain yield and percent of empty grains per panicle. In the wet season, the average grain yield (6.13 tons ha^{-1}) was significantly higher, and the average percent of empty grains per panicle (23%) was significantly lower than in the dry season (grain yield 4.37 tons ha^{-1} and percent of empty grains per panicle 31%). Priyadi and Nuryati (2019) assert that rice yield will be enhanced when cultivated in the wet season, owing to improved water availability and increased soil moisture during the growth period. Seasons had no significant effect on the traits total number of tillers, number of productive tillers, number of filled grains per panicle, and total number of grains per panicle, indicating that these

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traits produce equivalent results whether sown in the wet or dry season. This suggests that both seasons equally facilitate the growth of tiller numbers (Hindersah et al., 2022; Yuan et al., 2024).

The average grain yield from the optimum nitrogen dose (5.50 tons ha^{-1}) was significantly higher than the suboptimum nitrogen dose (5.00 tons ha^{-1}). This may facilitate the selection of multi-canopy genotypes for adaptation to optimum or suboptimum nitrogen conditions. On the other hand, the traits total number of tillers, number of productive tillers, number of filled grains per panicle, total number of grains per panicle, and percent of empty grains per panicle were not significantly influenced by variations in nitrogen doses administered.

The genotype combinations exhibited a highly significant effect on all measured traits, signifying genetic variation in multi-canopy rice. This study revealed the interaction between nitrogen and genotype combinations affecting the total number of tillers and number of productive tillers traits. However, no significant interactions were observed between season and nitrogen, season and genotype combinations, or among season, nitrogen, and genotype combinations for any of the observed traits. Huang et al. (2021) asserted that a genotype exhibiting better agronomic traits in one environmental condition may not exhibit the same superiority in other conditions.

The coefficient of variation (CV) for the examined traits ranges from 12.26 to 22.89%. A CV under 15% signifies reliability for the

Table 2. Average grain yield of short and tall genotypes across 4 environments

Comb. & Checks	Group	Genotypes	Grain yield (tons ha^{-1})		
			Short genotypes	Tall genotypes	Multi-canopy
Z1	T1-S1	IPB200-F-45 & Inpari 32	1.58^{bcd}	2.62^{c}	4.20^{abc}
Z2	T1-S1	IPB200-F-46 & Inpari 32	1.78^{bcd}	4.25^{ab}	6.02^{a}
Z3	T1-S1	IPB200-F-47 & Inpari 32	$1.94^{a\text{-}d}$	3.69^{abc}	5.62^{a}
Z4	T1-S1	IPB204-E-12 & Inpari 32	$1.98^{a\text{-}d}$	3.14^{abc}	5.12^{abc}
Z5	T1-S1	IPB200-F-48 & Inpari 32	1.83^{bcd}	3.98^{abc}	5.81^{a}
Z6	T1-S1	IPB200-F-49 & Inpari 32	$2.02^{a\text{-}d}$	3.58^{abc}	5.60^{a}
Z7	T1-S1	IPB200-F-50 & Inpari 32	$1.90^{a\text{-}d}$	3.33^{abc}	5.23^{abc}
Z8	T1-S1	IPB187-F-40 & Inpari 32	$1.98^{a\text{-}d}$	3.82^{abc}	5.80^{a}
Z9	T2-S2	IPB200-F-51 & IPB200-F-60	1.38^{d}	4.46^{a}	5.84^{a}
Z10	T2-S2	IPB200-F-52 & IPB200-F-60	1.36^{d}	3.86^{abc}	5.22^{abc}
Z11	T2-S2	IPB203-F-10 & IPB200-F-60	1.39^{d}	3.54^{abc}	4.93^{abc}
Z12	T2-S2	IPB202-F-3 & IPB200-F-60	1.58^{bcd}	4.00^{abc}	5.57^{ab}
Z13	T2-S2	IPB200-F-53 & IPB200-F-60	1.69^{bcd}	3.76^{abc}	5.45^{abc}
Z14	T2-S2	IPB200-F-54 & IPB200-F-60	1.53^{cd}	3.73^{abc}	5.25^{abc}
Z15	T2-S2	IPB202-F-4 & IPB200-F-60	1.63^{bcd}	3.92^{abc}	5.55^{ab}
Z16	T2-S2	IPB203-F-11 & IPB200-F-60	1.42^{d}	3.71^{abc}	5.13^{abc}
Z17	T3-S3	IPB205-F-1 & IPB200-F-43	$2.08^{a\text{-}d}$	3.25^{abc}	5.32^{abc}
Z18	T3-S3	IPB200-F-55 & IPB200-F-43	2.43^{ab}	3.09^{abc}	5.53^{ab}
Z19	T3-S3	IPB200-F-56 & IPB200-F-43	$2.06^{a\text{-}d}$	3.06^{abc}	5.13^{abc}
Z20	T3-S3	IPB200-F-57 & IPB200-F-43	$2.07^{a\text{-}d}$	2.85^{bc}	4.92^{abc}
Z21	T3-S3	IPB200-F-58 & IPB200-F-43	2.32^{abc}	3.44^{abc}	5.76^{a}
Z22	T3-S3	IPB201-F-17 & IPB200-F-43	$1.99^{a\text{-}d}$	3.07^{abc}	5.06^{abc}
Z23	T3-S3	IPB200-F-59 & IPB200-F-43	2.80^{a}	2.77^{bc}	5.57^{ab}
Z24	T3-S3	IPB202-F-5 & IPB200-F-43	2.78^{a}	2.92^{abc}	5.69^{a}
Z25	MC check	T5 (IPB187-F-40) & Inpari 32	1.88^{bcd}	3.70^{abc}	5.57^{ab}
Z26	MC check	T5 (IPB187-F-40) & Ciherang	$2.18^{a\text{-}d}$	3.02^{abc}	5.20^{abc}
Z27	MO check	Inpari 32 monoculture			3.43^{c}
Z28	MO check	Ciherang monoculture			3.51^{bc}
		Average (Z1-Z26)	1.91^{C}	3.48^{B}	5.39^{A}

Note: Comb. = Combination; MC = Multi-canopy; MO = Monoculture. Numbers followed by the same lowercase letter in the same column are not significantly different based on the Tukey HSD test at the 0.05 level; numbers followed by the same uppercase letter in the same row are not significantly different based on the LSD test at the 0.05 level

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Table 3. Combined ANOVA of the tall and short genotype combinations of multi-canopy rice, along with the checks

Source of variation	df	Mean square					
		GY	NTT	NPT	FGN	TGN	PEG
Season (S)	1	260.72**	0.28^{ns}	1.60^{ns}	6,097.22^{ns}	3,379.33^{ns}	0.60*
Urea (N)	1	20.90*	125.89^{ns}	92.71^{ns}	1,697.03^{ns}	1,797.63^{ns}	0.01^{ns}
N × S	1	4.93^{ns}	4.37^{ns}	0.39^{ns}	310.27^{ns}	5,873.56^{ns}	0.08^{ns}
Rep / N × S	8	2.11*	58.03**	41.49**	1,258.75*	1,636.63*	0.02**
Combination (C)	27	4.68**	29.18**	26.72**	2,052.43**	5,430.83**	0.02**
C × N	27	0.71^{ns}	11.25*	10.63*	355.21^{ns}	547.37^{ns}	0.005^{ns}
C × S	27	1.11^{ns}	6.16^{ns}	5.28^{ns}	369.62^{ns}	501.69^{ns}	0.005^{ns}
C × N × S	27	0.96^{ns}	7.24^{ns}	7.02^{ns}	271.98^{ns}	566.34^{ns}	0.005^{ns}
Error	216	0.90	5.65	5.29	337.15	547.04	0.004
CV%		18.07	12.31	12.26	15.37	14.05	22.89

Note: df = Degrees of freedom; GY = Grain yield; NTT = Total number of tillers; NPT = Number of productive tillers; FGN = Number of filled grains per panicle; TGN = Total number of grains per panicle; PEG = Percent of empty grains per panicle; CV = Coefficient of variation; * = Significant at the 0.05 probability level; ** = Significant at the 0.01 probability level; ns = Not significant

assessed traits, enabling breeders to select more rigorously (Aklilu et al., 2024). Selection can be performed directly and with greater rigor for traits exhibiting a low CV. For traits with a high CV, a more comprehensive strategy and an amalgamation of diverse selection strategies were essential to fully harness the potential variety within the population. The CV value indicates the extent of experimental error; a smaller CV number signifies greater accuracy in the results drawn (Nadim et al., 2025; Listiyanto et al., 2026).

Performance of genotype combinations

The evaluation results across 4 environments in Table 4 indicate a considerable variability among 26 combinations of tall and short rice genotypes in multi-canopy and 2 check varieties in monoculture. The Z15 combination had the highest number of filled grains per panicle and total number of grains per panicle, signifying that this genotype possessed superiority in grain numbers. The total number of tillers and number of productive tillers traits exhibited their maximum values of 22.5 and 21.8 in the Z11 combination, whereas their minimum values of 17.1 and 16.8 were observed in the Z15 combination. The Z4 combination showed the lowest empty grain percentage of 18.48%, whereas the Z12 combination displayed the highest at 37.16%. The results demonstrate that some genotype combinations perform better in the assessed traits.

The high tillering capacity of tall genotypes combined with the new plant type architecture of short genotypes in the T3-S3 group may be favored for multi-canopy systems. These results reinforce the importance of incorporating a higher tiller capacity trait in tall genotypes to enhance yield potential and number of productive tillers traits in short genotypes to improve performance. In wheat, shading from an extensive canopy can reduce the number of tillers (Abichou et al., 2019). While examining plant genotypes, it was crucial to account for the interaction between genotype and environment on the agronomic variables of interest (Shrestha et al., 2021; Williams et al., 2021).

Interaction of genotype combinations with nitrogen

Figure 2a illustrates the comparison of productive tiller counts among multi-canopy rice genotypes under 2 nitrogen conditions: optimum (light bar) and suboptimum (dark bar). Figure 2b illustrates the total number of tillers combined with multi-canopy rice genotypes. Nevertheless, several genotype combinations exhibit varying reactions to nitrogen conditions. For instance, in genotypes Z6, Z13, and Z22, the reduction in the number of productive tillers under suboptimum nitrogen conditions was comparatively minimal, indicating their resilience to suboptimum nitrogen conditions. This aligns with earlier research by Bala et al. (2025), which indicates that rice genotypes possessing specific adaptation traits can sustain vegetative growth in unfavorable environmental conditions. Conversely, genotypes Z1, Z18, and Z19 exhibited a marked reduction in productive tillers under suboptimum nitrogen conditions, signifying increased sensitivity to environmental stress. The drop was likely

Table 4. Average of multi-canopy rice genotype combinations and check varieties across 4 environments

Comb. & Checks	NTT	NPT	FGN	TGN	PEG
Z1	19.2^{a-f}	18.0^{b-e}	109.0^{b-e}	152.1^{d-h}	25.18^{b-g}
Z2	20.5^{a-f}	19.7^{a-e}	111.5^{b-e}	143.5^{e-h}	21.35^{d-g}
Z3	19.1^{a-f}	18.4^{a-e}	124.4^{a-e}	169.3^{a-g}	23.77^{b-g}
Z4	21.6^{abc}	21.4^{ab}	108.9^{b-e}	134.4^{gh}	18.48^{g}
Z5	21.9^{ab}	21.4^{ab}	103.5^{de}	132.2^{h}	20.69^{efg}
Z6	20.1^{a-f}	19.5^{a-e}	111.8^{b-e}	167.2^{b-h}	27.70^{b-g}
Z7	18.1^{c-f}	17.6^{cde}	135.5^{ab}	192.9^{abc}	25.77^{b-g}
Z8	17.6^{def}	17.1^{de}	122.3^{b-e}	165.8^{b-h}	23.86^{b-g}
Z9	17.4^{ef}	16.8^{e}	135.7^{ab}	186.8^{a-d}	26.61^{b-g}
Z10	18.7^{b-f}	18.3^{b-e}	110.1^{b-e}	159.4^{c-h}	31.21^{ab}
Z11	22.5^{a}	21.8^{a}	98.1^{e}	143.5^{e-h}	31.01^{abc}
Z12	18.8^{b-f}	18.5^{a-e}	104.4^{cde}	165.8^{b-h}	37.16^{a}
Z13	18.5^{b-f}	17.8^{cde}	115.0^{b-e}	159.4^{c-h}	28.20^{a-f}
Z14	19.6^{a-f}	18.9^{a-e}	121.2^{b-e}	154.0^{d-h}	21.65^{c-g}
Z15	17.1^{f}	16.8^{e}	152.5^{a}	204.2^{a}	24.71^{b-g}
Z16	21.2^{a-d}	20.8^{abc}	101.8^{de}	140.3^{fgh}	26.31^{b-g}
Z17	19.7^{a-f}	18.8^{a-e}	130.1^{a-d}	192.0^{abc}	31.51^{ab}
Z18	20.7^{a-f}	19.8^{a-e}	127.0^{a-d}	178.3^{a-e}	27.82^{a-g}
Z19	21.2^{a-d}	20.0^{a-e}	113.3^{b-e}	165.5^{b-h}	30.27^{a-d}
Z20	17.3^{ef}	16.8^{e}	131.9^{abc}	181.2^{a-d}	27.66^{b-g}
Z21	19.6^{a-f}	18.9^{a-e}	128.3^{a-d}	185.3^{a-d}	30.21^{a-d}
Z22	19.8^{a-f}	19.4^{a-e}	118.1^{b-e}	169.4^{a-g}	30.05^{a-d}
Z23	20.9^{a-e}	20.6^{a-d}	129.0^{a-d}	183.2^{a-d}	29.66^{a-e}
Z24	18.7^{b-f}	18.2^{b-e}	121.6^{b-e}	173.7^{a-f}	29.96^{a-e}
Z25	18.5^{b-f}	18.0^{b-e}	134.2^{ab}	190.9^{abc}	26.95^{b-g}
Z26	17.6^{def}	17.4^{cde}	132.9^{ab}	199.5^{ab}	31.25^{ab}
Z27	17.4^{ef}	17.3^{cde}	104.5^{cde}	132.2^{h}	19.76^{fg}
Z28	17.4^{ef}	17.3^{cde}	108.9^{b-e}	140.1^{fgh}	21.54^{d-g}

Note: Comb. = Combination (Z1-Z26 in multi-canopy, Z27 (Inpari 32) and Z28 (Ciherang) in monoculture); NTT = Total number of tillers; NPT = Number of productive tillers; FGN = Number of filled grains per panicle; TGN = Total number of grains per panicle; PEG = Percent of empty grains per panicle. Numbers followed by the same letter in the same column are not significantly different based on the Tukey HSD test at the $\alpha = 0.05$ level

attributable to constraints on photosynthesis or diminished nutrient absorption, as elucidated by Yoshida (1981), who demonstrated that abiotic stressors, such as water and nutrient scarcity, can inhibit the growth of rice seedlings.

Figure 2b illustrates the variations in genotype responses to optimum and suboptimum nitrogen conditions for the total number of tillers. Combination Z9 had identical responses under both nitrogen conditions. Certain genotype combinations, such as Z6 and Z7, showed a slight reduction in the overall number of tillers, suggesting their capacity to withstand suboptimum nitrogen conditions. This aligns with the findings of Qi et al. (2025), which indicated that specific rice genotypes exhibit significant tolerance to abiotic stressors, including drought and nutrient deficiency.

The study revealed that the interaction between genotype combinations and environmental conditions, including nitrogen dosage and season, significantly influenced yield and agronomic traits. Notably, the interaction between nitrogen and genotype combinations significantly affected traits like the total number of tillers and the number of productive tillers. In some cases, optimum conditions (200 kg ha^{-1} urea) yield a greater quantity of tillers than suboptimal conditions (75 kg ha^{-1} urea) (Figure 2). However, in some other cases, there were genotype combinations exhibiting a greater number of tillers under suboptimal conditions, namely Z3, Z4, Z10, Z12, Z14, Z26, and Z27. This phenomenon was also observed by Harahap and Harahap (2017), who found that applying urea at 75 kg ha^{-1} produced a greater number of

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productive tillers than at 200 kg ha^{-1}. This underscores the substantial influence of the environment on plant growth. Ria et al. (2025) assert that favorable conditions, including nutrition and water availability, promote plant vegetative growth, including tiller formation. These findings highlighted the importance of matching genotype characteristics with environmental conditions to maximize the number of tillers.

This disparity underscores the significance of genotype assessment in identifying productive combinations in good conditions and resilience in inferior environments. This method was essential for addressing the challenges of climate change and managing marginal areas to sustain rice yield (Surendran et al., 2021; Mir et al., 2025). The grain yield exhibits a notable difference in response to different dosages of nitrogen applied. To attain an elevated yield, it was preferable to be cultivated at optimum nitrogen conditions. The application of nitrogen at an optimal dosage of 200 kg ha^{-1} results in higher grain yield, likely because of enhanced nitrogen availability for the plants, which promotes vegetative growth, facilitates tiller formation, and improves rice quality (Luo et al., 2020; Zhou et al., 2021; Akter et al., 2022).

Variation within and between groups of pairings

Figure 3 presents a comparative analysis of performance among the 3 groups of pairings in multi-canopy, namely T1-S1, T2-S2, and T3-S3. Each group consisted of 8 genotype combinations, i.e., 8 tall genotypes combined with 1 short genotype. For the grain yield trait, the 3 groups had a similar average of 5.37 to 5.43 tons ha^{-1},

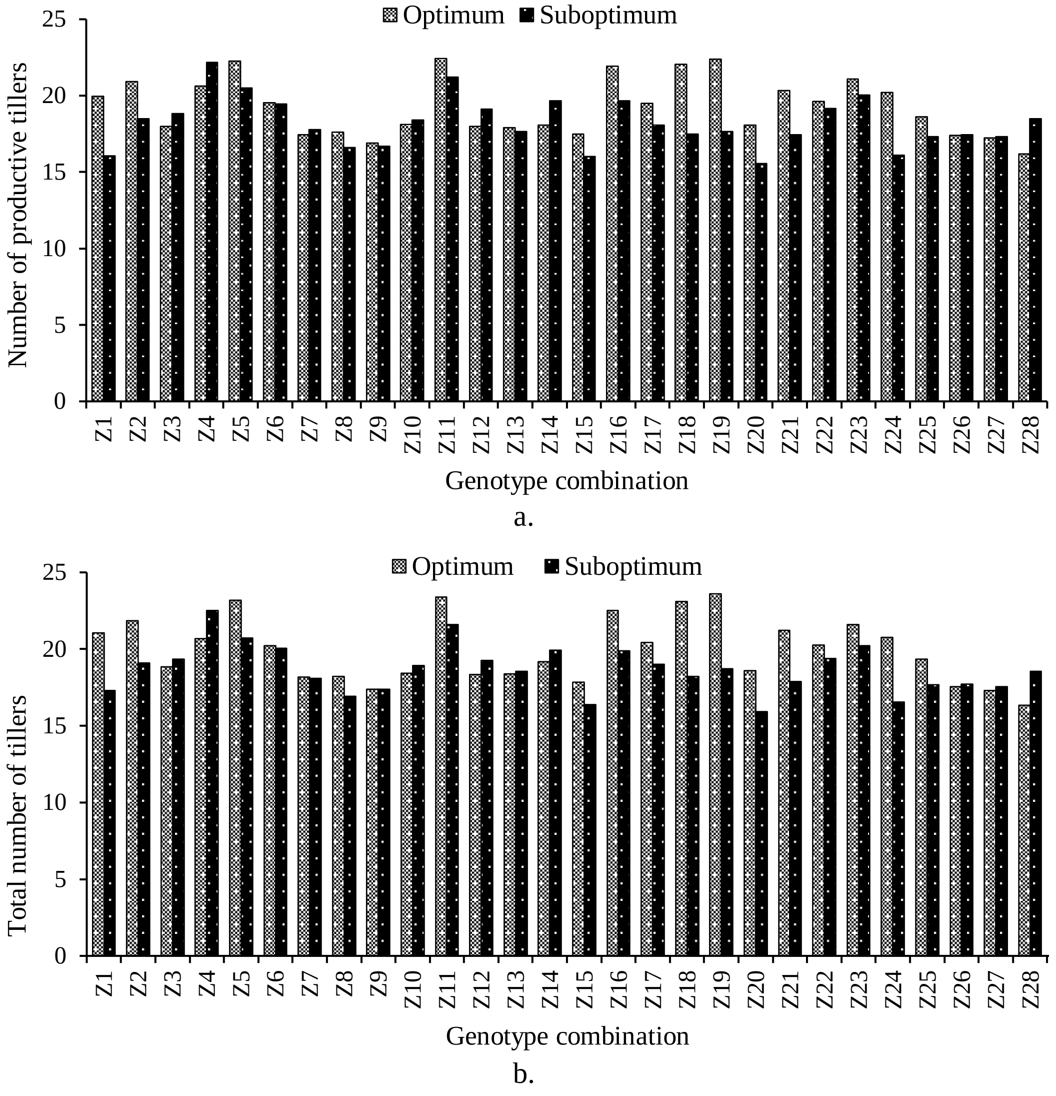

Figure 2. Number of productive tillers (a) and total number of tillers (b) of genotype combinations under optimum and suboptimum nitrogen conditions

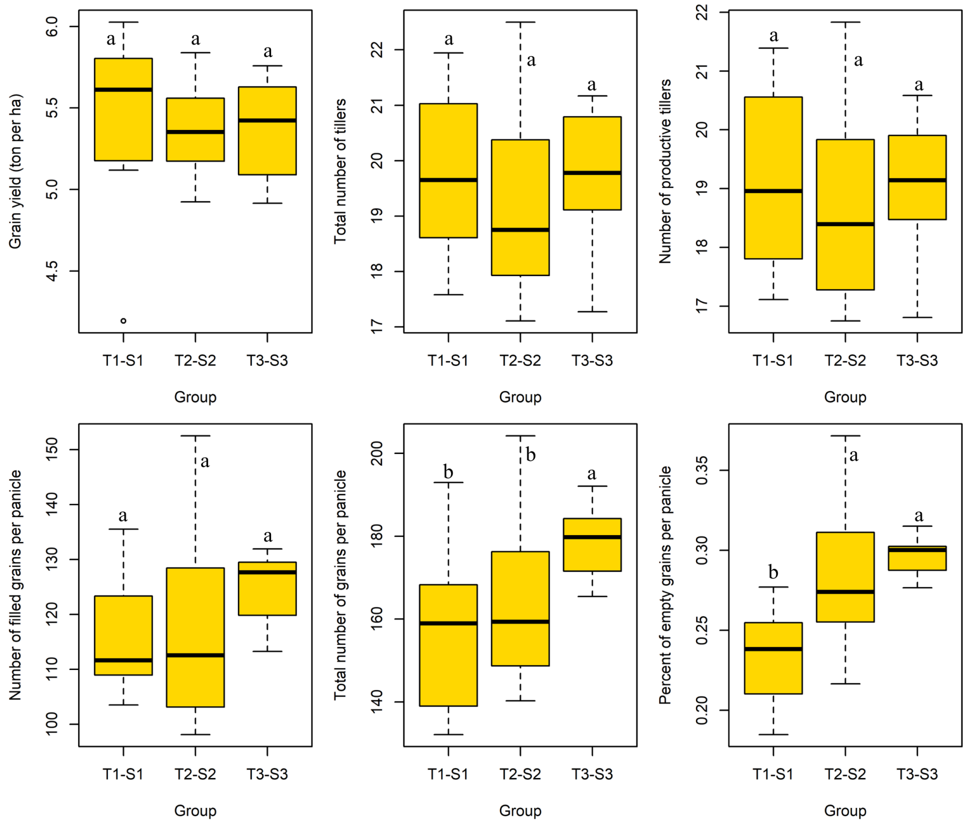

Figure 3. Variability between and within groups of pairings in a multi-canopy

Note: Numbers followed by the same letter in the same trait are not significantly different based on the Tukey HSD test at the 0.05 probability level; T1-S1 = Low-tillering tall genotype paired with green revolution type short genotype; T2-S2 = Medium-tillering tall genotype paired with dwarf stay-green short genotype; T3-S3 = High-tillering tall genotype paired with new plant type short genotype

significantly higher compared to monoculture (3.43 to 3.51 tons ha^{-1}). This suggests that a tiered canopy planting strategy may enhance rice crop yields. Incorporating panicles from tall genotypes in multi-canopy plantings can contribute to yield increase, even under stress conditions affecting short genotypes (Widyastuti et al., 2020; Hidayah et al., 2022; Listiyanto, 2026).

There were no significant variations across the groups in the grain yield, total number of tillers, number of productive tillers, and number of filled grains per panicle traits, as they showed similar averages. The T3-S3 group exhibited the highest value of total number of grains per panicle (178.6) and was significantly higher than the other 2 groups. Furthermore, the T1-S1 group had a significantly lower percent of empty grains per panicle than the other 2 groups (T2-S2 and T3-S3). Variation was present within each group based on the traits, underscoring the significance of genotype selection within a group to mitigate losses.

The T3-S3 genotype group had emerged as a promising group for the breeding program with multi-canopy objectives. This group demonstrated a superior number of total tillers for some traits compared to other groups, and it had a more restricted data dispersion. Simultaneously, the T1-S1 and T2-S2 groups had a broader data dispersion, signifying a heightened variability in genotype combinations within these groups (Figure 3). In groups with high genotypic variation, there were likely inherited traits (high heritability). This means that selection against certain traits can result significantly in subsequent generations. Without genetic variation, selection will be ineffective because the entire population tends to show a uniform response to specific environmental stresses or treatments (Yadi et al., 2021; Hassan et al., 2023).

Correlation and principal component analysis of multi-canopy rice

Figure 4 displays the findings of the Pearson correlation analysis for multi-canopy rice across four environments. Correlation analysis examines the correlations among traits and determines the factors affecting grain yield. The intensity of the linear correlation among traits was illustrated

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by a color gradient ranging from red to purple. Here, a stronger positive correlation between traits is visualized in a darker purple, whereas a stronger negative correlation is shown in a darker red. Taylor (1990) categorizes correlation based on the correlation coefficient values: weak ($r \leq 0.35$), moderate ($0.36 \leq r \leq 0.67$), high ($0.68 \leq r \leq 0.89$), and powerful ($r \geq 0.90$).

The grain yield exhibited a substantial positive association with the total grain count per panicle ($r = 0.41$, $p < 0.05$). Despite possessing a moderate correlation coefficient, this suggests that an increase in total number of grains per panicle may lead to a rise in the grain yield. Conversely, other traits exhibited feeble and inconsequential relationships. Nithya et al. (2020) found a significant positive correlation between grain yield and the number of grains per panicle under drought-stress conditions. This study emphasizes the importance of these morphophysiological traits in enhancing rice yield, particularly in water-limited environments. This aligns with the research by Sholehah et al. (2024), which showed that various features had an excellent impact on the yield of multi-canopy rice.

The PCA biplot is advantageous for illustrating the interrelations among genotypes and traits in rice (Aswidinnoor et al., 2023). Typically, a biplot constructed from the first two principal components (PC1 and PC2) is sufficient to visualize a multidimensional relationship when the proportion of explained variation is high. In the present study, PC1 and PC2 accounted for a cumulative variation of 79.3%, indicating that these 2 components adequately represent the multivariate structure of the dataset. Specifically, PC1 explained 50.1% of the total variance, whereas PC2 contributed 29.2% (Figure 5b). PC1 showed a positive correlation with the variables number of productive tillers and total number of tillers, with nearly identical coefficient values of 0.47 and 0.46, respectively (Table 5). This suggests that PC1 largely represents variation associated with vegetative growth capacity and tillering potential, traits that have been identified as major contributors to yield variation in rice (Salunkhe et al., 2023; Islam et al., 2024).

In contrast, PC2 was predominantly influenced by grain yield (-0.61) and percent empty grain (-0.44) (Table 5), indicating that this component reflects variation linked to grain filling efficiency and reproductive performance, a pattern consistent with multivariate trait interpretation in cereal crops (Akula et al., 2025). The number of significant components that may be relevant was contingent upon the extent of their contribution to the overall variance. For a reasonable interpretation, the cumulative variance explained by the 2 principal components should exceed 75% (Beriso et al., 2025; Matthew, 2025).

The scree plot further supports the retention of these 2 principal components, as a pronounced decline in explained variance was observed after PC2, followed by a gradual leveling of the curve (Figure 5a). This "elbow" in the scree plot suggests that additional components contribute only marginal information, consistent with criteria

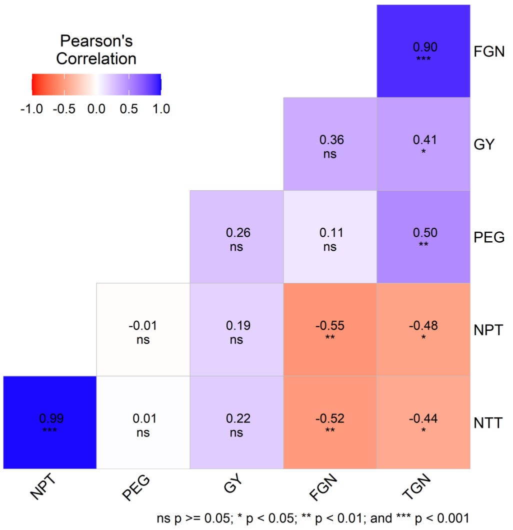
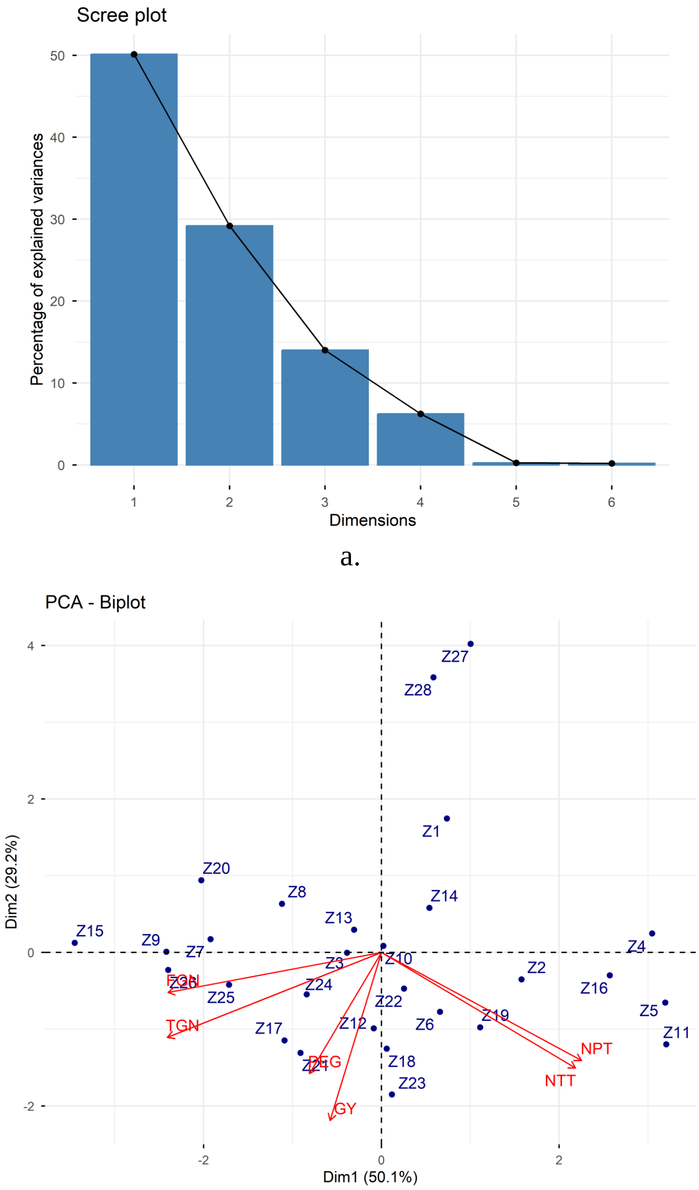


Figure 4. Correlation among traits of multi-canopy combinations across 4 environments

Note: GY = Grain yield; NTT = Total number of tillers; NPT = Number of productive tillers; FGN = Number of filled grains per panicle; TGN = Total number of grains per panicle; PEG = Percent of empty grains per panicle



a.

b.

Figure 5. Scree plot (a) and biplot of PCA (b) of multi-canopy combinations and agronomic traits from the average data of 4 environments

Table 5. Eigenvalues and factor loadings of agronomic traits based on PCA

Component	Eigenvalue	NTT	NPT	GY	FGN	TGN	PEG
PC1	3.01	0.46	0.47	-0.12	-0.51	-0.51	-0.17
PC2	1.75	-0.42	-0.39	-0.61	-0.14	-0.31	-0.44
PC3	0.84	0.08	0.08	0.41	0.36	-0.03	-0.83
PC4	0.37	0.33	0.33	-0.67	0.44	0.36	-0.09
PC5	0.01	0.57	-0.58	-0.00	-0.37	0.40	-0.18
PC6	0.01	-0.41	0.41	0.01	-0.51	0.59	-0.24

Note: PC = Principal component; NTT = Total number of tillers; NPT = Number of productive tillers; GY = Grain yield; FGN = Number of filled grains per panicle; TGN = Total number of grains per panicle; PEG = Percent of empty grains per panicle

for component retention in multivariate analyses (Cao et al., 2025). Moreover, the eigenvalues of PC1 and PC2 exceeded unity, satisfying the Kaiser criterion for component selection, a practice still reinforced in recent multivariate crop studies (Islam et al., 2024).

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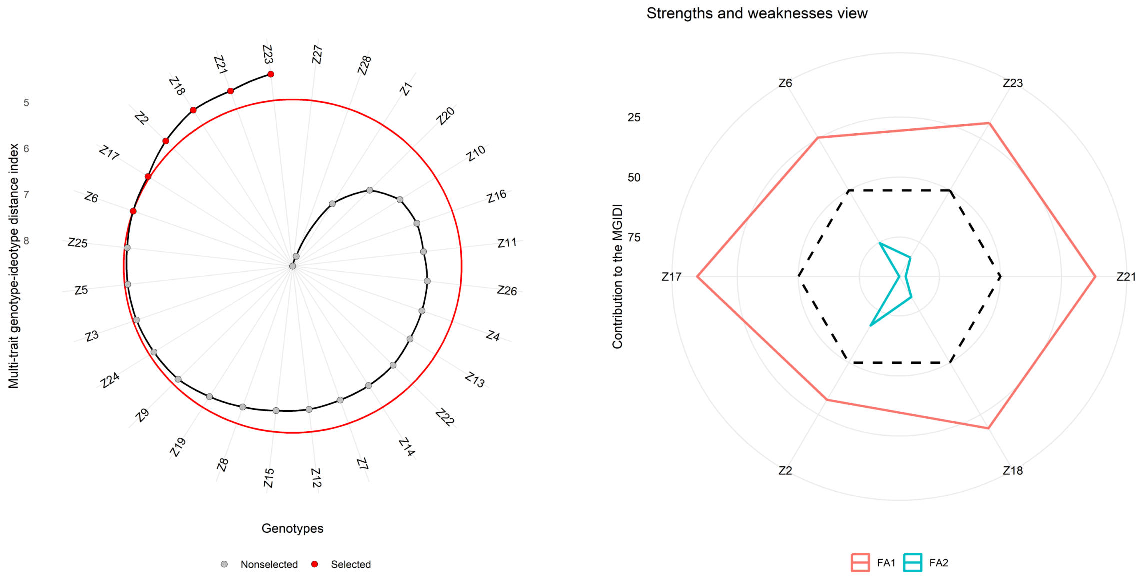

a. b.

Figure 6. Selection of 28 combinations of multi-canopy rice genotypes through the weighted MGIDI model (a); strengths and weaknesses of the selected multi-canopy rice genotype combinations (b)

The correlation analysis revealed a positive and significant relationship between grain yield and the total number of grains per panicle, suggesting that increasing total number of grains per panicle can enhance yield. PCA further validated these findings by identifying number of productive tillers and total number of tillers as key contributors to genetic variation. These analyses provide valuable insights into prioritizing traits for selection in multi-canopy breeding programs (Khan et al., 2021; Matthew, 2025). According to the concepts of PCA articulated by Jolliffe and Cadima (2016), principal component analysis facilitates the identification of predominant patterns in multivariate data by condensing it into many orthogonal principal components, thus enhancing interpretability through dimensional reduction.

MGIDI selection on multi-canopy rice genotypes

Figure 6a presents the 20% MGIDI selection for multi-canopy rice genotypes across 4 environments that involved 4 traits, namely grain yield, total number of tillers, total number of grains per panicle, and number of filled grains per panicle. The genotypes chosen according to MGIDI were Z23 (IPB200-F-59 and IPB200-F-43), Z21 (IPB200-F-58 and IPB200-F-43), Z18 (IPB200-F-55 and IPB200-F-43), Z2 (IPB200-F-46 and Inpari 32), Z17 (IPB205-F-1 and IPB200-F-43), and Z6 (IPB200-F-49 and Inpari 32) (Figure 6a). This finding was consistent with Figure 3, indicating potential genotype combinations in group T3-S3.

Figure 6b illustrates the strengths and weaknesses of each chosen multi-canopy genotype combination concerning a specific trait. FA1 pertains to total number of tillers, number of filled grains per panicle, and total number of grains per panicle, whereas FA2 pertains to grain yield. The contribution of FA1 to MGIDI was less than that of FA2 across all selected genotypes. This signifies that all chosen genotype combinations exhibit strength in FA1 but weakness in FA2. The pronounced disparity between the strengths and weaknesses of these genotypes was more apparent in Z21 and Z17 than in the other 4 genotypes.

MGIDI is a recent approach for a more efficient selection of genotypes involving multiple traits. This method provides a more thorough means of selecting potential genotypes (Olivoto and Nardino, 2021; Sholehah et al., 2024). Utilizing MGIDI in rice breeding can identify favorable genotypes based on multiple traits of interest. This method allows for the identification of strengths and weaknesses of the selected genotypes. In a multi-canopy rice breeding program, MGIDI may be able to assist in selecting favorable tall and short genotypes.

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CONCLUSIONS

Various combinations of tall and short in multi-canopy had higher grain yields than the check varieties in monoculture. High-tillering tall genotype combined with the new plant type short genotype (T3-S3) showed the highest average total grain number. The best multi-canopy combination within the T3-S3 group, Z21 (5.76 tons ha^{-1}), showed an increase of 64.1% compared to the Ciherang in monoculture (3.51 tons ha^{-1}). The multi-canopy rice genotypes selected according to the MGIDI at 20% pressure were Z23, Z21, Z18, Z2, Z17, and Z6. Overall, this research advances the development of multi-canopy rice cultivars that exhibit enhanced adaptability to diverse environmental circumstances.

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