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SELECTION IN RICE F_5 POPULATIONS UNDER LOW-FERTILIZER CONDITIONS USING GENOTYPE BY ENVIRONMENT INTERACTIONS AND TOLERANCE INDICES

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SUMMARY

Breeding for fertilizer-efficient rice is paramount. The succeeding research aimed to study the genetic makeup and selection procedure for tolerant rice genotypes in minimum fertilizer. The genetic material comprised 106 F_5 rice lines and five check genotypes grown under optimum and minimum fertilizer conditions. The experiment layout was in an augmented design with five replications. The results indicated genotype-by-environment interactions significantly ($p < 0.01$) affected rice yield-related traits, specifically productivity. The identified rice lines totaled 26 through multi-trait genotype-ideotype distance index (MGIDI) analysis using 25% selection intensity. The heritability value in the optimal environment (0.725) was higher than in the minimum environment (0.628). Similarly, values for genetic advance (GA) and genetic advance as a percentage of the mean (GAM) in the optimal environment (1.160% and 18.680%) were higher than those in the minimum environment (0.659% and 13.158%). The geometric mean productivity (GMP), harmonic mean (HM), mean productivity (MP), and stress tolerance index (STI) exhibited a significant positive correlation with the average yield under optimum conditions (Yp) and minimum conditions (Ys). However, the stress susceptibility index (SSI) and tolerance index (TOL) showed a negative correlation with Ys, indicating selection based on the tolerance index identified the best lines, G27 and G66.

Keywords: Rice (*O. sativa* L.), F_5 populations, minimum fertilizer, selection, heritability, genetic gain, tolerance indices, yield-related traits

Key findings: The study highlighted the use of the MGIDI method and tolerance indices (TOL, SSI, STI, MP, HM, and GMP) in identifying promising rice (*O. sativa* L.) genotypes better suited for low-fertilization conditions. These insights serve as a valuable resource for optimizing fertilizer efficiency to enhance sustainable rice production.

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INTRODUCTION

Rice (*Oryza sativa* L.) is an essential food commodity in the world. Indonesia is the fifth-largest consumer of rice globally, with an annual consumption of 35.6 million tons, fulfilling the basic dietary needs of the population (Shahbandeh, 2022). The annual increase in the world's population has led to a higher demand for food. Global food security faces threats from population growth, land-use competition, climate change, and the limited use of costly field inputs (Anisuzzaman *et al*., 2016).

An increase in rice production can be successful through intensification by improving the interactions between plants, soil, water, and nutrients. The fertilizers utilized by crop plants generally contain nitrogen (N), phosphorus (P), and potassium (K) (Stellacci *et al*., 2013). These nutrients are essential for rice production, and their nonuse can lead to decreased yield and trigger complex molecular and physiological processes (Jiang *et al*., 2019). These three major fertilizer elements (N, P, and K) are a common treatment as basic nutrients in substantial quantities (Masni and Wasli, 2019).

The deficiency of N, P, and K fertilizers disrupts various physiological and biochemical processes in crop plants and, therefore, becomes a limiting factor for crop production (Zorb *et al*., 2014). Fertilizer availability and its high cost are the primary constraints in rice production. Factors contributing to the scarcity of fertilizers include farmers' heavy reliance on inorganic fertilizers, land expansion, and the global political situation. Overreliance on mineral fertilizers can decline by exploring the crop genotypes that can adapt to nutrient deficiencies and serve as a potential strategy to develop nutrient-deficiency-tolerant crop genotypes (Francis *et al*., 2023).

Developing new high-yielding rice varieties that are adaptive to environments with low fertilizer inputs offers a promising solution for enhancing production efficiency amidst fluctuating fertilizer prices and availability. These adaptive varieties must undergo testing to assess their genetic potential and adaptability to varying environmental conditions. Such adaptation tests are crucial for identifying genotype-by-environment (G × E) interactions and determining yield stability of different genotypes. Rice varieties that exhibit minimal G × E effects have the potential to achieve consistent yields across diverse environments (Biswash and Haque, 2015). Therefore, it is necessary to evaluate the impact of G × E interactions on yield and agronomic traits of rice genotypes under optimal and suboptimal conditions, with varying fertilizer doses.

For effective selection results, the use of selection methods that consider various traits is appropriate and suitable. Additionally, assigning weights to particular traits ensures that the selected genotypes are more optimal (Anshori *et al*., 2022). The multi-trait genotype-ideotype distance index (MGIDI) is a quantitative measure that can apply to select promising genotypes based on multiple evaluated characteristics (Olivoto and Nardino, 2021). Plant breeding can proceed effectively and efficiently by evaluating and selecting rice genotypes under low-fertilizer stress conditions to identify those with optimal yield potentials. Evaluating and selecting genotypes that can thrive in such environments is essential. Tolerance indices are particularly helpful in identifying rice genotypes with solid resistance to low-fertilizer stress. Some commonly used tolerance indices include the tolerance index (TOL), harmonic mean (HM), mean productivity (MP), geometric mean productivity (GMP), stress tolerance index (STI), and stress susceptibility index (SSI). The following research aimed to study the genetic makeup and selection procedure to identify the tolerant rice genotypes in minimum fertilizer conditions.

MATERIALS AND METHODS

Breeding material and experimental site

The breeding material used in both environments (optimum and minimum fertilization) consisted of 106 rice lines obtained from the F_5 generation of five populations, viz., IPB198 (G1-G41), IPB199 (G42-G47), IPB200 (G48-G71), IPB201 (G72-

G91), IPB202 (G92-G98), and IPB203 (G99-G106). Likewise, check genotypes comprised five cultivars, i.e., Ciherang, Inpari 32, IPB 12S, IPB 14S, and IPB 15S. The checks' inclusion solely facilitated the statistical adjustment within the augmented design framework, serving as reference entries required for model calibration and variance estimation. The latest research work transpired at the IPB University Experimental Station, Bogor, West Java, Indonesia (6°33′ S, 106°43′ E, 201 masl). The soil type was latosol, and before the different treatments, the soil condition showed nutrient contents in the topsoil were pH (4.87–4.96), N-total (0.15%–0.22%), P_2O_5 P-available (1.96–6.41 ppm), exchangeable cation composition (1.39–1.46 cmol Mg/kg), and exchangeable K/kg (0.09–0.22 cmol). The conducted study was in a single season and with two different environmental conditions. The experiments began from August 2022 to January 2023, with seed sowing conducted in August 2022, rice seedling transplanting in September 2022, and harvesting in January 2023. The average rainfall, temperature, and relative humidity were 337.7 mm per month, 26 °C, and 85.5%, respectively.

Experimental design and procedure

The research project execution used the augmented randomized complete block design methodology. This methodology entails repetition for each check cultivar and without repetition for the tested lines. The number of replications, when calculating, used the following equation (Petersen, 1994):

$$r \geq \frac{10}{c-1} + 1$$

Where r is the number of replicates, and c denotes the number of comparisons.

Based on the above equation, each check cultivar acquired five replications, with the evaluated lines planted in five blocks. The planting of 15-day-old rice seedlings had a distance of 25 cm × 25 cm, and each tested line occupied a single row of 35 plants. The tested genotypes' planting in two different environments represented two different dose levels of fertilizers (Dou *et al*., 2021). In the optimal environment, the fertilizer doses utilized were 200 kg ha^{-1} urea (46% N), 150 kg ha^{-1} TSP (36% P_2O_5), and 100 kg ha^{-1} KCl (60% K_2O). In contrast, with the minimum fertilizer environment, the doses utilized were 50 kg ha^{-1} urea, 50 kg ha^{-1} TSP, and 50 kg ha^{-1} KCl. Fertilizer application proceeded in three stages. The first application ensued one week after planting (WAP); the second application continued three WAP; and the third application succeeded in implementation seven WAP. Fertilizer dosages for each application interval are available in Table 1. The management of pests and diseases and weed control took place optimally.

Observations and statistical analysis

Observations occurred on the agronomic and yield components by sampling five plants of each line. The traits observed were plant height, the total number of tillers, the number of productive tillers, panicle length, flowering, and harvesting age. Yield-related traits

Table 1. Fertilizer dosages for each application interval.

Environment	Application 1 (WAP)	Application 2 (WAP)	Application 3 (WAP)	Total Dosage
Environment 1	50 kg ha^{-1} Urea	100 kg ha^{-1} Urea	50 kg ha^{-1} Urea	200 kg ha^{-1} Urea
(Optimum	150 kg ha^{-1} TSP	0 kg ha^{-1} TSP	0 kg ha^{-1} TSP	150 kg ha^{-1} TSP
Fertilizer)	50 kg ha^{-1} KCl	0 kg ha^{-1} KCl	50 kg ha^{-1} KCl	100 kg ha^{-1} KCL
Environment 2	0 kg ha^{-1} Urea	50 kg ha^{-1} Urea	0 kg ha^{-1} Urea	50 kg ha^{-1} Urea
(Minimum	50 kg ha^{-1} TSP	0 kg ha^{-1} TSP	0 kg ha^{-1} TSP	50 kg ha^{-1} TSP
Fertilizer)	50 kg ha^{-1} KCl	0 kg ha^{-1} KCl	0 kg ha^{-1} KCl	50 kg ha^{-1} KCl

WAP= weeks after transplanting)

comprised the total number of grains per panicle, the number of filled and unfilled grains per panicle, 1000-grain weight, and productivity. The latter's measurement employed the following formula:

$$Y = \frac{\left(\frac{10000}{PS} \text{ x } GW\right) \text{x} \left(\frac{100-GM}{100-14}\right)}{1000}$$

Where Y is productivity, PS is plot size (the number of plants per row), GW is grain weight, and GM is the grain moisture content.

The data adjustment followed Petersen (1994) before further analysis. The adjusted data's subsequent employment to analyze the selected genotypes used the multiple trait genotype-ideotype distance index (MGIDI) (Olivoto and Nardino, 2021). The MGIDI method is a selection technique that utilizes multiple traits. In this study, MGIDI analysis continued using R version 4.4.1 software. Furthermore, the heritability values' assessment engaged the adjusted data, with the heritability value criteria determined based on Stansfield (1991), which classifies as high ($h^2 > 0.5$), medium ($0.2 < h^2 < 0.5$), and low ($h^2 < 0.2$).

$$h^2_{bs} = \frac{\sigma_g^2}{\sigma_p^2}$$

Where h^2_{bs} is the broad-sense heritability, σ_g^2 is the genetic variance, and σ_p^2 is the phenotypic variance. The genetic advance calculation is as follows:

$$GA = h^2_{bs} \times S$$

Where GA is the genetic advance, h^2_{bs} is the broad-sense heritability, and S is the selection differential. The genetic advance as a percentage of the mean reached the calculation as follows:

$$GAM = \frac{GA}{\bar{X}} \times 100\%$$

Where GAM is the genetic advance as a percentage of the mean, GA is the genetic advance, and $\bar{X}$ is the mean. Several parameters of stress indices, including tolerance index (TOL) (Rosielle and Hamblin, 1981), stress susceptibility index (SSI) (Fischer and Maurer, 1978), stress tolerance index (STI) (Fernandez, 1992), mean productivity (MP) (Schneider *et al*., 1997), harmonic mean (HM) (Fernandez, 1992), and geometric mean productivity (GMP) (Schneider *et al*., 1997), underwent calculations with the following formulas:

$$TOL = Y_p - Y_s$$

$$SSI = \frac{1-\frac{Y_s}{Y_p}}{1-\frac{\bar{Y}_s}{\bar{Y}_p}}$$

$$STI = \frac{Y_p \times Y_s}{(\bar{Y}_s)^2}$$

$$MP = \frac{(Y_p + Y_s)}{2}$$

$$HM = \frac{2(Y_p \times Y_s)}{(Y_p + Y_s)}$$

$$GMP = (Y_p \times Y_s)^{0,5}$$

Where Y_p is the mean yield under optimum conditions, Y_s is the mean yield under minimum conditions, $\bar{Y}_p$ is the grand mean yield under optimum conditions, and $\bar{Y}_s$ is the grand mean yield under minimum conditions.

RESULTS

The combined analysis of variance

The mean differences received influences from genotype-by-environment interactions under optimum and minimum fertilizer conditions for plant height, the total number of tillers, the number of productive tillers, panicle length, the number of filled grains, and productivity (Table 2). The analysis of variance showed the G × E interaction had a significant ($p < 0.01$) impact on plant height, the total number of tillers, the

Table 2. Combined analysis of variance for various traits under optimum and minimum fertilizer environments.

Traits	MS E	MS C	MS G	MS G × E	CV (%)	LSD$_{0.05}$
Plant height	449.55^{**}	18.27^{ns}	94.99^{**}	36.63^{**}	4.25	9.27
Total number of tillers	540.87^{**}	4.91^{ns}	10.50^{**}	7.61^{**}	12.72	3.77
Number of productive tillers	558.74^{**}	5.77^{ns}	10.93^{**}	7.99^{**}	13.69	3.81
Panicle length	32.25^{**}	2.4^{ns}	11.57^{**}	4.78^{*}	6.44	3.50
Total number of grains	9498.13^{**}	700.75^{ns}	1605.66^{*}	853.22^{ns}	19.08	63.73
Number of filled grains	13454.20^{**}	726.22^{*}	970.63^{**}	684.67^{**}	17.02	38.99
Number of unfilled grains	4585.18^{*}	282.97^{ns}	386.21^{ns}	346.97^{ns}	24.85	53.98
1000-grain weight	36.70^{**}	4.05^{ns}	4.70^{ns}	3.03^{ns}	8.34	4.47
Flowering age	0.63^{ns}	7.63^{ns}	5.81^{ns}	4.25^{ns}	2.55	4.25
Harvesting age	110.82^{**}	12.69^{ns}	9.03^{ns}	5.97^{ns}	2.42	5.71
Productivity	82.58^{**}	4.37^{**}	2.90^{**}	1.47^{**}	14.84	1.68

E = Environments, C = Blocks, G = Genotypes, CV = Coefficient of variation, LSD = Least significant difference, **** =** Significant at 1% level, *** =** Significant at 5% level, ns = Nonsignificant.

number of productive tillers, the number of filled grains, and productivity. Likewise, it had a significant ($p < 0.05$) effect on panicle length. The rice genotypes significantly affected plant height, the total number of tillers, the number of productive tillers, panicle length, the total number of grains, the number of filled grains, and productivity. The effect of environmental differences was evident on several traits, except for flowering age.

Genotypes selection based on MGIDI

The MGIDI selection progressed under optimal (Figure 1a) and minimum fertilizer conditions (Figure 2a). Under optimum and minimum fertilizer environments, the selection of MGIDI was dependent on several rice traits. These are plant height, the number of productive tillers, panicle length, the total grain number, the number of filled grains, 1000-grain weight, productivity, and flowering age. In the optimum environment, the rice genotypes selected based on 25% MGIDI selection are G85, G66, G11, G63, G103, G69, G57, G98, G12, G37, G16, G74, G55, G61, G26, G4, G48, G50, G8, G90, G88, G101, G32, G76, G97, and G13. Under a minimum fertilizer environment, the selected genotypes based on 25% MGIDI selection included G26, G63, G22, G20, G36, G21, G13, G23, G32, G62, G31, G65, G30, G66, G37, G25, G59, G46, G24, G73, G60, G33, G27, G29, G70, and G50. The strength and weakness of each MGIDI selection are available in Figures 1b and 2b. In an optimal environment, the factor analysis (FA) had four: FA1 (the total number of grains and the number of filled grains); FA2 (plant height and panicle length); FA3 (1000-grain weight and productivity); and FA4 (the number of productive tillers and flowering age). Meanwhile, in a minimum environment, three FAs occurred: FA1 (the total number of grains and the number of filled grains), FA2 (plant height, panicle length, and 1000-grain weight), and FA3 (the number of productive tillers, productivity, and flowering age).

Genetic parameters

The categories for heritability values consisted of low to high under optimum and medium to high in minimum fertilizer environments (Table 3). The heritability range was low to high (0.158–0.735) for the optimum environment, while it was medium to high (0.355–0.730) under the minimum fertilizer environment. In the optimum environment, the highest heritability value was notable for the number of productive tillers at 0.735. In contrast, the highest heritability appeared for plant height at 0.730 in the minimum environment. This indicates these traits gained more influence from genetic variation. In the optimum environment, the genetic advance values ranged from 0.121 to 10.869 for various traits;

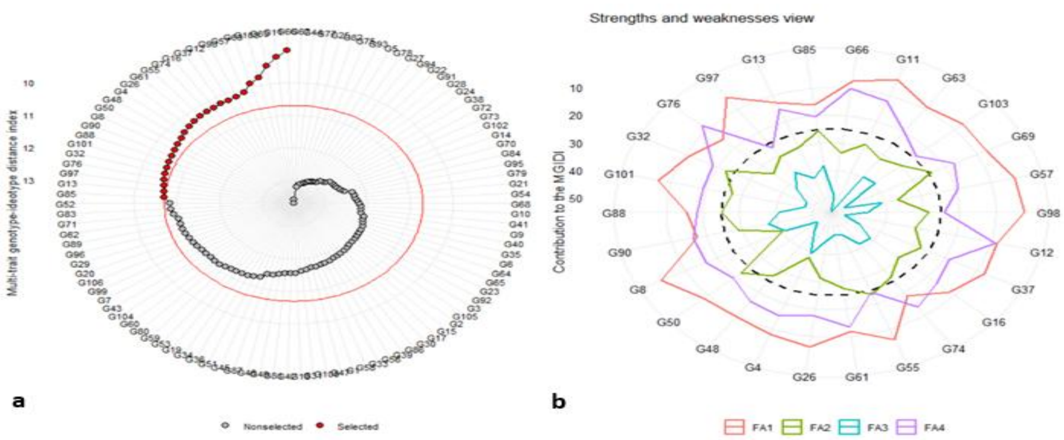

Figure 1. a) Ranked and selected rice lines through MGIDI considering 25% selection intensity; b) strength and weakness view of the selected rice genotypes under optimal fertilizer conditions.

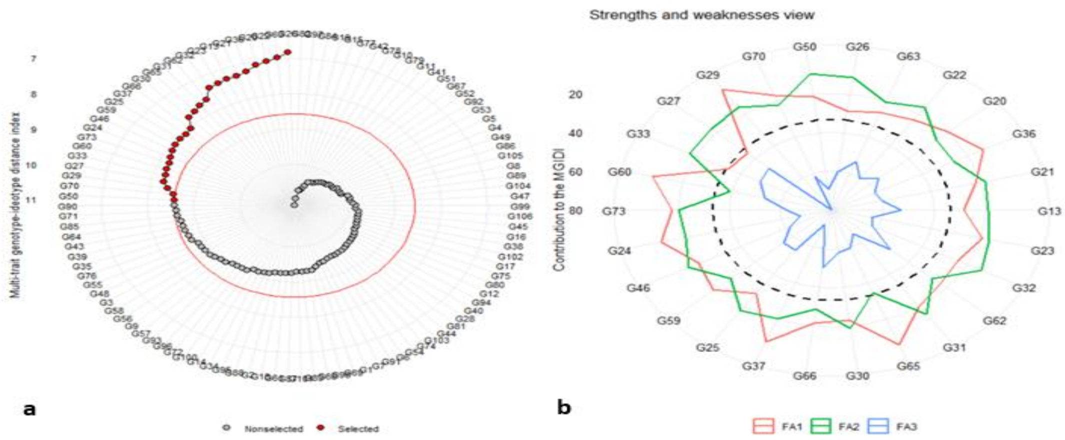

Figure 2. a) Ranked and selected lines through MGIDI considering 25% selection intensity, b) strength and weakness view of selected rice genotypes under minimum fertilizer conditions.

Table 3. Genetic parameters of various traits under optimum and minimum fertilizer environments.

Traits	Optimum fertilizer			Minimum fertilizer		
	h^2_{bs}	GA	GAM	h^2_{bs}	GA	GAM
Plant height	0.694	2.173	1.988	0.730	2.798	2.626
Total number of tillers	0.707	1.492	8.822	0.608	0.797	6.073
Number of productive tillers	0.735	1.947	12.700	0.605	1.271	10.411
Panicle length	0.646	1.259	4.623	0.534	1.036	3.910
Total number of grains	0.559	6.849	3.989	0.432	7.473	4.704
Number of filled grains	0.682	10.869	8.981	0.355	1.927	1.823
Number of unfilled grains	0.158	1.478	3.343	0.400	0.982	1.846
1000-grain weight	0.468	0.651	2.488	0.436	0.515	1.912
Flowering age	0.505	0.141	0.172	0.674	0.674	0.817
Harvesting age	0.564	0.121	0.103	0.533	0.545	0.469
Productivity	0.725	1.160	18.680	0.628	0.659	13.158

h^2_{bs} = Broad-sense heritability, GA = Genetic advance, GAM = Predicted genetic advance as percentage of mean.

in the minimum environment, it ranged from 0.515 to 7.473. The predicted genetic advance as a percentage of the mean under optimum environment ranged from 0.103 to 18.680, while under the minimum fertilizer environment, it ranged from 0.469 to 13.158. In the optimum fertilizer environment, several traits showed higher values of heritability, GA, and GAM than in the minimum fertilizer environment. These are the total number of tillers, the number of productive tillers, panicle length, the total number of grains, the number of filled grains, 1000-grain weight, harvesting age, and productivity. However, other traits exhibited higher values of h^2_{bs}, GA, and GAM under the minimum fertilizer environment.

Tolerance indices

Various analyses can be helpful to assess the tolerance of rice genotypes to low fertilizer conditions, including TOL, SSI, STI, MP, HM, and GMP (Table 4). Choosing the tolerance indices STI, MP, HM, and GMP came from the highest- to lowest-performing rice genotypes. In contrast, TOL and SSI selection resulted in the lowest- to highest-performing genotypes in an ascending order. The correlation analysis (Figure 3) showed HM (r=0.92), GMP (r=0.89), STI (r=0.88), and MP (r=0.84) had a strong positive correlation with yield in stress (Ys) and also a significant correlation with yield under non-stress (Yp) conditions, indicating their effectiveness as selection criteria for identifying superior genotypes. Conversely, TOL and SSI exhibited strong negative correlations with Ys, confirming that genotypes with high values for these indices tend to be more susceptible to stress and are less reliable for selection.

G27 exhibited the lowest TOL (-3.6) and SSI (-4.1) values among all the lines tested, indicating this line had higher productivity under the minimum fertilizer environment than in the optimum environment. G66 had the highest values among all the lines tested, with an STI of 1.9, MP of 8.6, HM of 8.3, and GMP of 8.5. It is indicative of G66 expressing the maximum productivity within the optimum environment while maintaining relatively high-yield performances compared with other genotypes in the minimum fertilizer environment.

DISCUSSION

The genotype-by-environment interaction effects indicated a genotype that performs well in one environment might not necessarily perform well in another, and ultimately the rankings of the rice genotypes for specific traits may vary across different testing environments (Jayaningsih *et al*., 2019). Genotype and environment (optimum and minimum fertilizer) interactions affected yield characters. The results showed genotypes with a high-yield potential in the environment with fertilizer only sometimes had higher yields than other genotypes with minimum fertilizer. In this study, the interaction between genotype and environment (G × E) modified productivity. In other words, variations in fertilizer application resulted in differences in productivity.

The different fertilizer environments did not change the flowering age of the genotypes, as well as the genotypes and their interactions. However, it is worth noting that out of the three sources of variance, only the environments significantly influenced the harvest age. Ye *et al*. (2019) reported the effects of N, P, and K fertilizers on flowering time in rice. Their findings revealed that increased nitrogen dose significantly delayed the flowering by 1–4 days, while the simultaneous application of P and K had no significant impact on flowering time. Another study revealed decreasing the dose of N fertilizer in rice significantly accelerated the flowering period (Lin and Tsay, 2017).

The multi-trait genotype-ideotype distance index (MGIDI) method, utilized for selecting genotypes, relied on data from a plant's characteristics (Olivoto and Nardino, 2021). This approach allows breeders to identify and select genotypes that exhibit desirable traits. The G26 and G37 lines became selections under both environmental conditions, demonstrating strong yield and agronomic performance in both optimal and suboptimal environments. Its productivity was

Table 4. The 106 rice genotypes evaluated based on TOL index and their values with low fertilizer.

Geno	YP	YS	TOL	SSI	STI	MP	HM	GMP	Geno	YP	YS	TOL	SSI	STI	MP	HM	GMP
G27	4.5	8.1	-3.6	-4.1	0.9	6.3	5.8	6.0	G90	6.5	5.8	0.7	0.5	1.0	6.2	6.2	6.2
G62	7.2	9.7	-2.5	-1.8	1.8	8.4	8.2	8.3	G44	4.1	3.4	0.7	0.9	0.4	3.8	3.8	3.8
G65	4.8	7.2	-2.4	-2.5	0.9	6.0	5.8	5.9	G79	4.9	4.2	0.7	0.7	0.5	4.5	4.5	4.5
G31	6.5	8.2	-1.8	-1.4	1.4	7.3	7.2	7.3	G9	4.8	4.1	0.8	0.8	0.5	4.4	4.4	4.4
G21	5.4	6.9	-1.5	-1.4	0.9	6.1	6.0	6.1	G87	6.5	5.7	0.8	0.6	1.0	6.1	6.1	6.1
G2	4.7	6.1	-1.5	-1.6	0.7	5.4	5.3	5.4	G93	5.5	4.6	0.8	0.8	0.7	5.1	5.0	5.0
G76	7.1	8.5	-1.4	-1.0	1.6	7.8	7.7	7.8	G94	4.3	3.4	0.8	1.0	0.4	3.9	3.8	3.8
G5	4.7	6.2	-1.4	-1.6	0.8	5.4	5.3	5.4	G88	7.0	6.1	0.9	0.6	1.1	6.6	6.5	6.6
G23	6.1	7.4	-1.3	-1.1	1.2	6.8	6.7	6.7	G89	6.2	5.3	0.9	0.7	0.8	5.8	5.7	5.7
G72	4.3	5.6	-1.2	-1.5	0.6	4.9	4.9	4.9	G63	8.3	7.4	0.9	0.6	1.6	7.8	7.8	7.8
G33	6.5	7.7	-1.2	-0.9	1.3	7.1	7.0	7.1	G7	6.3	5.3	0.9	0.8	0.9	5.8	5.8	5.8
G3	6.2	7.4	-1.2	-1.0	1.2	6.8	6.7	6.7	G20	7.2	6.2	1.0	0.7	1.2	6.7	6.7	6.7
G10	4.9	6.1	-1.2	-1.2	0.8	5.5	5.5	5.5	G91	4.7	3.7	1.1	1.1	0.5	4.2	4.1	4.2
G6	4.7	5.8	-1.1	-1.2	0.7	5.3	5.2	5.3	G102	6.0	4.9	1.1	1.0	0.7	5.4	5.4	5.4
G70	4.6	5.5	-0.9	-1.0	0.7	5.1	5.0	5.1	G22	6.7	5.5	1.2	0.9	1.0	6.1	6.0	6.1
G26	8.2	9.1	-0.8	-0.5	1.9	8.7	8.6	8.7	G39	5.5	4.3	1.3	1.2	0.6	4.9	4.8	4.9
G95	4.6	5.3	-0.7	-0.8	0.6	5.0	5.0	5.0	G43	6.5	5.0	1.5	1.2	0.8	5.8	5.7	5.7
G35	4.9	5.6	-0.7	-0.7	0.7	5.3	5.2	5.2	G57	7.4	5.8	1.6	1.1	1.1	6.6	6.5	6.5
G30	4.5	5.2	-0.6	-0.7	0.6	4.9	4.8	4.8	G40	5.3	3.7	1.6	1.6	0.5	4.5	4.4	4.5
G58	6.3	6.9	-0.6	-0.5	1.1	6.6	6.6	6.6	G81	6.7	5.0	1.7	1.3	0.9	5.8	5.7	5.8
G1	5.4	5.9	-0.5	-0.5	0.8	5.7	5.7	5.7	G17	5.3	3.6	1.8	1.7	0.5	4.5	4.3	4.4
G84	5.7	6.1	-0.4	-0.3	0.9	5.9	5.9	5.9	G61	6.5	4.7	1.8	1.4	0.8	5.6	5.4	5.5
G37	7.3	7.6	-0.4	-0.3	1.4	7.4	7.4	7.4	G13	7.3	5.4	1.8	1.3	1.0	6.3	6.2	6.3
G69	6.9	7.3	-0.4	-0.3	1.3	7.1	7.1	7.1	G78	5.4	3.5	1.9	1.8	0.5	4.5	4.3	4.4
G24	4.1	4.5	-0.3	-0.4	0.5	4.3	4.3	4.3	G55	7.0	5.0	2.0	1.5	0.9	6.0	5.9	5.9
G75	4.1	4.4	-0.3	-0.4	0.5	4.2	4.2	4.2	G92	5.1	3.1	2.0	2.0	0.4	4.1	3.9	4.0
G38	4.0	4.1	-0.2	-0.2	0.4	4.1	4.1	4.1	G100	5.2	3.1	2.1	2.0	0.4	4.1	3.9	4.0
G73	5.2	5.3	-0.1	-0.1	0.7	5.3	5.3	5.3	G71	6.1	4.0	2.1	1.8	0.6	5.0	4.8	4.9
G18	6.7	6.8	-0.1	-0.1	1.2	6.7	6.7	6.7	G16	8.2	6.1	2.1	1.3	1.3	7.1	7.0	7.1
G77	4.2	4.3	-0.1	-0.1	0.5	4.3	4.3	4.3	G80	6.4	4.3	2.1	1.7	0.7	5.4	5.2	5.3
G59	6.6	6.6	-0.1	-0.1	1.1	6.6	6.6	6.6	G105	5.7	3.5	2.1	1.9	0.5	4.6	4.4	4.5
G32	7.6	7.6	-0.1	0.0	1.5	7.6	7.6	7.6	G11	7.9	5.7	2.2	1.4	1.1	6.8	6.6	6.7
G67	4.4	4.3	0.1	0.2	0.5	4.3	4.3	4.3	G83	7.5	5.3	2.2	1.5	1.0	6.4	6.3	6.3
G14	5.9	5.7	0.2	0.2	0.9	5.8	5.8	5.8	G86	6.2	4.0	2.2	1.8	0.6	5.1	4.8	5.0
G25	4.6	4.4	0.2	0.3	0.5	4.5	4.5	4.5	G34	4.9	2.7	2.2	2.3	0.3	3.8	3.5	3.6
G60	6.0	5.7	0.3	0.3	0.9	5.9	5.9	5.9	G12	7.4	5.1	2.3	1.6	1.0	6.2	6.0	6.1
G85	8.0	7.6	0.4	0.3	1.6	7.8	7.8	7.8	G103	7.4	5.0	2.4	1.6	1.0	6.2	6.0	6.1
G28	5.1	4.7	0.4	0.4	0.6	4.9	4.9	4.9	G8	6.9	4.5	2.4	1.8	0.8	5.7	5.5	5.6
G36	7.6	7.1	0.4	0.3	1.4	7.3	7.3	7.3	G48	6.3	4.0	2.4	1.9	0.7	5.2	4.9	5.0
G56	5.5	5.1	0.5	0.4	0.7	5.3	5.3	5.3	G29	8.5	5.9	2.6	1.6	1.3	7.2	7.0	7.1
G46	5.9	5.4	0.5	0.4	0.8	5.7	5.7	5.7	G41	5.1	2.2	2.9	2.9	0.3	3.7	3.1	3.4
G64	6.4	5.9	0.5	0.4	1.0	6.1	6.1	6.1	G15	5.9	3.0	2.9	2.5	0.5	4.4	4.0	4.2
G68	5.7	5.2	0.5	0.5	0.8	5.5	5.5	5.5	G50	7.1	4.1	3.0	2.2	0.8	5.6	5.2	5.4
G90	6.5	5.8	0.7	0.5	1.0	6.2	6.2	6.2	G19	6.5	3.6	3.0	2.3	0.6	5.1	4.6	4.8
G44	4.1	3.4	0.7	0.9	0.4	3.8	3.8	3.8	G106	6.5	3.5	3.0	2.4	0.6	5.0	4.5	4.7
G79	4.9	4.2	0.7	0.7	0.5	4.5	4.5	4.5	G99	6.6	3.5	3.0	2.4	0.6	5.0	4.6	4.8
G9	4.8	4.1	0.8	0.8	0.5	4.4	4.4	4.4	G82	7.5	4.4	3.1	2.1	0.8	5.9	5.5	5.7
G87	6.5	5.7	0.8	0.6	1.0	6.1	6.1	6.1	G66	10.2	7.0	3.2	1.6	1.9	8.6	8.3	8.5
G93	5.5	4.6	0.8	0.8	0.7	5.1	5.0	5.0	G42	6.3	3.1	3.2	2.6	0.5	4.7	4.1	4.4
G94	4.3	3.4	0.8	1.0	0.4	3.9	3.8	3.8	G104	7.6	4.3	3.4	2.3	0.8	6.0	5.5	5.7
G88	7.0	6.1	0.9	0.6	1.1	6.6	6.5	6.6	G96	8.2	4.6	3.6	2.3	1.0	6.4	5.9	6.1
G89	6.2	5.3	0.9	0.7	0.8	5.8	5.7	5.7	G4	8.4	4.8	3.6	2.2	1.0	6.6	6.1	6.3
G63	8.3	7.4	0.9	0.6	1.6	7.8	7.8	7.8	G101	6.7	2.9	3.7	2.9	0.5	4.8	4.1	4.4
G7	6.3	5.3	0.9	0.8	0.9	5.8	5.8	5.8	G45	8.2	4.4	3.8	2.4	0.9	6.3	5.8	6.0
G20	7.2	6.2	1.0	0.7	1.2	6.7	6.7	6.7	G51	7.7	3.6	4.2	2.8	0.7	5.6	4.9	5.2
G91	4.7	3.7	1.1	1.1	0.5	4.2	4.1	4.2	G49	6.4	1.8	4.6	3.7	0.3	4.1	2.8	3.4
G102	6.0	4.9	1.1	1.0	0.7	5.4	5.4	5.4	G54	7.0	2.2	4.8	3.5	0.4	4.6	3.3	3.9
G22	6.7	5.5	1.2	0.9	1.0	6.1	6.0	6.1	G52	6.5	1.6	4.9	3.9	0.3	4.0	2.5	3.2
G39	5.5	4.3	1.3	1.2	0.6	4.9	4.8	4.9	G47	6.3	1.4	4.9	4.0	0.2	3.9	2.3	3.0
G43	6.5	5.0	1.5	1.2	0.8	5.8	5.7	5.7	G97	7.3	2.2	5.1	3.6	0.4	4.7	3.3	4.0
G57	7.4	5.8	1.6	1.1	1.1	6.6	6.5	6.5	G53	7.4	1.8	5.6	3.9	0.3	4.6	2.9	3.6
G40	5.3	3.7	1.6	1.6	0.5	4.5	4.4	4.5	G98	8.9	3.1	5.8	3.4	0.7	6.0	4.6	5.2
G81	6.7	5.0	1.7	1.3	0.9	5.8	5.7	5.8	G74	8.4	1.8	6.6	4.0	0.4	5.1	3.0	3.9

Yp = Yield under optimum conditions, Ys = Yield under minimum fertilizer conditions, TOL = Tolerance index, SSI = Stress susceptibility, STI = Stress tolerance index, MP = Mean productivity, HM = Harmonic mean, and GMP = Geometric mean productivity.

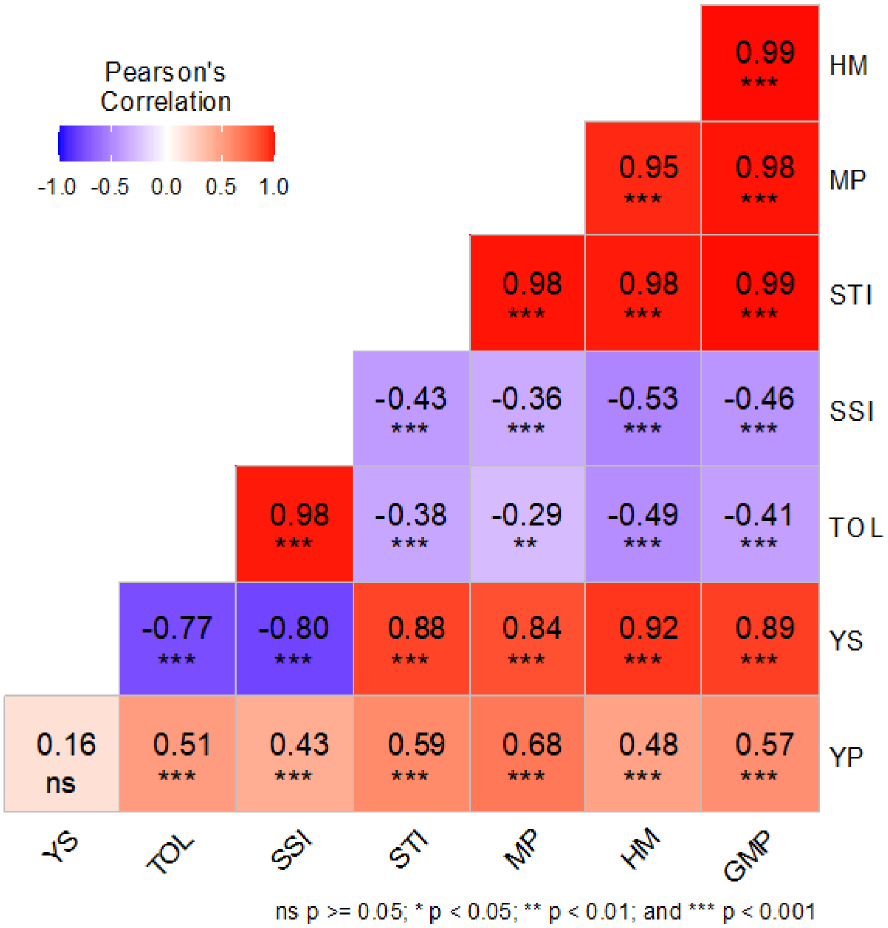

Figure 3. Pearson's correlation between tolerance indices and yield.

the highest under both conditions. In addition to choices across the two environments, both lines were also options based on all tolerance indices, implying their consistent stability and adaptability under varying fertilization levels. The MGIDI method has the advantage of mapping the selected genotypes in factor analysis. This enables the identification of each line's strength and weakness. The said method proved particularly useful in selecting genotypes under abiotic stress and mega-environments using several traits (Nardino *et al.*, 2016; Singamsetti *et al.*, 2023).

The MGIDI tool enables the breeders to evaluate the strengths and weaknesses of the different genotypes. The genotype's strength and weakness bore assessment using factor analysis (FA) in the MGIDI strength and weakness plot. The outer corner of the factor analysis polygon close to a genotype indicates the strength of the genotype in that specific analysis. In contrast, the factor analysis polygon away from the genotype implies weakness in that analysis. For example, in the optimal environment, the line G66 has strengths in FA1 (the total number of grains and the number of filled grains) but has weaknesses in FA3 (1000-grain weight and productivity). Meanwhile, in the minimum environment, the line G66 has strengths in FA1 (the total number of grains and the number of filled grains) but has weaknesses in FA3 (the number of productive tillers, productivity, and flowering age). This information can be beneficial to evaluate the strength and limitations of a character in a genotype (Zendrato *et al.*, 2024).

The selection success relies on several factors, such as knowledge of trait inheritance, the heritability value, the predicted genetic gain, and the percentage of predicted genetic gain. High heritability values indicate that the characters appearing in the plant obtained significant influences from genetic variations rather than environmental variations (Abebe *et al*., 2017). In this study, the optimum environment exhibited higher heritability values than the minimum environment. This suggests that, under optimum conditions, traits received stronger influences from genetic variation. Adequately and appropriately using fertilizers can create more stable environmental conditions, allowing genetic traits' expression more optimally. Optimum fertilizer environmental conditions can produce higher heritability values than the minimum environment, where environmental conditions with low fertilizer result in more significant environmental variation, and the use of appropriate fertilizers affects the environmental conditions (Al-Naggar *et al*., 2022). Characters with high heritability values can be favorable as selection criteria, while those with low heritability values should not apply for selection (Regmi *et al*., 2021). In this study, under optimal conditions, all traits, except the number of unfilled grains and 1000-grain weight, exhibit high heritability. Meanwhile, under minimum conditions, all traits display high heritability, except the total number of grains, the number of filled and unfilled grains, and 1000-grain weight. The predicted genetic gain is an essential indicator to assess the selection progress for relevant genotypes and traits. Heritability has a direct relation to the predicted genetic gain and predicted genetic advance as a percentage of the mean (Yunandra *et al*., 2017).

Selection of genotypes based on heritability values and tolerance indices is an important method used in field crops for selecting genotypes suitable for stressed environments in accordance with productivity under both optimum and minimum fertilizer conditions (Yemata and Bekele, 2024). The selected rice genotypes showed the lowest values for TOL and SSI, indicating better stress tolerance, while simultaneously showing the highest values for STI, GMP, HM, and MP, which reflect both high-yield potential and stability across environments. The correlation between tolerance indices can provide insight into which indices have relations with Yp and Ys (Figure 3). The tolerance indices that positively correlate with Yp and Ys have become the most effective in identifying the genotypes in stressful conditions (Sun *et al.,* 2023). In this study, the GMP, MP, STI, and HM demonstrated positive correlations with Yp and Ys, implying their potential in identifying the genotypes under stressful conditions (Yemata and Bekele, 2024).

CONCLUSIONS

Environments, genotypes, and genotype-by-environment interactions were significant for several agronomic and yield traits, particularly productivity trait. For productivity-related traits, the optimal environment resulted in higher values for heritability and genetic advance. The tolerance indices TOL, SSI, STI, HM, MP, and GMP showed positive correlations with grain yield (Yp). Based on three selection methods, the promising rice genotypes identified were G26 and G37, while G26 and G66 were selected using the tolerance parameters.

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REFERENCES

Abebe T, Alamerew S, Tulu L (2017). Genetic variability, heritability and genetic advance for yield and its related traits in rainfed lowland rice (*Oryza sativa* L.) genotypes at Fogera and Pawe, Ethiopia. *Adv. Crop Sci.*

Tech. 5(2): 272. doi: 10.4172/2329-8863.1000272.

Al-Naggar AMM, Atta MM, El-Moneim MLABD, Al-Metwally MS (2022). Heritability, genetic advance and trait interrelationships of *Chenopodium quinoa* under low, medium, and high n organic and mineral fertilizer conditions. *Plant Cell Biotech. Mol. Biol*. 23(5-6): 52–73.

Anisuzzaman MMA, Ali MG, Haque MM, Halder T (2016). Development of high-yielding rice varieties for favorable ecosystem with 40% higher yield than the present variety: A review paper. *Middle East J. Sci. Res*. 24(11): 3644–3653. doi: 10.5829/idosi.mejsr.2016.3644.3653.

Anshori MF, Purwoko BS, Dewi IS, Suwarno WB, Ardie SW (2022). Salinity tolerance selection of doubled-haploid rice lines based on selection index and factor analysis. *AIMS Agric. Food* 7(3): 520–535. doi: 10.3934/agrfood.2022032.

Biswash MR, Haque M (2015). Estimation of superiority of exotic hybrids of rice over check varieties in Bangladesh. *J. Agric. Environ. Sci*. 15(4): 659–663. doi: 10.5829/idosi.aejaes.2015.15.4.12581.

Dou Z, Li Y, Guo H, Chen L, Jiang J, Zhou Y, Zhang H (2021). Effects of mechanically transplanting methods and planting densities on yield and quality of Nanjing 2728 under rice-crayfish continuous production system. *Agronomy* 11(3): 488. https://doi.org/10.3390/agronomy11030488.

Fernandez GCJ (1992). Effective selection criteria for assessing plant stress tolerance. In Proceedings of the International Symposium on Adaptation of Vegetables and Other Food Crops in Temperature and Water Stress, Chapter 25, C.G. Kuo (Ed.). Tainan: Shanhua: AVRDC Publication. p. 257–270.

Fischer RA, Maurer R (1978). Drought resistance in spring wheat cultivars. I. grain yield responses. *Aust*. *J. Agric. Res*. 29: 897–912.

Francis B, Aravindakumar CT, Brewer PB, Simon S (2023). Plant nutrient stress adaptation: A prospect for fertilizer limited agriculture. *Env. Exp. Bot*. 213: 105431. https://doi.org/ 10.1016/j.envexpbot.2023.105431.

Jayaningsih ED, Suwarno WB, Nindita A, Aswidinnoor H (2019). Genotype x environment interaction on panicle morphology of heavy panicle rice genotypes (*Oryza sativa* L.). *J. Agron. Indonesia* 47(3): 240–247. https://doi.org/10.24831/jai.v47i3.26104.

Jiang W, Wang X, Xing Y, Liu X, Cui Z, Yang L (2019). Enhancing rice production by potassium management: recommended reasonable fertilization strategies in different inherent soil productivity levels for a sustainable rice production system. *Sustainability* 11(22): 1–13. https://doi.org/10.3390/su11226522.

Lin YL, Tsay YF (2017). Influence of differing nitrate and nitrogen availability on flowering control in *Arabidopsis*. *J. Exp. Bot*. 68(10): 2603–2609. https://doi.org/10.1093/jxb/erx053.

Masni Z, Wasli ME (2019). Yield performance and nutrient uptake of red rice variety (MRM 16) at different NPK fertilizer rates. *Int. J. Agron*. 2019: 1–6. https://doi.org/10.1155/2019/5134358.

Nardino M, Souza VQD, Baretta D, Konflanz VA, Carvalho IR, Follmann DN, Caron BO (2016). Association of secondary traits with yield in maize F1's. *Cienc. Rural.* 46: 776–782. doi: 10.1590/0103-8478cr20150253.

Olivoto T, Nardino M (2021). MGIDI: Toward an effective multivariate selection in biological experiments. *Bioinformatics* 37: 1383–1389. https://doi:10.1093/bioinformatics/btaa981

Petersen RG (1994). Agricultural Field Experiments: Design and Analysis. CRC Press.

Regmi S, Poudel B, Ojha BR, Kharel R, Joshi P, Khanal S, Kandel BP (2021). Estimation of genetic parameters of different wheat genotype traits in Chitwan, Nepal. *Int. J. Agron*. 2021: 1–10. https://doi.org/10.1155/2021/6651325.

Rosielle AA, Hamblin J (1981). Theoretical aspects of selection for yield in stress and non-stress environment. *Crop Sci.* 21: 943–946. https://doi:10.2135/cropsci1981.0011183X002100060033x.

Schneider KA, Serna RR, Perez FI, Enriquez BC, Gallegos JAA, Vallejo PR, Wassimi N, Kelly JD (1997). Improving common bean performance under drought stress. *Crop Sci*. 37(1):43-50. doi: https://doi.org/10.2135/cropsci1997.0011183X003700010007x .

Shahbandeh M (2022). Rice: Global Rice Consumption 2021/22 by Country. Statista Publisher, Hamburg.

Singamsetti A, Zaidi PH, Seetharam K, Vinayan MT, Olivoto T, Mahato A, Madankar K, Kumar M, Shikha K (2023). Genetic gains in tropical maize hybrids across moisture regimes with multi-trait-based index selection. *Front. Plant Sci*. 14: 1–16. https://doi.org/10.3389/fpls.2023.1147424.

Stansfield WD (1991). Theory and Problem of Genetics. (3rd Ed.). McGraw-Hill Inc, New York.

Stellacci AM, Cristiano G, Rubino P, Lucia BD, Cazzato E (2013). Nitrogen uptake, nitrogen partitioning and N-use efficiency of container - Grown Holmoak (*Quercus ilex* L.) under different nitrogen levels and fertilizer sources. *J. Food Agric. Environ*. 11:132–137.

Sun F, Chen Q, Chen Q, Jiang M, Qu Y (2023). Yield-based drought tolerance index evaluates the drought tolerance of cotton germplasm lines in the interaction of genotype-by-environment. *Peer J*. 11: e14367. https://doi.org/10.7717/peerj.14367.

Ye T, Li Y, Zhang J, Hou W, Zhou W, Lu J, Li X (2019). Nitrogen, phosphorus, and potassium fertilization affects the flowering time of rice (*Oryza sativa* L.). *Glob. Ecol. Conserv*. 20, e00753. https://doi.org/10.1016/j.gecco.2019. e00753.

Yemata G, Bekele T (2024). Evaluation of sesame (*Sesamum indicum* L.) varieties for drought tolerance using agromorphological traits and drought tolerance indices. *Peer J*. 12: e16840. https://doi.org/10.7717/peerj.16840.

Yunandra, Syukur M, Maharijaya A (2017). Selection and selection advance of yield component character in curly and large chilli pepper crossing. *J. Agron*. *Indonesia* 45(2): 169–174. https://doi.org/10.24831/jai.v45i2.12312.

Zendrato YM, Suwarno WB, Marwiyah S (2024). Multi-trait selection of tropical maize genotypes under optimum and acidic soil conditions. *SABRAO J. Breed. Genet.* 56(1): 142–155. http://doi.org/10.54910/sabrao2024.56.1.13.

Zorb C, Senbayram M, Peiter E (2014). Potassium in agriculture-status and perspectives. *J. Plant Physiol*. 171: 656–669. https://doi.org/10.1016/j.jplph.2013.08.008.