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SELECTION OF PROMISING POTATO (*SOLANUM TUBEROSUM* L.) GENOTYPES USING THE MULTI-TRAITS GENOTYPE-IDEOTYPE DISTANCE INDEX (MGIDI)

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SUMMARY

Potato (*Solanum tuberosum* L.) has become a major global food crop. Considerable population growth, food demand, and crop quality have encouraged the use of efficient technology to identify the high-yielding genotypes. The following study aimed to estimate the variances among the quantitative traits and the correlation among measured traits, as well as to identify the high-yielding potato genotypes using the multi-traits genotype-ideotype distance index (MGIDI). Ten potato genotypes generated through gamma-ray mutation from four cultivars and two commercial check cultivars underwent evaluation at Pangalengan, West Java, Indonesia, using a randomized complete block design. The results showed potato genotypes displayed significant differences for most traits, except economic tuber weight and leaf width. Tuber weight per plot revealed a significant positive correlation with tubers per plot, tubers per plant, economic tuber weight, stem diameter, tuber diameter, and economic amount of tubers. The MGIDI analysis successfully identified the two leading potato genotypes (G7 and G11) with a selection accuracy of 89.4% and heritability ranging from 23.8% to 92.7%. The MGIDI proved to be effective in selecting superior genotypes based on several quantitative traits, providing insight for future potato breeding programs.

Keywords: Potato (*S. tuberosum* L.), mutant genotypes, morphological and yield traits, MGIDI, multi-traits, PCA, selection accuracy, heritability

Key findings: Potato (*S. tuberosum* L.) mutant genotypes showed significant differences for most traits. The selection of two high-yielding potato clones was successful through the MGIDI analysis.

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INTRODUCTION

Potato (*Solanum tuberosum* L.) is one of the most widely cultivated food crops and has the highest carbohydrate content for a staple food worldwide (Gnanasekaran and Basalingappa, 2018; Reddy *et al.*, 2018). The potato is the fourth major food crop after rice, wheat, and corn globally (Jannah *et al*., 2024). The consumption and market demand for potatoes are very high, aligning with population growth each year (Devaux *et al.*, 2021). In Indonesia, consumer demand for potatoes increases while production stagnates (Pronk *et al.,* 2025). According to the Central Bureau of Statistics of Indonesia (2025), national potato production has decreased by 230 tons in 2024 compared with the crop season in 2022. This yield decline is also inversely proportional to the demand and fulfillment of national needs, which encourages researchers to find ways to overcome this challenging issue.

Induced mutation can be useful for trait modification in existing cultivars to further explore the genotypic diversity. Mutation induction appeared to be effective in increasing genetic variability among the potato genotypes for economically important traits such as the number and weight of tubers. The induced mutation in food crop improvement programs has produced more than 3,332 cultivars from 228 food crop species (Sarsu *et al.*, 2020). Mutation has contributed to improving the quality of food crops and the widespread distribution of promising cultivars for cultivation. However, mutation often produces a limited genetic base, especially through genetic recombination and segregation (Suprasanna *et al.*, 2015; Bharath *et al*., 2024). Gamma irradiation possesses high energy capable of inducing changes in the plant's DNA (point or small mutations) without causing fatal damage to tissues if properly controlling the dosage. These mutations are random but stable, resulting in new genetic diversity that can be selected for superior traits such as disease resistance, high productivity, or environmental adaptation. This mutation is random yet stable, resulting in new genetic diversity that can be selected for superior traits such as disease resistance, high productivity, or environmental adaptation.

Carrying out mutation breeding in potato plants in Indonesia sought to broaden the genetic diversity, which has long been scarce due to the use of introduced uniform varieties being vegetatively propagated for many generations. This lack of genetic variation makes potatoes susceptible to major diseases, particularly bacterial wilt (*Ralstonia solanacearum*), which poses a serious constraint in the country's highland production centers. Through artificial mutation techniques, such as gamma irradiation, the development of new clones can succeed with superior traits, including disease resistance, high productivity, and tuber quality, suitable for both consumption and industrial use (Maulana *et al.,* 2024). Moreover, this approach is considerably more efficient, cost-effective, and regulatory-friendly than genetic engineering. Hence, it supports national efforts to develop potato varieties adaptive to climate change and strengthens seed self-sufficiency and food security in Indonesia.

The potato cultivar 'Granola' is one of the most popular cultivars in Indonesia, and 90% of the farming community use this genotype for cultivation (Kartasih and Suwandi, 2014; Saadah *et al.,* 2023). The said potato cultivar has very desirable traits, including early maturity (90 to 100 days) and the highest tuber yield (Satria, 2020), along with resistance to various potato viruses (Bonierbale *et al.,* 2020). Efforts to meet the need for potatoes have also encountered several problems, such as low production of cultivars due to low-quality seeds and the issues related to pests and diseases (Sayaka *et al.,* 2016). Therefore, the advanced breeding program is vital to overcome these issues in potato crops.

In plant breeding programs, genetic variation, heritability, genetic gain, phylogenetic relationship, and other genetic parameters play a pivotal role in the development and selection of promising genotypes (Okasa *et al.,* 2021). However, it is very difficult to determine the genotypes with a complex of several desired traits. Therefore, an appropriate method is necessary to select the superior genotypes based on multi-trait indices. The multi-trait genotype-ideotype distance index (MGIDI) has been applicable as an innovative method to identify superior genotypes with a combination of various desirable traits (Olivoto and Nardino, 2021). The MGIDI analysis in integration with quantitative traits assessment offers a comprehensive and powerful approach to investigate the hidden genetic possibilities in potato mutant genotypes (Olivoto and Nardino, 2021).

Unlike conventional selection indices prone to multicollinearity and complexity in determining economic weights (Smith, 1936; Hazel, 1943), MGIDI offers a weight-free genotype-ideotype distance-based approach and can be a more effective and stable approach for multi-trait selection (Olivoto and Nardino, 2021). The presented study may be the first investigation on the application of MGIDI to gamma-ray potato mutant genotypes in Indonesia. Therefore, this study aimed to estimate the variances due to quantitative traits in potato mutant genotypes and the correlation among the measured traits, as well as identify and select the potential potato genotypes based on all traits measured using MGIDI.

MATERIALS AND METHODS

Plant materials and experimental design

The genetic material comprised 10 potato (*S. tuberosum* L.) mutant genotypes generated through gamma-ray irradiation and induced mutation in four potato commercial cultivars, i.e., Papita, Medians, Repita, and Vega, and two check cultivars (Granola and Medians). The check cultivars are the widely cultivated varieties of the farming community in various regions of Indonesia (Table 1). The gamma irradiation performed on stem cuttings derived from plantlets at a dose of 30 Gy used a Gammacell 220 irradiator belonging to the Center for Isotope and Radiation Technology Research and Development, National Nuclear Energy Agency of Indonesia (BATAN). Then the stem cuttings underwent subculturing every four weeks on ½ MS medium supplemented with 0.5 ppm kinetin. Their maintenance occurs in an incubation room at a temperature of 18 °C–23 °C with a fluorescent light intensity of 1500 lux for 16 h per day. The experiment comprised field testing plots, as conducted in Pangalengan, West Java, Indonesia. The field test location has an altitude of 1470 meters above sea level (masl) with coordinates 7°18′41″S 107°58′37″E. The field experiment layout was in a randomized complete block design with three replications. Each experimental plot had a size of 5 m^2 × 3 m^2, with a planting distance of 25 cm × 25 cm. The weather conditions of the experimental area appear in Figure 1.

Table 1. Potato genotypes used in the experiment.

No.	Code	Initial variety	Cultivar
1	G1	M-120	Medians
2	G2	M-163	Medians
3	G3	M-59	Medians
4	G4	M-145	Medians
5	G5	P-91	Papita
6	G6	R-6	Repita
7	G7	R-8	Repita
8	G8	V-9	Vega
9	G9	R-78	Repita
10	G10	M-275	Medians
11	G11	Medians	Commercial cultivar
12	G12	Granola	Commercial cultivar

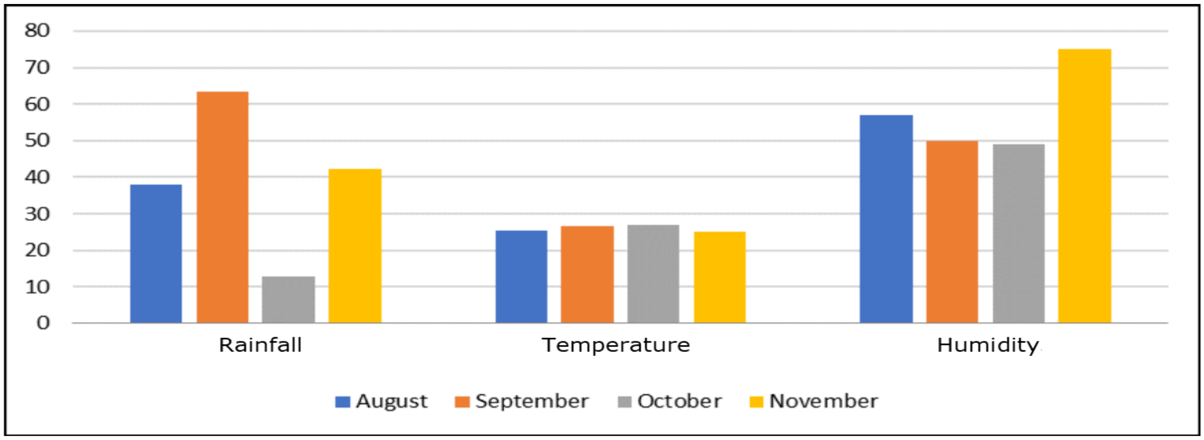

Figure 1. Weather conditions during the experiment.

Traits measurement

In potato plants, the data recorded included the morphological traits, such as leaf length, leaf width, and stem diameter, measured at 40 days after planting (DAP). Yield and yield attributes (tubers per plant and per plot, tuber length and diameter, economic weight of tubers, tuber weight per plot, and economic tuber weight) entailed measurement at harvest time at 105 DAP. The calculation of yield of each genotype used a digital scale before converting to tons/ha.

Data analysis

Analysis of variance (ANOVA) follows the equation:

$$Y_{ij} = \mu + B_j + T_i + \varepsilon_{ij}$$

Where Y_{ij} is the observed value of the i-th treatment in the j-th replication, μ is the grand mean, T_i is the effect of the i-th treatment, B_j is the effect of the j-th block/replication, and ε_{ij} is the experimental error.

The coefficient of variation (CV) calculation relied on the equation:

$$CV\ (\%) = \frac{SD_e}{\bar{Y}}\ x\ 100\%$$

Where SDe is the standard deviation of error, and Y is the grand mean of all observations.

Based on various morphological and yield-related traits, all the collected data reached analysis using R-programming software in Google Colab. The "Agricolae" package aided in performing the ANOVA for each trait separately. The use of the Pearson correlation algorithm helped construct correlation plots to evaluate the strength and direction of associations among variables. The principal component analysis (PCA), as performed, used the R packages/libraries "Ggally," "factoextra," and "ggfortify" via the Google Colab Integrated Development Environment (IDE). The visualization of PCA results engaged a two-way matrix containing the genotypes and their associated traits, focusing on the first two principal components. The usage of eigenvectors of each principal component revealed the distribution of these traits.

In the MGIDI index, the factor analysis for the selection process (Olivoto and Nardino, 2021) considered a selection intensity of approximately 15%. All the traits entailed equal weights to achieve positive desired gains. Factor analysis computation with X accounted for data correlation and reduced dimensionality. The variance components obtained from the analysis served to formulate the broad-sense heritability (h^2_b) based on the genotype means.

The MGIDI index calculation for the 12 genotypes sought to determine the best-performing genotypes by using the following formula (Olivoto and Nardino, 2021):

$$\mathrm{MGIDI}_{i} = \left[\sum_{j=i}^{f}\left(\gamma_{j=i} - \gamma_{j}\right)^{2}\right]_{0.5}$$

In this equation, γ_{ij} represents the jth score of the ith genotype, and γ_{j} represents the jth score of the ideotype. The index underwent computation for each genotype (i = 1, 2, …. t), where t was the total number of genotypes and j ranges from 1 to f, which was the number of traits. Meanwhile, j represents the traits, i represents the genotype, and f represents the number of observed traits.

The assessment of strengths and weaknesses of the genotypes under study utilized crucial assessment techniques. Measuring the contribution of the jth trait to the ith genotype employed the calculation of the proportion (ωij) of MGIDI as follows:

$$\omega_{ij} = \frac{\sqrt{D_{ij}^{2}}}{\sum_{j=i}^{f}\sqrt{D_{ij}^{2}}}$$

Where D_{ij} denotes the genetic distance between the ith genotype and the ideal genotype according to the MGIDI, with ω calculations performed using the "mgidi" and "gamem" functions available in the "metan" package (Olivoto and Lúcio, 2020) in R software. These calculations allowed us to measure how closely each genotype aligns with the ideotype for a given trait, providing valuable insights into the performance of the genotypes for the traits of interest. Low values of ω_{ij} indicate that the genotype in that particular trait provided high alignment with the ideal genotype, indicating considerable performance for that particular trait.

RESULTS

Analysis of variance

Analysis of variance showed potato (*Solanum tuberosum* L.) mutant genotypes revealed significant differences for most quantitative traits, except for economic tuber weight and leaf width (Table 2). In the estimation of genetic traits, the potato traits, tubers per plant, economic amount of tubers, tuber length, and tuber diameter showed a low coefficient of variation (CV: <10%). The tubers per plot, tuber weight per plot, leaf length, and stem diameter received a medium category recording (CV: 10%–20%), while the traits, economic tuber weight, and leaf width, emerged with the highest category (CV: >20%).

Relationship between measured traits

The correlation analysis showed several potato traits have significantly positive correlations with each other. The potato trait, tuber weight per plot, displayed a significant positive association with tubers per plot, tubers per plant, economic amount of tubers, stem diameter, tuber diameter, and economic tuber weight. The tubers per plant expressed a considerable positive correlation with the economic amount of tubers, tubers per plot, economic tuber weight, stem diameter, tuber diameter, and tuber weight per plot (Figure 2). The darker blue in each trait indicates a higher positive correlation value. The results revealed targeting genotypes that show desirable values for these traits can be useful in identifying the potato genotypes with better performance through indirect selection.

Genetic diversity in potato genotypes

Each potato trait value in the principal component (PC) showed its contribution to the diversity. The positive and negative values were useful to separate one group from another, with the positive values providing the maximum contribution to the diversity. The negative value indicates that the trait contributes but not optimally to the diversity (Razvy *et al.,* 2007). On the potato trait effects on diversity, the number of PCs listed were those PCs with an eigenvalue >1.00 (Table 3).

The potato traits, tubers per plant, tubers per plot, economic amount of tubers, tuber diameter, leaf width, and stem diameter, affected potato genotype diversity on PC1

Table 2. Analysis of variance for all traits in the potato genotypes.

Traits	Means	Significance	CV (%)
Tubers per plant (NTPG)	4.85±32.98	**	0.68
Tubers per plot (NTP)	21.59±2.197	**	10.17
Economic amount of tubers (EAT)	59.38 ±10.95	**	2.03
Tuber weight per plot (TWP) (Kg)	13.49±2.45	*	18.16
Economic tuber weight (ETW) (Kg)	1.29±0.88	Ns	27.90
Tuber length (TL)	103.40±5.07	**	4.90
Tuber diameter (TD)	135.80±3.13	***	2.30
Leaf length (LL)	7.36 ±1.46	**	19.84
Leaf width (LW)	1.57±1.10	Ns	29.99
Stem diameter (SD)	4.46 ±0.72	***	16.11

* *P* < 0.05, ** *P* < 0.01, *** *P* < 0.001. ns = nonsignificant, CV = coefficient of variations.

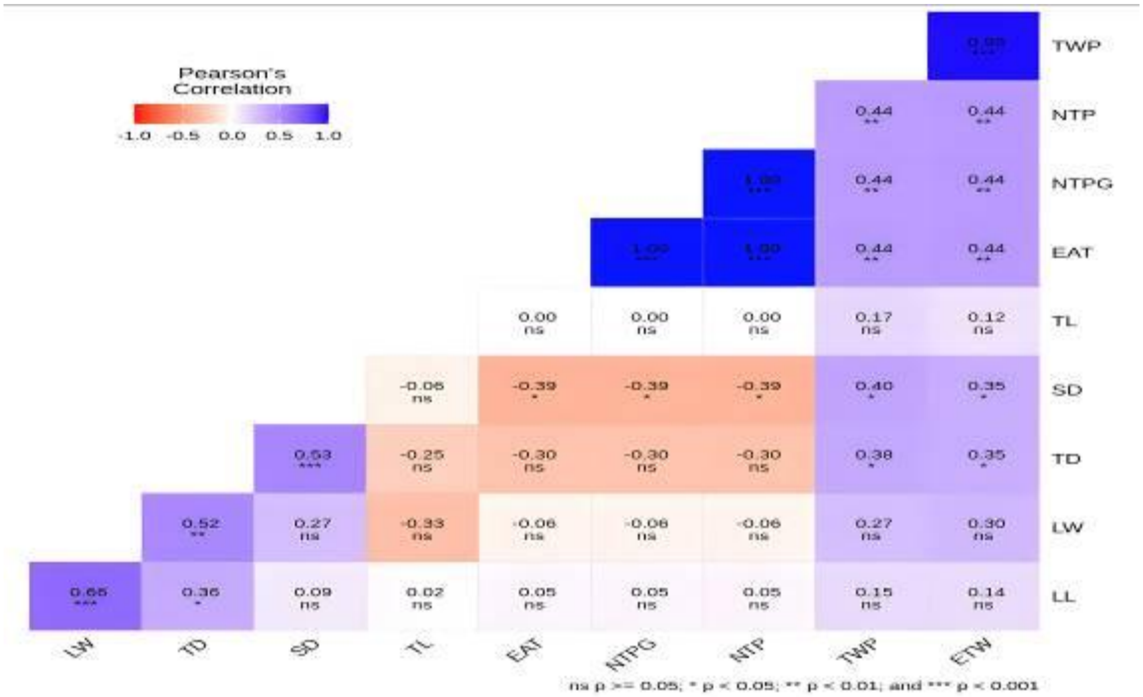

Figure 2. Visualization of Pearson's correlation coefficient matrix for quantitative traits in potato genotypes. NTPG = Tubers per plant, NTP = Tubers per plot, EAT = Economic amount of tubers, TWP = Tuber weight per plot, ETW = Economic tuber weight, TL = Tuber length, TD = Tuber diameter, LL = Leaf length, LW = Leaf width, and SD = Stem diameter.

(Table 3). The traits, tubers per plant, tubers per plot, economic amount of tubers, tuber weight per plot, and economic tuber weight influenced the genotype diversity on PC2. Meanwhile, the variables of tuber length, leaf length, and leaf width altered the genotype diversity on PC3. The traits, tubers per plant, tubers per plot, and economic amount of tubers, showed the same values on all PCs, indicating these three traits had the same potential role in genetic diversity of the potato genotypes.

Graphical representation of the first two principal components (PC 1 and PC 2) shows that 42.9% accounts for PC 1 and 29.5% for PC 2 of the total variance (Figure 3). This revealed a significant contribution of the traits across all the tested plots. The potato

Table 3. Trait values that influence the potato genotype diversity.

Traits	PC1	PC2	PC3
Tubers per plant (NTPG)	-0.80	0.54	0.23
Tubers per plot (NTP)	-0.80	0.54	0.23
Economic amount of tubers (EAT)	-0.80	0.54	0.23
Tuber weight per plot (TWP)	0.25	0.88	-0.36
Economic tuber weight (ETW)	0.23	0.91	-0.36
Tuber length (TL)	-0.35	-0.32	-0.59
Tuber diameter (TD)	0.85	0.35	0.30
Leaf length (LL)	0.38	-0.11	0.61
Leaf width (LW)	0.79	0.29	0.50
Stem diameter (SD)	0.77	0.33	-0.48
Eigenvalue	4.29	2.95	1.70
Variability (%)	42.9	29.5	17.0
Cumulative (%)	42.9	72.4	89.4

Note: PC = Principal Component; Numbers in bold indicate a discriminant of > 0.5 or <−0.5 that contributed to the variance.

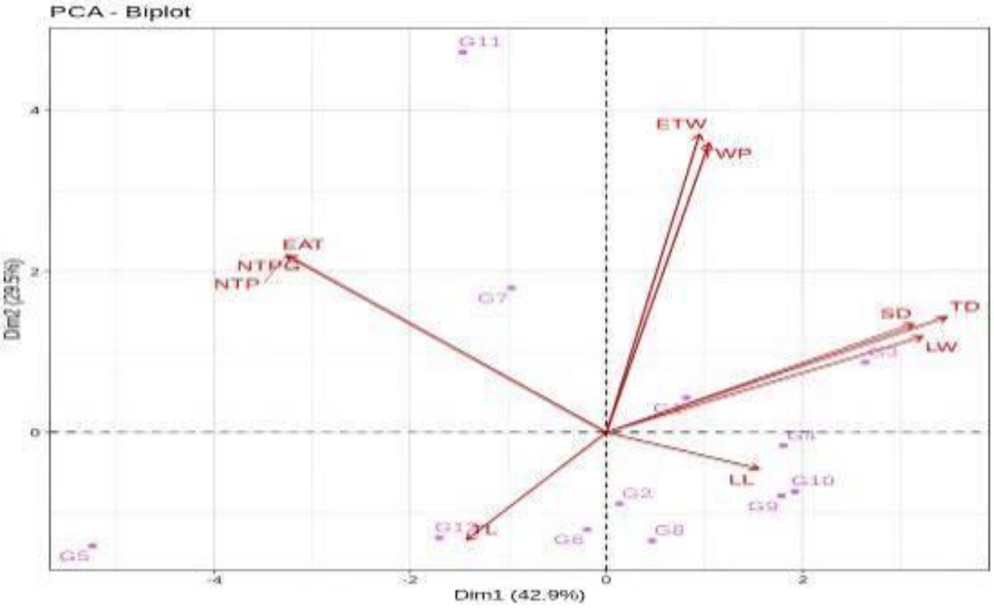

Figure 3. PCA biplot for all the traits and potato genotypes; red arrow: vector angle; purple dot: Genotype. NTPG = Tubers per plant, NTP = Tubers per plot, EAT = Economic amount of tubers, TWP = Tuber weight per plot, ETW = Economic tuber weight, TL = Tuber length, TD = Tuber diameter, LL = Leaf length, LW = Leaf width, and SD = Stem diameter.

traits relationship incurred measuring based on the vector angle analysis, where the tubers per plant, tubers per plot, and economic amount of tubers have very sharp angles (have the same vector line). These three traits have a considerable positive relationship (Figure 3). Furthermore, the traits of economic tuber weight, tuber weight per plot, stem diameter, tuber diameter, and leaf width also showed sharp vector angles. Conversely, the traits with obtuse vector angles exhibited the negative association. Additionally, PCA can indicate the dominance of a trait over a specific genotype, such as the dominant leaf width trait for the G3 potato genotype.

Table 4. Selection differentials for 10 traits tested among the potato genotypes.

Traits	FA1	FA2	FA3	Sense	h^2(%)	Communality	Uniquenesses
NTPG	-0.99	-0.06	-0.12	Increase	77.7	1	0
NTP	-0.99	-0.06	-0.12	Increase	77.7	1	0
EAT	-0.99	-0.06	-0.12	Increase	77.7	1	0
TWP	-0.14	-0.98	0.07	Increase	55.4	0.98	0.02
ETW	-0.19	-0.97	0.11	Increase	40.2	0.98	0.02
TL	0.12	-0.1	-0.75	Increase	88.4	0.58	0.42
TD	0.36	-0.43	0.80	Increase	75.2	0.95	0.05
LL	0.13	0.26	0.68	Increase	92.7	0.54	0.46
LW	0.27	-0.26	0.91	Increase	71.1	0.97	0.03
SD	0.59	-0.76	0.11	Increase	23.8	0.95	0.05
Cumulative (%)	42.9	72.4	89.4				

FA: Factor analysis; h^2: heritability; Tubers per plant (NTPG); Tubers per plot (NTP); Economic amount of tubers (EAT); Tuber weight per plot (TWP); Economic tuber weight (ETW); Tuber length (TL); Tuber diameter (TD); Leaf length (LL); Leaf width (LW); and Stem diameter (SD).

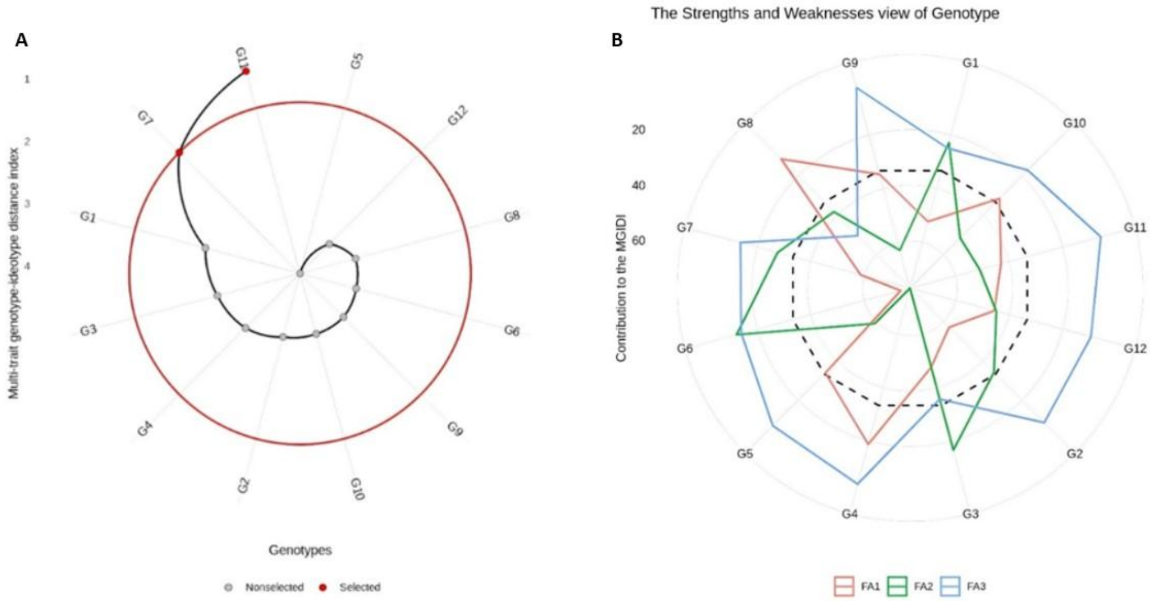

Figure 4. Selection of potato mutants using MGIDI; A. Ranking of selected potato mutants, B. Visualization of strengths and weaknesses of the potato mutants.

Heritability and multi-traits selection

The results revealed three factor analyses (FA1-3) were responsible for the total variation (89.4%) of all studied potato variables (Table 4). Factor analysis is a multivariate statistical technique used to reduce the dimension of data and identify the hidden structures in a set of traits. All the potato genotypes gained assessment based on the desired trait values using the MGIDI analysis. Eight potato traits (tubers per plant, tubers per plot, economic amount of tubers, tuber weight per plot, tuber length, tuber diameter, leaf length, and leaf width) gave the highest heritability (>50%), while two potato traits (economic tuber weight and stem diameter) showed moderate heritability values (20%–50%).

In the identification of potato genotypes approaching the ideotype through MGIDI analysis, it resulted in two main genotypes (G7 and G11) that exceeded and were on the red line (Figure 4A). However, genotype G7 was the best test genotype, and genotype G11 was the check cultivar. The potato genotype G1 approaches the selection threshold, which was the red line, indicating the possibility that this genotype may have specific traits. Meanwhile, genotype G5 was on the trajectory, and the said genotype was the farthest from the desired criteria. This extraordinary success exceeds it by 80%. The desirable trait values investigated in the presented study were also indicative of the selected potato mutant genotypes.

Strengths and weaknesses of potato mutants

Visualization of the strengths and weaknesses of potato mutant genotypes assessed through MGIDI analysis appears in Figure 4B. A consideration of the magnitude of each trait existed. Factors with greater contribution expressed a plotting closer to the edge. In the factor analysis, the study also expected that selected genotypes would show higher values for all traits, such as potato genotype G11 showing dominance in FA3. This means that genotype G11 occurred dominantly for the tuber length, tuber diameter, leaf length and leaf width. Then, the factor analyses FA2 and FA3 showed moderate values, which means that genotype G11 has no dominance for all traits. The said comprehensive analysis provides an overview of genotypes' performance and emphasizes strength and room for further improvement in these potato genotypes for various traits.

DISCUSSION

According to the analysis of variance, significant differences were evident among the potato (*S. tuberosum* L.) genotypes for most traits, except for economic tuber weight and leaf width (Table 2). The significant variations among the sweet potato genotypes indicate the highest level of genetic variability, which plays a crucial role in the selection process and in the success of breeding programs (Maulana *et al.,* 2022). These results were in line with the previous research by Maulana *et al.* (2024), who reported that gamma-ray-induced potato mutant genotypes showed significant differences in tuber yield during several growing seasons. In other past studies, genotypic differences, environmental influences, and their interactions could be the main causes for variations among the genotypes for various traits (Al-Mamun *et al.,* 2024). Thus, further selection was essential to identify the superior potato genotypes for the expected target traits and to choose traits with high correlations (Ahmadikhah *et al.,* 2008). In the presented study, numerous traits emerged to be significantly positively correlated with tuber weight per plot, including tubers per plot, tubers per plant, economic amount of tubers, stem diameter, tuber diameter, and economic tuber weight. The considerable correlation allows for using these traits as an effective indirect selection criterion to identify high-yielding genotypes (Joshi *et al.,* 2020). Overall, the pertinent study underscores that the high genetic variation was vital for predicting the potential and performance of the potato genotypes.

The principal component analysis showed PC1 and PC2 collectively explain 82.4% of the total genetic variation, indicating these two components emerged as crucial for understanding the genotypic diversity. The PCA biplot served to visualize the correlations among traits, where the angles between the vectors revealed the strength of these associations (Maulana *et al.,* 2023). Potato genotypes with a small variation among their vectors can help identify effective methods to obtain genotypes with higher yield potential.

In the PCA, some traits have positive and negative PC values. These positive and negative values helped separate one group from another and identify the potato traits with a maximum contribution to the diversity. Conversely, the traits with negative values indicate these traits could contribute, but not optimally, to diversity in potato genotypes (Razvy *et al.,* 2007). In traits effect on PC, it was evident that the traits of tubers per plant, tubers per plot, economic amount of tubers, tuber diameter, leaf width, and stem diameter affected the genotype diversity on PC1. Meanwhile, the traits tubers per plant, tubers per plot, economic amount of tubers, tuber weight per plot, and economic tuber weight influenced the genotype diversity on PC2. Moreover, the traits tuber length, leaf length, and leaf width altered the genotype diversity on PC3. PCA visualization showed the distribution of genotypes and the measured traits. PCA biplot helps us understand the relationship among the traits and individuals in complex data through vector angle analysis (Maulana *et al.*, 2023). The tubers per plant trait displayed a considerable positive correlation with tubers per plot and economic amount of tubers, as seen from their proximity. Similarly, the trait economic tuber weight appeared closer to the tuber weight per plot, and stem diameter lies near to the traits, viz., tuber diameter and leaf width. This proximity revealed the dominance of a genotype over certain traits, such as the G3 genotype being close to the leaf width vector, indicating genotype G3 has an advantage in that trait.

The quantitative genetic approach has proven to be effective in selecting the best genotypes from a diverse population, although its application proved limited in the advanced breeding lines (Jahufer and Casler, 2015). In this study, the MGIDI analysis application in a potato breeding program addressed these limitations (Olivoto and Nardino, 2021). The MGIDI analysis helped in the identification of superior genotypes by analyzing multi-trait data, using eigenvalues as the main criterion to determine relevant factors (Olivoto and Lúcio, 2020). The values of the selected analysis factors detailed each had an eigenvalue greater than one (Joshi *et al.,* 2020).

The MGIDI analysis identified G7 and G11 as superior potato genotypes that best meet the ideal criteria. The potato genotype G11 is the check cultivar Medians, selected for their highest productivity and local market preference. In other research, this variety also has a good agronomic performance when planted on medium plains (Supriatna *et al.*, 2018). Similarly, G7 occurred as a promising new genotype with high-yield potential and resistance to bacterial wilt disease. This characteristic is crucial, considering that 90% of farmers currently rely on the disease-susceptible potato cultivar Granola (Kartasih and Suwandi*,* 2014). The utilization of genotype G7, which is disease-resistant and has large tubers, could reduce dependence on seed imports by up to 40%. Morphologically, genotype G7 showed superiority in tuber length and diameter, as well as a significant increase in leaf length and width. Large leaf size positively correlates with tuber enlargement due to the vital role of leaves in photosynthesis (Rozentsvet *et al.,* 2022).

The MGIDI analysis also successfully identified the unique potato genotypes like G1 and G5 that were far from the ideal criteria, identifying them as of interest to breeders for further exploration (Olivoto and Nardino, 2021). The MGIDI analysis has been aiding in the selection of superior genotypes in various crops, such as wheat (Pour-Aboughadareh and Poczai, 2021), guar (Benakanahalli *et al.,* 2021), eggplant (Uddin *et al.,* 2021), soybeans (Maranna *et al.,* 2021), corn (Yue *et al.,* 2022), and rice (Al-Mamun *et al.,* 2024). The MGIDI application has even succeeded in detecting soil microbes in sweet potatoes (Nafi’ah *et al.,* 2025). In the latest study, eight traits exhibited the highest heritability (>50%), which proved highly favorable for the traits’ transmission to the next generation. The high heritability values of the traits tubers per plant (77.7%) and tuber diameter (75.2%) were particularly crucial, as they considerably helped in early-generation selection and saved time of up to two planting seasons used in the breeding program.

The MGIDI analysis revealed the strengths and weaknesses of each potato genotype, enabling the identification of traits that need further improvement. Factor Analysis 1 (FA1) focuses on traits with positive gains, with the selected potato genotypes expected to exhibit higher values. Factors with a greater contribution provide a strategic location near the edge of the plot. Potato genotypes G7 and G11 showed dominance in Factor Analysis 3 (FA3), indicating superiority in the tuber length, tuber diameter, leaf length and leaf width. The accuracy of MGIDI selection (89.4%) in potatoes was comparable to the success reported in rice (91.2%) (Al Mamun *et* *al.,* 2024) and corn (85.7%) (Yue *et al.,* 2022) crops, confirming the method's reliability in primary food crops. The integration of the superior potato genotype G7, with the highest leaf length heritability and significant PCA variance accumulation, received high recommendations for consideration in the national potato seed production and distribution strategies to improve efficiency and crop yield quality. The relevant study represents the first report on using the MGIDI analysis in potato breeding in Indonesia. Given the limitation of a single location, multi-location validation will be crucial to confirm the stability of the potato genotype G7.

CONCLUSIONS

The analysis of variance showed significant differences for most traits, except for the economic tuber weight and leaf width. The correlation analysis exhibited the considerable positive association of tuber weight per plot with the traits of tubers per plot, tubers per plant, economic tuber weight, stem diameter, tuber diameter, and economic amount of tubers. The MGIDI analysis successfully identified the highest heritability in leaf length (92.7%) and accumulated the PCA variance of 89.4%. The MGIDI analysis also succeeded in identifying the two leading potato genotypes (G7 and G11) with the desired traits profile.

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